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SciPy (pronounced “Sigh Pie”) is open-source software for mathematics, science, and engineering.
CHAPTER
ONE

INSTALLING AND UPGRADING

Information on how to install SciPy and/or the SciPy Stack (a larger set of packages for scientific computing with Python) can be found at https://scipy.org/install.html.

It is recommended that users use a scientific Python distribution or binaries for their platform. If building from source is required, documentation about that can be found at Building from sources.

If you already have SciPy installed and want to upgrade to a newer version, use the same install mechanism as you have used to install SciPy before. Before upgrading to a newer version, it is recommended to check that your own code does not use any deprecated SciPy functionality. To do so, run your code with python -Wd.
In Python the distinction between what is the public API of a library and what are private implementation details is not always clear. Unlike in other languages like Java, it is possible in Python to access “private” function or objects. Occasionally this may be convenient, but be aware that if you do so your code may break without warning in future releases. Some widely understood rules for what is and isn’t public in Python are:

- Methods / functions / classes and module attributes whose names begin with a leading underscore are private.
- If a class name begins with a leading underscore none of its members are public, whether or not they begin with a leading underscore.
- If a module name in a package begins with a leading underscore none of its members are public, whether or not they begin with a leading underscore.
- If a module or package defines __all__ that authoritatively defines the public interface.
- If a module or package doesn’t define __all__ then all names that don’t start with a leading underscore are public.

**Note:** Reading the above guidelines one could draw the conclusion that every private module or object starts with an underscore. This is not the case; the presence of underscores do mark something as private, but the absence of underscores do not mark something as public.

In Scipy there are modules whose names don’t start with an underscore, but that should be considered private. To clarify which modules these are we define below what the public API is for Scipy, and give some recommendations for how to import modules/functions/objects from Scipy.

### 2.1 Guidelines for importing functions from Scipy

The scipy namespace itself only contains functions imported from numpy. These functions still exist for backwards compatibility, but should be imported from numpy directly.

Everything in the namespaces of scipy submodules is public. In general, it is recommended to import functions from submodule namespaces. For example, the function `curve_fit` (defined in scipy/optimize/minpack.py) should be imported like this:

```python
from scipy import optimize
result = optimize.curve_fit(...)
```

This form of importing submodules is preferred for all submodules except `scipy.io` (because `io` is also the name of a module in the Python stdlib):
from scipy import interpolate
from scipy import integrate
import scipy.io as spio

In some cases, the public API is one level deeper. For example the scipy.sparse.linalg module is public, and the functions it contains are not available in the scipy.sparse namespace. Sometimes it may result in more easily understandable code if functions are imported from one level deeper. For example, in the following it is immediately clear that lomax is a distribution if the second form is chosen:

```python
# first form
from scipy import stats
stats.lomax(...)  
# second form
from scipy.stats import distributions
distributions.lomax(...)
```

In that case the second form can be chosen, if it is documented in the next section that the submodule in question is public.

## 2.2 API definition

Every submodule listed below is public. That means that these submodules are unlikely to be renamed or changed in an incompatible way, and if that is necessary a deprecation warning will be raised for one Scipy release before the change is made.

- **scipy.cluster**
  - `scipy.cluster.vq`
  - `scipy.cluster.hierarchy`
- **scipy.constants**
- **scipy.fftpack**
- **scipy.integrate**
- **scipy.interpolate**
- **scipy.io**
  - `scipy.io.arff`
  - `scipy.io.harwell_boeing`
  - `scipy.io.idl`
  - `scipy.io.matlab`
  - `scipy.io.netcdf`
  - `scipy.io.wavfile`
- **scipy.linalg**
  - `scipy.linalg.blas`
  - `scipy.linalg.cython_blas`
  - `scipy.linalg.lapack`
- `scipy.linalg.cython_lapack`
- `scipy.linalg.interpolative`

- `scipy.misc`
- `scipy.ndimage`
- `scipy.odr`
- `scipy.optimize`
- `scipy.signal`
  - `scipy.signal.windows`
- `scipy.sparse`
  - `scipy.sparse.linalg`
  - `scipy.sparse.csgraph`
- `scipy.spatial`
  - `scipy.spatial.distance`
  - `scipy.spatial.transform`
- `scipy.special`
- `scipy.stats`
  - `scipy.stats.distributions`
  - `scipy.stats.mstats`
3.1 SciPy 1.2.0 Release Notes

SciPy 1.2.0 is the culmination of 6 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Before upgrading, we recommend that users check that their own code does not use deprecated SciPy functionality (to do so, run your code with python -Wd
and check for `DeprecationWarning` s). Our development attention will now shift to bug-fix releases on the 1.2.x branch, and on adding new features on the master branch.

This release requires Python 2.7 or 3.4+ and NumPy 1.8.2 or greater.

**Note:** This will be the last SciPy release to support Python 2.7. Consequently, the 1.2.x series will be a long term support (LTS) release; we will backport bug fixes until 1 Jan 2020.

For running on PyPy, PyPy3 6.0+ and NumPy 1.15.0 are required.

### 3.1.1 Highlights of this release

- 1-D root finding improvements with a new solver, `toms748`, and a new unified interface, `root_scalar`
- New `dual_annealing` optimization method that combines stochastic and local deterministic searching
- A new optimization algorithm, `shgo` (simplicial homology global optimization) for derivative free optimization problems
- A new category of quaternion-based transformations are available in `scipy.spatial.transform`

### New features

#### 3.1.2 scipy.ndimage improvements

Proper spline coefficient calculations have been added for the `mirror`, `wrap`, and `reflect` modes of `scipy.ndimage.rotate`.

#### 3.1.3 scipy.fftpack improvements

DCT-IV, DST-IV, DCT-I, and DST-I orthonormalization are now supported in `scipy.fftpack`.

#### 3.1.4 scipy.interpolate improvements

`scipy.interpolate.pade` now accepts a new argument for the order of the numerator.

#### 3.1.5 scipy.cluster improvements

`scipy.cluster.vq.kmeans2` gained a new initialization method, kmeans++.

#### 3.1.6 scipy.special improvements

The function `softmax` was added to `scipy.special`.

#### 3.1.7 scipy.optimize improvements

The one-dimensional nonlinear solvers have been given a unified interface `scipy.optimize.root_scalar`, similar to the `scipy.optimize.root` interface for multi-dimensional solvers. `scipy.optimize.root_scalar(f, bracket=[a ,b], method="brenth")` is equivalent to `scipy.optimize.brenth(f, a , b)`. If no `method` is specified, an appropriate one will be selected based upon the bracket and the number of derivatives available.

The so-called Algorithm 748 of Alefeld, Potra and Shi for root-finding within an enclosing interval has been added as `scipy.optimize.toms748`. This provides guaranteed convergence to a root with convergence rate per function evaluation of approximately 1.65 (for sufficiently well-behaved functions.)
differential_evolution now has the **updating** and **workers** keywords. The first chooses between continuous updating of the best solution vector (the default), or once per generation. Continuous updating can lead to faster convergence. The **workers** keyword accepts an int or map-like callable, and parallelises the solver (having the side effect of updating once per generation). Supplying an int evaluates the trial solutions in N parallel parts. Supplying a map-like callable allows other parallelisation approaches (such as mpi4py, or joblib) to be used.

**dual_annealing** (and **shgo** below) is a powerful new general purpose global optimization (GO) algorithm. **dual_annealing** uses two annealing processes to accelerate the convergence towards the global minimum of an objective mathematical function. The first annealing process controls the stochastic Markov chain searching and the second annealing process controls the deterministic minimization. So, dual annealing is a hybrid method that takes advantage of stochastic and local deterministic searching in an efficient way.

**shgo** (simplicial homology global optimization) is a similar algorithm appropriate for solving black box and derivative free optimization (DFO) problems. The algorithm generally converges to the global solution in finite time. The convergence holds for non-linear inequality and equality constraints. In addition to returning a global minimum, the algorithm also returns any other global and local minima found after every iteration. This makes it useful for exploring the solutions in a domain.

**scipy.optimize.newton** can now accept a scalar or an array

MINPACK usage is now thread-safe, such that MINPACK + callbacks may be used on multiple threads.

### 3.1.8 scipy.signal improvements

Digital filter design functions now include a parameter to specify the sampling rate. Previously, digital filters could only be specified using normalized frequency, but different functions used different scales (e.g. 0 to 1 for **butter** vs 0 to \(\pi\) for **freqz**), leading to errors and confusion. With the **fs** parameter, ordinary frequencies can now be entered directly into functions, with the normalization handled internally.

**find_peaks** and related functions no longer raise an exception if the properties of a peak have unexpected values (e.g. a prominence of 0). A **PeakPropertyWarning** is given instead.

The new keyword argument **plateau_size** was added to **find_peaks**. **plateau_size** may be used to select peaks based on the length of the flat top of a peak.

**welch()** and **csd()** methods in **scipy.signal** now support calculation of a median average PSD, using **average='mean'** keyword

### 3.1.9 scipy.sparse improvements

The **scipy.sparse.bsr_matrix.tocsr** method is now implemented directly instead of converting via COO format, and the **scipy.sparse.bsr_matrix.tocsc** method is now also routed via CSR conversion instead of COO. The efficiency of both conversions is now improved.

The issue where SuperLU or UMFPACK solvers crashed on matrices with non-canonical format in **scipy.sparse.linalg** was fixed. The solver wrapper canonicalizes the matrix if necessary before calling the SuperLU or UMFPACK solver.

The **largest** option of **scipy.sparse.linalg.lobpcg()** was fixed to have a correct (and expected) behavior. The order of the eigenvalues was made consistent with the ARPACK solver (**eigs()**), i.e. ascending for the smallest eigenvalues, and descending for the largest eigenvalues.

The **scipy.sparse.random** function is now faster and also supports integer and complex values by passing the appropriate value to the **dtype** argument.
3.1.10 scipy.spatial improvements

The function `scipy.spatial.distance.jaccard` was modified to return 0 instead of `np.nan` when two all-zero vectors are compared.

Support for the Jensen Shannon distance, the square-root of the divergence, has been added under `scipy.spatial.distance.jensenshannon`.

An optional keyword was added to the function `scipy.spatial.cKDTree.query_ball_point()` to sort or not sort the returned indices. Not sorting the indices can speed up calls.

A new category of quaternion-based transformations are available in `scipy.spatial.transform`, including spherical linear interpolation of rotations (`slerp`), conversions to and from quaternions, Euler angles, and general rotation and inversion capabilities (`spatial.transform.Rotation`), and uniform random sampling of 3D rotations (`spatial.transform.Rotation.random`).

3.1.11 scipy.stats improvements

The Yeo-Johnson power transformation is now supported (`yeojohnson`, `yeojohnson_llf`, `yeojohnson_normmax`, `yeojohnson_normplot`). Unlike the Box-Cox transformation, the Yeo-Johnson transformation can accept negative values.

Added a general method to sample random variates based on the density only, in the new function `rvs_ratio_uniforms`.

The Yule-Simon distribution (`yulesimon`) was added – this is a new discrete probability distribution.

`stats` and `mstats` now have access to a new regression method, `siegelslopes`, a robust linear regression algorithm.

`scipy.stats.gaussian_kde` now has the ability to deal with weighted samples, and should have a modest improvement in performance.

Levy Stable Parameter Estimation, PDF, and CDF calculations are now supported for `scipy.stats.levy_stable`.

The Brunner-Munzel test is now available as `brunnermunzel` in `stats` and `mstats`.

3.1.12 scipy.linalg improvements

`scipy.linalg.lapack` now exposes the LAPACK routines using the Rectangular Full Packed storage (RFP) for upper triangular, lower triangular, symmetric, or Hermitian matrices; the upper trapezoidal fat matrix RZ decomposition routines are now available as well.

Deprecated features

The functions `hyp2f0`, `hyp1f2` and `hyp3f0` in `scipy.special` have been deprecated.

Backwards incompatible changes

LAPACK version 3.4.0 or later is now required. Building with Apple Accelerate is no longer supported.

The function `scipy.linalg.subspace_angles(A, B)` now gives correct results for all angles. Before this, the function only returned correct values for those angles which were greater than pi/4.

Support for the Bento build system has been removed. Bento has not been maintained for several years, and did not have good Python 3 or wheel support, hence it was time to remove it.

The required signature of `scipy.optimize.lingprog` method=`simplex` callback function has changed. Before iteration begins, the simplex solver first converts the problem into a standard form that does not, in general, have the same variables or constraints as the problem defined by the user. Previously, the simplex solver...
would pass a user-specified callback function several separate arguments, such as the current solution vector \( \mathbf{x}_k \), corresponding to this standard form problem. Unfortunately, the relationship between the standard form problem and the user-defined problem was not documented, limiting the utility of the information passed to the callback function.

In addition to numerous bug fix changes, the simplex solver now passes a user-specified callback function a single :class:`OptimizeResult` object containing information that corresponds directly to the user-defined problem. In future releases, this :class:`OptimizeResult` object may be expanded to include additional information, such as variables corresponding to the standard-form problem and information concerning the relationship between the standard-form and user-defined problems.

The implementation of :func:`scipy.sparse.random` has changed, and this affects the numerical values returned for both :func:`sparse.random` and :func:`sparse.rand` for some matrix shapes and a given seed.

\[ \text{scipy.optimize.newton} \] will no longer use Halley’s method in cases where it negatively impacts convergence.

**Other changes**

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3.1. SciPy 1.2.0 Release Notes
• Ted Pudlik
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• Eric Quintero
• Pradeep Reddy Raamana +
• Vyas Ramasubramani +
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• Pauli Virtanen
• Stefan van der Walt
• Warren Weckesser
• Joshua Wharton +
• Bernhard M. Wiedemann +
• Eric Wieser
• Josh Wilson
3.1.13 Issues closed for 1.2.0

- #9520: signal.correlate with method='fft' doesn’t benefit from long...
- #9547: signature of dual_annealing doesn’t match other optimizers
- #9540: SciPy v1.2.0rc1 cannot be imported on Python 2.7.15
- #1240: Allowing multithreaded use of minpack through scipy.optimize...
- #1432: scipy.stats.mode extremely slow (Trac #905)
- #3372: Please add Sphinx search field to online scipy html docs
- #3678: _clough_tocher_2d_single direction between centroids
- #4174: lobpcg “largest” option invalid?
- #5493: anderson_ksamp p-values>1
- #5743: slsqp fails to detect infeasible problem
- #6139: scipy.optimize.linprog failed to find a feasible starting point...
- #6358: stats: docstring for vonmises_line points to vonmises_line...
- #6386: runtests.py is missing in pypi distfile
- #7246: scipy.stats.ksone(n).pdf(x) returns nan for positive values of...
- #7455: scipy.stats.ksone.pdf(2,x) return incorrect values for x near...
- #7456: scipy.special.smirnov and scipy.special.smirnovi have accuracy...
- #7492: scipy.special.kolmogorov(x)/kolmogi(p) inefficient, inaccurate...
- #7914: TravisCI not failing when it should for -OO run
- #8064: linalg.solve test crashes on Windows
- #8212: LAPACK Rectangular Full Packed routines
- #8256: differential_evolution bug converges to wrong results in complex...
- #8443: Deprecate hyp2f0, hyp1f2, and hyp3f0?!
- #8452: DOC: ARPACK tutorial has two conflicting equations
- #8680: scipy fails compilation when building from source
- #8686: Division by zero in _trustregion.py when x0 is exactly equal...
- #8700: _MINPACK_LOCK not held when calling into minpack from least_squares
- #8786: erroneous moment values for t-distribution
- #8789: Checking COLA condition in istft should be optional (or omitted)
- #8843: imresize cannot be deprecated just yet
- #8844: Inverse Wishart Log PDF Incorrect for Non-diagonal Scale Matrix?
• #8878: vonmises and vonmises_line in stats: vonmises wrong and superfluous?
• #8895: v1.1.0 ndi.rotate documentation – reused parameters not filled...
• #8900: Missing complex conjugation in scipy.sparse.linalg.LinearOperator
• #8904: BUG: if zero derivative at root, then Newton fails with RuntimeWarning
• #8911: make_interp_spline bc_type incorrect input interpretation
• #8942: MAINT: Refactor _linprog.py and _linprog_ip.py to remove...
• #8947: np.int64 in scipy.fftpack.next_fast_len
• #9020: BUG: linalg.subspace_angles gives wrong results
• #9033: scipy.stats.normaltest sometimes gives incorrect returns b/c...
• #9036: Bizarre times for scipy.sparse.rand function with ‘low’ density...
• #9044: optimize.minimize(method=‘trust-constr’) result dict does not...
• #9071: doc/linalg: add cho_solve_banded to see also of cholesky_banded
• #9082: eigenvalue sorting in scipy.sparse.linalg.eigsh
• #9086: signaltools.py:491: FutureWarning: Using a non-tuple sequence...
• #9091: test_spline_filter failure on 32-bit
• #9122: Typo on scipy minimization tutorial
• #9135: doc error at https://docs.scipy.org/doc/scipy/reference/tutorial/stats/discrete_poisson.html
• #9167: DOC: BUG: typo in ndimage LowLevelCallable tutorial example
• #9169: truncnorm does not work if b < a in scipy.stats
• #9250: scipy.special.tests.test_mpmath::TestSystematic::test_pcfw fails...
• #9259: rv.expect() == rv.mean() is false for rv.mean() == nan (and inf)
• #9286: DOC: Rosenbrock expression in optimize.minimize tutorial
• #9316: SLSQP fails in nested optimization
• #9337: scipy.signal.find_peaks key typo in documentation
• #9345: Example from documentation of scipy.sparse.linalg.eigs raises...
• #9383: Default value for “mode” in “ndimage.shift”
• #9419: dual_annnealing off by one in the number of iterations
• #9442: Error in Defintion of Rosenbrock Function
• #9453: TST: test_eigs_consistency() doesn’t have consistent results

3.1.14 Pull requests for 1.2.0
• #9526: TST: relax precision requirements in signal.correlate tests
• #9507: CI: MAINT: Skip a ckdtest tree on pypy
• #9512: TST: test_random_sampling 32-bit handling
• #9494: TST: test_kolmogorov xfail 32-bit
• #9486: BUG: fix sparse random int handling
• #9550: BUG: scipy/_lib/_numpy_compat: get_randint
#9549: MAINT: make dual_annealing signature match other optimizers
#9541: BUG: fix SyntaxError due to non-ascii character on Python 2.7
#7352: ENH: add Brunner Munzel test to scipy.stats.
#7373: BUG: Jaccard distance for all-zero arrays would return np.nan
#7374: ENH: Add PDF, CDF and parameter estimation for Stable Distributions
#8098: ENH: Add shgo for global optimization of NLPs.
#8203: ENH: adding simulated dual annealing to optimize
#8259: Option to follow original Storn and Price algorithm and its parallelisation
#8293: ENH add ratio-of-uniforms method for rv generation to scipy.stats
#8294: BUG: Fix slowness in stats.mode
#8295: ENH: add Jensen Shannon distance to scipy.spatial.distance
#8357: ENH: vectorize scalar zero-search-functions
#8397: Add fs= parameter to filter design functions
#8537: ENH: Implement mode parameter for spline filtering.
#8558: ENH: small speedup for stats.gaussian_kde
#8560: BUG: fix p-value calc of anderson_ksamp in scipy.stats
#8614: ENH: correct p-values for stats.kendalltau and stats.mstats.kendalltau
#8670: ENH: Require Lapack 3.4.0
#8725: MAINT: Cleanup scipy.optimize.leastsq
#8726: BUG: Fix _get_output in scipy.ndimage to support string
#8733: MAINT: stats: A bit of clean up.
#8737: BUG: Improve numerical precision/convergence failures of smirnov/kolmogorov
#8738: MAINT: stats: A bit of clean up in test_distributions.py.
#8740: BF/ENH: make minpack thread safe
#8742: BUG: Fix division by zero in trust-region optimization methods
#8746: MAINT: signal: Fix a docstring of a private function, and fix...
#8750: DOC clarified description of norminvgauss in scipy.stats
#8753: DOC: signal: Fix a plot title in the chirp docstring.
#8755: DOC: MAINT: Fix link to the wheel documentation in developer...
#8760: BUG: stats: boltzmann wasn’t setting the upper bound.
#8763: [DOC] Improved scipy.cluster.hierarchy documentation
#8765: DOC: added example for scipy.stat.mstats.tmin
#8788: DOC: fix definition of optional disp parameter
#8802: MAINT: Suppress dd_real unused function compiler warnings.
#8803: ENH: Add full_output support to optimize.newton()
• #8804: MAINT: stats cleanup
• #8808: DOC: add note about isinstance for frozen rvs
• #8812: Updated numpydoc submodule
• #8813: MAINT: stats: Fix multinomial docstrings, and do some clean up.
• #8816: BUG: fixed _stats of t-distribution in scipy.stats
• #8817: BUG: ndimage: Fix validation of the origin argument in correlate...
• #8822: BUG: integrate: Fix crash with repeated t values in odeint.
• #8832: Hyperlink DOIs against preferred resolver
• #8837: BUG: sparse: Ensure correct dtype for sparse comparison operations.
• #8839: DOC: stats: A few tweaks to the linregress docstring.
• #8846: BUG: stats: Fix logpdf method of invwishart.
• #8849: DOC: signal: Fixed mistake in the firwin docstring.
• #8854: DOC: fix type descriptors in ltit sys documentation
• #8865: Fix tiny typo in docs for chi2 pdf
• #8870: Fixes related to invertibility of STFT
• #8872: ENH: special: Add the softmax function
• #8874: DOC correct gamma function in docstrings in scipy.stats
• #8876: ENH: Added TOMS Algorithm 748 as 1-d root finder; 17 test function...
• #8882: ENH: Only use Halley’s adjustment to Newton if close enough.
• #8883: FIX: optimize: make jac and hess truly optional for ‘trust-constr’
• #8885: TST: Do not error on warnings raised about non-tuple indexing.
• #8887: MAINT: filter out np.matrix PendingDeprecationWarning’s in numpy...
• #8889: DOC: optimize: separate legacy interfaces from new ones
• #8890: ENH: Add optimize.root_scalar() as a universal dispatcher for...
• #8899: DCT-IV, DST-IV and DCT-I, DST-I orthonormalization support in...
• #8901: MAINT: Reorganize flapack.pyf.src file
• #8907: BUG: ENH: Check if guess for newton is already zero before checking...
• #8908: ENH: Make sorting optional for cKDTree.query_ball_point()
• #8910: DOC: sparse.csgraph simple examples.
• #8914: DOC: interpolate: fix equivalences of string aliases
• #8918: add float__control(precise, on) to _fpumode.c
• #8919: MAINT: interpolate: improve error messages for common be_type...
• #8920: DOC: update Contributing to SciPy to say “prefer no PEP8 only...
• #8924: MAINT: special: deprecate hyp2f0, hyp1f2, and hyp3f0
• #8927: MAINT: special: remove errprint
• #8932: Fix broadcasting scale arg of entropy
• #8936: Fix (some) non-tuple index warnings
• #8937: ENH: implement sparse matrix BSR to CSR conversion directly.
• #8938: DOC: add @_ni_docstrings.docfiller in ndimage.rotate
• #8940: Update _discrete_distns.py
• #8943: DOC: Finish dangling sentence in convolve docstring
• #8944: MAINT: Address tuple indexing and warnings
• #8945: ENH: spatial.transform.Rotation [GSOC2018]
• #8950: csgraph Dijkstra function description rewording
• #8953: DOC, MAINT: HTTP -> HTTPS, and other linkrot fixes
• #8955: BUG: np.int64 in scipy.fftpack.next_fast_len
• #8958: MAINT: Add more descriptive error message for phase one simplex.
• #8962: BUG: sparse.linalg: add missing conjugate to _ScaledLinearOperator.adjoint
• #8963: BUG: sparse.linalg: downgrade LinearOperator TypeError to warning
• #8965: ENH: Wrapped RFP format and RZ decomposition routines
• #8969: MAINT: doc and code fixes for optimize.newton
• #8970: Added ‘average’ keyword for welch/csd to enable median averaging
• #8971: Better imresize deprecation warning
• #8972: MAINT: Switch np.where(c) for np.nonzero(c)
• #8975: MAINT: Fix warning-based failures
• #8979: DOC: fix description of count_sort keyword of dendrogram
• #8982: MAINT: optimize: Fixed minor mistakes in test_linprog.py (#8978)
• #8984: BUG: sparse.linalg: ensure expm casts integer inputs to float
• #8986: BUG: optimize/slsqp: do not exit with convergence on steps where...
• #8989: MAINT: use collections.abc in basinhopping
• #8990: ENH extend p-values of anderson_ksamp in scipy.stats
• #8991: ENH: Weighted kde
• #8993: ENH: spatial.transform.Rotation.random [GSOC 2018]
• #8994: ENH: spatial.transform.Slerp [GSOC 2018]
• #8995: TST: time.time in test
• #9007: Fix typo in fftpack.rst
• #9013: Added correct plotting code for two sided output from spectrogram
• #9014: BUG: differential_evolution with inf objective functions
• #9017: BUG: fixed #8446 corner case for asformat(array|dense)
• #9018: MAINT: _lib/ccallback: remove unused code
• #9021: BUG: Issue with subspace_angles
• #9022: DOC: Added “See Also” section to lombscargle docstring
• #9034: BUG: Fix tolerance printing behavior, remove meaningless tol...
• #9035: TST: improve signal.bsplines test coverage
• #9037: ENH: add a new init method for k-means
• #9039: DOC: Add examples to fftpack.irfft docstrings
• #9048: ENH: scipy.sparse.random
• #9050: BUG: scipy.io.hb_write: fails for matrices not in csc format
• #9051: MAINT: Fix slow sparse.rand for k < mn/3 (#9036).
• #9054: MAINT: spatial: Explicitly initialize LAPACK output parameters.
• #9055: DOC: Add examples to scipy.special docstrings
• #9056: ENH: Use one thread in OpenBLAS
• #9059: DOC: Update README with link to Code of Conduct
• #9060: BLD: remove support for the Bento build system.
• #9062: DOC add sections to overview in scipy.stats
• #9066: BUG: Correct “remez” error message
• #9069: DOC: update linalg section of roadmap for LAPACK versions.
• #9079: MAINT: add spatial.transform to refguide check; complete some...
• #9081: MAINT: Add warnings if pivot value is close to tolerance in linprog(method='simplex')
• #9084: BUG fix incorrect p-values of kurtosistest in scipy.stats
• #9095: DOC: add sections to mstats overview in scipy.stats
• #9096: BUG: Add test for Stackoverflow example from issue 8174.
• #9101: ENH: add Siegel slopes (robust regression) to scipy.stats
• #9125: interpolative: correctly reconstruct full rank matrices
• #9131: DOC: Correct the typo in scipy.optimize tutorial page
• #9133: FIX: Avoid use of bare except
• #9137: DOC: typo fixes for discrete Poisson tutorial
• #9139: FIX: Doctest failure in optimize tutorial
• #9143: DOC: missing sigma in Pearson r formula
• #9145: MAINT: Refactor linear programming solvers
• #9149: FIX: Make scipy.odr.ODR ifixx equal to its data.fix if given
• #9156: DOC: special: Mention the sigmoid function in the `expit` docstring.
• #9160: Fixed a latex delimiter error in `levy()`
• #9170: DOC: correction / update of docstrings of distributions in `scipy.stats`
• #9171: better description of the hierarchical clustering parameter
• #9174: domain check for \( a < b \) in `stats.truncnorm`
• #9175: DOC: Minor grammar fix
• #9176: BUG: CloughTocher2DInterpolator: fix miscalculation at neighborless...
• #9177: BUILD: Document the “clean” target in the `doc/Makefile`
• #9178: MAINT: make `refguide-check` more robust for printed `numpy` arrays
• #9186: MAINT: Remove `np.ediff1d` occurrence
• #9188: DOC: correct typo in extending ndimage with `C`
• #9190: ENH: Support specifying axes for `fftfconvolve`
• #9192: MAINT: optimize: fixed @pv style suggestions from #9112
• #9200: Fix `make_interp_spline(..., k=0 or 1, axis<0)`
• #9201: BUG: `sparse.linalg/gmres`: use machine eps in breakdown check
• #9204: MAINT: fix up `stats.spearmanr` and match `mstats.spearmanr` with...
• #9206: MAINT: include benchmarks and dev files in `sdist`
• #9208: TST: signal: bump bsplines test tolerance for complex data
• #9210: TST: mark tests as slow, fix missing random seed
• #9211: ENH: add capability to specify orders in `pade` func
• #9217: MAINT: Include `success` and `nit` in `OptimizeResult` returned...
• #9222: ENH: interpolate: Use `scipy.spatial.distance` to speed-up `Rbf`
• #9229: BENCH: Fix Fourier filter double case
• #9233: BUG: spatial/distance: fix `pdist/cdist` performance regression...
• #9234: FIX: Proper suppression
• #9235: BENCH: rationalize slow benchmarks + miscellaneous fixes
• #9238: BENCH: limit number of parameter combinations in `spatial.*KDTree`
• #9239: DOC: stats: Fix `LaTeX` markup of a couple distribution PDFs.
• #9241: ENH: Evaluate plateau size during peak finding
• #9242: ENH: stats: Implement `_ppf` and `_logpdf` for `crystalball`, and do...
• #9246: DOC: Properly render version added directive in HTML documentation
• #9255: DOC: mention `RootResults` in optimization reference guide
• #9260: TST: relax some tolerances so tests pass with x87 math
• #9264: TST Use `assert_raises` “match” parameter instead of the “message”...
• #9267: DOC: clarify `expect()` return val when moment is inf/nan
• #9272: DOC: Add description of default bounds to `linprog`
• #9277: MAINT: sparse/linalg: make test deterministic
• #9278: MAINT: interpolate: pep8 cleanup in test_polyint
• #9279: Fixed docstring for resample
• #9280: removed first check for float in get_sum_dtype
• #9281: BUG: only accept 1d input for bartlett / levene in scipy.stats
• #9282: MAINT: dense_output and t_eval are mutually exclusive inputs
• #9283: MAINT: add docs and do some cleanups in interpolate.Rbf
• #9288: Run distance_transform_edt tests on all types
• #9294: DOC: fix the formula typo
• #9298: MAINT: optimize/trust-constr: restore .niter attribute for backward-compat
• #9299: DOC: clarification of default rvs method in scipy.stats
• #9301: MAINT: removed unused import sys
• #9302: MAINT: removed unused imports
• #9303: DOC: signal: Refer to fs instead of nyq in the firwin docstring.
• #9305: ENH: Added Yeo-Johnson power transformation
• #9306: ENH - add dual annealing
• #9309: ENH add the yulesimon distribution to scipy.stats
• #9317: Nested SLSQP bug fix.
• #9320: MAINT: stats: avoid underflow in stats.geom.ppf
• #9326: Add example for Rosenbrock function
• #9332: Sort file lists
• #9340: Fix typo in find_peaks documentation
• #9343: MAINT Use np.full when possible
• #9344: DOC: added examples to docstring of dirichlet class
• #9346: DOC: Fix import of scipy.sparse.linalg in example (#9345)
• #9350: Fix interpolate read only
• #9351: MAINT: special.erf: use the x->-x symmetry
• #9356: Fix documentation typo
• #9358: DOC: improve doc for ksone and kstwobign in scipy.stats
• #9362: DOC: Change datatypes of A matrices in linprog
• #9364: MAINT: Adds implicit none to fftpack fortran sources
• #9369: DOC: minor tweak to CoC (updated NumFOCUS contact address).
• #9373: Fix exception if python is called with -OO option
• #9374: FIX: AIX compilation issue with NAN and INFINITY
• #9376: COBLYA -> COBYLA in docs
• #9377: DOC: Add examples integrate: fixed_quad and quadrature
• #9379: MAINT: TST: Make tests NumPy 1.8 compatible
• #9385: CI: On Travis matrix “OPTIMIZE=-OO” flag ignored
• #9387: Fix default value for ‘mode’ in ‘ndimage.shift’ in the doc
• #9392: BUG: rank has to be integer in rank_filter: fixed issue 9388
• #9399: DOC: Misc. typos
• #9400: TST: stats: Fix the expected r-value of a linregress test.
• #9405: BUG: np.hstack does not accept generator expressions
• #9408: ENH: linalg: Shorter ill-conditioned warning message
• #9418: DOC: Fix ndimage docstrings and reduce doc build warnings
• #9421: DOC: Add missing docstring examples in scipy.spatial
• #9422: DOC: Add an example to integrate.newton_cotes
• #9427: BUG: Fixed defect with maxiter #9419 in dual annealing
• #9431: BENCH: Add dual annealing to scipy benchmark (see #9415)
• #9435: DOC: Add docstring examples for stats.binom_test
• #9443: DOC: Fix the order of indices in optimize tutorial
• #9444: MAINT: interpolate: use operator.index for checking/coercing...
• #9445: DOC: Added missing example to stats.mstats.kruskal
• #9446: DOC: Add note about version changed for jaccard distance
• #9447: BLD: version-script handling in setup.py
• #9448: TST: skip a problematic linalg test
• #9449: TST: fix missing seed in lobpcg test.
• #9456: TST: test_eigs_consistency() now sorts output

3.2 SciPy 1.1.0 Release Notes
SciPy 1.1.0 is the culmination of 7 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Before upgrading, we recommend that users check that their own code does not use deprecated SciPy functionality (to do so, run your code with `python -Wd` and check for `DeprecationWarning` s). Our development attention will now shift to bug-fix releases on the 1.1.x branch, and on adding new features on the master branch.

This release requires Python 2.7 or 3.4+ and NumPy 1.8.2 or greater.

This release has improved but not necessarily 100% compatibility with the PyPy Python implementation. For running on PyPy, PyPy 6.0+ and Numpy 1.15.0+ are required.

### 3.2.1 New features

**scipy.integrate improvements**

The argument `tfirst` has been added to the function `scipy.integrate.odeint`. This allows `odeint` to use the same user functions as `scipy.integrate.solve_ivp` and `scipy.integrate.ode` without the need for wrapping them in a function that swaps the first two arguments.

Error messages from `quad()` are now clearer.

**scipy.linalg improvements**

The function `scipy.linalg.ldl` has been added for factorization of indefinite symmetric/hermitian matrices into triangular and block diagonal matrices.

Python wrappers for LAPACK `sygst`, `hegst` added in `scipy.linalg.lapack`.

Added `scipy.linalg.null_space`, `scipy.linalg.cdf2rdf`, `scipy.linalg.rsf2csf`.

**scipy.misc improvements**

An electrocardiogram has been added as an example dataset for a one-dimensional signal. It can be accessed through `scipy.misc.electrocardiogram`.

**scipy.ndimage improvements**

The routines `scipy.ndimage.binary_opening`, and `scipy.ndimage.binary_closing` now support masks and different border values.

**scipy.optimize improvements**

The method `trust-constr` has been added to `scipy.optimize.minimize`. The method switches between two implementations depending on the problem definition. For equality constrained problems it is an implementation of a trust-region sequential quadratic programming solver and, when inequality constraints are
imposed, it switches to a trust-region interior point method. Both methods are appropriate for large scale problems. Quasi-Newton options BFGS and SR1 were implemented and can be used to approximate second order derivatives for this new method. Also, finite-differences can be used to approximate either first-order or second-order derivatives.

Random-to-Best/1/bin and Random-to-Best/1/exp mutation strategies were added to `scipy.optimize.differential_evolution` as `randtobest1bin` and `randtobest1exp`, respectively. Note: These names were already in use but implemented a different mutation strategy. See Backwards incompatible changes, below. The `init` keyword for the `scipy.optimize.differential_evolution` function can now accept an array. This array allows the user to specify the entire population.

Add an adaptive option to Nelder-Mead to use step parameters adapted to the dimensionality of the problem.

Minor improvements in `scipy.optimize.basinhopping`.

**scipy.signal improvements**

Three new functions for peak finding in one-dimensional arrays were added. `scipy.signal.find_peaks` searches for peaks (local maxima) based on simple value comparison of neighbouring samples and returns those peaks whose properties match optionally specified conditions for their height, prominence, width, threshold and distance to each other. `scipy.signal.peak_prominences` and `scipy.signal.peak_widths` can directly calculate the prominences or widths of known peaks.


Added `scipy.signal.windows.dpss`, `scipy.signal.windows.general_cosine` and `scipy.signal.windows.general_hamming`.

**scipy.sparse improvements**

Previously, the reshape method only worked on `scipy.sparse.lil_matrix`, and in-place reshaping did not work on any matrices. Both operations are now implemented for all matrices. Handling of shapes has been made consistent with `numpy.matrix` throughout the `scipy.sparse` module (shape can be a tuple or splatted, negative number acts as placeholder, padding and unpadding dimensions of size 1 to ensure length-2 shape).

**scipy.special improvements**

Added Owen’s T function as `scipy.special.owens_t`.

Accuracy improvements in `chndtr`, `digamma`, `gammaincinv`, `lambertw`, `zetac`.

**scipy.stats improvements**

The Moyal distribution has been added as `scipy.stats.moyal`.

Added the normal inverse Gaussian distribution as `scipy.stats.norminvgauss`.

### 3.2.2 Deprecated features

The iterative linear equation solvers in `scipy.sparse.linalg` had a sub-optimal way of how absolute tolerance is considered. The default behavior will be changed in a future Scipy release to a more standard and less surprising one. To silence deprecation warnings, set the `atol=` parameter explicitly.

`scipy.signal.windows.slepian` is deprecated, replaced by `scipy.signal.windows.dpss`.

The window functions in `scipy.signal` are now available in `scipy.signal.windows`. They will remain also available in the old location in the `scipy.signal` namespace in future Scipy versions. However, importing them from `scipy.signal.windows` is preferred, and new window functions will be added only there.
Indexing sparse matrices with floating-point numbers instead of integers is deprecated.

The function `scipy.stats.itemfreq` is deprecated.

### 3.2.3 Backwards incompatible changes

Previously, `scipy.linalg.orth` used a singular value cutoff value appropriate for double precision numbers also for single-precision input. The cutoff value is now tunable, and the default has been changed to depend on the input data precision.

In previous versions of Scipy, the `randtobest1bin` and `randtobest1exp` mutation strategies in `scipy.optimize.differential_evolution` were actually implemented using the Current-to-Best/1/bin and Current-to-Best/1/exp strategies, respectively. These strategies were renamed to `currenttobest1bin` and `currenttobest1exp` and the implementations of `randtobest1bin` and `randtobest1exp` strategies were corrected.

Functions in the ndimage module now always return their output array. Before this most functions only returned the output array if it had been allocated by the function, and would return `None` if it had been provided by the user.

Distance metrics in `scipy.spatial.distance` now require non-negative weights.

`scipy.special.loggamma` returns now real-valued result when the input is real-valued.

### 3.2.4 Other changes

When building on Linux with GNU compilers, the `.so` Python extension files now hide all symbols except those required by Python, which can avoid problems when embedding the Python interpreter.

### 3.2.5 Authors

- Saurabh Agarwal +
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• Ilhan Polat
• Robert Pollak +
• Anant Prakash +
• Anan Pratik
• Sean Quinn +
• Giftlin Rajaiah +
• Tyler Reddy
• Joscha Reimer
• Antonio H Ribeiro +
• Antonio Horta Ribeiro
• Benjamin Rose +
• Fabian Rost
• Divakar Roy +
• Scott Sievert
• Leo Singer
• Sourav Singh
• Martino Sorbaro +
• Eric Stansifer +
• Martin Thoma
A total of 122 people contributed to this release. People with a “+” by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.
Issues closed for 1.1.0

- #979: Allow Hermitian matrices in lobpcg (Trac #452)
- #2694: Solution of iterative solvers can be less accurate than tolerance...
- #3164: RectBivariateSpline usage inconsistent with other interpolation...
- #4161: Missing ITMAX optional argument in scipy.optimize.nnls
- #4354: signal.slepian should use definition of digital window
- #4866: Shouldn’t scipy.linalg.sqrtm raise an error if matrix is singular?
- #4953: The dirichlet distribution unnecessarily requires strictly positive...
- #5336: sqrtm on a diagonal matrix can warn “Matrix is singular and may..."
- #5922: Suboptimal convergence of Halley’s method?
- #6036: Incorrect edge case in scipy.stats.triang.pdf
- #6202: Enhancement: Add LDLt factorization to scipy
- #6589: sparse.random with custom rvs callable does pass on arg to subclass
- #6654: Spearman’s rank correlation coefficient slow with nan values...
- #6794: Remove NumarrayType struct with numarray type names from ndimage
- #7136: The dirichlet distribution unnecessarily rejects probabilities...
- #7169: Will it be possible to add LDL’ factorization for Hermitian indefinite...
- #7291: fsolve docs should say it doesn’t handle over- or under-determined...
- #7453: binary_opening/binary_closing missing arguments
- #7500: linalg.solve test failure on OS X with Accelerate
- #7555: Integrating a function with singularities using the quad routine
- #7624: allow setting both absolute and relative tolerance of sparse...
- #7724: odeint documentation refers to t0 instead of t
- #7746: False CDF values for skew normal distribution
- #7750: mstats.winsorize documentation needs clarification
- #7787: Documentation error in spherical Bessel, Neumann, modified spherical...
- #7836: Scipy mmwrite incorrectly writes the zeros for skew-symmetric,...
- #7839: sqrtm is unable to compute square root of zero matrix
- #7847: solve is very slow since #6775
- #7888: Scipy 1.0.0b1 prints spurious DVODE/ZVODE/lsoda messages
- #7909: bessel kv function in 0 is nan
- #7915: LinearOperator’s __init__ runs two times when instantiating the...
- #7958: integrate.quad could use better error messages when given bad...
- #7968: integrate.quad handles decreasing limits (b<a) inconsistently
- #7970: ENH: matching return dtype for loggamma/gammaln
- #7991: lfilter segfaults for integer inputs
• #8076: “make dist” for the docs doesn’t complete cleanly
• #8080: Use JSON in special/​_generate_pyx.py?
• #8127: scipy.special.psi(x) very slow for some values of x
• #8145: BUG: ndimage geometric_transform and zoom using deprecated NumPy...
• #8158: BUG: romb print output requires correction
• #8181: loadmat() raises TypeError instead of FileNotFound when reading...
• #8228: bug for log1p on csr_matrix
• #8235: scipy.stats multionomial pmf return nan
• #8271: scipy.io.mmwrite raises type error for uint16
• #8288: Should tests be written for scipy.sparse.linalg.solve.minres...
• #8298: Broken links on scipy API web page
• #8329: __gels fails for fat A matrix
• #8346: Avoidable overflow in scipy.special.binom(n, k)
• #8371: BUG: special: zetac(x) returns 0 for x < -30.8148
• #8382: collections.OrderedDict in test_mio.py
• #8492: Missing documentation for brute_force parameter in scipy.ndimage.morphology
• #8532: leastsq needlessly appends extra dimension for scalar problems
• #8544: [feature request] Convert complex diagonal form to real block...
• #8561: [Bug?] Example of Bland’s Rule for optimize.linprog (simplex)...  
• #8562: CI: Appveyor builds fail because it can’t import ConvexHull from...
• #8576: BUG: optimize: show_options(solver=’minimize’, method=’Newton-CG’)...
• #8603: test_roots_gegenbauer/chebyt/chebyc failures on manylinux
• #8604: Test failures in scipy.sparse test_inplace_dense
• #8616: special: ellpj.c code can be cleaned up a bit
• #8625: scipy 1.0.1 no longer allows overwriting variables in netcdf...
• #8629: gcrotmk.test_atol failure with MKL
• #8632: Sigma clipping on data with the same value
• #8646: scipy.special.sinpi test failures in test_zero_sign on old MSVC
• #8663: linprog with method=interior-point produced incorrect answer...
• #8694: linalg:TestSolve.test_all_type_size_routine_combinations fails...
• #8703: Q: Does runtests.py --refguide-check need env (or other) variables...

Pull requests for 1.1.0

• #6590: BUG: sparse: fix custom rvs callable argument in sparse.random
• #7004: ENH: scipy.linalg.eigh cannot get all eigenvalues
• #7120: ENH: implemented Owen’s T function
• #7483: ENH: Addition/multiplication operators for StateSpace systems
• #7566: Informative exception when passing a sparse matrix
• #7592: Adaptive Nelder-Mead
• #7729: WIP: ENH: optimize: large-scale constrained optimization algorithms...
• #7802: MRG: Add dpss window function
• #7803: DOC: Add examples to spatial.distance
• #7821: Add Returns section to the docstring
• #7833: ENH: Performance improvements in scipy.linalg.special_matrices
• #7864: MAINT: sparse: Simplify sutils.isintlike
• #7865: ENH: Improved speed of copy into L, U matrices
• #7871: BENCH: split spatial benchmark imports

• #7900: API: Soft deprecate signal.* windows
• #7910: ENH: allow sqrtm to compute the root of some singular matrices
• #7911: MAINT: Avoid unnecessary array copies in xdist
• #7913: DOC: Clarifies the meaning of initial of scipy.integrate.cumtrapz()
• #7916: BUG: sparse.linalg: fix wrong use of __new__ in LinearOperator
• #7921: BENCH: split spatial benchmark imports
• #7927: ENH: added sygst/hegst routines to lapack
• #7934: MAINT: add io/_test_fortranmodule to gitignore
• #7936: DOC: Fixed typo in scipy.special.roots_jacobi documentation
• #7937: MAINT: special: Mark a test that fails on i686 as a known failure.
• #7941: ENH: LDLt decomposition for indefinite symmetric/hermitian matrices
• #7945: ENH: Implement reshape method on sparse matrices
• #7947: DOC: update docs on releasing and installing/upgrading
• #7954: Basin-hopping changes
• #7964: BUG: test_falker not robust against numerical fuss in eigenvalues
• #7967: QUADPACK Errors - human friendly errors to replace ‘Invalid Input’
• #7975: Make sure integrate.quad doesn’t double-count singular points
• #7981: BUG: special: fix hyp2f1 behavior in certain circumstances
• #7983: ENH: special: Add a real dispatch to loggamma
• #7989: BUG: special: make kv return inf at a zero real argument
• #7990: TST: special: test ufuncs in special at nan inputs
• #7994: DOC: special: fix typo in spherical Bessel function documentation
• #7995: ENH: linalg: add null_space for computing null spaces via svd
• #7999: BUG: optimize: Protect _minpack calls with a lock.
• #8003: MAINT: consolidate c99 compatibility
• #8004: TST: special: get all cython_special tests running again
• #8006: MAINT: Consolidate an additional _c99compat.h
• #8011: Add new example of integrate.quad
• #8015: DOC: special: remove jn from the refguide (again)
• #8018: BUG - Issue with uint datatypes for array in get_index_dtype
• #8021: DOC: spatial: Simplify Delaunay plotting
• #8024: Documentation fix
• #8027: BUG: io.matlab: fix saving unicode matrix names on py2
• #8028: BUG: special: some fixes for lambertw
• #8030: MAINT: Bump Cython version
• #8034: BUG: sparse.linalg: fix corner-case bug in expm
• #8035: MAINT: special: remove complex division hack
• #8038: ENH: Cythonize pyx files if pxd dependencies change
• #8042: TST: stats: reduce required precision in test_fligner
• #8043: TST: Use diff. values for decimal keyword for single and doubles
• #8044: TST: accuracy of tests made different for singles and doubles
• #8049: Unhelpful error message when calling scipy.sparse.save_npz on...
• #8052: TST: spatial: add a regression test for gh-8051
• #8059: BUG: special: fix ufunc results for nan arguments
• #8066: MAINT: special: reimplement inverses of incomplete gamma functions
• #8072: Example for scipy.fftpack.ifft, https://github.com/scipy/scipy/issues/7168
• #8073: Example for ifftn, https://github.com/scipy/scipy/issues/7168
• #8078: Link to CoC in contributing.rst doc
• #8085: BLD: Fix nppy_isnan of integer variables in cephes
• #8088: DOC: note version for which new attributes have been added to...
• #8090: BUG: special: add nan check to _legacy_cast_check functions
• #8091: Doxy Typos + trivial comment typos (2nd attempt)
• #8096: TST: special: simplify Arg
• #8101: MAINT: special: run _generate_pyx.py when add_newdocs.py...
• #8104: Input checking for scipy.sparse.linalg.inverse()
• #8105: DOC: special: Update the ‘euler’ docstring.
• #8109: MAINT: fixing code comments and hyp2f1 docstring: see issues...
• #8112: More trivial typos
• #8113: MAINT: special: generate test data npz files in setup.py and...
• #8116: DOC: add build instructions
• #8120: DOC: Clean up README
• #8121: DOC: Add missing colons in docstrings
• #8123: BLD: update Bento build config files for recent C99 changes.
• #8124: Change to avoid use of fmod in scipy.signal.chebwin
• #8126: Added examples for mode arg in geometric_transform
• #8128: relax relative tolerance parameter in TestMinimumPhase.test_hilbert
• #8129: ENH: special: use rational approximation for digamma on $^4[1,...$
• #8137: DOC Correct matrix width
• #8141: MAINT: optimize: remove unused __main__ code in L-BSGS-B
• #8147: BLD: update Bento build for removal of .npz scipy.special test...
• #8148: Alias hanning as an explanatory function of hann
• #8149: MAINT: special: small fixes for digamma
• #8159: Update version classifiers
• #8164: BUG: riccati solvers don’t catch ill-conditioned problems sufficiently...
• #8168: DOC: release note for sparse resize methods
• #8170: BUG: correctly pad netCDF files with null bytes
• #8171: ENH added normal inverse gaussian distribution to scipy.stats
• #8175: DOC: Add example to scipy.ndimage.zoom
• #8177: MAINT: diffev small speedup in ensure constraint
• #8178: FIX: linalg._qz String formatter syntax error
• #8179: TST: Added pdist to asv spatial benchmark suite
• #8180: TST: ensure constraint test improved
• #8183: 0d conj correlate
• #8186: BUG: special: fix derivative of spherical_jn(1, 0)
• #8194: Fix warning message
• #8196: BUG: correctly handle inputs with nan’s and ties in spearmanr
• #8198: MAINT: stats.triang edge case fixes #6036
• #8200: DOC: Completed “Examples” sections of all linalg funcs
• #8201: MAINT: stats.trapz edge cases
• #8204: ENH: sparse.linalg/lobpcg: change .T to .T.conj() to support...
• #8206: MAINT: missed trianq edge case.
• #8214: BUG: Fix memory corruption in linalg._decomp_update C extension
• #8222: DOC: recommend scipy.integrate.solve_ivp
• #8223: ENH: added Moyal distribution to scipy.stats
- #8232: BUG: sparse: Use deduped data for numpy ufuncs
- #8236: Fix #8235
- #8253: BUG: optimize: fix bug related with function call calculation...
- #8264: ENH: Extend peak finding capabilities in scipy.signal
- #8273: BUG fixed printing of convergence message in minimize_scalar...
- #8276: DOC: Add notes to explain constrains on overwrite_<>
- #8279: CI: fixing doctests
- #8282: MAINT: weightedtau, change search for nan
- #8287: Improving documentation of solve_ivp and the underlying solvers
- #8291: DOC: fix non-ascii characters in docstrings which broke the doc...
- #8292: CI: use numpy 1.13 for refguide check build
- #8296: Fixed bug reported in issue #8181
- #8297: DOC: Examples for linalg/decomp eigvals function
- #8300: MAINT: Housekeeping for minimizing the linalg compiler warnings
- #8301: DOC: make public API documentation cross-link to refguide.
- #8302: make sure _onenorm_matrix_power_nnm actually returns a float
- #8313: Change copyright to outdated 2008-2016 to 2008-year
- #8315: TST: Add tests for scipy.sparse.linalg.solve.minres
- #8318: ENH: odeint: Add the argument ‘tfirst’ to odeint.
- #8328: ENH: optimize: trust-constr optimization algorithms [GSoC...
- #8330: ENH: add a maxiter argument to NNLS
- #8331: DOC: tweak the Moyal distribution docstring
- #8333: FIX: Rewrapped ?gels and ?gels_lwork routines
- #8336: MAINT: integrate: handle b < a in quad
- #8337: BUG: special: Ensure zetac(1) returns inf.
- #8347: BUG: Fix overflow in special.binom. Issue #8346
- #8356: DOC: Corrected Documentation Issue #7750 winsorize function
- #8358: ENH: stats: Use explicit MLE formulas in lognorm.fit and expon.fit
- #8374: BUG: gh7854, maxiter for l-bfgs-b closes #7854
- #8379: CI: enable gcov coverage on travis
- #8383: Removed collections.OrderedDict import ignore.
- #8384: TravisCI: tool pep8 is now pycodestyle
- #8387: MAINT: special: remove unused specfun code for Struve functions
- #8393: DOC: Replace old type names in ndimage tutorial.
- #8400: Fix tolerance specification in sparse.linalg iterative solvers
- #8402: MAINT: Some small cleanups in ndimage.
- #8403: FIX: Make scipy.optimize.zeros run under PyPy
- #8407: BUG: sparse.linalg: fix termination bugs for cg, cgs
- #8409: MAINT: special: add a pxd file for Cephes functions
- #8412: MAINT: special: remove cephes/protos.h
- #8421: Setting “unknown” message in OptimizeResult when calling MINPACK.
- #8423: FIX: Handle unsigned integers in mmio
- #8426: DOC: correct FAQ entry on Apache license compatibility. Closes...
- #8433: MAINT: add pytest_cache to the gitignore
- #8436: MAINT: scipy.sparse: less copies at transpose method
- #8437: BUG: correct behavior for skew-symmetric matrices in io.mmwrite
- #8440: DOC: Add examples to integrate.quadpack docstrings
- #8441: BUG: sparse.linalg/gmres: deal with exact breakdown in gmres
- #8442: MAINT: special: clean up Cephes header files
- #8448: TST: Generalize doctest stopwords .axis(. .plot()
- #8457: MAINT: special: use JSON for function signatures in _generate_pxd.py
- #8461: MAINT: Simplify return value of ndimage functions.
- #8464: MAINT: Trivial typos
- #8474: BUG: spatial: make qhull.pyx more pypy-friendly
- #8476: TST: __lib: disable refcounting tests on PyPy
- #8479: BUG: io/matlab: fix issues in matlab i/o on pypy
- #8481: DOC: Example for signal.cmplx_sort
- #8482: TST: integrate: use integers instead of PyCapsules to store pointers
- #8483: ENH: io/netcdf: make mmap=False the default on PyPy
- #8484: BUG: io/matlab: work around issue in to_writeable on PyPy
- #8488: MAINT: special: add const/static specifiers where possible
- #8489: BUG: ENH: use common halley’s method instead of parabolic variant
- #8491: DOC: fix typos
- #8496: ENH: special: make Chebyshev nodes symmetric
- #8501: BUG: stats: Split the integral used to compute skewnorm.cdf.
- #8502: WIP: Port CircleCI to v2
- #8507: DOC: Add missing description to brute_force parameter.
- #8509: BENCH: forgot to add nelder-mead to list of methods
- #8512: MAINT: Move spline interpolation code to spline.c
- #8513: TST: special: mark a slow test as xslow
- #8514: CircleCI: Share data between jobs
- #8515: ENH: special: improve accuracy of zetac for negative arguments
• #8520: TST: Decrease the array sizes for two linalg tests
• #8522: TST: special: restrict range of test_besselk/test_besselk_int
• #8527: Documentation - example added for voronoi_plot_2d
• #8528: DOC: Better, shared docstrings in ndimage
• #8533: BUG: Fix PEP8 errors introduced in #8528.
• #8534: ENH: Expose additional window functions
• #8538: MAINT: Fix a couple mistakes in .pyf files.
• #8540: ENH: interpolate: allow string aliases in make_interp_spline...
• #8541: ENH: Cythonize peak_prominences
• #8542: Remove numerical arguments from convolve2d / correlate2d
• #8546: ENH: New arguments, documentation, and tests for ndimage.binary_opening
• #8547: Giving both size and input now raises UserWarning (#7334)
• #8549: DOC: stats: inweibull is also known as Frechet or type II extreme...
• #8550: add cdf2rdf function
• #8551: ENH: Port of most of the dd_real part of the qd high-precision...
• #8553: Note in docs to address issue #3164.
• #8554: ENH: stats: Use explicit MLE formulas in uniform.fit()
• #8555: MAINT: adjust benchmark config
• #8557: [DOC]: fix Nakagami density docstring
• #8559: DOC: Fix docstring of diric(x, n)
• #8563: [DOC]: fix gamma density docstring
• #8564: BLD: change default Python version for doc build from 2.7 to...
• #8568: BUG: Fixes Bland’s Rule for pivot row/leaving variable, closes...
• #8572: ENH: Add previous/next to interp1d
• #8578: Example for linalg.eig()
• #8580: DOC: update link to asv docs
• #8584: filter_design: switch to explicit arguments, keeping None as...
• #8586: DOC: stats: Add parentheses that were missing in the exponnorm...
• #8587: TST: add benchmark for newton, secant, halley
• #8588: DOC: special: Remove heaviside from “functions not in special”...
• #8591: DOC: cdf2rdf Added version info and “See also”
• #8594: ENH: Cythonize peak_widths
• #8595: MAINT/ENH/BUG/TST: cdf2rdf: Address review comments made after...
• #8597: DOC: add versionadded 1.1.0 for new keywords in ndimage.morphology
• #8605: MAINT: special: improve implementations of sinpi and cospi
• #8607: MAINT: add 2D benchmarks for convolve
• #8608: FIX: Fix int check
• #8613: fix typo in doc of signal.peak_widths
• #8615: TST: fix failing linalg.qz float32 test by decreasing precision.
• #8617: MAINT: clean up code in ellpj.c
• #8618: add fsolve docs it doesn’t handle over- or under-determined problems
• #8620: DOC: add note on dtype attribute of aslinearoperator() argument
• #8627: ENH: Add example 1D signal (ECG) to scipy.misc
• #8630: ENH: Remove unnecessary copying in stats.percentileofscore
• #8631: BLD: fix pdf doc build. closes gh-8076
• #8633: BUG: fix regression in io.netcdf_file with append mode.
• #8635: MAINT: remove spurious warning from (z)vode and lsoda. Closes...
• #8636: BUG: sparse.linalg/gcrotmk: avoid rounding error in termination...
• #8637: For pdf build
• #8639: CI: build pdf documentation on circleci
• #8640: TST: fix special test that was importing np.testing.utils (deprecated)
• #8641: BUG: optimize: fixed sparse redundancy removal bug
• #8645: BUG: modified sigmaclip to avoid clipping of constant input in...
• #8647: TST: sparse: skip test_inplace_dense for numpy<1.13
• #8657: Latex reduce left margins
• #8659: TST: special: skip sign-of-zero test on 32-bit win32 with old...
• #8661: Fix dblquad and tplquad not accepting float boundaries
• #8666: DOC: fixes #8532
• #8667: BUG: optimize: fixed issue #8663
• #8668: Fix example in docstring of netcdf_file
• #8671: DOC: Replace deprecated matplotlib kwarg
• #8673: BUG: special: Use a stricter tolerance for the chndtr calculation.
• #8674: ENH: In the Dirichlet distribution allow x_i to be 0 if alpha_i...
• #8676: BUG: optimize: partial fix to linprog fails to detect infeasibility...
• #8685: DOC: Add interp1d-next/previous example to tutorial
• #8687: TST: netcdf: explicit mmap=True in test
• #8688: BUG: signal, stats: use Python sum() instead of np.sum for summing...
• #8689: TST: bump tolerances in tests
• #8690: DEP: deprecate stats.itemfreq
• #8691: BLD: special: fix build vs. dd_real.h package
• #8695: DOC: Improve examples in signal.find_peaks with ECG signal
• #8697: BUG: Fix setup.py build install egg_info, which did not previously...
3.3 SciPy 1.0.1 Release Notes

SciPy 1.0.1 is a bug-fix release with no new features compared to 1.0.0. Probably the most important change is a fix for an incompatibility between SciPy 1.0.0 and numpy.f2py in the NumPy master branch.

3.3.1 Authors

- Saurabh Agarwal +
- Alessandro Pietro Bardelli
- Philip DeBoer
- Ralf Gommers
- Matt Haberland
- Eric Larson
- Denis Laxalde
- Mihai Capotă +
- Andrew Nelson
- Oleksandr Pavlyk
- Ilhan Polat
- Anant Prakash +
- Pauli Virtanen
- Warren Weckesser
- @xoviat
- Ted Ying +
A total of 16 people contributed to this release. People with a “+” by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 1.0.1

- #7493: ndimage.morphology functions are broken with numpy 1.13.0
- #8118: minimize_cobyla broken if disp=True passed
- #8142: scipy-v1.0.0 pdist with metric='minkowski' raises 'ValueError:'...
- #8173: scipy.stats.ortho_group produces all negative determinants...
- #8207: gaussian_filter seg faults on float16 numpy arrays
- #8234: scipy.optimize.linprog interior-point presolve bug with trivial...
- #8243: Make csgraph importable again via from scipy.sparse import*
- #8320: scipy.optimize.root segfaults with optimizer 'lm'

Pull requests for 1.0.1

- #8068: BUG: fix numpy deprecation test failures
- #8082: BUG: fix solve_lyapunov import
- #8144: MRG: Fix for cobyla
- #8150: MAINT: resolve UPDATEIFCOPY deprecation errors
- #8156: BUG: missing check on minkowski w kwarg
- #8187: BUG: Sign of elements in random orthogonal 2D matrices in “ortho_group_gen”...
- #8197: CI: uninstall oclint
- #8215: Fixes Numpy datatype compatibility issues
- #8237: BUG: optimize: fix bug when variables fixed by bounds are inconsistent...
- #8248: BUG: declare “gfk” variable before call of terminate() in newton-cg
- #8280: REV: reintroduce csgraph import in scipy.sparse
- #8322: MAINT: prevent scipy.optimize.root segfault closes #8320
- #8334: TST: stats: don’t use exact equality check for hdmedian test
- #8477: BUG: signal/signaltools: fix wrong refcounting in PyArray_OrderFilterND
- #8566: CI: Temporarily pin Cython version to 0.27.3
- #8573: Backports for 1.0.1
- #8581: Fix Cython 0.28 build break of qhull.pyx

3.4 SciPy 1.0.0 Release Notes
We are extremely pleased to announce the release of SciPy 1.0, 16 years after version 0.1 saw the light of day. It has been a long, productive journey to get here, and we anticipate many more exciting new features and releases in the future.

### 3.4.1 Why 1.0 now?

A version number should reflect the maturity of a project - and SciPy was a mature and stable library that is heavily used in production settings for a long time already. From that perspective, the 1.0 version number is long overdue.

Some key project goals, both technical (e.g. Windows wheels and continuous integration) and organisational (a governance structure, code of conduct and a roadmap), have been achieved recently.

Many of us are a bit perfectionist, and therefore are reluctant to call something “1.0” because it may imply that it’s “finished” or “we are 100% happy with it”. This is normal for many open source projects, however that doesn’t make it right. We acknowledge to ourselves that it’s not perfect, and there are some dusty corners left (that will probably always be the case). Despite that, SciPy is extremely useful to its users, on average has high quality code and documentation, and gives the stability and backwards compatibility guarantees that a 1.0 label imply.
3.4.2 Some history and perspectives

- 2001: the first SciPy release
- 2005: transition to NumPy
- 2007: creation of scikits
- 2008: scipy.spatial module and first Cython code added
- 2010: moving to a 6-monthly release cycle
- 2011: SciPy development moves to GitHub
- 2011: Python 3 support
- 2012: adding a sparse graph module and unified optimization interface
- 2012: removal of scipy.maxentropy
- 2013: continuous integration with TravisCI
- 2015: adding Cython interface for BLAS/LAPACK and a benchmark suite
- 2017: adding a unified C API with scipy.LowLevelCallable; removal of scipy.weave
- 2017: SciPy 1.0 release

Pauli Virtanen is SciPy’s Benevolent Dictator For Life (BDFL). He says:

Truthfully speaking, we could have released a SciPy 1.0 a long time ago, so I’m happy we do it now at long last. The project has a long history, and during the years it has matured also as a software project. I believe it has well proved its merit to warrant a version number starting with unity.

Since its conception 15+ years ago, SciPy has largely been written by and for scientists, to provide a box of basic tools that they need. Over time, the set of people active in its development has undergone some rotation, and we have evolved towards a somewhat more systematic approach to development. Regardless, this underlying drive has stayed the same, and I think it will also continue propelling the project forward in future. This is all good, since not long after 1.0 comes 1.1.

Travis Oliphant is one of SciPy’s creators. He says:

I’m honored to write a note of congratulations to the SciPy developers and the entire SciPy community for the release of SciPy 1.0. This release represents a dream of many that has been patiently pursued by a stalwart group of pioneers for nearly 2 decades. Efforts have been broad and consistent over that time from many hundreds of people. From initial discussions to efforts coding and packaging to documentation efforts to extensive conference and community building, the SciPy effort has been a global phenomenon that it has been a privilege to participate in.

The idea of SciPy was already in multiple people’s minds in 1997 when I first joined the Python community as a young graduate student who had just fallen in love with the expressibility and extensibility of Python. The internet was just starting to bringing together like-minded mathematicians and scientists in nascent electronically-connected communities. In 1998, there was a concerted discussion on the matrix-SIG, python mailing list with people like Paul Barrett, Joe Harrington, Perry Greenfield, Paul Dubois, Konrad Hinsen, David Ascher, and others. This discussion encouraged me in 1998 and 1999 to procrastinate my PhD and spend a lot of time writing extension modules to Python that mostly wrapped battle-tested Fortran and C-code making it available to the Python user. This work attracted the help of others like Robert Kern, Pearu Peterson and Eric Jones who joined their efforts with mine in 2000 so that by 2001, the first SciPy release was ready. This was long before Github simplified collaboration and input from others and the “patch” command and email was how you helped a project improve.

Since that time, hundreds of people have spent an enormous amount of time improving the SciPy library and the community surrounding this library has dramatically grown. I stopped being able to participate actively in developing the SciPy library around 2010. Fortunately, at that time, Pauli Virtanen and Ralf
Gommers picked up the pace of development supported by dozens of other key contributors such as David Cournapeau, Evgeni Burovski, Josef Perktold, and Warren Weckesser. While I have only been able to admire the development of SciPy from a distance for the past 7 years, I have never lost my love of the project and the concept of community-driven development. I remain driven even now by a desire to help sustain the development of not only the SciPy library but many other affiliated and related open-source projects. I am extremely pleased that SciPy is in the hands of a world-wide community of talented developers who will ensure that SciPy remains an example of how grass-roots, community-driven development can succeed.

Fernando Perez offers a wider community perspective:

The existence of a nascent Scipy library, and the incredible –if tiny by today’s standards– community surrounding it is what drew me into the scientific Python world while still a physics graduate student in 2001. Today, I am awed when I see these tools power everything from high school education to the research that led to the 2017 Nobel Prize in physics.

Don't be fooled by the 1.0 number: this project is a mature cornerstone of the modern scientific computing ecosystem. I am grateful for the many who have made it possible, and hope to be able to contribute again to it in the future. My sincere congratulations to the whole team!

### 3.4.3 Highlights of this release

Some of the highlights of this release are:

- Major build improvements. Windows wheels are available on PyPI for the first time, and continuous integration has been set up on Windows and OS X in addition to Linux.
- A set of new ODE solvers and a unified interface to them (*scipy.integrate.solve_ivp*).
- Two new trust region optimizers and a new linear programming method, with improved performance compared to what *scipy.optimize* offered previously.
- Many new BLAS and LAPACK functions were wrapped. The BLAS wrappers are now complete.

### 3.4.4 Upgrading and compatibility

There have been a number of deprecations and API changes in this release, which are documented below. Before upgrading, we recommend that users check that their own code does not use deprecated SciPy functionality (to do so, run your code with `python -Wd` and check for `DeprecationWarning`s).

This release requires Python 2.7 or >=3.4 and NumPy 1.8.2 or greater.

This is also the last release to support LAPACK 3.1.x - 3.3.x. Moving the lowest supported LAPACK version to >=3.2.x was long blocked by Apple Accelerate providing the LAPACK 3.2.1 API. We have decided that it’s time to either drop Accelerate or, if there is enough interest, provide shims for functions added in more recent LAPACK versions so it can still be used.

### New features

#### 3.4.5 scipy.cluster improvements

*scipy.cluster.hierarchy.optimal_leaf_ordering*, a function to reorder a linkage matrix to minimize distances between adjacent leaves, was added.

#### 3.4.6 scipy.fftpack improvements

N-dimensional versions of the discrete sine and cosine transforms and their inverses were added as *dctn, idctn, dstn* and *idstn*. 
3.4.7 *scipy.integrate* improvements

A set of new ODE solvers have been added to *scipy.integrate*. The convenience function *scipy.integrate.solve_ivp* allows uniform access to all solvers. The individual solvers (RK23, RK45, Radau, BDF and LSODA) can also be used directly.

3.4.8 *scipy.linalg* improvements

The BLAS wrappers in *scipy.linalg.blas* have been completed. Added functions are *gbmv, hbmv, hpmv, hpr, hpr2, spmv, spr, tbmv, tbsv, tspv, trsm, trsv, sbmv, spr2, gbmv, hbmv, hpmv, hpr, hpr2, spmv, spr, tbmv, tbsv, tspv, trsm, trsv, sbmv, spr2, gbmv, hbmv, hpmv, hpr, hpr2, spmv, spr, tbmv, tbsv, tspv, trsm, trsv, sbmv, spr2,*

Wrappers for the LAPACK functions *gels, stev, sytrd, hetrd, sytf2, hetrf, sytrf, sycon, hecon, gglse, stebz, stemr, sterf, and stein* have been added.

The function *scipy.linalg.subspace_angles* has been added to compute the subspace angles between two matrices.

The function *scipy.linalg.clarkson_woodruff_transform* has been added. It finds low-rank matrix approximation via the Clarkson-Woodruff Transform.

The functions *scipy.linalg.eigh_tridiagonal* and *scipy.linalg.eigvalsh_tridiagonal*, which find the eigenvalues and eigenvectors of tridiagonal hermitian/symmetric matrices, were added.

3.4.9 *scipy.ndimage* improvements

Support for homogeneous coordinate transforms has been added to *scipy.ndimage.affine_transform*. The *ndimage* C code underwent a significant refactoring, and is now a lot easier to understand and maintain.

3.4.10 *scipy.optimize* improvements

The methods *trust-region-exact* and *trust-krylov* have been added to the function *scipy.optimize.minimize*. These new trust-region methods solve the subproblem with higher accuracy at the cost of more Hessian factorizations (compared to dogleg) or more matrix vector products (compared to ncg) but usually require less nonlinear iterations and are able to deal with indefinite Hessians. They seem very competitive against the other Newton methods implemented in scipy.

*scipy.optimize.linprog* gained an interior point method. Its performance is superior (both in accuracy and speed) to the older simplex method.

3.4.11 *scipy.signal* improvements

An argument *fs* (sampling frequency) was added to the following functions: *firwin, firwin2, firls, and remez*. This makes these functions consistent with many other functions in *scipy.signal* in which the sampling frequency can be specified.

*scipy.signal.freqz* has been sped up significantly for FIR filters.

3.4.12 *scipy.sparse* improvements

Iterating over and slicing of CSC and CSR matrices is now faster by up to ~35%.

The *tocsr* method of COO matrices is now several times faster.

The *diagonal* method of sparse matrices now takes a parameter, indicating which diagonal to return.
3.4.13 **scipy.sparse.linalg** improvements

A new iterative solver for large-scale nonsymmetric sparse linear systems, `scipy.sparse.linalg.gcrotmk`, was added. It implements GCROT(m,k), a flexible variant of GCROT.

`scipy.sparse.linalg.lsmr` now accepts an initial guess, yielding potentially faster convergence.

SuperLU was updated to version 5.2.1.

3.4.14 **scipy.spatial** improvements

Many distance metrics in `scipy.spatial.distance` gained support for weights.

The signatures of `scipy.spatial.distance.pdist` and `scipy.spatial.distance.cdist` were changed to `*args, **kwargs` in order to support a wider range of metrics (e.g., string-based metrics that need extra keywords). Also, an optional `out` parameter was added to `pdist` and `cdist` allowing the user to specify where the resulting distance matrix is to be stored.

3.4.15 **scipy.stats** improvements

The methods `cdf` and `logcdf` were added to `scipy.stats.multivariate_normal`, providing the cumulative distribution function of the multivariate normal distribution.

New statistical distance functions were added, namely `scipy.stats.wasserstein_distance` for the first Wasserstein distance and `scipy.stats.energy_distance` for the energy distance.

**Deprecated features**

The following functions in `scipy.misc` are deprecated: `bytescale`, `fromimage`, `imfilter`, `imread`, `imresize`, `imrotate`, `imsave`, `imshow` and `toimage`. Most of those functions have unexpected behavior (like rescaling and type casting image data without the user asking for that). Other functions simply have better alternatives.

`scipy.interpolate.interpolate_wrapper` and all functions in that submodule are deprecated. This was a never finished set of wrapper functions which is not relevant anymore.

The `fillvalue` of `scipy.signal.convolve2d` will be cast directly to the dtypes of the input arrays in the future and checked that it is a scalar or an array with a single element.

`scipy.spatial.distance.matching` is deprecated. It is an alias of `scipy.spatial.distance.hamming`, which should be used instead.

Implementation of `scipy.spatial.distance.wminkowski` was based on a wrong interpretation of the metric definition. In scipy 1.0 it has been just deprecated in the documentation to keep retro-compatibility but is recommended to use the new version of `scipy.spatial.distance.minkowski` that implements the correct behaviour.

Positional arguments of `scipy.spatial.distance.pdist` and `scipy.spatial.distance.cdist` should be replaced with their keyword version.

**Backwards incompatible changes**

The following deprecated functions have been removed from `scipy.stats`: `betai`, `chisqprob`, `f_value`, `histogram`, `histogram2`, `pdf_fromgamma`, `signaltonoise`, `square_of_sums`, `ss` and `threshold`.

The following deprecated functions have been removed from `scipy.stats.mstats`: `betai`, `f_value_wilks_lambda`, `signaltonoise` and `threshold`.

The deprecated `a` and `reta` keywords have been removed from `scipy.stats.shapiro`.

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The deprecated functions `scipy.sparse.csgraph.cs_graph_components` and `scipy.linalg.symeig` have been removed from `scipy.sparse`.

The following deprecated keywords have been removed in `scipy.sparse.linalg`: `drop_tol` from `splu`, and `xtype` from `bicg`, `bicgstab`, `cg`, `cgs`, `gmres`, `qmr`, and `minres`.

The deprecated functions `expm2` and `expm3` have been removed from `scipy.linalg`. The deprecated keyword `q` was removed from `scipy.linalg.expm`. And the deprecated submodule `linalg.calc_lwork` was removed.

The deprecated functions `C2K`, `K2C`, `F2C`, `C2F`, `F2K` and `K2F` have been removed from `scipy.constants`.

The deprecated `ppform` class was removed from `scipy.interpolate`.

The deprecated keyword `iprint` was removed from `scipy.optimize.fmin_cobyla`.

The default value for the `zero_phase` keyword of `scipy.signal.decimate` has been changed to True.

The `kmeans` and `kmeans2` functions in `scipy.cluster.vq` changed the method used for random initialization, so using a fixed random seed will not necessarily produce the same results as in previous versions.

`scipy.special.gammain` does not accept complex arguments anymore.

The deprecated functions `sph_jn`, `sph_yn`, `sph_jnyn`, `sph_in`, `sph_kn`, and `sph_inkn` have been removed. Users should instead use the functions `spherical_jn`, `spherical_yn`, `spherical_in`, and `spherical_kn`. Be aware that the new functions have different signatures.

The cross-class properties of `scipy.signal.lti` systems have been removed. The following properties/setters have been removed:

Name - (accessing/setting has been removed) - (setting has been removed)

- StateSpace - (num, den, gain) - (zeros, poles)
- TransferFunction (A, B, C, D, gain) - (zeros, poles)
- ZerosPolesGain (A, B, C, D, num, den) - ()

`signal.freqz(b, a)` with b or a > 1-D raises a `ValueError`. This was a corner case for which it was unclear that the behavior was well-defined.

The method `var` of `scipy.stats.dirichlet` now returns a scalar rather than an ndarray when the length of alpha is 1.

Other changes

SciPy now has a formal governance structure. It consists of a BDFL (Pauli Virtanen) and a Steering Committee. See the governance document for details.

It is now possible to build SciPy on Windows with MSVC + gfortran! Continuous integration has been set up for this build configuration on Appveyor, building against OpenBLAS.

Continuous integration for OS X has been set up on TravisCI.

The SciPy test suite has been migrated from `nose` to `pytest`.

`scipy/_distributor_init.py` was added to allow redistributors of SciPy to add custom code that needs to run when importing SciPy (e.g. checks for hardware, DLL search paths, etc.).

Support for PEP 518 (specifying build system requirements) was added - see `pyproject.toml` in the root of the SciPy repository.

In order to have consistent function names, the function `scipy.linalg.solve_lyapunov` is renamed to `scipy.linalg.solve_continuous_lyapunov`. The old name is kept for backwards-compatibility.
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• Aman Pratik
• Eric Quintero
• Vedant Rathore +
• Tyler Reddy
• Joscha Reimer
• Philipp Rentzsch +
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• Ned Richards +
• Kevin Rose +
• Benoit Rostykus +
• Matt Ruffalo +
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• Nico Schlömer +
• Klaus Sembritzki +
• Nikolay Shebanov +
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• Scott Sievert
• Max Silbiger +
• Mandeep Singh +
• Michael Stewart +
• Jonathan Sutton +
• Deep Tavker +
• Martin Thoma
3.4.16 Issues closed for 1.0.0

- #2300: scipy.misc.toimage (and therefore imresize) converts to uint32...
- #2347: Several misc.im* functions incorrectly handle 3 or 4-channeled...
- #2442: scipy.misc.pilutil -> scipy.ndimage?
- #2829: Mingw Gfortran on Windows?
- #3154: scipy.misc.imsave creates wrong bitmap header
- #3505: scipy.linalg.lstsq() residual’s help text is a lil strange
- #3808: Is Brent’s method for minimizing the value of a function implemented...
- #4121: Add cdf() method to stats.multivariate_normal
- #4458: scipy.misc.imresize changes image range
- #4575: Docs for L-BFGS-B mention non-existent parameter
- #4893: misc.imsave does not work with file type defined
- #5231: Discrepancies in scipy.optimize.minimize(method='L-BFGS-B')
- #5238: Optimal leaf ordering in scipy.cluster.hierarchy.dendrogram
- #5305: Wrong image scaling in scipy/misc/pilutil.py with misc.imsave?
- #5823: test failure in filter_design
- #6061: scipy.stats.spearmanr return values outside range -1 to 1
- #6242: Inconsistency / duplication for imread and imshow, imsave
- #6265: BUG: signal.iirfilter of bandpass type is unstable when high...
- #6370: scipy.optimize.linear_sum_assignment hangs on undefined matrix
• #6417: scipy.misc.imresize converts images to uint8
• #6618: splrep and splprep inconsistent
• #6854: Support PEP 519 in I/O functions
• #6921: [Feature request] Random unitary matrix
• #6930: uniform_filter1d appears to truncate rather than round when output...
• #6949: interp2d function crashes python
• #6959: scipy.interpolate.LSQUnivariateSpline - check for increasing...
• #7005: linear_sum_assignment in scipy.optimize never return if one of...
• #7010: scipy.statsbinned_statistic_2d: incorrect binnumbers returned
• #7049: expm_multiply is excessively slow when called for intervals
• #7050: Documenting _argcheck for rv_discrete
• #7077: coo_matrix.tocsr() still slow
• #7093: Wheels licensing
• #7122: Sketching-based Matrix Computations
• #7133: Discontinuity of a scipy special function
• #7141: Improve documentation for Elliptic Integrals
• #7181: A change in numpy.poly1d is causing the scipy tests to fail.
• #7220: String Formatting Issue in LinearOperator.__init__
• #7239: Source tarball distribution
• #7247: genlaguerre poly1d-object doesn’t respect ‘monic’ option at evaluation
• #7248: BUG: regression in Legendre polynomials on master
• #7316: dgels is missing
• #7381: Krogh interpolation fails to produce derivatives for complex...
• #7416: scipy.stats.kappa4(h,k) raise a ValueError for positive integer...
• #7421: scipy.stats.arcsine().pdf and scipy.stats.beta(0.5, 0.5).pdf...
• #7429: test_matrix_norms() in scipy/linalg/tests/test_basic.py calls...
• #7444: Doc: stats.dirichlet.var output description is wrong
• #7475: Parameter amax in scalar_search_wolfe2 is not used
• #7510: Operations between numpy.array and scipy.sparse matrix return...
• #7550: DOC: signal tutorial: Typo in explanation of convolution
• #7551: stdint.h included in SuperLU header files, but does not exist...
• #7553: Build for master broken on OS X
• #7557: Error in scipy.signal.periodogram example
• #7590: OSX test fail - test_ltisys.TestPlacePoles.test_real
• #7658: optimize.BenchGlobal broken
• #7669: nan result from multivariate_normal.cdf
• #7733: Inconsistent usage of indices, indptr in Delaunay.vertex_neighbor_vertices
• #7747: Numpy changes in np.random.dirichlet cause test failures
• #7772: Fix numpy lstsq rcond= parameter
• #7776: tests require nose
• #7798: contributor names for 1.0 release notes
• #7828: 32-bit Linux test errors on TestCephes
• #7893: scipy.spatial.distance.wminkowski behaviour change in 1.0.0b1
• #7898: DOC: Window functions
• #7959: BUG maybe: fmin_bfgs possibly broken in 1.0
• #7969: scipy 1.0.0rc1 windows wheels depend on missing msvcp140.dll

3.4.17 Pull requests for 1.0.0

• #4978: WIP: add pre_center and normalize options to lombscargle
• #5796: TST: Remove all permanent filter changes from tests
• #5910: ENH: sparse.linalg: add GCROT(m,k)
• #6326: ENH: New ODE solvers
• #6480: ENH: Make signal.decimate default to zero_phase=True
• #6705: ENH: add initial guess to sparse.linalg.lsqr
• #6706: ENH: add initial guess to sparse.linalg.lsmr
• #6769: BUG: optimize: add sufficient descent condition check to CG line...
• #6855: Handle objects supporting PEP 519 in I/O functions
• #6945: MAINT: ckdtree codebase clean up
• #6953: DOC: add a SciPy Project Governance document
• #6998: fix documentation of spearman rank corcoef
• #7017: ENH: add methods logcdf and cdf to scipy.stats.multivariate_normal
• #7027: Add random unitary matrices
• #7030: ENH: Add strictly-increasing checks for x to 1D splines
• #7031: BUG: Fix linear_sum_assignment hanging on an undefined matrix
• #7041: DOC: Clarify that windows are DFT-even by default
• #7048: DOC: modified docs for find_peak_cwt. Fixes #6922
• #7056: Fix insufficient precision when calculating spearman/kendall...
• #7057: MAINT: change dtype comparison in optimize.linear_sum_assignment.
• #7059: TST: make Xdist_deprecated_args cover all metrics
• #7061: Fix msvc 9 and 10 compile errors
• #7070: ENH: sparse: optimizing CSR/CSC slicing fast paths
• #7078: ENH: sparse: defer sum_duplicates to csr/csc
• #7079: ENH: sparse: allow subclasses to override specific math operations
• #7081: ENH: sparse: speed up CSR/CSC toarray()
• #7082: MAINT: Add missing PyType_Ready(&SuperLUGlobalType) for Py3
• #7083: Corrected typo in the doc of scipy.linalg.lstsq()
• #7086: Fix bug #7049 causing excessive slowness in expm_multiply
• #7088: Documented _argcheck for rv_discrete
• #7094: MAINT: Fix mistake in PR #7082
• #7098: BF: return NULL from failed Py3 module check
• #7105: MAINT: Customize ?TRSYL call in lyapunov solver
• #7111: Fix error message typo in UnivariateSpline
• #7113: FIX: Add add float to return type in documentation
• #7119: ENH: sparse.linalg: remove _count_nonzero hack
• #7123: ENH: added “interior-point” method for scipy.optimize.linprog
• #7137: DOC: clarify stats.linregress docstring, closes gh-7074
• #7138: DOC: special: Add an example to the airy docstring.
• #7139: DOC: stats: Update stats tutorial
• #7142: BUG: special: prevent segfault in pbwa
• #7143: DOC: special: warn about alternate elliptic integral parameterizations
• #7146: fix docstring of NearestNDInterpolator
• #7148: DOC: special: Add Parameters, Returns and Examples to gamma docstring
• #7152: MAINT: spatial: Remove two unused variables in ckdtrtree/src/distance.h
• #7153: MAINT: special: remove deprecated variant of gammaln
• #7154: MAINT: Fix some code that generates C compiler warnings
• #7155: DOC: linalg: Add examples for solve_banded and solve_triangular
• #7156: DOC: fix docstring of NearestNDInterpolator
• #7159: BUG: special: fix sign of derivative when x < 0 in pbwa
• #7161: MAINT: interpolate: make Rbf.A array a property
• #7163: MAINT: special: return nan for inaccurate regions of pbwa
• #7165: ENH: optimize: changes to make BFGS implementation more efficient.
• #7166: BUG: Prevent infinite loop in optimize._lsq.trf_linear.py
• #7173: BUG: sparse: return a numpy matrix from _add_dense
• #7179: DOC: Fix an error in sparse argmax docstring
• #7180: MAINT: interpolate: A bit of clean up in interpolate/src/_interpolate.cpp
• #7182: Allow homogeneous coordinate transforms in affine_transform
• #7184: MAINT: Remove hack modifying a readonly attr
• #7185: ENH: Add evaluation of periodic splines #6730
• #7186: MAINT: PPoly: improve error messages for wrong shape/axis

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- #7187: DEP: interpolate: deprecate interpolate_wrapper
- #7198: DOC: linalg: Add examples for solve_banded and solve_toeplitz.
- #7200: DOC: stats: Added tutorial documentation for the generalized...
- #7208: DOC: Added docstrings to issparse/isspmatrix(...) methods and...
- #7213: DOC: Added examples to circmean, circvar, circstd
- #7215: DOC: Adding examples to scipy.sparse.linalg.... docstrings
- #7223: DOC: special: Add examples for expit and logit.
- #7224: BUG: interpolate: fix integer overflow in fitpack.bispev
- #7225: DOC: update 1.0 release notes for several recent PRs.
- #7226: MAINT: update docs and code for mailing list move to python.org
- #7233: Fix issue #7232: Do not mask exceptions in objective func evaluation
- #7234: MAINT: cluster: cleaning up VQ/k-means code
- #7236: DOC: Fixed typo
- #7238: BUG: fix syntaxerror due to unicode character in trustregion_exact.
- #7243: DOC: Update docstring in misc/pilutil.py
- #7246: DEP: misc: deprecate imported names
- #7249: DOC: Add plotted example to scipy.cluster.vq.kmeans
- #7252: Fix 5231: docs of factr, ftol in sync w/ code
- #7254: ENH: SphericalVoronoi Input Handling
- #7256: fix for issue #7255 - Circular statistics functions give wrong...
- #7263: CI: use python’s faulthandler to ease tracing segfaults
- #7290: BUG: stats: Fix spurious warnings in genextreme.
- #7292: ENH: optimize: added trust region method trust-trlib
- #7296: DOC: stats: Add an example to the ttest_ind_from_stats docstring.
- #7297: DOC: signal: Add examples for chirp() and sweep_poly().
- #7299: DOC: Made difference between brent and fminbound clearer
- #7305: Simplify if-statements and constructor calls in integrate._ode
- #7309: Comply with PEP 518.
- #7313: REL: add python_requires to setup.py, fix Python version check.
- #7315: BUG: Fixed bug with Laguerre and Legendre polynomials
- #7320: DOC: clarify meaning of flags in ode.integrate
- #7333: DOC: Add examples to scipy.ndimage.gaussian_filter1d
- #7337: ENH: add n-dimensional DCT and IDCT to fftpack
- #7353: Add _gels functions
- #7357: DOC: linalg: Add examples to the svdvals docstring.

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• #7359: Bump Sphinx version to 1.5.5
• #7361: DOC: linalg: Add some ‘See Also’ links among special matrices...
• #7362: TST: Fix some Fedora 25 test failures.
• #7363: DOC: linalg: tweak the docstring example of svd
• #7365: MAINT: fix refguide_check.py for Sphinx >= 1.5
• #7367: BUG: odrpack: fix invalid stride checks in d_lpkbls.f
• #7368: DOC: constants: Add examples to the ‘find’ docstring.
• #7369: MAINT: fix refguide_check.py for Sphinx >= 1.5
• #7370: DOC: optimize: Better name for trust-region-exact method.
• #7371: MAINT: bundle Mathjax with built docs
• #7372: DOC: optimize: A few tweaks of the examples in the curve_fit
• #7373: DOC: Add examples to scipy.stats
• #7374: “Weight” is actually mass. Add slugs and slinches/blobs to mass
• #7375: DOC: Correct minor typo in optimize.{brenth,brentq}
• #7376: DOC: zeta only accepts real input
• #7377: MAINT: fix error messages in _minimize_trustregion_exact
• #7378: DOC: fix ndimage.distance_transform_bf docstring [ci skip]
• #7379: DOC: fix skew docstring [ci skip]
• #7380: Expand binnumbers with correct dimensions
• #7381: BUG: Extend scipy.stats.arcsine.pdf to endpoints 0 and 1 #7427
• #7382: DOC: Add examples to scipy.cluster.hierarchy
• #7383: ENH: stats: Implement the survival function for pareto.
• #7384: FIX Replaced np.assert_allclose with imported assert_allclose
• #7385: TST: fix integrate.ivp test that fails on 32-bit Python.
• #7386: Doc: Added tutorial documentation for stats distributions ksone
• #7387: DOC: Fix typos and remove trailing whitespace
• #7388: Fix some ndimage.interpolation endianness bugs
• #7389: del redundance in interpolate.py
• #7400: Initialize “info” in minpack_lmdif
• #7391: Added more testing of smirnov/smirnovi functions
• #7392: MAINT: update for new FutureWarning’s in numpy 1.13.0
• #7393: DOC: correctly describe output shape of dirichlet.mean() and...
• #7394: signal.lti: Remove deprecated cross-system properties
• #7395: MAINT: Clean-up uses of np.asarray in ndimage

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- #7485: ENH: support any order \(\geq 0\) in \texttt{ndimage.gaussian\_filter}
- #7486: ENH: Support \(k!\geq 0\) for \texttt{sparse.diagonal()}
- #7498: BUG: sparse: pass \texttt{assumeSortedIndices} option to \texttt{scikit.umfpack}
- #7501: ENH: add optimal leaf ordering for linkage matrices
- #7506: MAINT: remove overflow in Metropolis fixes #7495
- #7507: TST: speed up full test suite by less eval points in \texttt{mpmath} tests.
- #7509: BUG: fix issue when using \texttt{python setup.py somecommand --force}.
- #7511: fix some alerts found with \texttt{lgtm}
- #7514: Add explanation what the integer returned mean.
- #7516: BUG: Fix roundoff errors in \texttt{ndimage.uniform\_filter1d}.
- #7517: TST: fix \texttt{signal.convolve} test that was effectively being skipped.
- #7523: ENH: \texttt{linAlg}: allow \texttt{lstsq} to work with 0-shaped arrays
- #7525: TST: Warning cleanup
- #7526: DOC: params in \texttt{ndimage.interpolation} functions not optional
- #7527: MAINT: Encapsulate error message handling in \texttt{NI\_LineBuffer}.
- #7528: MAINT: Remove \texttt{ndimage} aliases for \texttt{NPY\_MAXDIMS}.
- #7529: MAINT: Remove \texttt{NI\_\_UNLIKELY} macros in favor of \texttt{numpy} ones.
- #7537: MAINT: Use accessor function for \texttt{numpy} array internals
- #7541: MAINT: Remove some uses of \texttt{Numarray} types in \texttt{ndimage}.
- #7543: MAINT: Replace all \texttt{Numarray} uses in \texttt{ni\_fourier.c}
- #7544: MAINT: Replace all uses of \texttt{Numarray} in \texttt{ni\_interpolation.c}
- #7545: MAINT: Replace all uses of \texttt{Numarray} in \texttt{ni\_measure.c}
- #7546: MAINT: Replace all uses of \texttt{Numarray} in \texttt{ni\_morphology.c}
- #7548: DOC: make a note in benchmarks \texttt{README} on how to run without rebuilding.
- #7549: MAINT: Get rid of \texttt{Numarray}.
- #7552: TST: Fix new warnings -> error bugs found on OSX
- #7554: Update superlu to 5.2.1 + fix \texttt{stdint.h} issue on MSVC
- #7556: MAINT: Fix some types from #7549 + miscellaneous warnings.
- #7558: MAINT: Use correct \#define \texttt{NO\_IMPORT\_ARRAY}, not \texttt{NO\_ARRAY\_IMPORT}...
- #7562: BUG: Copy \texttt{import\_nose} from \texttt{numpy}.
- #7563: ENH: Add the first Wasserstein and the Cramér-von Mises statistical...
- #7568: Test \texttt{janitoring}
- #7571: Test \texttt{janitoring pt. 2}
- #7572: Pytesting...
- #7574: TST: Remove ignore warnings filters from \texttt{stats}
- #7577: MAINT: Remove unused code in \texttt{ndimage/ni\_measure.c} and \texttt{h}
• #7578: TST: Remove ignore warnings filters from sparse, clean up warning...
• #7581: BUG: properly deallocate memory from PyArray_IntpConverter.
• #7582: DOC: signal tutorial: Typo in explanation of convolution
• #7583: Remove remaining ignore warnings filters
• #7586: DOC: add note to HACKING.rst on where to find build docs.
• #7587: DOC: Add examples to scipy.optimize
• #7594: TST: Add tests for ndimage converter functions.
• #7596: Added a sanity check to signal.savgol_filter
• #7599: __upfirdn_apply stopping condition bugfix
• #7601: MAINT: special: remove sph_jn et al.
• #7602: TST: fix test failures in trimmed statistics tests with numpy...
• #7605: Be clear about required dimension order
• #7606: MAINT: Remove unused function NI_NormalizeType.
• #7607: TST: add osx to travis matrix
• #7608: DOC: improve HACKING guide - mention reviewing PRs as contribution.
• #7609: MAINT: Remove unnecessary warning filter by avoiding unnecessary...
• #7610: #7557 : fix example code in periodogram
• #7611: #7220 : fix TypeError while raising ValueError for invalid shape
• #7612: Convert yield tests to pytest parametrized tests
• #7613: Add distributor init file
• #7614: fixup header
• #7615: BUG: sparse: Fix assignment w/ non-canonical sparse argument
• #7617: DOC: Clarify digital filter functions
• #7619: ENH: scipy.sparse.spmatrix.astype: casting and copy parameter...
• #7621: Expose VODE/ZVODE/LSODE IDID return code to user
• #7622: MAINT: special: remove out-of-date comment for ellpk
• #7625: TST: Add a test for “ignore” warning filters
• #7628: MAINT: refactoring and cleaning distance.py/.c/.h
• #7629: DEP: deprecate args usage in xdist
• #7630: ENH: weighted metrics
• #7634: Follow-up to #6855
• #7635: interpolate.splprep: Test some error cases, give slightly better...
• #7642: Add an example to interpolate.lagrange
• #7643: ENH: Added wrappers for LAPACK <s,d>stev
• #7649: Fix #7636, add PEP 519 test coverage to remaining I/O functions
• #7650: DOC: signal: Add ‘Examples’ to the docstring for sosfiltfilt.
• #7651: Fix up ccache usage on Travis + try enabling on OSX
• #7653: DOC: transition of examples from 2 to 3. Closes #7366
• #7662: CI: speed up continuous integration builds
• #7664: Update odr documentation
• #7665: BUG: wofle2 line/scalar search now uses amax parameter
• #7671: MAINT: _lib/ccallback.h: PyCapsule_GetName returns const char*
• #7672: TST: interpolate: test integrating periodic b-splines against...
• #7674: Tests tuning
• #7675: CI: move refguide-check to faster build
• #7676: DOC: bump scip-sphinx-theme to fix copybutton.js
• #7678: Note the zero-padding of the results of splrep and splprep
• #7681: MAINT: _lib: add user-overridable available memory determination
• #7684: TST: linalg: explicitly close opened npz files
• #7686: MAINT: remove unnecessary shebang lines and executable bits
• #7687: BUG: stats: don’t emit invalid warnings if moments are infinite
• #7690: ENH: allow int-like parameters in several routines
• #7691: DOC: Drop non-working source links from docs
• #7694: fix ma.rray to ma.array in func median_cihs
• #7698: BUG: stats: fix nan result from multivariate_normal.cdf (#7669)
• #7703: DOC: special: Update the doctstrings for noncentral F functions.
• #7709: BLD: integrate: avoid symbol clash between lsoda and vode
• #7711: TST: _lib: make test_parallel_threads to not fail falsely
• #7712: TST: stats: bump test tolerance in TestMultivariateNormal.test_broadcasting
• #7715: MAINT: fix deprecated use of numpy.issubdtype
• #7716: TST: integrate: drop timing tests
• #7717: MAINT: mstats.winsorize inclusion bug fix
• #7719: DOC: stats: Add a note about the special cases of the rdist distribution.
• #7720: DOC: Add example and math to stats.pearsonr
• #7723: DOC: Added Mann-Whitney U statistic reference
• #7727: BUG: special/cdflib: deal with nan and nonfinite inputs
• #7728: BLD: spatial: fix ckdtree depends header list
• #7732: BLD: update Bento build for optimal_leaf_ordering addition
• #7734: DOC: signal: Copy-edit and add examples to the Kaiser-related...
• #7736: BUG: Fixes #7735: Prevent integer overflow in concatenated index...
• #7737: DOC: rename indices/indptr for spatial.Delaunay vertex_neighbor_vertices
- #7738: ENH: Speed up freqz computation
- #7739: TST: ignore ncfdtridfn failure in win32 and warn on FPU mode changes
- #7740: Fix overflow in Anderson-Darling k-sample test
- #7742: TST: special: limit expm1 mpmath comparison range
- #7748: TST: stats: don’t pass invalid alpha to np.random.dirichlet
- #7749: BUG/DOC: optimize: method is ‘interior-point’, not ‘interior’
- #7751: BUG: optimize: show_options(‘linprog’, method=’interior-point’)...
- #7753: ENH: io: easier syntax for FortranFile read/write of mixed records
- #7754: BLD: add _lib._fpumode extension to Bento build.
- #7756: DOC: Show probability density functions as math
- #7757: MAINT: remove outdated OS X build scripts. Fixes pytest failure.
- #7758: MAINT: stats: pep8, wrap lines
- #7760: DOC: special: add instructions on how to add special functions
- #7761: DOC: allow specifying Python version for Sphinx makefile
- #7765: TST: fix test coverage of mstats_extras.py
- #7767: DOC: update 1.0 release notes.
- #7768: DOC: update notes on how to release. Also change paver file to...
- #7769: Add the _sf and _logsf function for planck dist
- #7770: DOC: Replace rotten links in the docstring of minres
- #7771: MAINT: f2py build output cleanup
- #7773: DOC: optimize: Some copy-editing of linprog docs.
- #7774: MAINT: set rcond explicitly for np.linalg.lstsq calls
- #7777: remove leftover nose imports
- #7780: ENH: Wrap LAPACK’s dsytrd
- #7781: DOC: Link rfft
- #7782: MAINT: run pyx autogeneration in cythonize & remove autogen files
- #7783: FIX: Disallow Wn=1 in digital filters
- #7790: Fix test errors introduced by gh-5910
- #7792: MAINT: fix syntax in pyproject.toml
- #7809: ENH: sketches - Clarkson Woodruff Transform
- #7810: ENH: Add eig(vals)_tridiagonal
- #7811: BUG: stats: Fix warnings in binned_statistics_dd
- #7814: ENH: signal: Replace ‘nyq’ and ‘Hz’ arguments with ‘fs’.
- #7820: DOC: update 1.0 release notes and mailmap
- #7823: BUG: memory leak in messagestream / qhull.pyx
- #7830: DOC: linalg: Add an example to the lstsq docstring.
• #7835: ENH: Automatic FIR order for decimate
• #7838: MAINT: stats: Deprecate frechet_l and frechet_r.
• #7841: slsqp PEP8 formatting fixes, typos, etc.
• #7843: ENH: Wrap all BLAS routines
• #7844: DOC: update LICENSE.txt with licenses of bundled libs as needed.
• #7851: ENH: Add wrappers for ?GGLSE, ?(HE/SY)CON, ?SYTF2, ?(HE/SY)TRF
• #7856: ENH: added out argument to Xdist
• #7858: BUG: special/cdflib: fix fatal loss of precision issues in cumfnc
• #7859: FIX: Squash place_poles warning corner case
• #7861: dummy statement for undefined WITH_THREAD
• #7863: MAINT: add license texts to binary distributions
• #7866: DOC, MAINT: fix links in the doc
• #7867: DOC: fix up descriptions of pdf's in distribution docstrings.
• #7869: DEP: deprecate misc.pilutil functions
• #7870: DEP: remove deprecated functions
• #7872: TST: silence RuntimeWarning for stats.truncnorm test marked as...
• #7874: TST: fix an optimize.linprog test that fails intermittently.
• #7875: TST: filter two integration warnings in stats tests.
• #7876: GEN: Add comments to the tests for clarification
• #7891: ENH: backport #7879 to 1.0.x
• #7902: MAINT: signal: Make freqz handling of multidim. arrays match...
• #7905: REV: restore wminkowski
• #7908: FIX: Avoid bad __del__ (close) behavior
• #7918: TST: mark two optimize.linprog tests as xfail. See gh-7877.
• #7929: MAINT: changed defaults to lower in sytf2, sytrf and hetrf
• #7939: Fix umfpack solver construction for win-amd64
• #7948: DOC: add note on checking for deprecations before upgrade to...
• #7952: DOC: update SciPy Roadmap for 1.0 release and recent discussions.
• #7960: BUG: optimize: revert changes to bfgs in gh-7165
• #7962: TST: special: mark a failing hyp2f1 test as xfail
• #7973: BUG: fixed keyword in ‘info’ in _get_mem_available utility
• #8001: TST: fix test failures from Matplotlib 2.1 update
• #8010: BUG: signal: fix crash in lfilter
• #8019: MAINT: fix test failures with NumPy master
3.5 SciPy 0.19.1 Release Notes

SciPy 0.19.1 is a bug-fix release with no new features compared to 0.19.0. The most important change is a fix for a severe memory leak in integrate.quad.

3.5.1 Authors

- Evgeni Burovski
- Patrick Callier +
- Yu Feng
- Ralf Gommers
- Ilhan Polat
- Eric Quintero
- Scott Sievert
- Pauli Virtanen
- Warren Weckesser

A total of 9 people contributed to this release. People with a “+” by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 0.19.1

- #7214: Memory use in integrate.quad in scipy-0.19.0
- #7258: linalg.matrix_balance gives wrong transformation matrix
- #7262: Segfault in daily testing
- #7273: scipy.interpolate._bspl.evaluate_spline gets wrong type
- #7335: scipy.signal.dlti(A,B,C,D).freqresp() fails

Pull requests for 0.19.1

- #7211: BUG: convolve may yield inconsistent dtypes with method changed
- #7216: BUG: integrate: fix refcounting bug in quad()
- #7229: MAINT: special: Rewrite a test of wrightomega
- #7261: FIX: Corrected the transformation matrix permutation
- #7265: BUG: Fix broken axis handling in spectral functions
- #7266: FIX 7262: ckdmtree crashes in query_knn.
- #7279: Upcast half- and single-precision floats to doubles in BSpline...
- #7336: BUG: Fix signal.dfreqresp for StateSpace systems
- #7419: Fix several issues in sparse.load_npz, save_npz
- #7420: BUG: stats: allow integers as kappa4 shape parameters
3.6 SciPy 0.19.0 Release Notes

SciPy 0.19.0 is the culmination of 7 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.19.x branch, and on adding new features on the master branch.

This release requires Python 2.7 or 3.4-3.6 and NumPy 1.8.2 or greater.

Highlights of this release include:

- A unified foreign function interface layer, `scipy.LowLevelCallable`.
- Cython API for scalar, typed versions of the universal functions from the `scipy.special` module, via `cimport scipy.special.cython_special`.

3.6.1 New features
Foreign function interface improvements

`scipy.LowLevelCallable` provides a new unified interface for wrapping low-level compiled callback functions in the Python space. It supports Cython imported “api” functions, ctypes function pointers, CFFI function pointers, PyCapsules, Numba jitted functions and more. See gh-6509 for details.

`scipy.linalg` improvements

The function `scipy.linalg.solve` obtained two more keywords `assume_a` and `transposed`. The underlying LAPACK routines are replaced with “expert” versions and now can also be used to solve symmetric, hermitian and positive definite coefficient matrices. Moreover, ill-conditioned matrices now cause a warning to be emitted with the estimated condition number information. Old `sym_pos` keyword is kept for backwards compatibility reasons however it is identical to using `assume_a='pos'`. Moreover, the `debug` keyword, which had no function but only printing the `overwrite_<a, b>` values, is deprecated.

The function `scipy.linalg.matrix_balance` was added to perform the so-called matrix balancing using the LAPACK xGEBAL routine family. This can be used to approximately equate the row and column norms through diagonal similarity transformations.

The functions `scipy.linalg.solve_continuous_are` and `scipy.linalg.solve_discrete_are` have numerically more stable algorithms. These functions can also solve generalized algebraic matrix Riccati equations. Moreover, both gained a balanced keyword to turn balancing on and off.

`scipy.spatial` improvements

`scipy.spatial.SphericalVoronoi.sort_vertices_of_regions` has been re-written in Cython to improve performance.

`scipy.spatial.SphericalVoronoi` can handle > 200 k points (at least 10 million) and has improved performance.

The function `scipy.spatial.distance.directed_hausdorff` was added to calculate the directed Hausdorff distance.

`count_neighbors` method of `scipy.spatial.cKDTree` gained an ability to perform weighted pair counting via the new keywords `weights` and `cumulative`. See gh-5647 for details.

`scipy.spatial.distance.pdist` and `scipy.spatial.distance.cdist` now support non-double custom metrics.

`scipy.ndimage` improvements

The callback function C API supports PyCapsules in Python 2.7

Multidimensional filters now allow having different extrapolation modes for different axes.

`scipy.optimize` improvements

The `scipy.optimize.basinhopping` global minimizer obtained a new keyword, `seed`, which can be used to seed the random number generator and obtain repeatable minimizations.

The keyword `sigma` in `scipy.optimize.curve_fit` was overloaded to also accept the covariance matrix of errors in the data.

`scipy.signal` improvements

The function `scipy.signal.correlate` and `scipy.signal.convolve` have a new optional parameter `method`. The default value of `auto` estimates the fastest of two computation methods, the direct approach and the Fourier transform approach.
A new function has been added to choose the convolution/correlation method, `scipy.signal.choose_conv_method` which may be appropriate if convolutions or correlations are performed on many arrays of the same size.

New functions have been added to calculate complex short time fourier transforms of an input signal, and to invert the transform to recover the original signal: `scipy.signal.stft` and `scipy.signal.istft`. This implementation also fixes the previously incorrect output of `scipy.signal.spectrogram` when complex output data were requested.

The function `scipy.signal.sosfreqz` was added to compute the frequency response from second-order sections.

The function `scipy.signal.unit_impulse` was added to conveniently generate an impulse function.

The function `scipy.signal.iirnotch` was added to design second-order IIR notch filters that can be used to remove a frequency component from a signal. The dual function `scipy.signal.iirpeak` was added to compute the coefficients of a second-order IIR peak (resonant) filter.

The function `scipy.signal.minimum_phase` was added to convert linear-phase FIR filters to minimum phase.

The functions `scipy.signal.upfirdn` and `scipy.signal.resample_poly` are now substantially faster when operating on some n-dimensional arrays when n > 1. The largest reduction in computation time is realized in cases where the size of the array is small (<1k samples or so) along the axis to be filtered.

**scipy.fftpack improvements**

Fast Fourier transform routines now accept `np.float16` inputs and upcast them to `np.float32`. Previously, they would raise an error.

**scipy.cluster improvements**

Methods "centroid" and "median" of `scipy.cluster.hierarchy.linkage` have been significantly sped up. Long-standing issues with using `linkage` on large input data (over 16 GB) have been resolved.

**scipy.sparse improvements**

The functions `scipy.sparse.save_npz` and `scipy.sparse.load_npz` were added, providing simple serialization for some sparse formats.

The `prune` method of classes `bsr_matrix`, `csc_matrix`, and `csr_matrix` was updated to reallocate backing arrays under certain conditions, reducing memory usage.

The methods `argmin` and `argmax` were added to classes `coo_matrix`, `csc_matrix`, `csr_matrix`, and `bsr_matrix`.

New function `scipy.sparse.csgraph.structural_rank` computes the structural rank of a graph with a given sparsity pattern.

New function `scipy.sparse.linalg.spsolve_triangular` solves a sparse linear system with a triangular left hand side matrix.

**scipy.special improvements**

Scalar, typed versions of universal functions from `scipy.special` are available in the Cython space via `cimport` from the new module `scipy.special.cython_special`. These scalar functions can be expected to be significantly faster than the universal functions for scalar arguments. See the `scipy.special` tutorial for details.

Better control over special-function errors is offered by the functions `scipy.special.geterr` and `scipy.special.seterr` and the context manager `scipy.special.errstate`. 
The names of orthogonal polynomial root functions have been changed to be consistent with other functions relating to orthogonal polynomials. For example, `scipy.special.j_roots` has been renamed `scipy.special.roots_jacobi` for consistency with the related functions `scipy.special.jacobi` and `scipy.special.eval_jacobi`. To preserve back-compatibility the old names have been left as aliases.

Wright Omega function is implemented as `scipy.special.wrightomega`.

### scipy.stats improvements

The function `scipy.stats.weightedtau` was added. It provides a weighted version of Kendall’s tau.

New class `scipy.stats.multinomial` implements the multinomial distribution.

New class `scipy.stats.rv_histogram` constructs a continuous univariate distribution with a piecewise linear CDF from a binned data sample.

New class `scipy.stats.argus` implements the Argus distribution.

### scipy.interpolate improvements

New class `scipy.interpolate.BSpline` represents splines. BSpline objects contain knots and coefficients and can evaluate the spline. The format is consistent with FITPACK, so that one can do, for example:

```python
>>> t, c, k = splrep(x, y, s=0)
>>> spl = BSpline(t, c, k)
>>> np.allclose(spl(x), y)
```

**spl* functions**, `scipy.interpolate.splev`, `scipy.interpolate.splint`, `scipy.interpolate.splder` and `scipy.interpolate.splantider`, accept both BSpline objects and `(t, c, k)` tuples for backwards compatibility.

For multidimensional splines, `c.ndim > 1`, BSpline objects are consistent with piecewise polynomials, `scipy.interpolate.PPoly`. This means that BSpline objects are not immediately consistent with `scipy.interpolate.splprep`, and one cannot do `>>> BSpline(*splprep([x, y])[0])`. Consult the `scipy.interpolate` test suite for examples of the precise equivalence.

In new code, prefer using `scipy.interpolate.BSpline` objects instead of manipulating `(t, c, k)` tuples directly.

New function `scipy.interpolate.make_interp_spline` constructs an interpolating spline given data points and boundary conditions.

New function `scipy.interpolate.make_lsq_spline` constructs a least-squares spline approximation given data points.

### scipy.integrate improvements

Now `scipy.integrate.fixed_quad` supports vector-valued functions.

#### 3.6.2 Deprecated features

`scipy.interpolate.splmake`, `scipy.interpolate.spleval` and `scipy.interpolate.spline` are deprecated. The format used by splmake/spleval was inconsistent with splrep/splev which was confusing to users.

`scipy.special.errprint` is deprecated. Improved functionality is available in `scipy.special.seterr`.

Calling `scipy.spatial.distance.pdist` or `scipy.spatial.distance.cdist` with arguments not needed by the chosen metric is deprecated. Also, metrics “old_cosine” and “old_cos” are deprecated.
3.6.3 Backwards incompatible changes

The deprecated `scipy.weave` submodule was removed.

`scipy.spatial.distance.squareform` now returns arrays of the same dtype as the input, instead of always float64.

`scipy.special.errprint` now returns a boolean.

The function `scipy.signal.find_peaks_cwt` now returns an array instead of a list.

`scipy.stats.kendalltau` now computes the correct p-value in case the input contains ties. The p-value is also identical to that computed by `scipy.stats.mstats.kendalltau` and by R. If the input does not contain ties there is no change w.r.t. the previous implementation.

The function `scipy.linalg.block_diag` will not ignore zero-sized matrices anymore. Instead it will insert rows or columns of zeros of the appropriate size. See gh-4908 for more details.

3.6.4 Other changes

SciPy wheels will now report their dependency on `numpy` on all platforms. This change was made because Numpy wheels are available, and because the pip upgrade behavior is finally changing for the better (use `--upgrade-strategy=only-if-needed` for `pip >= 8.2`; that behavior will become the default in the next major version of `pip`).

Numerical values returned by `scipy.interpolate.interp1d` with `kind="cubic"` and "quadratic" may change relative to previous scipy versions. If your code depended on specific numeric values (i.e., on implementation details of the interpolators), you may want to double-check your results.

3.6.5 Authors

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• Evan Limanto +
A total of 121 people contributed to this release. People with a “+” by their names contributed a patch for
the first time. This list of names is automatically generated, and may not be fully complete.
Issues closed for 0.19.0

- #1767: Function definitions in __fitpack.h should be moved. (Trac #1240)
- #1774: _kmeans chokes on large thresholds (Trac #1247)
- #2089: Integer overflows cause segfault in linkage function with large...
- #2190: Are odd-length window functions supposed to be always symmetrical?...
- #2251: solve_discrete_are in scipy.linalg does (sometimes) not solve...
- #2580: scipy.interpolate.UnivariateSpline (or a new superclass of it)...
- #2592: scipy.stats.anderson assumes gumbel_1
- #3054: scipy.linalg.eig does not handle infinite eigenvalues
- #3160: multinomial pmf / logpmf
- #3904: scipy.special.ellipj dn wrong values at quarter period
- #4044: Inconsistent code book initialization in kmeans
- #4234: scipy.signal.flattop documentation doesn’t list a source for...
- #4831: Bugs in C code in __quadpack.h
- #4908: bug: unnessesary validity check for block dimension in scipy.sparse.block_diag
- #4917: BUG: indexing error for sparse matrix with ix_
- #4938: Docs on extending ndimage need to be updated.
- #5056: sparse matrix element-wise multiplying dense matrix returns dense...
- #5337: Formula in documentation for correlate is wrong
- #5537: use OrderedDict in io.netcdf
- #5750: [doc] missing data index value in KDTree, cKDTree
- #5755: p-value computation in scipy.stats.kendalltau() in broken in...
- #5757: BUG: Incorrect complex output of signal.spectrogram
- #5964: ENH: expose scalar versions of scipy.special functions to cython
- #6107: scipy.cluster.hierarchy.single segmentation fault with 2**16...
- #6278: optimize.basinhopping should take a RandomState object
- #6296: InterpolatedUnivariateSpline: check_finite fails when w is unspecified
- #6306: Anderson-Darling bad results
- #6314: scipy.stats.kendalltau() p value not in agreement with R, SPSS...
- #6340: Curve_fit bounds and maxfev
- #6377: expm_multiply, complex matrices not working using start,stop,etc...
- #6428: scipy.stats.mstats.mode modifies input
• #6440: Figure out ABI break policy for scipy.special Cython API
• #6441: Using Qhull for halfspace intersection: segfault
• #6442: scipy.spatial: In incremental mode volume is not recomputed
• #6451: Documentation for scipy.cluster.hierarchy.to_tree is confusing...
• #6490: interp1d (kind=zero) returns wrong value for rightmost interpolation...
• #6521: scipy.stats.entropy does not calculate the KL divergence
• #6530: scipy.stats.spearmanr unexpected NaN handling
• #6541: Test runner does not run scipy._lib/tests?
• #6551: scipy.stats.entropy does not calculate the KL divergence
• #6552: BUG: misc.bytescale returns unexpected results when using cmin/cmax...
• #6556: RectSphereBivariateSpline(u, v, r) fails if min(v) >= pi
• #6559: Differential_evolution maxiter causing memory overflow
• #6565: Coverage of spectral functions could be improved
• #6628: Incorrect parameter name in binomial documentation
• #6634: Expose LAPACK’s xGESVX family for linalg.solve ill-conditioned...
• #6657: Confusing documentation for scipy.special.sph_harm
• #6676: Documentation for scipy.stats.norm.fit is incorrect
• #6652: BUG: scipy.io.wavfile.read stays in infinite loop, warns on wav...
• #6700: BUG: scipy.io.wavfile.read stays in infinite loop, warns on wav...
• #6701: scipy.stats.entropy(N) throw a ‘TypeError’ when N > 64
• #6721: scipy.spatial.SphericalVoronoi fails for large number of points
• #6727: Documentation for scipy.stats.norm.fit is incorrect
• #6759: scipy.stats.entropy(N) throw a ‘TypeError’ when N > 64
• #6764: Documentation for scipy.spatial.Delaunay is partially incorrect
• #6811: scipy.spatial.SphericalVoronoi fails for large number of points
• #6841: spearmanr fails when nan_policy='omit' is set
• #6849: Currently in gaussian_kde, the logpdf function is calculated...
• #6850: SLSQP inconsistent handling of invalid bounds
• #6856: Python stopped working (Segfault?) with minimum/maximum filter...
• #6889: dblquad gives different results under scipy 0.17.1 and 0.18.1
• #6898: BUG: dblquad ignores error tolerances
• #6901: Solving sparse linear systems in CSR format with complex values
• #6903: issue in spatial.distance.pdist docstring
• #6926: signature mismatches for LowLevelCallable
• #6961: scipy contains shebang pointing to /usr/bin/python and /bin/bash...
• #6972: BUG: special: generate_ufuncs.py is broken
• #6984: Assert raises test failure for test_ill_condition_warning
• #6990: BUG: sparse: Bad documentation of the k argument in sparse.linalg.eigs
• #6991: Division by zero in linregress()
• #7011: possible speed improvement in rv_continuous.fit()
• #7015: Test failure with Python 3.5 and numpy master
• #7055: SciPy 0.19.0rc1 test errors and failures on Windows
• #7096: macOS test failures for test_solve_continuous_are
• #7100: test_distance.test_Xdist_deprecated_args test error in 0.19.0rc2

Pull requests for 0.19.0
• #2908: Scipy 1.0 Roadmap
• #3174: add b-splines
• #4606: ENH: Add a unit impulse waveform function
• #5608: Adds keyword argument to choose faster convolution method
• #5647: ENH: Faster count_neighbour in cKDTree / + weighted input data
• #6021: Netcdf append
• #6058: ENH: scipy.signal - Add stft and istft
• #6059: ENH: More accurate signal.freqresp for zpk systems
• #6195: ENH: Cython interface for special
• #6234: DOC: Fixed a typo in ward() help
• #6261: ENH: add docstring and clean up code for signal.normalize
• #6270: MAINT: special: add tests for cdflib
• #6271: Fix for scipy.cluster.hierarchy.is_isomorphic
• #6273: optimize: rewrite while loops as for loops
• #6279: MAINT: Bessel tweaks
• #6291: Fixes gh-6219: remove runtime warning from genextreme distribution
• #6294: STY: Some PEP8 and cleaning up imports in stats/_continuous_distns.py
• #6297: Clarify docs in misc/__init__.py
• #6300: ENH: sparse: Loosen input validation for diags with empty inputs
• #6301: BUG: standardizes check_finite behavior re optional weights,...
• #6303: Fixing example in _lazyselect docstring.
• #6307: MAINT: more improvements to gammaine/gammaincc
• #6308: Clarified documentation of hypergeometric distribution.
• #6309: BUG: stats: Improve calculation of the Anderson-Darling statistic.
• #6315: ENH: Descending order of x in PPoly
• #6317: ENH: stats: Add support for nan_policy to stats.median_test
• #6321: TST: fix a typo in test name
• #6328: ENH: sosfreqz
• #6335: Define LinregressResult outside of linregress
• #6337: In anderson test, added support for right skewed gumbel distribution.
• #6341: Accept several spellings for the curve_fit max number of function...
• #6342: DOC: cluster: clarify hierarchy.linkage usage
• #6352: DOC: removed brentq from its own ‘see also’
• #6362: ENH: stats: Use explicit formulas for sf, logsf, etc in weibull...
• #6369: MAINT: special: add a comment to hyp0f1_complex
• #6375: Added the multinomial distribution.
• #6387: MAINT: special: improve accuracy of ellipj’s dn at quarter...
• #6388: BenchmarkGlobal - getting it to work in Python3
• #6394: ENH: scipy.sparse: add save and load functions for sparse matrices
• #6400: MAINT: moves global benchmark run from setup_cache to track_all
• #6403: ENH: seed kwd for basinhopping. Closes #6278
• #6404: ENH: signal: added irnootch and irpeak functions.
• #6406: ENH: special: extend sici/shichi to complex arguments
• #6407: ENH: Window functions should not accept non-integer or negative...
• #6408: MAINT: _differentialevolution now uses _lib._util.check_random_state
• #6427: MAINT: Fix gmpy build & test that mpmath uses gmpy
• #6439: MAINT: ndimage: update callback function c api
• #6443: BUG: Fix volume computation in incremental mode
• #6447: Fixes issue #6413 - Minor documentation fix in the entropy function...
• #6448: ENH: Add halfspace mode to Qhull
• #6449: ENH: rtol and atol for differential_evolution termination fixes...
• #6453: DOC: Add some See Also links between similar functions
• #6454: DOC: linalg: clarify callable signature in ordfz
• #6457: ENH: spatial: enable non-double dtypes in squareform
• #6459: BUG: Complex matrices not handled correctly by expm_multiply...
• #6465: TST DOC Window docs, tests, etc.
• #6469: ENH: linalg: better handling of infinite eigenvalues in eig/eigvals
• #6475: DOC: calling interp1d/interp2d with NaNs is undefined
• #6477: Document magic numbers in optimize.py
• #6481: TST: Supress some warnings from test_windows
• #6485: DOC: spatial: correct typo in procrustes
• #6487: Fix Bray-Curtis formula in pdist docstring
• #6493: ENH: Add covariance functionality to scipy.optimize.curve_fit
• #6494: ENH: stats: Use log1p() to improve some calculations.
• #6495: BUG: Use MST algorithm instead of SLINK for single linkage clustering
• #6497: MRG: Add minimum_phase filter function
• #6505: reset scipy.signal.resample window shape to 1-D
• #6507: BUG: linkage: Raise exception if y contains non-finite elements
• #6509: ENH: _lib: add common machinery for low-level callback functions
• #6520: scipy.sparse.base.__mul__ non-numpy/scipy objects with ‘shape’...
• #6522: Replace kl_div by rel_entr in entropy
• #6524: DOC: add next_fast_len to list of functions
• #6527: DOC: Release notes to reflect the new covariance feature in optimize.curve_fit
• #6532: ENH: Simplify _cos_win, document it, add symmetric/periodic arg
• #6535: MAINT: sparse.csgraph: updating old cython loops
• #6540: DOC: add to documentation of orthogonal polynomials
• #6544: TST: Ensure tests for scipy._lib are run by scipy.test()
• #6546: updated docstring of stats.linregress
• #6553: committed changes that I originally submitted for scipy.signal.cspline...
• #6561: BUG: modify signal.find_peaks_cwt() to return array and accept...
• #6562: DOC: Negative binomial distribution clarification
• #6563: MAINT: be more liberal in requiring numpy
• #6567: MAINT: use xrange for iteration in differential_evolution fixes...
• #6572: BUG: “sp.linalg.solve_discrete_are” fails for random data
• #6578: BUG: misc: allow both cmin/cmax and low/high params in bytescale
• #6581: Fix some unfortunate typos
• #6582: MAINT: linalg: make handling of infinite eigenvalues in ordqz...
• #6585: DOC: interpolate: correct seealso links to ndimage
• #6588: Update docstring of scipy.spatial.distance_matrix
• #6592: DOC: Replace ‘first’ by ‘smallest’ in mode
• #6593: MAINT: remove scipy.weave submodule
• #6594: DOC: distance.squareform: fix html docs, add note about dtype...
• #6598: [DOC] Fix incorrect error message in medfilt2d
• #6599: MAINT: linalg: turn a solve_discrete_are test back on
• #6600: DOC: Add SOS goals to roadmap
• #6601: DEP: Raise minimum numpy version to 1.8.2
• #6605: MAINT: ‘new’ module is deprecated, don’t use it
• #6607: DOC: add note on change in wheel dependency on numpy and pip...
• #6609: Fixes #6602 - Typo in docs
• #6616: ENH: generalization of continuous and discrete Riccati solvers...
• #6621: DOC: improve cluster.hierarchy docstrings.
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- #6623: CS matrix prune method should copy data from large unpruned arrays
- #6625: DOC: special: complete documentation of `eval_*` functions
- #6626: TST: special: silence some deprecation warnings
- #6631: fix parameter name doc for discrete distributions
- #6632: MAINT: stats: change some instances of `special` to `sc`
- #6633: MAINT: refguide: py2k long integers are equal to py3k integers
- #6638: MAINT: change type declaration in cluster.linkage, prevent overflow
- #6640: BUG: fix issue with duplicate values used in `cluster.vq.kmeans`
- #6641: BUG: fix corner case in `cluster.vq.kmeans` for large thresholds
- #6643: MAINT: clean up truncation modes of dendrogram
- #6645: MAINT: special: rename `*_roots` functions
- #6646: MAINT: clean up mpmath imports
- #6647: DOC: add `sqrt` to Mahalanobis description for `pdist`
- #6648: DOC: special: add a section on `cython_special` to the tutorial
- #6649: ENH: Added `scipy.spatial.distance.directed_hausdorff`
- #6650: DOC: add Sphinx roles for DOI and arXiv links
- #6651: BUG: mstats: make sure `mode(..., None)` does not modify its input
- #6652: DOC: special: add section to tutorial on functions not in `special`
- #6653: ENH: `special`: add the Wright Omega function
- #6656: ENH: don’t coerce input to double with custom metric in `cdist`...
- #6658: Faster/shorter code for computation of discordances
- #6659: DOC: special: make `__init__` summaries and html summaries match
- #6661: general.rst: Fix a typo
- #6664: TST: Spectral functions’ window correction factor
- #6665: [DOC] Conditions on `v` in `RectSphereBivariateSpline`
- #6668: DOC: Mention negative masses for center of mass
- #6675: MAINT: special: remove outdated README
- #6677: BUG: Fixes computation of p-values.
- #6679: BUG: optimize: return correct Jacobian for method ‘SLSQP’ in...
- #6680: ENH: Add structural rank to `sparse.csgraph`
- #6686: TST: Added Airspeed Velocity benchmarks for `SphericalVoronoi`
- #6687: DOC: add section “deciding on new features” to developer guide.
- #6691: ENH: Clearer error when `fmin_slsqp` obj doesn’t return scalar
- #6702: TST: Added airspeed velocity benchmarks for `scipy.spatial.distance.cdist`
- #6707: TST: interpolate: test fitpack wrappers, not `_impl`
- #6709: TST: fix a number of test failures on 32-bit systems
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- #6711: MAINT: move function definitions from __fitpack.h to _fitpackmodule.c
- #6712: MAINT: clean up wishlist in stats.morestats, and copyright statement.
- #6715: DOC: update the release notes with BSpine et al.
- #6716: MAINT: scipy.io.wavfile: No infinite loop when trying to read...
- #6717: some style cleanup
- #6723: BUG: special: cast to float before in-place multiplication in...
- #6726: address performance regressions in interp1d
- #6728: DOC: made code examples in integrate tutorial copy-pasteable
- #6731: DOC: scipy.optimize: Added an example for wrapping complex-valued...
- #6732: MAINT: cython_special: remove errprint
- #6733: MAINT: special: fix some pyflakes warnings
- #6734: DOC: sparse.linalg: fixed matrix description in biegstab doc
- #6737: BLD: update cythonize.py to detect changes in pxi files
- #6740: DOC: special: some small fixes to docstrings
- #6741: MAINT: remove dead code in interpolate.py
- #6742: BUG: fix linalg.block_diag to support zero-sized matrices.
- #6744: ENH: interpolate: make PPoly.from_spline accept BSpline objects
- #6746: DOC: special: clarify use of Condon-Shortley phase in sph_harm/lpmv
- #6750: ENH: sparse: avoid densification on broadcasted elem-wise mult
- #6751: sinm doc explained cosm
- #6753: ENH: special: allow for more fine-tuned error handling
- #6759: Move logsumexp and pade from scipy.misc to scipy.special and...
- #6761: ENH: argmax and argmin methods for sparse matrices
- #6762: DOC: Improve docstrings of sparse matrices
- #6763: ENH: Weighted tau
- #6768: ENH: cythonized spherical Voronoi region polygon vertex sorting
- #6770: Correction of Delaunay class' documentation
- #6775: ENH: Integrating LAPACK “expert” routines with conditioning warnings...
- #6776: MAINT: Removing the trivial f2py warnings
- #6777: DOC: Update rv_continuous.fit doc.
- #6778: MAINT: cluster.hierarchy: Improved wording of error msgs
- #6786: BLD: increase minimum Cython version to 0.23.4
- #6787: DOC: expand on linalg.block_diag changes in 0.19.0 release...
- #6789: ENH: Add further documentation for norm.fit
- #6790: MAINT: Fix a potential problem in nn_chain linkage algorithm
- #6791: DOC: Add examples to scipy.ndimage.fourier
• #6792: DOC: fix some numpydoc / Sphinx issues.
• #6793: MAINT: fix circular import after moving functions out of misc
• #6796: TST: test importing each submodule. Regression test for gh-6793.
• #6799: ENH: stats: Argus distribution
• #6801: ENH: stats: Histogram distribution
• #6803: TST: make sure tests for _build_utils are run.
• #6804: MAINT: more fixes in loggamma
• #6806: ENH: Faster linkage for ‘centroid’ and ‘median’ methods
• #6810: ENH: speed up upfirdn and resample_poly for n-dimensional arrays
• #6812: TST: Added ConvexHull asv benchmark code
• #6814: ENH: Different extrapolation modes for different dimensions in...
• #6826: Signal spectral window default fix
• #6828: BUG: SphericalVoronoi Space Complexity (Fixes #6811)
• #6830: RealData docstring correction
• #6834: DOC: Added reference for skewtest function. See #6829
• #6836: DOC: Added mode=mirror in the docstring for the functions accepting...
• #6838: MAINT: sparse: start removing old BSR methods
• #6844: handle incompatible dimensions when input is not an ndarray in...
• #6847: Added maxiter to golden search.
• #6850: BUG: added check for optional param scipy.stats.spearmanr
• #6858: MAINT: Removing redundant tests
• #6861: DEP: Fix escape sequences deprecated in Python 3.6.
• #6862: DOC: dx should be float, not int
• #6863: updated documentation curve_fit
• #6866: DOC : added some documentation to j1 referring to spherical_jn
• #6867: DOC: cdist move long examples list into Notes section
• #6868: BUG: Make stats.mode return a ModeResult namedtuple on empty...
• #6871: Corrected documentation.
• #6874: ENH: gaussian_kde.logpdf based on logsumexp
• #6877: BUG: ndimage: guard against footprints of all zeros
• #6881: python 3.6
• #6885: Vectorized integrate.fixed_quad
• #6886: fixed typo
• #6891: TST: fix failures for linalg.dare/care due to tightened test...
• #6892: DOC: fix a bunch of Sphinx errors.
• #6894: TST: Added asv benchmarks for scipy.spatial.Voronoi

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• #6908: BUG: Fix return dtype for complex input in spsolve
• #6909: ENH: fftpack: use float32 routines for float16 inputs.
• #6911: added min/max support to binned_statistic
• #6913: Fix 6875: SLSQP raise ValueError for all invalid bounds.
• #6914: DOCS: GH6903 updating docs of Spatial.distance.pdist
• #6916: MAINT: fix some issues for 32-bit Python
• #6924: BLD: update Bento build for scipy.LowLevelCallable
• #6932: ENH: Use OrderedDict in io.netcdf. Closes gh-5537
• #6933: BUG: fix LowLevelCallable issue on 32-bit Python.
• #6936: BUG: sparse: handle size-1 2D indexes correctly
• #6938: TST: fix test failures in special on 32-bit Python.
• #6939: Added attributes list to cKDTree docstring
• #6940: improve efficiency of dok_matrix.tocoo
• #6942: DOC: add link to liac-arff package in the io.arff docstring.
• #6943: MAINT: Docstring fixes and an additional test for linalg.solve
• #6944: DOC: Add example of odeint with a banded Jacobian to the integrate...
• #6946: ENH: hypergeom.logpmf in terms of betain
• #6947: TST: speedup distance tests
• #6948: DEP: Deprecate the keyword “debug” from linalg.solve
• #6950: BUG: Correctly treat large integers in MMIO (fixes #6397)
• #6952: ENH: Minor user-friendliness cleanup in LowLevelCallable
• #6956: DOC: improve description of ‘output’ keyword for convolve
• #6957: ENH more informative error in sparse.bmat
• #6962: Shebang fixes
• #6964: DOC: note argmin/argmax addition
• #6965: BUG: Fix issues passing error tolerances in dblquad and tplquad.
• #6971: fix the docstring of signaltools.correlate
• #6973: Silence expected numpy warnings in scipy.ndimage.interpolation.zoom()
• #6975: BUG: special: fix regex in generate__ufuncs.py
• #6976: Update docstring for griddata
• #6978: Avoid division by zero in zoom factor calculation
• #6979: BUG: ARE solvers did not check the generalized case carefully
• #6985: ENH: sparse: add scipy.sparse.linalg.spsolve_triangular
• #6994: MAINT: spatial: updates to plotting utils
• #6995: DOC: Bad documentation of k in sparse.linalg.eigs See #6990
• #6997: TST: Changed the test with a less singular example
• #7000: DOC: clarify interp1d ‘zero’ argument
• #7007: BUG: Fix division by zero in linregress() for 2 data points
• #7009: BUG: Fix problem in passing drop__rule to scipy.sparse.linalg.spilu
• #7012: speed improvement in _distn_infrastructure.py
• #7014: Fix Typo: add a single quotation mark to fix a slight typo
• #7021: MAINT: stats: use machine constants from np.finfo, not machar
• #7026: MAINT: update .mailmap
• #7032: Fix layout of rv_histogram docs
• #7035: DOC: update 0.19.0 release notes
• #7036: ENH: Add more boundary options to signal.stft
• #7040: TST: stats: skip too slow tests
• #7042: MAINT: sparse: speed up setdiag tests
• #7043: MAINT: refactor and code cleaning Xdist
• #7053: Fix msvc 9 and 10 compile errors
• #7060: DOC: updated release notes with #7043 and #6656
• #7062: MAINT: Change default STFT boundary kwarg to “zeros”
• #7064: Fix ValueError: path is on mount ‘X:’, start on mount ‘D:’ on...
• #7067: TST: Fix PermissionError: [Errno 13] Permission denied on Windows
• #7068: TST: Fix UnboundLocalError: local variable ‘data’ referenced...
• #7069: Fix OverflowError: Python int too large to convert to C long...
• #7071: TST: silence RuntimeWarning for nan test of stats.spearmanr
• #7072: Fix OverflowError: Python int too large to convert to C long...
• #7084: TST: linalg: bump tolerance in test_falker
• #7095: TST: linalg: bump more tolerances in test_falker
• #7101: TST: Relax solve_continuous_are test case 2 and 12
• #7106: BUG: stop cdist “correlation” modifying input
• #7116: Backports to 0.19.0rc2

3.7 SciPy 0.18.1 Release Notes

SciPy 0.18.1 is a bug-fix release with no new features compared to 0.18.0.

3.7.1 Authors

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• Yu Feng
• Ralf Gommers
• Johannes Schmitz +
• Josh Wilson
• Nathan Woods

A total of 9 people contributed to this release. People with a “+” by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

**Issues closed for 0.18.1**

* #6357: scipy 0.17.1 piecewise cubic hermite interpolation does not return...
* #6420: circmean() changed behaviour from 0.17 to 0.18
* #6421: scipy.linalg.solve_banded overwrites input ‘b’ when the inversion...
* #6425: cKDTree INF bug
* #6435: scipy.stats.ks_2samp returns different values on different computers
* #6458: Error in scipy.integrate.dblquad when using variable integration...

**Pull requests for 0.18.1**

* #6405: BUG: sparse: fix elementwise divide for CSR/CSC
* #6431: BUG: result for insufficient neighbours from cKDTree is wrong.
* #6432: BUG Issue #6421: scipy.linalg.solve_banded overwrites input ‘b’...
* #6455: DOC: add links to release notes
* #6462: BUG: interpolate: fix .roots method of PchipInterpolator
* #6492: BUG: Fix regression in dblquad: #6458
* #6543: fix the regression in circmean
* #6545: Revert gh-5938, restore ks_2samp
* #6557: Backports for 0.18.1

### 3.8 SciPy 0.18.0 Release Notes

**Contents**

- *SciPy 0.18.0 Release Notes*
  - New features
    * scipy.integrate improvements
    * scipy.interpolate improvements
    * scipy.fftpack improvements
    * scipy.signal improvements
      - Discrete-time linear systems
SciPy 0.18.0 is the culmination of 6 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecation and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.19.x branch, and on adding new features on the master branch.

This release requires Python 2.7 or 3.4-3.5 and NumPy 1.7.1 or greater.

Highlights of this release include:

- A new ODE solver for two-point boundary value problems, `scipy.optimize.solve_bvp`.
- A new class, `CubicSpline`, for cubic spline interpolation of data.
- Spherical Voronoi diagrams, `scipy.spatial.SphericalVoronoi`.
- Support for discrete-time linear systems, `scipy.signal.dlti`.

### 3.8.1 New features

#### scipy.integrate improvements

A solver of two-point boundary value problems for ODE systems has been implemented in `scipy.integrate.solve_bvp`. The solver allows for non-separated boundary conditions, unknown parameters and certain singular terms. It finds a C1 continuous solution using a fourth-order collocation algorithm.
**scipy.interpolate improvements**

Cubic spline interpolation is now available via `scipy.interpolate.CubicSpline`. This class represents a piecewise cubic polynomial passing through given points and C2 continuous. It is represented in the standard polynomial basis on each segment.

A representation of n-dimensional tensor product piecewise polynomials is available as the `scipy.interpolate.NdPPoly` class.

Univariate piecewise polynomial classes, `PPoly` and `Bpoly`, can now be evaluated on periodic domains. Use `extrapolate="periodic"` keyword argument for this.

**scipy.fftpack improvements**

`scipy.fftpack.next_fast_len` function computes the next “regular” number for FFTPACK. Padding the input to this length can give significant performance increase for `scipy.fftpack.fft`.

**scipy.signal improvements**

Resampling using polyphase filtering has been implemented in the function `scipy.signal.resample_poly`. This method upsamples a signal, applies a zero-phase low-pass FIR filter, and downsamples using `scipy.signal.upfirdn` (which is also new in 0.18.0). This method can be faster than FFT-based filtering provided by `scipy.signal.resample` for some signals.

`scipy.signal.firls`, which constructs FIR filters using least-squares error minimization, was added.

`scipy.signal.sosfiltfilt`, which does forward-backward filtering like `scipy.signal.filtfilt` but for second-order sections, was added.

**Discrete-time linear systems**

`scipy.signal.dlti` provides an implementation of discrete-time linear systems. Accordingly, the `StateSpace`, `TransferFunction` and `ZerosPolesGain` classes have learned a the new keyword, `dt`, which can be used to create discrete-time instances of the corresponding system representation.

**scipy.sparse improvements**

The functions `sum`, `max`, `mean`, `min`, `transpose`, and `reshape` in `scipy.sparse` have had their signatures augmented with additional arguments and functionality so as to improve compatibility with analogously defined functions in `numpy`.

Sparse matrices now have a `count_nonzero` method, which counts the number of nonzero elements in the matrix. Unlike `getnnz()` and `nnz` property, which return the number of stored entries (the length of the data attribute), this method counts the actual number of non-zero entries in data.

**scipy.optimize improvements**

The implementation of Nelder-Mead minimization, `scipy.minimize(..., method="Nelder-Mead")`, obtained a new keyword, `initial_simplex`, which can be used to specify the initial simplex for the optimization process.

Initial step size selection in CG and BFGS minimizers has been improved. We expect that this change will improve numeric stability of optimization in some cases. See pull request gh-5536 for details.

Handling of infinite bounds in SLSQP optimization has been improved. We expect that this change will improve numeric stability of optimization in the some cases. See pull request gh-6024 for details.

A large suite of global optimization benchmarks has been added to `scipy/benchmarks/go_benchmark_functions`. See pull request gh-4191 for details.

Nelder-Mead and Powell minimization will now only set defaults for maximum iterations or function evaluations if neither limit is set by the caller. In some cases with a slow converging function and only 1 limit
set, the minimization may continue for longer than with previous versions and so is more likely to reach
convergence. See issue gh-5966.

**scipy.stats improvements**

Trapezoidal distribution has been implemented as `scipy.stats.trapz`. Skew normal distribution has been
implemented as `scipy.stats.skewnorm`. Burr type XII distribution has been implemented as `scipy.stats.
burr12`. Three- and four-parameter kappa distributions have been implemented as `scipy.stats.kappa3`
and `scipy.stats.kappa4`, respectively.

New `scipy.stats.iqr` function computes the interquartile region of a distribution.

**Random matrices**

`scipy.stats.special_ortho_group` and `scipy.stats.ortho_group` provide generators of random matrices
in the SO(N) and O(N) groups, respectively. They generate matrices in the Haar distribution, the only
uniform distribution on these group manifolds.

`scipy.stats.random_correlation` provides a generator for random correlation matrices, given specified
eigenvalues.

**scipy.linalg improvements**

`scipy.linalg.svd` gained a new keyword argument, `lapack_driver`. Available drivers are `gesdd` (default)
and `gesvd`.

`scipy.linalg.lapack.ilaver` returns the version of the LAPACK library SciPy links to.

**scipy.spatial improvements**

Boolean distances, `scipy.spatial.pdist`, have been sped up. Improvements vary by the function and the input
size. In many cases, one can expect a speed-up of x2–x10.

New class `scipy.spatial.SphericalVoronoi` constructs Voronoi diagrams on the surface of a sphere. See
pull request gh-5232 for details.

**scipy.cluster improvements**

A new clustering algorithm, the nearest neighbor chain algorithm, has been implemented for `scipy.cluster.
hierarchy.linkage`. As a result, one can expect a significant algorithmic improvement (\(O(N^2)\) instead of
\(O(N^3)\)) for several linkage methods.

**scipy.special improvements**

The new function `scipy.special.loggamma` computes the principal branch of the logarithm of the Gamma
function. For real input, `loggamma` is compatible with `scipy.special.gammaln`. For complex input, it has
more consistent behavior in the complex plane and should be preferred over `gammaln`.

Vectorized forms of spherical Bessel functions have been implemented as `scipy.special.spherical_jn`,
`scipy.special.spherical_kn`, `scipy.special.spherical_in` and `scipy.special.spherical_yn`. They
are recommended for use over `sph_*` functions, which are now deprecated.

Several special functions have been extended to the complex domain and/or have seen domain/stability
improvements. This includes `spence`, `digamma`, `log1p` and several others.

### 3.8.2 Deprecated features

The cross-class properties of `lti` systems have been deprecated. The following properties/setters will raise a
`DeprecationWarning`:
Name - (accessing/setting raises warning) - (setting raises warning) * StateSpace - (num, den, gain) - (zeros, poles) * TransferFunction (A, B, C, D, gain) - (zeros, poles) * ZerosPolesGain (A, B, C, D, num, den) - ()

Spherical Bessel functions, sph_in, sph_jn, sph_kn, sph_yn, sph_jnyn and sph_inkn have been deprecated in favor of scipy.special.spherical_jn and spherical_kn, spherical_yn, spherical_in.

The following functions in scipy.constants are deprecated: C2K, K2C, C2F, F2C, F2K and K2F. They are superceded by a new function scipy.constants.convert_temperature that can perform all those conversions plus to/from the Rankine temperature scale.

3.8.3 Backwards incompatible changes

scipy.optimize

The convergence criterion for optimize.bisect, optimize.brentq, optimize.brenth, and optimize.ridder now works the same as numpy.allclose.

scipy.ndimage

The offset in ndimage.interpolation.affine_transform is now consistently added after the matrix is applied, independent of if the matrix is specified using a one-dimensional or a two-dimensional array.

scipy.stats

stats.ks_2samp used to return nonsensical values if the input was not real or contained nans. It now raises an exception for such inputs.

Several deprecated methods of scipy.stats distributions have been removed: est_loc_scale, vecfunc, veccdf and vec_generic_moment.

Deprecated functions nanmean, nanstd and nanmedian have been removed from scipy.stats. These functions were deprecated in scipy 0.15.0 in favor of their numpy equivalents.

A bug in the rvs() method of the distributions in scipy.stats has been fixed. When arguments to rvs() were given that were shaped for broadcasting, in many cases the returned random samples were not random. A simple example of the problem is stats.norm.rvs(loc=np.zeros(10)). Because of the bug, that call would return 10 identical values. The bug only affected code that relied on the broadcasting of the shape, location and scale parameters.

The rvs() method also accepted some arguments that it should not have. There is a potential for backwards incompatibility in cases where rvs() accepted arguments that are not, in fact, compatible with broadcasting. An example is

    stats.gamma.rvs([2, 5, 10, 15], size=(2,2))

The shape of the first argument is not compatible with the requested size, but the function still returned an array with shape (2, 2). In scipy 0.18, that call generates a ValueError.

scipy.io

scipy.io.netcdf masking now gives precedence to the _FillValue attribute over the missing_value attribute, if both are given. Also, data are only treated as missing if they match one of these attributes exactly: values that differ by roundoff from _FillValue or missing_value are no longer treated as missing values.

scipy.interpolate

scipy.interpolate.PiecewisePolynomial class has been removed. It has been deprecated in scipy 0.14.0, and scipy.interpolate.BPoly.from_derivatives serves as a drop-in replacement.
3.8.4 Other changes
Scipy now uses setuptools for its builds instead of plain distutils. This fixes usage of install_requires='scipy' in the setup.py files of projects that depend on Scipy (see Numpy issue gh-6551 for details). It potentially affects the way that build/install methods for Scipy itself behave though. Please report any unexpected behavior on the Scipy issue tracker.

PR #6240 changes the interpretation of the maxfun option in L-BFGS-B based routines in the scipy.optimize module. An L-BFGS-B search consists of multiple iterations, with each iteration consisting of one or more function evaluations. Whereas the old search strategy terminated immediately upon reaching maxfun function evaluations, the new strategy allows the current iteration to finish despite reaching maxfun.

The bundled copy of Qhull in the scipy.spatialsubpackage has been upgraded to version 2015.2.

The bundled copy of ARPACK in the scipy.sparse.linalgsubpackage has been upgraded to arpack-ng 3.3.0.

The bundled copy of SuperLU in the scipy.sparsesubpackage has been upgraded to version 5.1.1.

3.8.5 Authors
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• Nikolay Mayorov
• Matthieu Melot +
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• Eric Moore
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• Maniteja Nandana
• Tavi Nathanson +
3.8. SciPy 0.18.0 Release Notes
A total of 99 people contributed to this release. People with a “+” by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 0.18.0

- #1484: SVD using *GESVD* lapack drivers (Trac #957)
- #1547: Inconsistent use of offset in ndimage.interpolation.affine_transform()
- #1609: special.hyp0f1 returns nan (Trac #1082)
- #1656: fmin_slsqp enhancement (Trac #1129)
- #2069: stats broadcasting in rvs (Trac #1544)
- #2165: sph_jn returns false results for some orders/values (Trac #1640)
- #2255: Incorrect order of translation and rotation in affine_transform...
- #2332: hyp0f1 args and return values are unnumpyic (Trac #1813)
- #2534: The sparse .sum() method with uint8 dtype does not act like the...
- #3113: Implement ufuncs for CSPHJY, SPHJ, SPHY, CSPHIK, PHI, SPHIK...
- #3568: SciPy 0.13.3 - CentOS5 - Errors in test__arpack
- #3581: optimize: stepsize in fmin_bfgs is “bad”
- #4476: scipy.sparse non-native endian bug
- #4484: ftol in optimize.fmin fails to work
- #4510: sparsetools.cxx call_thunk can segfault due to out of bounds...
- #5051: ftol and xtol for _minimize_neldermead are absolute instead of...
- #5097: proposal: spherical Voronoi diagrams
- #5123: Call to scipy.sparse.coo_matrix fails when passed Cython typed...
- #5220: scipy.cluster.hierarchy.{ward,median,centroid} does not work...
- #5379: Add a build step at the end of .travis.yml that uploads working...
- #5440: scipy.optimize.basinhopping: accept_test returning numpy.bool_...
- #5452: Error in scipy.integrate.nquad when using variable integration...
- #5520: Cannot inherit csr_matrix properly
- #5533: Kendall tau implementation uses Python mergesort
- #5553: stats.tiecorrect overflows
- #5589: Add the Type XII Burr distribution to stats.
- #5612: sparse.linalg factorizations slow for small k due to default...
- #5626: io.netcdf masking should use masked_equal rather than masked_value
- #5637: Simple cubic spline interpolation?
- #5683: BUG: Akima1DInterpolator may return nans given multidimensional...
- #5686: scipy.stats.ttest_ind_from_stats does not accept arrays
• #5702: scipy.ndimage.interpolation.affine_transform lacks documentation...
• #5718: Wrong computation of weighted minkowski distance in cdist
• #5745: move to setuptools for next release
• #5752: DOC: solve_discrete_lyapunov equation puts transpose in wrong...
• #5760: signal.ss2tf doesn’t handle zero-order state-space models
• #5764: Hypergeometric function hyp0f1 behaves incorrectly for complex...
• #5814: stats NaNa Policy Error message inconsistent with code
• #5833: docstring of stats.binom_test() needs an update
• #5853: Error in scipy.linalg.expm for complex matrix with shape (1,1)
• #5856: Specify Nelder-Mead initial simplex
• #5865: scipy.linalg.expm fails for certain numpy matrices
• #5915: optimize.basinhopping - variable referenced before assignment.
• #5916: LSQUnivariateSpline fitting failed with knots generated from...
• #5927: unicode vs. string comparison in scipy.stats.binned_statistic_dd
• #5936: faster implementation of ks_2samp
• #5948: csc matrix .mean returns single element matrix rather than scalar
• #5959: BUG: optimize test error for root when using lgmres
• #5972: Test failures for sparse sum tests on 32-bit Python
• #5976: Unexpected exception in scipy.sparse.bmat while using 0 x 0 matrix
• #6008: scipy.special.kl_div not available in 0.14.1
• #6011: The von-Mises entropy is broken
• #6016: python crashes for linalg.interpolative.svd with certain large...
• #6017: Wilcoxon signed-rank test with zero_method=”pratt” or “zsplit”...
• #6028: stats.distributions does not have trapezoidal distribution
• #6035: Wrong link in f_oneway
• #6056: BUG: signal.decimate should only accept discrete LTI objects
• #6093: Precision error on Linux 32 bit with openblas
• #6101: Barycentric transforms test error on Python3, 32-bit Linux
• #6105: scipy.misc.face docstring is incorrect
• #6113: scipy.linalg.logm fails for a trivial matrix
• #6128: Error in dot method of sparse COO array, when used with numpy...
• #6132: Failures with latest MKL
• #6136: Failures on master with MKL
• #6162: fmin_l_bfgs_b returns inconsistent results (fmin ≠ f(xmin)) and...
• #6165: optimize.minimize infinite loop with Newton-CG
• #6167: incorrect distribution fitting for data containing boundary values.
• #6194: lstsq() and others detect numpy.complex256 as real
• #6216: ENH: improve accuracy of ppf cdf roundtrip for bradford
• #6217: BUG: weibull_min.logpdf return nan for c=1 and x=0
• #6218: Is there a method to cap shortest path search distances?
• #6222: PchipInterpolator no longer handles a 2-element array
• #6226: ENH: improve accuracy for logistic.pp and logistic.isf
• #6227: ENH: improve accuracy for rayleigh.logpdf and rayleigh.logsf...
• #6228: ENH: improve accuracy of ppf cdf roundtrip for gumbel_1
• #6235: BUG: alpha.pdf and alpha.logpdf returns nan for x=0
• #6245: ENH: improve accuracy for ppf-cdf and sf-isf roundtrips for invgamma
• #6263: BUG: stats: Inconsistency in the multivariate_normal docstring
• #6292: Python 3 unorderable type errors in test_sparsetools.TestInt32Overflow
• #6316: TestCloughTocher2DInterpolator.test Dense crashes python3.5.2rc1_64bit...
• #6318: Scipy interp1d ‘nearest’ not working for high values on x-axis

Pull requests for 0.18.0
• #3226: DOC: Change nb and na to conventional m and n
• #3867: allow cKDTree.query taking a list input in k.
• #4191: ENH: Benchmarking global optimizers
• #4356: ENH: add PPoly.solve(y) for solving p(x) == y
• #4370: DOC separate boolean distance functions for clarity
• #4678: BUG: sparse: ensure index dtype is large enough to pass all parameters...
• #4881: scipy.signal: Add the class dlti for linear discrete-time systems....
• #4901: MAINT: add benchmark and improve docstring for signal.lfilter
• #5043: ENH: sparse: add count_nonzero method
• #5136: Attribute kurtosistest() to Anscombe & Glynn (1983)
• #5186: ENH: Port upfirdn
• #5232: ENH: adding spherical Voronoi diagram algorithm to scipy.spatial
• #5279: ENH: Bessel filters with different normalizations, high order
• #5384: BUG: Closes #5027 distance function always casts bool to double
• #5392: ENH: Add zero_phase kwarg to signal.decimate
• #5394: MAINT: sparse: non-canonical test cleanup and fixes
• #5424: DOC: add Scipy developers guide
• #5442: STY: PEP8 amendments
• #5472: Online QR in LGMRES
• #5526: BUG: stats: Fix broadcasting in the rvs() method of the distributions.
• #5530: MAINT: sparse: set format attr explicitly
• #5536: optimize: fix up cg/bfgs initial step sizes
• #5548: PERF: improves performance in stats.kendalltau
• #5549: ENH: Nearest-neighbor chain algorithm for hierarchical clustering
• #5554: MAINT/BUG: closes overflow bug in stats.tiecorrect
• #5557: BUG: modify optimize.bisect to achieve desired tolerance
• #5581: DOC: Tutorial for least_squares
• #5606: ENH: differential._evolution - moving core loop of solve method...
• #5609: [MRG] test against numpy dev
• #5611: use setuptools for bdist_egg distributions
• #5615: MAINT: linalg: tighten _decomp_update + special: remove unused...
• #5622: Add SO(N) rotation matrix generator
• #5623: ENH: special: Add vectorized spherical Bessel functions.
• #5627: Response to issue #5160, implements the skew normal distribution...
• #5628: DOC: Align the description and operation
• #5632: DOC: special: Expanded docs for Airy, elliptic, Bessel functions.
• #5633: MAINT: linalg: unchecked malloc in _decomp_update
• #5634: MAINT: optimize: tighten __group__columns
• #5640: Fixes for io.netcdf masking
• #5645: MAINT: size 0 vector handling in cKDTree range queries
• #5649: MAINT: update license text
• #5650: DOC: Clarify Exponent Order in ltisys.py
• #5651: DOC: Clarify Documentation for scipy.special.gamma
• #5652: DOC: Fixed scipy.special.betain Doc
• #5653: [MRG] ENH: CubicSpline interpolator
• #5654: ENH: Burr12 distribution to stats module
• #5659: DOC: Define BEFORE/AFTER in runtests.py -h for bench-compare
• #5660: MAINT: remove functions deprecated before 0.16.0
• #5662: ENH: Circular statistic optimization
• #5663: MAINT: remove uses of np.testing.rand
• #5665: MAINT: spatial: remove matching distance implementation
• #5667: Change some HTTP links to HTTPS
• #5669: DOC: zpk2sos can’t do analog, array_like, etc.
• #5670: Update conf.py
• #5672: MAINT: move a sample distribution to a subclass of rv_discrete
• #5678: MAINT: stats: remove est_loc_scale method
• #5679: MAINT: DRY up generic computations for discrete distributions
• #5680: MAINT: stop shadowing builtins in stats.distributions
• #5681: forward port ENH: Re-enable broadcasting of fill_value
• #5684: BUG: Fix Akima1DInterpolator returning nans
• #5690: BUG: fix stats.ttest_ind_from_stats to handle arrays.
• #5691: BUG: fix generator in io._loadarff to comply with PEP 0479
• #5693: ENH: use math.factorial for exact factorials
• #5695: DOC: dx might be a float, not only an integer
• #5699: MAINT: io: micro-optimize Matlab reading code for size
• #5701: Implement OptimizeResult.__dir__
• #5703: ENH: stats: make R^2 printing optional in probplot
• #5704: MAINT: typo ouf->out
• #5705: BUG: fix typ in query_pairs
• #5707: DOC: Add some explanation for ftol xtol in scipy.optimize.fmin
• #5708: DOC: optimize: PEP8 minimize docstring
• #5709: MAINT: optimize Cython code for speed and size
• #5713: [DOC] Fix broken link to reference
• #5717: DOC: curve_fit raises RuntimeError on failure.
• #5724: forward port gh-5720
• #5728: STY: remove a blank line
• #5729: ENH: spatial: speed up boolean distances
• #5732: MAINT: differential_evolution changes to default keywords break...
• #5733: TST: differential_evolution - population initiation tests
• #5736: Complex number support in log1p, expm1, and xlog1py
• #5741: MAINT: sparse: clean up extraction functions
• #5742: DOC: signal: Explain fttbins in get_window
• #5748: ENH: Add O(N) random matrix generator
• #5749: ENH: Add polyphase resampling
• #5756: RFC: Bump the minimum numpy version, drop older python versions
• #5761: DOC: Some improvements to least squares docstrings
• #5762: MAINT: spatial: distance refactoring
• #5768: DOC: Fix io.loadmat docstring for mdict param
• #5770: BUG: Accept anything np.dtype can handle for a dtype in sparse.random
• #5772: Update sparse.csgraph.laplacian docstring
• #5777: BUG: fix special.hyp0f1 to work correctly for complex inputs.
• #5780: DOC: Update PIL error install URL
• #5781: DOC: Fix documentation on solve_discrete_lyapunov
• #5782: DOC: cKDTree and KDTree now reference each other
• #5783: DOC: Clarify finish behaviour in scipy.optimize.brute
• #5784: MAINT: Change default tolerances of least_squares to 1e-8
• #5787: BUG: Allow Processing of Zero Order State Space Models in signal.ss2tf
• #5788: DOC, BUG: Clarify and Enforce Input Types to ‘Data’ Objects
• #5789: ENH: sparse: speedup LIL matrix slicing (was #3338)
• #5791: DOC: README: remove coveralls.io
• #5792: MAINT: remove uses of deprecated np.random.random_integers
• #5794: fix affine_transform (fixes #1547 and #5702)
• #5795: DOC: Removed uniform method from kmeans2 doc
• #5797: DOC: Clarify the computation of weighted minkowski
• #5798: BUG: Ensure scipy’s _asfarray returns ndarray
• #5799: TST: Mpmath testing patch
• #5801: allow reading of certain IDL 8.0 .sav files
• #5803: DOC: fix module name in error message
• #5804: DOC: special: Expanded docs for special functions.
• #5805: DOC: Fix order of returns in __spectral_helper
• #5806: ENH: sparse: vectorized coo_matrix.diagonal
• #5808: ENH: Added iqr function to compute IQR metric in scipy/stats/stats.py
• #5810: MAINT/BENCH: sparse: Benchmark cleanup and additions
• #5811: DOC: sparse.linalg: shape, not size
• #5813: Update sparse ARPACK functions min ncv value
• #5815: BUG: Error message contained wrong values
• #5816: remove dead code from stats tests
• #5820: “in”->”a” in order_filter docstring
• #5821: DOC: README: INSTALL.txt was renamed in 2014
• #5825: DOC: typo in the docstring of least_squares
• #5826: MAINT: sparse: increase test coverage
• #5827: NdPPoly rebase
• #5828: Improve numerical stability of hyp0f1 for large orders
• #5829: ENH: sparse: Add copy parameter to all .toXXX() methods in sparse...
• #5830: DOC: rework INSTALL.rst.txt
• #5831: Adds plotting options to voronoi_plot_2d
• #5834: Update stats.binom_test() docstring
• #5836: ENH, TST: Allow SIMO tf’s for tf2ss
• #5837: DOC: Image examples
- #5838: ENH: sparse: add eliminate_zeros() to coo_matrix
- #5839: BUG: Fixed name of NumpyVersion.__repr__
- #5845: MAINT: Fixed typos in documentation
- #5847: Fix bugs in sparsetools
- #5848: BUG: sparse.linalg: add locks to ensure ARPACK thread safety
- #5849: ENH: sparse.linalg: upgrade to superlu 5.1.1
- #5851: ENH: expose lapack’s ilaver to python to allow lapack version...
- #5852: MAINT: runtests.py: ensure Ctrl-C interrupts the build
- #5854: DOC: Minor update to documentation
- #5855: Pr 5640
- #5859: ENH: Add random correlation matrix generator
- #5862: BUG: Allow expm for complex matrix with shape (1, 1)
- #5863: FIX: Fix test
- #5864: DOC: add a little note about the Normal survival function (Q-function)
- #5867: Fix for #5865
- #5869: extend normal distribution cdf to complex domain
- #5872: DOC: Note that morlet and cwt don’t work together
- #5875: DOC: interp2d class description
- #5876: MAINT: spatial: remove a stray print statement
- #5878: MAINT: Fixed noisy UserWarnings in ndimage tests. Fixes #5877
- #5879: MAINT: sparse.linalg/superlu: add explicit casts to resolve compiler...
- #5880: MAINT: signal: import gcd from math and not fractions when on...
- #5887: Neldermead initial simplex
- #5894: BUG: __CustomLinearOperator unpickalable in python3.5
- #5895: DOC: special: slightly improve the multigammaln docstring
- #5900: Remove duplicate assignment.
- #5901: Update bundled ARPACK
- #5904: ENH: Make convolve and correlate order-agnostic
- #5905: ENH: sparse.linalg: further LGMRES cleanups
- #5906: Enhancements and cleanup in scipy.integrate (attempt #2)
- #5907: ENH: Change sparse sum and mean dtype casting to match...
- #5909: changes for convolution symmetry
- #5913: MAINT: basinhopping remove instance test closes #5440
- #5919: MAINT: uninitialised var if basinhopping niter=0. closes #5915
- #5920: BLD: Fix missing lsame.c error for MKL
- #5921: DOC: interpolate: add example showing how to work around issue...
• #5926: MAINT: spatial: upgrade to Qhull 2015.2
• #5928: MAINT: sparse: optimize DIA sum/diagonal, csgraph.laplacian
• #5929: Update info/URL for octave-maintainers discussion
• #5930: TST: special: silence DeprecationWarnings from sph_yy
• #5931: ENH: implement the principle branch of the logarithm of Gamma.
• #5934: Typo: “mush” => “must”
• #5935: BUG:string comparison stats._binned_statistic closes #5927
• #5938: Cythonize stats.ks_2samp for a ~33% gain in speed.
• #5939: DOC: fix optimize.fmin convergence docstring
• #5941: Fix minor typo in squareform docstring
• #5942: Update linregress stderr description.
• #5943: ENH: Improve numerical accuracy of lognorm
• #5944: Merge vonmises into stats.pyx
• #5945: MAINT: interpolate: Tweak declaration to avoid cython warning...
• #5946: MAINT: sparse: clean up format conversion methods
• #5949: BUG: fix sparse .mean to return a scalar instead of a matrix
• #5955: MAINT: Replace calls to hanning with hann
• #5956: DOC: Missing periods interfering with parsing
• #5958: MAINT: add a test for lognorm.sf underflow
• #5961: MAINT _centered(): rename size to shape
• #5962: ENH: constants: Add multi-scale temperature conversion function
• #5965: ENH: special: faster way for calculating comb() for exact=True
• #5975: ENH: Improve FIR path of signal.decimate
• #5977: MAINT/BUG: sparse: remove overzealous bmat checks
• #5978: minimize_neldermead() stop at user requested maxiter or maxfev
• #5983: ENH: make sparse sum cast dtypes like NumPy sum for 32-bit...
• #5985: BUG, API: Add jac parameter to curve_fit
• #5989: ENH: Add firls least-squares fitting
• #5990: BUG: read tries to handle 20-bit WAV files but shouldn’t
• #5991: DOC: Cleanup wav read/write docs and add tables for common types
• #5994: ENH: Add gesvd method for svd
• #5996: MAINT: Wave cleanup
• #5997: TST: Break up upfirdn tests & compare to lfilter
• #6001: Filter design docs
• #6002: COMPAT: Expand compatibility fromnumeric.py
• #6007: ENH: Skip conversion of TF to TF in freqresp
• #6009: DOC: fix incorrect versionadded for entr, rel_entr, kl_div
• #6013: Fixed the entropy calculation of the von Mises distribution.
• #6014: MAINT: make gamma, rgamma use loggamma for complex arguments
• #6020: WIP: ENH: add exact=True factorial for vectors
• #6022: Added 'lanczos' to the image interpolation function list.
• #6024: BUG: optimize: do not use dummy constraints in SLSQP when no...
• #6025: ENH: Boundary value problem solver for ODE systems
• #6029: MAINT: Future imports for optimize._lsq
• #6030: ENH: stats.trap - adding trapezoidal distribution closes #6028
• #6031: MAINT: Some improvements to optimize._numdiff
• #6032: MAINT: Add special/_comb.c to .gitignore
• #6033: BUG: check the requested approximation rank in interpolative.svd
• #6034: DOC: Doc for mannwhitneyu in stats.py corrected
• #6040: FIX: Edit the wrong link in f_oneway
• #6044: BUG: (ordqz) always increase parameter lwork by 1.
• #6047: ENH: extend special.spence to complex arguments.
• #6049: DOC: Add documentation of PR #5640 to the 0.18.0 release notes
• #6050: MAINT: small cleanups related to loggamma
• #6070: Add asarray to explicitly cast list to numpy array in wilcoxon...
• #6071: DOC: antialiasing filter and link decimate resample, etc.
• #6075: MAINT: reimplement special.digamma for complex arguments
• #6080: avoid multiple computation in kstest
• #6081: Clarified pearson correlation return value
• #6085: ENH: allow long indices of sparse matrix with umfpack in spsolve()
• #6086: fix description for associated Laguerre polynomials
• #6087: Corrected docstring of splrep.
• #6094: ENH: special: change zeta signature to zeta(x, q=1)
• #6095: BUG: fix integer overflow in special.spence
• #6106: Fixed Issue #6105
• #6116: BUG: matrix logarithm edge case
• #6119: TST: DeprecationWarnings in stats on python 3.5 closes #5885
• #6120: MAINT: sparse: clean up sutils.isintlike
• #6122: DOC: optimize: linprog docs should say minimize instead of maximize
• #6123: DOC: optimize: document the fun field in scipy.optimize.OptimizeResult
• #6124: Move FFT zero-padding calculation from signaltools to fftpack
• #6125: MAINT: improve special.gammaine in the a ~ x regime.
• #6130: BUG: sparse: Fix COO dot with zero columns
• #6138: ENH: stats: Improve behavior of genextreme.sf and genextreme.isf
• #6146: MAINT: simplify the expit implementation
• #6151: MAINT: special: make generate_ufuncs.py output deterministic
• #6152: TST: special: better test for gammainc at large arguments
• #6153: ENH: Make next_fast_len public and faster
• #6154: fix typo “mush”–>”must”
• #6155: DOC: Fix some incorrect RST definition lists
• #6160: make logsumexp error out on a masked array
• #6161: added missing bracket to rosen documentation
• #6163: ENH: Added “kappa4” and “kappa3” distributions.
• #6164: DOC: Minor clean-up in integrate._bvp
• #6169: Fix mpfr_assert_allclose to handle iterable results, such as maps
• #6170: Fix pchip_interpolate convenience function
• #6172: Corrected misplaced bracket in doc string
• #6175: ENH: sparse.csgraph: Pass indices to shortest_path
• #6178: TST: increase test coverage of sf and isf of a generalized extreme...
• #6179: TST: avoid a deprecation warning from numpy
• #6181: ENH: Boundary conditions for CubicSpline
• #6182: DOC: Add examples/graphs to max_len_seq
• #6183: BLD: update Bento build config files for recent changes.
• #6184: BUG: fix issue in io/wavfile for float96 input.
• #6186: ENH: Periodic extrapolation for PPoly and BPoly
• #6192: MRG: Add circle-CI
• #6193: ENH: sparse: avoid setitem densification
• #6196: Fixed missing sqrt in docstring of Mahalanobis distance in cdist,...
• #6206: MAINT: Minor changes in solve_bvp
• #6207: BUG: linalg: for BLAS, downcast complex256 to complex128, not...
• #6209: BUG: io.matlab: avoid buffer overflows in read_element_into
• #6210: BLD: use setuptools when building.
• #6214: BUG: sparse.linalg: fix bug in LGMRES breakdown handling
• #6215: MAINT: special: make loggamma use zdiv
• #6220: DOC: Add parameter
• #6221: ENH: Improve Newton solver for solve_bvp
• #6223: pchip should work for length-2 arrays
• #6224: signal.lti: deprecate cross-class properties/setters
• #6229: BUG: optimize: avoid an infinite loop in Newton-CG
• #6230: Add example for application of gaussian filter
• #6236: MAINT: gumbel_l accuracy
• #6237: MAINT: rayleigh accuracy
• #6238: MAINT: logistic accuracy
• #6239: MAINT: bradford distribution accuracy
• #6240: MAINT: avoid bad fmin in l-bfgs-b due to maxfun interruption
• #6241: MAINT: weibull_min accuracy
• #6246: ENH: Add _support_mask to distributions
• #6247: fixed a print error for an example of ode
• #6249: MAINT: change x-axis label for stats.probplot to “theoretical…
• #6250: DOC: fix typos
• #6251: MAINT: constants: filter out test noise from deprecated conversions
• #6252: MAINT: io/arff: remove unused variable
• #6253: Add examples to scipy.ndimage.filters
• #6254: MAINT: special: fix some build warnings
• #6258: MAINT: inverse gamma distribution accuracy
• #6260: MAINT: signal.decimate - Use discrete-time objects
• #6262: TST: fix some test issues in interpolate and stats.
• #6269: TST: fix some warnings in the test suite
• #6274: ENH: Add sosfiltfilt
• #6276: DOC: update release notes for 0.18.0
• #6277: MAINT: update the author name mapping
• #6282: DOC: Correcting references for scipy.stats.normaltest
• #6283: DOC: some more additions to 0.18.0 release notes.
• #6284: Add versionadded:: directive to loggamma.
• #6285: BUG: stats: Inconsistency in the multivariate_normal docstring...
• #6290: Add author list, gh-lists to 0.18.0 release notes
• #6293: TST: special: relax a test’s precision
• #6295: BUG: sparse: stop comparing None and int in bsr_matrix constructor
• #6313: MAINT: Fix for python 3.5 travis-ci build problem.
• #6327: TST: signal: use assert_allclose for testing near-equality in...
• #6330: BUG: spatial/qhull: allocate qhT via malloc to ensure CRT likes...
• #6332: TST: fix stats.iqr test to not emit warnings, and fix line lengths.
• #6334: MAINT: special: fix a test for hyp0f1
• #6347: TST: spatial.qhull: skip a test on 32-bit platforms
• #6350: BUG: optimize/slsqp: don’t overwrite an array out of bounds
• #6351: BUG: #6318 Interp1d ‘nearest’ integer x-axis overflow issue fixed
• #6355: Backports for 0.18.0

3.9 SciPy 0.17.1 Release Notes

SciPy 0.17.1 is a bug-fix release with no new features compared to 0.17.0.

3.9.1 Issues closed for 0.17.1

• #5817: BUG: skew, kurtosis return np.nan instead of “propagate”
• #5850: Test failed with sgelsy
• #5898: interpolate.interp1d crashes using float128
• #5953: Massive performance regression in cKDTree.query with L_inf distance...
• #6062: mannwhitneyu breaks backward compatibility in 0.17.0
• #6134: T test does not handle nans

3.9.2 Pull requests for 0.17.1

• #5902: BUG: interpolate: make interp1d handle np.float128 again
• #5957: BUG: slow down with p=np.inf in 0.17 cKDTree.query
• #5970: Actually propagate nans through stats functions with nan_policy="propagate"
• #5971: BUG: linalg: fix lwork check in *gelsy
• #6074: BUG: special: fixed violation of strict aliasing rules.
• #6083: BUG: Fix dtype for sum of linear operators
• #6100: BUG: Fix mannwhitneyu to be backward compatible
• #6135: Don’t pass null pointers to LAPACK, even during workspace queries.
• #6148: stats: fix handling of nan values in T tests and kendalltau

3.10 SciPy 0.17.0 Release Notes

Contents

• SciPy 0.17.0 Release Notes
  – New features
    – scipy.cluster improvements
    – scipy.io improvements
    – scipy.optimize improvements
      · Linear assignment problem solver
SciPy 0.17.0 is the culmination of 6 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.17.x branch, and on adding new features on the master branch.

This release requires Python 2.6, 2.7 or 3.2-3.5 and NumPy 1.6.2 or greater. Release highlights:

- New functions for linear and nonlinear least squares optimization with constraints: `scipy.optimize.lsq_linear` and `scipy.optimize.least_squares`
- Support for fitting with bounds in `scipy.optimize.curve_fit`.
- Significant improvements to `scipy.stats`, providing many functions with better handling of inputs which have NaNs or are empty, improved documentation, and consistent behavior between `scipy.stats` and `scipy.stats.mstats`.
- Significant performance improvements and new functionality in `scipy.spatial.cKDTree`.

### 3.10.1 New features

**scipy.cluster improvements**

A new function `scipy.cluster.hierarchy.cut_tree`, which determines a cut tree from a linkage matrix, was added.

**scipy.io improvements**

`scipy.io.mmwrite` gained support for symmetric sparse matrices.

`scipy.io.netcdf` gained support for masking and scaling data based on data attributes.

**scipy.optimize improvements**
Linear assignment problem solver
`scipy.optimize.linear_sum_assignment` is a new function for solving the linear sum assignment problem. It uses the Hungarian algorithm (Kuhn-Munkres).

Least squares optimization
A new function for nonlinear least squares optimization with constraints was added: `scipy.optimize.least_squares`. It provides several methods: Levenberg-Marquardt for unconstrained problems, and two trust-region methods for constrained ones. Furthermore, it provides different loss functions. New trust-region methods also handle sparse Jacobians.

A new function for linear least squares optimization with constraints was added: `scipy.optimize.lsq_linear`. It provides a trust-region method as well as an implementation of the Bounded-Variable Least-Squares (BVLS) algorithm.

`scipy.optimize.curve_fit` now supports fitting with bounds.

scipy.signal improvements
A mode keyword was added to `scipy.signal.spectrogram`, to let it return other spectrograms than power spectral density.

scipy.stats improvements
Many functions in `scipy.stats` have gained a `nan_policy` keyword, which allows specifying how to treat input with NaNs in them: propagate the NaNs, raise an error, or omit the NaNs.

Many functions in `scipy.stats` have been improved to correctly handle input arrays that are empty or contain inf/nans.

A number of functions with the same name in `scipy.stats` and `scipy.stats.mstats` were changed to have matching signature and behavior. See gh-5474 for details.

`scipy.stats.binom_test` and `scipy.stats.mannwhitneyu` gained a keyword `alternative`, which allows specifying the hypothesis to test for. Eventually all hypothesis testing functions will get this keyword.

For methods of many continuous distributions, complex input is now accepted.

Matrix normal distribution has been implemented as `scipy.stats.matrix_normal`.

scipy.sparse improvements
The `axis` keyword was added to sparse norms, `scipy.sparse.linalg.norm`.

scipy.spatial improvements
`scipy.spatial.cKDTree` was partly rewritten for improved performance and several new features were added to it:

- the `query_ball_point` method became significantly faster
- `query` and `query_ball_point` gained an `n_jobs` keyword for parallel execution
- build and query methods now release the GIL
- full pickling support
- support for periodic spaces
- the `sparse_distance_matrix` method can now return and sparse matrix type
**scipy.interpolate** improvements

Out-of-bounds behavior of `scipy.interpolate.interp1d` has been improved. Use a two-element tuple for the `fill_value` argument to specify separate fill values for input below and above the interpolation range. Linear and nearest interpolation kinds of `scipy.interpolate.interp1d` support extrapolation via the `fill_value`="extrapolate" keyword.

`fill_value` can also be set to an array-like (or a two-element tuple of array-likes for separate below and above values) so long as it broadcasts properly to the non-interpolated dimensions of an array. This was implicitly supported by previous versions of scipy, but support has now been formalized and gets compatibility-checked before use. For example, a set of y values to interpolate with shape (2, 3, 5) interpolated along the last axis (2) could accept a `fill_value` array with shape (,) (singleton), (1,), (2, 1), (1, 3), (3,), or (2, 3); or it can be a 2-element tuple to specify separate below and above bounds, where each of the two tuple elements obeys proper broadcasting rules.

**scipy.linalg** improvements

The default algorithm for `scipy.linalg.leastsq` has been changed to use LAPACK’s function *gelsd*. Users wanting to get the previous behavior can use a new keyword `lapack_driver="gelss"` (allowed values are “gelss”, “gelsd” and “gelsy”).

`scipy.sparse` matrices and linear operators now support the matmul (\@) operator when available (Python 3.5+). See [PEP 465](https://legacy.python.org/dev/peps/pep-0465/)

A new function `scipy.linalg.orqz`, for QZ decomposition with reordering, has been added.

### 3.10.2 Deprecated features

`scipy.stats.histogram` is deprecated in favor of `np.histogram`, which is faster and provides the same functionality.

`scipy.stats.threshold` and `scipy.mstats.threshold` are deprecated in favor of `np.clip`. See issue #617 for details.

`scipy.stats.ss` is deprecated. This is a support function, not meant to be exposed to the user. Also, the name is unclear. See issue #663 for details.

`scipy.stats.square_of_sums` is deprecated. This too is a support function not meant to be exposed to the user. See issues #665 and #663 for details.

`scipy.stats.f_value`, `scipy.stats.f_value_multivariate`, `scipy.stats.f_value_wilks_lambda`, and `scipy.mstats.f_value_wilks_lambda` are deprecated. These are related to ANOVA, for which `scipy.stats` provides quite limited functionality and these functions are not very useful standalone. See issues #660 and #650 for details.

`scipy.stats.chisqprob` is deprecated. This is an alias. `stats.chi2.sf` should be used instead.

`scipy.stats.betai` is deprecated. This is an alias for `special.betainc` which should be used instead.

### 3.10.3 Backwards incompatible changes

The functions `stats.trim1` and `stats.trimboth` now make sure the elements trimmed are the lowest and/or highest, depending on the case. Slicing without at least partial sorting was previously done, but didn’t make sense for unsorted input.

When `variable_names` is set to an empty list, `scipy.io.loadmat` now correctly returns no values instead of all the contents of the MAT file.

Element-wise multiplication of sparse matrices now returns a sparse result in all cases. Previously, multiplying a sparse matrix with a dense matrix or array would return a dense matrix.
The function `misc.lena` has been removed due to license incompatibility.

The constructor for `sparse.coo_matrix` no longer accepts `(None, (m,n))` to construct an all-zero matrix of shape `(m,n)`. This functionality was deprecated since at least 2007 and was already broken in the previous SciPy release. Use `coo_matrix((m,n))` instead.

The Cython wrappers in `linalg.cython_lapack` for the LAPACK routines `*gegs`, `*gegv`, `*gelsx`, `*geqpf`, `*ggsvd`, `*ggsy`, `*lahrd`, `*latzm`, `*tzrqf` have been removed since these routines are not present in the new LAPACK 3.6.0 release. With the exception of the routines `*ggsy` and `*ggsy`, these were all deprecated in favor of routines that are currently present in our Cython LAPACK wrappers.

Because the LAPACK `*gegv` routines were removed in LAPACK 3.6.0. The corresponding Python wrappers in `scipy.linalg.lapack` are now deprecated and will be removed in a future release. The source files for these routines have been temporarily included as a part of `scipy.linalg` so that SciPy can be built against LAPACK versions that do not provide these deprecated routines.

### 3.10.4 Other changes

Html and pdf documentation of development versions of Scipy is now automatically rebuilt after every merged pull request.

`scipy.constants` is updated to the CODATA 2014 recommended values.

Usage of `scipy.fftpack` functions within Scipy has been changed in such a way that PyFFTW can easily replace `scipy.fftpack` functions (with improved performance). See gh-5295 for details.

The `imread` functions in `scipy.misc` and `scipy.ndimage` were unified, for which a mode argument was added to `scipy.misc.imread`. Also, bugs for 1-bit and indexed RGB image formats were fixed.

`runtests.py`, the development script to build and test Scipy, now allows building in parallel with `--parallel`.

### 3.10.5 Authors

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• Luke Zoltan Kelley +
• Jason King +
• Andreas Kopecky +
• Eric Larson
• Denis Laxalde
• Antony Lee
• Gregory R. Lee
• Josh Levy-Kramer +
A total of 101 people contributed to this release. People with a “+” by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

**Issues closed for 0.17.0**

- #1923: problem with numpy 0’s in stats.poisson.rvs (Trac #1398)
- #2138: scipy.misc.imread segfaults on 1 bit png (Trac #1613)
- #2237: distributions do not accept complex arguments (Trac #1718)
- #2282: scipy.special.hyp1f1(0.5, 1.5, -1000) fails (Trac #1763)
- #2618: poisson.pmf returns NaN if mu is 0
- #2957: hyp1f1 precision issue
- #2997: FAIL: test_qhull.TestUtilities.test_more_barycentric_transforms
- #3129: No way to set ranges for fitting parameters in Optimize functions
- #3191: interp1d should contain a fill_value_below and a fill_value_above...
- #3453: PchipInterpolator sets slopes at edges differently than Matlab’s...
- #4106: ndimage._ni_support._normalize_sequence() fails with numpy.int64
- #4118: scipy.integrate.ode.set_solout called after scipy.integrate.ode.set_initial_value fails silently
- #4233: 1D scipy.interpolate.griddata using method=nearest produces nans...
- #4375: All tests fail due to bad file permissions
- #4580: scipy.ndimage.filters.convolve documentation is incorrect
- #4627: logsumexp with sign indicator - enable calculation with negative...
- #4702: logsumexp with zero scaling factor
- #4834: gammainc should return 1.0 instead of NaN for infinite x
- #4838: enh: exprel special function
- #4862: the scipy.special.boxcox function is inaccurate for denormal...
- #4887: Spherical harmonic incongruences
- #4895: some scipy ufuncs have inconsistent output dtypes?
- #4923: logm does not aggressively convert complex outputs to float
- #4932: BUG: stats: The fit method of the distributions silently ignores...
- #4956: Documentation error in scipy.special.bi_zeros
- #4957: Docstring for pbvv_seq is wrong
- #4967: block_diag should look at dtypes of all arguments, not only the...
- #5037: scipy.optimize.minimize error messages are printed to stdout...
- #5039: Cubic interpolation: On entry to DGESDD parameter number 12 had...
- #5163: Base case example of Hierarchical Clustering (offer)
- #5181: BUG: stats.genextreme.entropy should use the explicit formula
- #5184: Some? wheels don’t express a numpy dependency
- #5197: mstats: test_kurtosis fails (ULP max is 2)
- #5260: Typo causing an error in splrep
- #5263: Default epsilon in rbf.py fails for colinear points
- #5276: Reading empty (no data) arff file fails
- #5280: 1d scipy.signal.convolve much slower than numpy.convolve
- #5326: Implementation error in scipy.interpolate.PchipInterpolator
- #5370: Test issue with test_quadpack and libm.so as a linker script
- #5426: ERROR: test_stats.test_chisquare_masked_arrays
- #5427: Automate installing correct numpy versions in numpy-vendor image
- #5430: Python3 : Numpy scalar types “not iterable”; specific instance...
- #5450: BUG: spatial.ConvexHull triggers a seg. fault when given nans.
- #5478: clarify the relation between matrix normal distribution and multivariate_normal
- #5539: lstsq related test failures on windows binaries from numpy-vendor
- #5560: doc: scipy.stats.burr pdf issue
- #5571: lstsq test failure after lapack_driver change
- #5577: ordqz segfault on Python 3.4 in Wine
- #5578: scipy.linalg test failures on python 3 in Wine
- #5607: Overloaded ‘isnan(double&)’ is ambiguous when compiling with...
- #5629: Test for lstsq randomly failed
- #5630: memory leak with scipy 0.16 spatial cKDEtree
- #5689: isnan errors compiling scipy/special/Faddeeva.cc with clang++
- #5694: fftpack test failure in test_import
Pull requests for 0.17.0

- #3022: hyp1f1: better handling of large negative arguments
- #3107: ENH: Add ordered QZ decomposition
- #4390: ENH: Allow axis and keepdims arguments to be passed to scipy.linalg.norm.
- #4671: ENH: add axis to sparse norms
- #4796: ENH: Add cut tree function to scipy.cluster.hierarchy
- #4809: MAINT: cauchy moments are undefined
- #4821: ENH: stats: make distribution instances picklable
- #4839: ENH: Add scipy.special.exprel relative error exponential ufunc
- #4859: Logsumexp fixes - allows sign flags and b==0
- #4865: BUG: scipy.io.mmio.write: error with big indices and low precision
- #4869: add as_inexact option to __lib__.util._asarray_validated
- #4884: ENH: Finite difference approximation of Jacobian matrix
- #4890: ENH: Port cKDTree query methods to C++, allow pickling on Python...
- #4892: how much doctesting is too much?
- #4896: MAINT: work around a possible numpy ufunc loop selection bug
- #4898: MAINT: A bit of pyflakes-driven cleanup.
- #4899: ENH: add ‘alternative’ keyword to hypothesis tests in stats
- #4903: BENCH: Benchmarks for interpolate module
- #4905: MAINT: prepend underscore to mask_to_limits; delete masked_var.
- #4906: MAINT: Benchmarks for optimize.leastsq
- #4910: WIP: Trimmed statistics functions have inconsistent API.
- #4924: MAINT: if the imaginary part of logm of a real matrix is small,...
- #4930: BENCH: Benchmarks for signal module
- #4941: ENH: update find_repeats.
- #4942: MAINT: use np.float64_t instead of np.float_t in cKDTree
- #4944: BUG: integer overflow in correlate_nd
- #4951: do not ignore invalid kwargs in distributions fit method
- #4958: Add some detail to docstrings for special functions
- #4961: ENH: stats.describe: add bias kw and empty array handling
- #4963: ENH: scipy.sparse.coo.coo_matrix.__init__: less memory needed
- #4968: DEP: deprecate stats.f_value* and mstats.f_value* functions.
- #4969: ENH: review stats.relfreq and stats.cumfreq; fixes to stats.histogram
• #4971: Extend github source links to line ranges
• #4972: MAINT: improve the error message in validate_runtests_log
• #4976: DEP: deprecate scipy.stats.threshold
• #4977: MAINT: more careful dtype treatment in block diagonal matrix...
• #4978: ENH: distributions, complex arguments
• #4992: MAINT: more careful dtype treatment in block diagonal matrix...
• #4996: DOC: fix stats.spearmanr docs
• #4997: Fix up boxcox for underflow / loss of precision
• #4998: DOC: improved documentation for stats.ppcc_max
• #5000: ENH: added empty input handling scipy.moment; doc enhancements
• #5003: ENH: improves rankdata algorithm
• #5005: scipy.stats: numerical stability improvement
• #5007: ENH: nan handling in functions that use stats._chk_asarray
• #5009: remove coveralls.io
• #5010: Hypergeometric distribution log survival function
• #5014: Patch to compute the volume and area of convex hulls
• #5015: DOC: Fix mistaken variable name in sawtooth
• #5016: DOC: resample example
• #5017: DEP: deprecate stats.betai and stats.chisqprob
• #5018: ENH: Add test on random input to volume computations
• #5026: BUG: Fix return dtype of lil_matrix.getnnz(axis=0)
• #5030: DOC: resample slow for prime output too
• #5033: MAINT: integrate, special: remove unused R1MACH and Makefile
• #5034: MAINT: signal: lift max_len_seq validation out of Cython
• #5035: DOC/MAINT: refguide / doctest drudgery
• #5041: BUG: fixing some small memory leaks detected by cppcheck
• #5044: [GSoC] ENH: New least-squares algorithms
• #5050: MAINT: C fixes, trimmed a lot of dead code from Cephes
• #5052: ENH: sparse: avoid densifying on sparse/dense elementwise mult
• #5058: TST: stats: add a sample distribution to the test loop
• #5061: ENH: spatial: faster 2D Voronoi and Convex Hull plotting
• #5065: TST: improve test coverage for stats.mvsdist and stats.bayes_mvs
• #5066: MAINT: fitpack: remove a noop
• #5067: ENH: empty and nan input handling for stats.kstat and stats.kstatvar
• #5071: DOC: optimize: Correct paper reference, add doi
• #5072: MAINT: scipy.sparse cleanup
• #5073: DOC: special: Add an example showing the relation of diric to...
• #5075: DOC: clarified parameterization of stats.lognorm
• #5076: use int, float, bool instead of np.int, np.float, np.bool
• #5078: DOC: Rename fftpack docs to README
• #5081: BUG: Correct handling of scalar ‘b’ in lsmr and lsqr
• #5082: loadmat variable_names: don’t confuse [] and None.
• #5083: Fix integrate.fixed_quad docstring to indicate None return value
• #5086: Use solve() instead of inv() for gaussian_kde
• #5090: MAINT: stats: add explicit _sf, _isf to gengamma distribution
• #5094: ENH: scipy.interpolate.NearestNDInterpolator: cKDTree configurable
• #5098: DOC: special: fix typesetting in *_roots quadrature functions
• #5099: DOC: make the docstring of stats.moment raw
• #5104: DOC/ENH fixes and micro-optimizations for scipy.linalg
• #5105: enh: made l-bfgs-b parameter for the maximum number of line search...
• #5106: TST: add NIST test cases to stats.f_oneway
• #5110: [GSoC]: Bounded linear least squares
• #5111: MAINT: special: Cephes cleanup
• #5118: BUG: FIR path failed if len(x) < len(b) in lfilter.
• #5124: ENH: move the filliben approximation to a publicly visible function
• #5126: StatisticsCleanup: stats.kruskal review
• #5131: DOC: differential_evolution, improve docstring for mutation and...
• #5132: MAINT: differential_evolution improve init_population_lhs comments...
• #5133: MRG: rebased mmio refactoring
• #5135: MAINT: stats.mstats consistency with stats.stats
• #5139: TST: linalg: add a smoke test for gh-5039
• #5140: ENH: Update constants.codata to CODATA 2014
• #5145: added ValueError to docstring as possible error raised
• #5146: MAINT: Improve implementation details and doc in stats.shapiro
• #5147: [GSoC] ENH: Upgrades to curve_fit
• #5150: Fix misleading wavelets/cwt example
• #5152: BUG: cluster.hierarchy.dendrogram: missing font size doesn’t...
• #5153: add keywords to control the summation in discrete distributions...
• #5156: DOC: added comments on algorithms used in Legendre function
• #5158: ENH: optimize: add the Hungarian algorithm
• #5162: FIX: Remove lena
• #5164: MAINT: fix cluster.hierarchy.dendrogram issues and docs
• #5166: MAINT: changed stats.pointbiserialr to delegate to stats.pearsonr
• #5167: ENH: add nan_policy to stats.kendalltau.
• #5168: TST: added nist test case (Norris) to stats.linregress.
• #5169: update lpmv docstring
• #5171: Clarify metric parameter in linkage docstring
• #5172: ENH: add mode keyword to signal.spectrogram
• #5177: DOC: graphical example for KDTree.query_ball_point
• #5179: MAINT: stats: tweak the formula for ncx2.pdf
• #5188: MAINT: linalg: A bit of clean up.
• #5189: BUG: stats: Use the explicit formula in stats.genextreme.entropy
• #5193: BUG: fix uninitialized use in lartg
• #5194: BUG: properly return error to fortran from ode_jacobian_function
• #5198: TST: Fix TestCtypesQuad failure on Python 3.5 for Windows
• #5201: allow extrapolation in interp1d
• #5209: MAINT: Change complex parameter to boolean in Y_()
• #5213: BUG: sparse: fix logical comparison dtype conflicts
• #5216: BUG: sparse: fixing unbound local error
• #5218: DOC and BUG: Bessel function docstring improvements, fix array_like,...
• #5222: MAINT: sparse: fix COO ctor
• #5224: DOC: optimize: type of OptimizeResult.hess_inv varies
• #5228: ENH: Add maskandscale support to netcdf; based on pupynere and...
• #5229: DOC: sparse.linalg.svds doc typo fixed
• #5234: MAINT: sparse: simplify COO ctor
• #5235: MAINT: sparse: warn on todia() with many diagonals
• #5236: MAINT: ndimage: simplify thread handling/recursion + constness
• #5239: BUG: integrate: Fixed issue 4118
• #5241: qr_insert fixes, closes #5149
• #5246: Doctest tutorial files
• #5247: DOC: optimize: typo/import fix in linear_sum_assignment
• #5248: remove inspect.getargspec and test python 3.5 on Travis CI
• #5250: BUG: Fix sparse multiply by single-element zero
• #5261: Fix bug causing a TypeError in splrep when a runtime warning...
• #5262: Follow up to 4489 (Addition LAPACK routines in linalg.l lstsq)
• #5264: ignore zero-length edges for default epsilon
• #5269: DOC: Typos and spell-checking
• #5272: MAINT: signal: Convert array syntax to memoryviews
• #5273: DOC: raw strings for docstrings with math
• #5274: MAINT: sparse: update cython code for MST
• #5278: BUG: io: Stop guessing the data delimiter in ARFF files.
• #5289: BUG: misc: Fix the Pillow work-around for 1-bit images.
• #5291: ENH: call np.correlate for 1d in scipy.signal.correlate
• #5294: DOC: special: Remove a potentially misleading example from the...
• #5295: Simplify replacement of fftpack by pyfftw
• #5296: ENH: Add matrix normal distribution to stats
• #5297: Fixed leaf_rotation and leaf_font_size in Python 3
• #5303: MAINT: stats: rewrite find_repeats
• #5307: MAINT: stats: remove unused Fortran routine
• #5313: BUG: sparse: fix diags for nonsquare matrices
• #5315: MAINT: special: Cephes cleanup
• #5316: fix input check for sparse.linalg.svds
• #5319: MAINT: Cython code maintenance
• #5328: BUG: Fix place_poles return values
• #5329: avoid a spurious divide-by-zero in Student t stats
• #5334: MAINT: integrate: miscellaneous cleanup
• #5340: MAINT: Printing Error Msg to STDERR and Removing iterate.dat
• #5347: ENH: add Py3.5-style matmul operator (e.g. A @ B) to sparse linear...
• #5350: FIX error, when reading 32-bit float wav files
• #5351: refactor the PCHIP interpolant’s algorithm
• #5354: MAINT: construct csr and csc matrices from integer lists
• #5359: add a fast path to interp1d
• #5364: Add two fill_values to interp1d.
• #5365: ABCD docstrings
• #5366: Fixed typo in the documentation for scipy.signal.cwt() per #5290.
• #5367: DOC updated scipy.spatial.Delaunay example
• #5368: ENH: Do not create a throwaway class at every function call
• #5372: DOC: spectral: fix reference formatting
• #5375: PEP8 amendments to fftpack.basic.py
• #5377: BUG: integrate: builtin name no longer shadowed
• #5381: PEP8ified fftpack.pseudo_diffs.py
• #5385: BLD: fix Bento build for changes to optimize and spatial
• #5386: STY: PEP8 amendments to interpolate.py
• #5387: DEP: deprecate stats.histogram
• #5388: REL: add “make upload” command to doc/Makefile.
• #5389: DOC: updated origin param of scipy.ndimage.filters.convolve
• #5395: BUG: special: fix a number of edge cases related to $x = np.inf$.
• #5398: MAINT: stats: avoid spurious warnings in lognorm.pdf(0, s)
• #5407: ENH: stats: Handle mu=0 in stats.poisson
• #5409: Fix the behavior of discrete distributions at the right-hand...
• #5412: TST: stats: skip a test to avoid a spurious log(0) warning
• #5413: BUG: linalg: work around LAPACK single-precision lwork computation...
• #5414: MAINT: stats: move creation of namedtuples outside of function...
• #5415: DOC: fix up sections in ToC in the pdf reference guide
• #5416: TST: fix issue with a ctypes test for integrate on Fedora.
• #5419: MAINT: sparse: fix usage of NotImplementedError
• #5420: Raise proper error if maxiter < 1
• #5422: DOC: changed documentation of brent to be consistent with bracket
• #5444: BUG: gaussian_filter, BPoly.from_derivatives fail on numpy int...
• #5445: MAINT: stats: fix incorrect deprecation warnings and test noise
• #5446: DOC: add note about PyFFTW in fftpack tutorial.
• #5459: DOC: integrate: Some improvements to the differential equation...
• #5465: BUG: Relax mstats kurtosis test tolerance by a few ulp
• #5471: ConvexHull should raise ValueError for NaNs.
• #5473: MAINT: update decorators.py module to version 4.0.5
• #5476: BUG: imsave searches for wrong channel axis if image has 3 or...
• #5477: BLD: add mumpy to setup/install_.requires for OS X wheels
• #5479: ENH: return Jacobian/Hessian from BasinHopping
• #5484: BUG: fix ttest zero division handling
• #5486: Fix crash on kmeans2
• #5491: MAINT: Expose parallel build option to runtests.py
• #5494: Sort OptimizeResult.__repr__ by key
• #5496: DOC: update the author name mapping
• #5497: Enhancement to binned_statistic: option to unraveled returned...
• #5498: BUG: sparse: fix a bug in spaceroots input dtype resolution
• #5500: DOC: detect unprintable characters in docstrings
• #5505: BUG: misc: Ensure fromimage converts mode ‘P’ to ‘RGB’ or ‘RGBA’.
- #5514: DOC: further update the release notes
- #5515: ENH: optionally disable fixed-point acceleration
- #5517: DOC: Improvements and additions to the matrix_normal doc
- #5518: Remove wrappers for LAPACK deprecated routines
- #5521: TST: skip a linalg.orth memory test on 32-bit platforms.
- #5523: DOC: change a few floats to integers in docstring examples
- #5524: DOC: more updates to 0.17.0 release notes.
- #5525: Fix to minor typo in documentation for scipy.integrate.ode
- #5527: TST: bump arccosh tolerance to allow for inaccurate numpy or...
- #5535: DOC: signal: minor clarification to docstring of TransferFunction.
- #5538: DOC: signal: fix find_peaks_cwt documentation
- #5545: MAINT: Fix typo in linalg/basic.py
- #5547: TST: mark TestEig.test_singular as knownfail in master.
- #5550: MAINT: work around lstsq driver selection issue
- #5556: BUG: Fixed broken dogbox trust-region radius update
- #5561: BUG: eliminate warnings, exception (on Win) in test_maskandscale;
- #5567: TST: a few cleanups in the test suite; run_module_suite and clearer...
- #5568: MAINT: simplify poisson’s _argcheck
- #5569: TST: bump GMean test tolerance to make it pass on Wine
- #5572: TST: lstsq: bump test tolerance for TravisCI
- #5573: TST: remove use of np.fromfile from cluster.vq tests
- #5576: Lapack deprecations
- #5579: TST: skip tests of linalg.norm axis keyword on numpy <= 1.7.x
- #5582: Clarify language of survival function documentation
- #5583: MAINT: stats/tests: A bit of clean up.
- #5588: DOC: stats: Add a note that stats.burr is the Type III Burr distribution.
- #5595: TST: fix test_lamch failures on Python 3
- #5600: MAINT: Ignore spatial/ckdtree.cxx and .h
- #5602: Explicitly numbered replacement fields for maintainability
- #5605: MAINT: collection of small fixes to test suite
- #5614: Minor doc change.
- #5624: FIX: Fix interpolate
- #5625: BUG: msvc9 binaries crash when indexing std::vector of size 0
- #5635: BUG: misspelled __dealloc__ in cKDTree.
- #5642: STY: minor fixup of formatting of 0.17.0 release notes.
- #5643: BLD: fix a build issue in special/Faddeeva.cc with isnan.
• #5661: TST: linalg tests used stdlib random instead of numpy.random.
• #5682: backports for 0.17.0
• #5696: Minor improvements to least_squares’ docstring.
• #5697: BLD: fix for isnan/isinf issues in special/Faddeeva.cc
• #5720: TST: fix for file opening error in fftpack test_import.py
• #5722: BUG: Make curve_fit respect an initial guess with bounds
• #5726: Backports for v0.17.0rc2
• #5727: API: Changes to least_squares API

3.11 SciPy 0.16.1 Release Notes
SciPy 0.16.1 is a bug-fix release with no new features compared to 0.16.0.

3.11.1 Issues closed for 0.16.1
• #5077: cKDTree not indexing properly for arrays with too many elements
• #5127: Regression in 0.16.0: solve_banded errors out in patsy test suite
• #5149: linalg tests apparently cause python to crash with numpy 1.10.0b1
• #5154: 0.16.0 fails to build on OS X; can’t find Python.h
• #5173: failing stats.histogram test with numpy 1.10
• #5191: Scipy 0.16.x - TypeError: _asarray_validated() got an unexpected...
• #5195: tarballs missing documentation source
• #5363: FAIL: test_orthogonal.test_j_roots, test_orthogonal.test_js_roots

3.11.2 Pull requests for 0.16.1
• #5088: BUG: fix logic error in cKDTree.sparse_distance_matrix
• #5089: BUG: Don’t overwrite b in lfilter’s FIR path
• #5128: BUG: solve_banded failed when solving 1x1 systems
• #5155: BLD: fix missing Python include for Homebrew builds.
• #5192: BUG: backport as_inexact kwarg to _asarray_validated
• #5203: BUG: fix uninitialized use in lartg 0.16 backport
• #5204: BUG: properly return error to fortran from ode_jacobian_function...
• #5207: TST: Fix TestCtypesQuad failure on Python 3.5 for Windows
• #5352: TST: sparse: silence warnings about boolean indexing
• #5355: MAINT: backports for 0.16.1 release
• #5356: REL: update Paver file to ensure sdist contents are OK for releases.
• #5382: 0.16.x backport: MAINT: work around a possible numpy ufunc loop...
• #5393: TST:special: bump tolerance levels for test_j_roots and test_js_roots
• #5417: MAINT: stats: move namedtuple creating outside function calls.
SciPy 0.16.0 is the culmination of 7 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.16.x branch, and on adding new features on the master branch.

This release requires Python 2.6, 2.7 or 3.2-3.4 and NumPy 1.6.2 or greater.

Highlights of this release include:

- A Cython API for BLAS/LAPACK in `scipy.linalg`
- A new benchmark suite. It’s now straightforward to add new benchmarks, and they’re routinely included with performance enhancement PRs.
- Support for the second order sections (SOS) format in `scipy.signal`.

### 3.12.1 New features

**Benchmark suite**

The benchmark suite has switched to using Airspeed Velocity for benchmarking. You can run the suite locally via `python runtests.py --bench`. For more details, see `benchmarks/README.rst`.

**scipy.linalg improvements**

A full set of Cython wrappers for BLAS and LAPACK has been added in the modules `scipy.linalg.cython_blas` and `scipy.linalg.cython_lapack`. In Cython, these wrappers can now be cimported from their corresponding modules and used without linking directly against BLAS or LAPACK.
The functions \texttt{scipy.linalg.qr\_delete}, \texttt{scipy.linalg.qr\_insert} and \texttt{scipy.linalg.qr\_update} for updating QR decompositions were added.

The function \texttt{scipy.linalg.solve\_circulant} solves a linear system with a circulant coefficient matrix.

The function \texttt{scipy.linalg.inv\_pascal} computes the inverse of a Pascal matrix.

The function \texttt{scipy.linalg.solve\_toeplitz}, a Levinson-Durbin Toeplitz solver, was added.

Added wrapper for potentially useful LAPACK function \texttt{*lasd4}. It computes the square root of the i-th updated eigenvalue of a positive symmetric rank-one modification to a positive diagonal matrix. See its LAPACK documentation and unit tests for it to get more info.

Added two extra wrappers for LAPACK least-square solvers. Namely, they are \texttt{*gelsd} and \texttt{*gelsy}.

Wrappers for the LAPACK \texttt{*lange} functions, which calculate various matrix norms, were added.

Wrappers for \texttt{*gtsv} and \texttt{*ptsv}, which solve $A\times X = B$ for tri-diagonal matrix $A$, were added.

\texttt{scipy.signal} improvements

Support for second order sections (SOS) as a format for IIR filters was added. The new functions are:

- \texttt{scipy.signal.sosfilt}
- \texttt{scipy.signal.sosfilt\_zi},
- \texttt{scipy.signal.sos2tf}
- \texttt{scipy.signal.sos2zpk}
- \texttt{scipy.signal.tf2sos}
- \texttt{scipy.signal.zpk2sos}.

Additionally, the filter design functions \texttt{iirdesign}, \texttt{iirfilter}, \texttt{butter}, \texttt{cheby1}, \texttt{cheby2}, \texttt{ellip}, and \texttt{bessel} can return the filter in the SOS format.

The function \texttt{scipy.signal.place\_poles}, which provides two methods to place poles for linear systems, was added.

The option to use Gustafsson’s method for choosing the initial conditions of the forward and backward passes was added to \texttt{scipy.signal.filt\_filt}.

New classes \texttt{TransferFunction}, \texttt{StateSpace} and \texttt{ZerosPolesGain} were added. These classes are now returned when instantiating \texttt{scipy.signal.lti}. Conversion between those classes can be done explicitly now.

An exponential (Poisson) window was added as \texttt{scipy.signal.exponential}, and a Tukey window was added as \texttt{scipy.signal.tukey}.

The function for computing digital filter group delay was added as \texttt{scipy.signal.group\_delay}.

The functionality for spectral analysis and spectral density estimation has been significantly improved: \texttt{scipy.signal.welch} became ~8x faster and the functions \texttt{scipy.signal.spectrogram}, \texttt{scipy.signal.coherence} and \texttt{scipy.signal.csd} (cross-spectral density) were added.

\texttt{scipy.signal.lsim} was rewritten - all known issues are fixed, so this function can now be used instead of \texttt{lsim2}; \texttt{lsim} is orders of magnitude faster than \texttt{lsim2} in most cases.

\texttt{scipy.sparse} improvements

The function \texttt{scipy.sparse.norm}, which computes sparse matrix norms, was added.

The function \texttt{scipy.sparse.random}, which allows to draw random variates from an arbitrary distribution, was added.
SciPy Reference Guide, Release 1.2.0

**scipy.spatial improvements**

*scipy.spatial.cKDTree* has seen a major rewrite, which improved the performance of the *query* method significantly, added support for parallel queries, pickling, and options that affect the tree layout. See pull request 4374 for more details.

The function *scipy.spatial.procrustes* for Procrustes analysis (statistical shape analysis) was added.

**scipy.stats improvements**

The Wishart distribution and its inverse have been added, as *scipy.stats.wishart* and *scipy.stats.invwishart*.

The Exponentially Modified Normal distribution has been added as *scipy.stats.exponnorm*.

The Generalized Normal distribution has been added as *scipy.stats.gennorm*.

All distributions now contain a *random_state* property and allow specifying a specific *numpy.random.RandomState* random number generator when generating random variates.

Many statistical tests and other *scipy.stats* functions that have multiple return values now return *namedtuples*. See pull request 4709 for details.

**scipy.optimize improvements**

A new derivative-free method DF-SANE has been added to the nonlinear equation system solving function *scipy.optimize.root*.

### 3.12.2 Deprecated features

*scipy.stats.pdf_fromgamma* is deprecated. This function was undocumented, untested and rarely used. Statsmodels provides equivalent functionality with *statsmodels.distributions.ExpandedNormal*.

*scipy.stats.fastsort* is deprecated. This function is unnecessary, *numpy.argsort* can be used instead.

*scipy.stats.signaltonoise* and *scipy.stats.mstats.signaltonoise* are deprecated. These functions did not belong in *scipy.stats* and are rarely used. See issue #609 for details.

*scipy.stats.histogram2* is deprecated. This function is unnecessary, *numpy.histogram2d* can be used instead.

### 3.12.3 Backwards incompatible changes

The deprecated global optimizer *scipy.optimize.anneal* was removed.

The following deprecated modules have been removed: *scipy.lib.blas*, *scipy.lib.lapack*, *scipy.linalg.cblas*, *scipy.linalg.fblas*, *scipy.linalg.clapack*, *scipy.linalg.flapack*. They had been deprecated since Scipy 0.12.0, the functionality should be accessed as *scipy.linalg.blas* and *scipy.linalg.lapack*.

The deprecated function *scipy.special.all_mat* has been removed.

The deprecated functions *fprob*, *ksprob*, *zprob*, *randwcdf* and *randwppf* have been removed from *scipy.stats*.

### 3.12.4 Other changes

The version numbering for development builds has been updated to comply with PEP 440.

Building with *python setup.py develop* is now supported.
3.12.5 Authors

- @axiru +
- @endolith
- Elliott Sales de Andrade +
- Anne Archibald
- Yoshiki Vázquez Baeza +
- Sylvain Bellemare
- Felix Berkenkamp +
- Raoul Bourquin +
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- Lars Buitinck
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- Steven Byrnes
- CJ Carey
- George Castillo +
- Alex Conley +
- Liam Damewood +
- Rupak Das +
- Abraham Escalante +
- Matthias Feurer +
- Eric Firing +
- Clark Fitzgerald
- Chad Fulton
- André Gaul
- Andreea Georgescu +
- Christoph Gohlke
- Andrey Golovizin +
- Ralf Gommers
- J.J. Green +
- Alex Griffing
- Alexander Grigorievski +
- Hans Moritz Gunther +
- Jonas Hahndorf +
- Charles Harris
• Ian Henriksen
• Andreas Hilboll
• Åsmund Hjulstad +
• Jan Schlüter +
• Janko Slavič +
• Daniel Jensen +
• Johannes Ballé +
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• Amato Kasahara +
• Eric Larson
• Denis Laxalde
• Antony Lee
• Gregory R. Lee
• Perry Lee +
• Loïc Estève
• Martin Manns +
• Eric Martin +
• Matěj Kocián +
• Andreas Mayer +
• Nikolay Mayorov +
• Robert McGibbon +
• Sturla Molden
• Nicola Montecchio +
• Eric Moore
• Jamie Morton +
• Nikolas Moya +
• Maniteja Nandana +
• Andrew Nelson
• Joel Nothman
• Aldrian Obaja
• Regina Ongowarsito +
• Paul Ortyl +
• Pedro López-Adeva Fernández-Layos +
• Stefan Peterson +
• Irvin Probst +
• Eric Quintero +
A total of 93 people contributed to this release. People with a “+” by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 0.16.0

- #1063: Implement a whishart distribution (Trac #536)
- #1885: Rbf: floating point warnings - possible bug (Trac #1360)
- #2020: Rbf default epsilon too large (Trac #1495)
- #2325: extending distributions, hypergeom, to degenerate cases (Trac...)
- #3502: [ENH] linalg.hessenberg should use ORGHR for calc_q= True
- #3603: Passing array as window into signal.resample() fails
- #3675: Intermittent failures for signal.slepian on Windows
- #3742: Pchipinterpolator inconvenient as ppoly
- #3786: add procrustes?
- #3798: scipy.io.savemat fails for empty dicts
- #3975: Use RandomState in scipy.stats
- #4022: savemat incorrectly saves logical arrays
- #4028: scipy.stats.geom.logpmf(1,1) returns nan. The correct value is...
- #4030: simplify scipy.stats.betaprime.pdf
- #4031: improve accuracy of scipy.stats.gompertz distribution for small...
- #4033: improve accuracy of scipy.stats.lomax distribution for small...
- #4034: improve accuracy of scipy.stats.rayleigh distribution for large...
- #4035: improve accuracy of scipy.stats.truncexpon distribution for small...
- #4081: Error when reading matlab file: buffer is too small for requested...
- #4100: Why does qr(a, lwork=0) not fail?
- #4134: scipy.stats: rv_frozen has no expect() method
- #4204: Please add docstring to scipy.optimize.RootResults
- #4206: Wrap LAPACK tridiagonal solve routine gtsv
- #4208: Empty sparse matrices written to MAT file cannot be read by MATLAB
- #4217: use a TravisCI configuration with numpy built with NPY_RELAXED_STRIDES_CHECKING=1
- #4282: integrate.odeint raises an exception when full_output=1 and the...
- #4301: scipy and numpy version names do not follow pep 440
- #4355: PPoly.antiderivative() produces incorrect output
- #4391: spsolve becomes extremely slow with large b matrix
- #4393: Documentation glitch in sparse.linalg.spilu
- #4408: Vector-valued constraints in minimize() et al
- #4412: Documentation of scipy.signal.cwt error
- #4428: dok.__setitem__ problem with negative indices
- #4434: Incomplete documentation for sparse.linalg.spsolve
- #4438: linprog() documentation example wrong
- #4445: Typo in scipy.special.expit doc
- #4467: Documentation Error in scipy.optimize options for TNC
- #4492: solve_toeplitz benchmark is bitrotting already
- #4506: lobpcg/sparse performance regression Jun 2014?
- #4520: g77_abi_wrappers needed on Linux for MKL as well
- #4521: Broken check in uses_mkl for newer versions of the library
- #4523: rbf with gaussian kernel seems to produce more noise than original...
- #4526: error in site documentation for poisson.pmf() method
- #4527: KDTree example doesn’t work in Python 3
- #4550: scipy.stats.mode - UnboundLocalError on empty sequence
- #4554: filter out convergence warnings in optimization tests
• #4565: odeint messages
• #4569: remez: “ValueError: Failure to converge after 25 iterations....
• #4582: DOC: optimize: __minimize_scalar_brent does not have a disp option
• #4585: DOC: Erroneous latex-related characters in tutorial.
• #4590: sparse.linalg.svds should throw an exception if which not in...
• #4594: scipy.optimize.linprog IndexError when a callback is provide
• #4596: scipy.linalg.block_diag misbehavior with empty array inputs (v0.13.3)
• #4599: scipy.integrate.nquad should call __OptFunc when called with only...
• #4612: Crash in signal.lfilter on nd input with wrong shaped zi
• #4613: scipy.io.readsav error on reading sav file
• #4673: scipy.interpolate.RectBivariateSpline construction locks PyQt...
• #4681: Broadcasting in signal.lfilter still not quite right.
• #4705: kmeans k_or_guess parameter error if guess is not square array
• #4719: Build failure on 14.04.2
• #4724: GenGamma __munp function fails due to overflow
• #4726: FAIL: test_cobyla.test_vector_constraints
• #4734: Failing tests in stats with numpy master.
• #4736: qr__update bug or incompatibility with numpy 1.10?
• #4746: linprog returns solution violating equality constraint
• #4757: optimize.leastsq docstring mismatch
• #4774: Update contributor list for v0.16
• #4779: circmean and others do not appear in the documentation
• #4788: problems with scipy sparse linalg solve iterative.py when complex
• #4791: BUG: scipy.spatial: incremental Voronoi doesn’t increase size...

Pull requests for 0.16.0
• #3116: sparse: enhancements for DIA format
• #3157: ENH: linalg: add the function ‘solve_circulant’ for solving a...
• #3442: ENH: signal: Add Gustafsson’s method as an option for the filtfilt...
• #3679: WIP: fix sporadic slepian failures
• #3680: Some cleanups in stats
• #3717: ENH: Add second-order sections filtering
• #3741: Dltisys changes
• #3956: add note to scipy.signal.resample about prime sample numbers
• #3980: Add check_finite flag to UnivariateSpline
• #3996: MAINT: stricter linalg argument checking
• #4001: BUG: numerical precision in dirichlet
• #4012: ENH: linalg: Add a function to compute the inverse of a Pascal...
• #4021: ENH: Cython api for lapack and blas
• #4089: Fixes for various PEP8 issues.
• #4116: MAINT: fitpack: trim down compiler warnings (unused labels, variables)
• #4129: ENH: stats: add a random_state property to distributions
• #4135: ENH: Add Wishart and inverse Wishart distributions
• #4195: improve the interpolate docs
• #4200: ENH: Add t-test from descriptive stats function.
• #4202: Dendrogram threshold color
• #4205: BLD: fix a number of Bento build warnings.
• #4211: add an ufunc for the inverse Box-Cox transform
• #4212: MRG: fix for gh-4208
• #4213: ENH: specific warning if matlab file is empty
• #4215: Issue #4209: splprep documentation updated to reflect dimensional...
• #4219: DOC: silence several Sphinx warnings when building the docs
• #4223: MAINT: remove two redundant lines of code
• #4226: try forcing the numpy rebuild with relaxed strides
• #4228: BLD: some updates to Bento config files and docs. Closes gh-3978.
• #4232: wrong references in the docs
• #4242: DOC: change example sample spacing
• #4245: Arff fixes
• #4246: MAINT: C fixes
• #4247: MAINT: remove some unused code
• #4249: Add routines for updating QR decompositions
• #4250: MAINT: Some pyflakes-driven cleanup in linalg and sparse
• #4252: MAINT trim away >10 kLOC of generated C code
• #4253: TST: stop shadowing ellip* tests vs boost data
• #4254: MAINT: special: use NPY_PI, not M_PI
• #4255: DOC: INSTALL: use Py3-compatible print syntax, and don’t mention...
• #4256: ENH: spatial: reimplement cdist_cosine using np.dot
• #4258: BUG: io.arff #4429 #2088
• #4261: MAINT: signal: PEP8 and related style clean up.
• #4262: BUG: newton_krylov() was ignoring norm_tol argument, closes #4259
• #4263: MAINT: clean up test noise and optimize tests for docstrings...
• #4266: MAINT: io: Give an informative error when attempting to read...
• #4268: MAINT: fftpack benchmark integer division vs true division
• #4269: MAINT: avoid shadowing the eigvals function
• #4272: BUG: sparse: Fix bench_sparse.py
• #4276: DOC: remove confusing parts of the documentation related to writing...
• #4281: Sparse matrix multiplication: only convert array if needed (with...
• #4284: BUG: integrate: odeint crashed when the integration time was...
• #4286: MRG: fix matlab output type of logical array
• #4291: DOC: linalg: fix layout in cholesky_banded docstring
• #4292: BUG: allow empty dict as proxy for empty struct
• #4293: MAINT: !=- > not_ _equal in hamming distance implementation
• #4295: Pole placement
• #4296: MAINT: some cleanups in tests of several modules
• #4302: ENH: Solve toepplitz linear systems
• #4306: Add benchmark for conjugate gradient solver.
• #4307: BLD: PEP 440
• #4310: BUG: make stats.geom.logpmf(1,1) return 0.0 instead of nan
• #4311: TST: restore a test that uses slogdet now that we have dropped...
• #4313: Some minor fixes for stats.wishart addition.
• #4315: MAINT: drop nump_1.5 compatibility code in sparse matrix tests
• #4318: ENH: Add random_ _state to multivariate distributions
• #4319: MAINT: fix hamming distance regression for exotic arrays, with...
• #4320: TST: a few changes like self.assertTrue(x == y, message) -> assert_ _equal(x,...
• #4321: TST: more changes like self.assertTrue(x == y, message) -> assert_ _equal(x,...
• #4322: TST: in test_ _signaltools, changes like self.assertTrue(x == y,...
• #4323: MAINT: clean up benchmarks so they can all be run as single files.
• #4324: Add more detailed committer guidelines, update MAINTAINERS.txt
• #4326: TST: use numpy.testing in test_ _hierarchy.py
• #4329: MAINT: stats: rename check_ _random_ _state test function
• #4330: Update distance tests
• #4333: MAINT: import comb, factorial from scipy.special, not scipy.misc
• #4338: TST: more conversions from nose to numpy.testing
• #4339: MAINT: remove the deprecated all_ _mat function from special_ _matrices.py
• #4340: add several features to frozen distributions
• #4344: BUG: Fix/test invalid lwork param in qr
• #4345: Fix test noise visible with Python 3.x
• #4347: Remove deprecated blas/lapack imports, rename lib to _lib
• #4349: DOC: add a nontrivial example to stats.binned_statistic.
• #4350: MAINT: remove optimize.anneal for 0.16.0 (was deprecated in 0.14.0).
• #4351: MAINT: fix usage of deprecated Numpy C API in optimize...
• #4352: MAINT: fix a number of special test failures
• #4353: implement cdf for betaprime distribution
• #4357: BUG: piecewise polynomial antiderivative
• #4358: BUG: integrate: fix handling of banded Jacobians in odeint, plus...
• #4359: MAINT: remove a code path taken for Python version < 2.5
• #4360: MAINT: stats.mstats: Remove some unused variables (thanks, pyflakes).
• #4362: Removed erroneous reference to smoothing parameter #4072
• #4363: MAINT: interpolate: clean up in fitpack.py
• #4364: MAINT: lib: don’t export “partial” from decorator
• #4365: svdvals now returns a length-0 sequence of singular values given...
• #4367: DOC: slightly improve TeX rendering of wishart/invwishart docstring
• #4373: ENH: wrap gtsv and ptsv for solve_banded and solveh_banded.
• #4374: ENH: Enhancements to spatial.cKDTree
• #4376: BF: fix reading off-spec matlab logical sparse
• #4377: MAINT: integrate: Clean up some Fortran test code.
• #4378: MAINT: fix usage of deprecated Numpy C API in signal
• #4380: MAINT: scipy.optimize, removing further anneal references
• #4381: ENH: Make DCT and DST accept int and complex types like fft
• #4392: ENH: optimize: add DF-SANE nonlinear derivative-free solver
• #4394: Make reordering algorithms 64-bit clean
• #4396: BUG: bundle cblas.h in Accelerate ABI wrappers to enable compilation...
• #4398: FIX pdist bug where wminkowski’s w.dtype != double
• #4402: BUG: fix stat.hypergeom argcheck
• #4404: MAINT: Fill in the full symmetric squareform in the C loop
• #4405: BUG: avoid X += X.T (refs #4401)
• #4407: improved accuracy of gompertz distribution for small x
• #4414: DOC:fix error in scipy.signal.cwt documentation.
• #4415: ENH: Improve accuracy of lomax for small x.
• #4416: DOC: correct a parameter name in docstring of SuperLU.solve....
• #4419: Restore scipy.linalg.calc_lwork also in master
• #4420: fix a performance issue with a sparse solver
• #4423: ENH: improve rayleigh accuracy for large x.
• #4424: BUG: optimize.minimize: fix overflow issue with integer x0 input.
- #4425: ENH: Improve accuracy of truncexpon for small x
- #4426: ENH: improve rayleigh accuracy for large x.
- #4427: MAINT: optimize: cleanup of TNC code
- #4429: BLD: fix build failure with numpy 1.7.x and 1.8.x.
- #4430: BUG: fix a sparse.dok_matrix set/get copy-paste bug
- #4433: Update __minimize__.py
- #4435: ENH: release GIL around batch distance computations
- #4436: Fixed incomplete documentation for spsolve
- #4439: MAINT: integrate: Some clean up in the tests.
- #4440: Fast permutation t-test
- #4442: DOC: optimize: fix wrong result in docstring
- #4447: DOC: signal: Some additional documentation to go along with the...
- #4448: DOC: tweak the docstring of lapack.linalg module
- #4449: fix a typo in the expit docstring
- #4451: ENH: vectorize distance loops with gcc
- #4456: MAINT: don’t fail large data tests on MemoryError
- #4461: CI: use travis_retry to deal with network timeouts
- #4462: DOC: rationalize minimize() et al. documentation
- #4470: MAINT: sparse: inherit dok_matrix.toarray from spmatrix
- #4473: BUG: signal: Fix validation of the zi shape in sosfilt.
- #4475: BLD: setup.py: update min numpy version and support “setup.py...
- #4481: ENH: add a new linalg special matrix: the Helmert matrix
- #4485: MRG: some changes to allow reading bad mat files
- #4490: [ENH] linalg.hessenberg: use orghr - rebase
- #4491: ENH: linalg: Adding wrapper for potentially useful LAPACK function...
- #4493: BENCH: the solve_toeplitz benchmark used outdated syntax and...
- #4494: MAINT: stats: remove duplicated code
- #4496: References added for watershed_ift algorithm
- #4499: DOC: reshuffle stats distributions documentation
- #4501: Replace benchmark suite with airspeed velocity
- #4502: SLSQP should strictly satisfy bound constraints
- #4503: DOC: forward port 0.15.x release notes and update author name...
- #4504: ENH: option to avoid computing possibly unused svd matrix
- #4505: Rebase of PR 3303 (sparse matrix norms)
- #4507: MAINT: fix lobpcg performance regression
- #4509: DOC: sparse: replace dead link
• #4511: Fixed differential evolution bug
• #4512: Change to fully PEP440 compliant dev version numbers (always...)
• #4525: made tiny style corrections (pep8)
• #4533: Add exponentially modified gaussian distribution (scipy.stats.expongauss)
• #4534: MAINT: benchmarks: make benchmark suite importable on all scipy...
• #4535: BUG: Changed zip() to list(zip()) so that it could work in Python...
• #4536: Follow up to pr 4348 (exponential window)
• #4540: ENH: spatial: Add procrustes analysis
• #4541: Bench fixes
• #4542: TST: NumpyVersion dev -> dev0
• #4543: BUG: Overflow in savgol_coeffs
• #4544: pep8 fixes for stats
• #4546: MAINT: use reduction axis arguments in one-norm estimation
• #4549: ENH : Added group_delay to scipy.signal
• #4553: ENH: Significantly faster moment function
• #4556: DOC: document the changes of the sparse.linalg.svds (optional...)
• #4559: DOC: stats: describe loc and scale parameters in the docstring...
• #4563: ENH: rewrite of stats.ppcc_plot
• #4564: Be more (or less) forgiving when user passes +-inf instead of...
• #4566: DEP: remove a bunch of deprecated function from scipy.stats,...
• #4570: MNT: Suppress LineSearchWarning’s in scipy.optimize tests
• #4572: ENH: Extract inverse hessian information from L-BFGS-B
• #4576: ENH: Split signal.lti into subclasses, part of #2912
• #4578: MNT: Reconcile docstrings and function signatures
• #4581: Fix build with Intel MKL on Linux
• #4583: DOC: optimize: remove references to unused disp kwarg
• #4584: ENH: scipy.signal - Tukey window
• #4587: Hermite asymptotic
• #4593: DOC - add example to RegularGridInterpolator
• #4595: DOC: Fix erroneous latex characters in tutorial/optimize.
• #4600: Add return codes to optimize.tnc docs
• #4603: ENH: Wrap LAPACK *lange functions for matrix norms
• #4604: scipy.stats: generalized normal distribution
• #4609: MAINT: interpolate: fix a few inconsistencies between docstrings...
• #4610: MAINT: make runtest.py –bench-compare use asv continuous and...
• #4611: DOC: stats: explain rice scaling; add a note to the tutorial...
- #4614: BUG: lfilter, the size of zi was not checked correctly for nd...
- #4617: MAINT: integrate: Clean the C code behind odeint.
- #4618: FIX: Raise error when window length != data length
- #4619: Issue #4550: scipy.stats.mode - UnboundLocalError on empty...
- #4620: Fixed a problem (#4590) with svds accepting wrong eigenvalue...
- #4621: Speed up special.ai_zeros/bi_zeros by 10x
- #4623: MAINT: some tweaks to spatial.procrustes (private file, html...
- #4628: Speed up signal.lfilter and add a convolution path for FIR filters
- #4629: Bug: integrate.nquad; resolve issue #4599
- #4631: MAINT: integrate: Remove unused variables in a Fortran test function.
- #4633: MAINT: Fix convergence message for remez
- #4635: PEP8: indentation (so that pep8 bot does not complain)
- #4637: MAINT: generalize a sign function to do the right thing for complex...
- #4639: Amended typo in apple_sgemv_fix.c
- #4642: MAINT: use lapack for scipy.linalg.norm
- #4643: RBF default epsilon too large 2020
- #4646: Added atleast_1d around poly in invres and invresz
- #4647: fix doc pdf build
- #4648: BUG: Fixes #4408: Vector-valued constraints in minimize() et...
- #4649: Vonmisesfix
- #4650: Signal example clean up in Tukey and place_poles
- #4652: DOC: Fix the error in convolve for same mode
- #4653: improve erf performance
- #4655: DEP: deprecate scipy.stats.histogram2 in favour of np.histogram2d
- #4656: DEP: deprecate scipy.stats.signaltonoise
- #4660: Avoid extra copy for sparse compressed [:, seq] and [seq, :]...
- #4661: Clean, rebase of #4478, adding ?gelsy and ?gelsd wrappers
- #4662: MAINT: Correct odeint messages
- #4664: Update _monotone.py
- #4672: fix behavior of scipy.linalg.block_diag for empty input
- #4675: Fix lsim
- #4676: Added missing colon to :math: directive in docstring.
- #4679: ENH: sparse randn
- #4682: ENH: scipy.signal - Addition of CSD, coherence; Enhancement of...
- #4684: BUG: various errors in weight calculations in orthogonal.py
- #4685: BUG: Fixes #4594: optimize.linprog IndexError when a callback...
• #4686: MAINT: cluster: Clean up duplicated exception raising code.
• #4688: Improve is_distance_dm exception message
• #4692: MAINT: stats: Simplify the calculation in tukeylambda._ppf
• #4693: ENH: added functionality to handle scalars in stats._chk_asarray
• #4694: Vectorization of Anderson-Darling computations.
• #4696: Fix singleton expansion in lfilter.
• #4698: MAINT: quiet warnings from cephes.
• #4701: add Bpoly.antiderivatives / integrals
• #4703: Add citation of published paper
• #4706: MAINT: special: avoid out-of-bounds access in specfun
• #4707: MAINT: fix issues with np.matrix as input to functions related...
• #4709: ENH: scipy.stats now returns namedtuples.
• #4710: scipy.io.idl: make reader more robust to missing variables in...
• #4711: Fix crash for unknown chunks at the end of file
• #4712: Reduce onenormest memory usage
• #4713: MAINT: interpolate: no need to pass dtype around if it can be...
• #4714: BENCH: Add benchmarks for stats module
• #4715: MAINT: polish signal.place_poles and signal/test_ltabsys.py
• #4716: DEP: deprecate mstats.signaltoisie
• #4717: MAINT: basinhopping: fix error in tests, silence /0 warning, ...
• #4718: ENH: stats: can specify f-shapes to fix in fitting by name
• #4721: Document that imresize converts the input to a PIL image
• #4722: MAINT: PyArray_BASE is not an lvalue unless the deprecated API...
• #4725: Fix gengamma _nump failure
• #4728: DOC: add poch to the list of scipy special function descriptions
• #4735: MAINT: stats: avoid (a spurious) division-by-zero in skew
• #4738: TST: silence runtime warnings for some corner cases in stats...
• #4739: BLD: try to build numpy instead of using the one on TravisCI
• #4740: DOC: Update some docstrings with `versionadded`.
• #4742: BLD: make sure that relaxed strides checking is in effect on...
• #4750: DOC: special: TeX typesetting of rel_ent, kl_div and pseudo_huber
• #4751: BENCH: add sparse null slice benchmark
• #4753: BUG: Fixed compilation with recent Cython versions.
• #4756: BUG: Fixes #4733: optimize.brute finish option is not compatible...
• #4758: DOC: optimize.leastsq default maxfev clarification
• #4759: improved stats mle fit
- #4760: MAINT: count bfgs updates more carefully
- #4762: BUGS: Fixes #4746 and #4594: linprog returns solution violating...
- #4763: fix small linprog bugs
- #4766: BENCH: add signal.lsim benchmark
- #4768: fix python syntax errors in docstring examples
- #4769: Fixes #4726: test_cobyla.test_vector_constraints
- #4770: Mark FITPACK functions as thread safe.
- #4771: edited scipy/stats/stats.py to fix doctest for fisher_exact
- #4773: DOC: update 0.16.0 release notes.
- #4775: DOC: linalg: add funn_psd as a docstring example
- #4778: Use a dictionary for function name synonyms
- #4780: Include apparently-forgotten functions in docs
- #4783: Added many missing special functions to docs
- #4784: add an axis attribute to PPoly and friends
- #4785: Brief note about origin of Lena image
- #4786: DOC: reformat the Methods section of the KDE docstring
- #4787: Add rice cdf and ppf.
- #4792: CI: add a kludge for detecting test failures which try to disguise...
- #4795: Make refguide_check smarter about false positives
- #4797: BUG/TST: numpoints not updated for incremental Voronoi
- #4799: BUG: spatial: Fix a couple edge cases for the Mahalanobis metric...
- #4801: BUG: Fix TypeError in scipy.optimize._trust-region.py when disp=True.
- #4803: Issues with relaxed strides in QR updating routines
- #4806: MAINT: use an informed initial guess for cauchy fit
- #4810: PEP8ify codata.py
- #4812: BUG: Relaxed strides cleanup in decomp_update.pyx.in
- #4820: BLD: update Bento build for sgemv fix and install cython blas/lapack...
- #4823: ENH: scipy.signal - Addition of spectrogram function
- #4827: DOC: add csd and coherence to __init__.py
- #4833: BLD: fix issue in linalg *lange wrappers for g77 builds.
- #4841: TST: fix test failures in scipy.special with mingw32 due to test...
- #4842: DOC: update site.cfg.example. Mostly taken over from Numpy
- #4845: BUG: signal: Make spectrogram’s return values order match the...
- #4849: DOC:Fix error in ode docstring example
- #4856: BUG: fix typo causing memleak
3.13 SciPy 0.15.1 Release Notes

SciPy 0.15.1 is a bug-fix release with no new features compared to 0.15.0.

3.13.1 Issues fixed

- #4413: BUG: Tests too strict, f2py doesn’t have to overwrite this array
- #4417: BLD: avoid using NPY_API_VERSION to check not using deprecated...
- #4418: Restore and deprecate scipy.linalg.calc_work

3.14 SciPy 0.15.0 Release Notes

Contents

- SciPy 0.15.0 Release Notes
  - New features
    * Linear Programming Interface
    * Differential evolution, a global optimizer
    * scipy.signal improvements
    * scipy.integrate improvements
    * scipy.linalg improvements
    * scipy.sparse improvements
    * scipy.special improvements
    * scipy.sparse.csgraph improvements
    * scipy.stats improvements
  - Deprecated features
  - Backwards incompatible changes
    * scipy.ndimage
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  - Authors
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SciPy 0.15.0 is the culmination of 6 months of hard work. It contains several new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.16.x branch, and on adding new features on the master branch.

This release requires Python 2.6, 2.7 or 3.2-3.4 and NumPy 1.5.1 or greater.

3.14.1 New features
Linear Programming Interface

The new function `scipy.optimize.linprog` provides a generic linear programming similar to the way `scipy.optimize.minimize` provides a generic interface to nonlinear programming optimizers. Currently the only method supported is `simplex` which provides a two-phase, dense-matrix-based simplex algorithm. Callbacks functions are supported, allowing the user to monitor the progress of the algorithm.

Differential evolution, a global optimizer

A new `scipy.optimize.differential_evolution` function has been added to the `optimize` module. Differential Evolution is an algorithm used for finding the global minimum of multivariate functions. It is stochastic in nature (does not use gradient methods), and can search large areas of candidate space, but often requires larger numbers of function evaluations than conventional gradient based techniques.

scipy.signal improvements

The function `scipy.signal.max_len_seq` was added, which computes a Maximum Length Sequence (MLS) signal.

scipy.integrate improvements

It is now possible to use `scipy.integrate` routines to integrate multivariate ctypes functions, thus avoiding callbacks to Python and providing better performance.

scipy.linalg improvements

The function `scipy.linalg.orthogonal_procrustes` for solving the procrustes linear algebra problem was added.

BLAS level 2 functions `her`, `syr`, `her2` and `syr2` are now wrapped in `scipy.linalg`.

scipy.sparse improvements

`scipy.sparse.linalg.svds` can now take a `LinearOperator` as its main input.

scipy.special improvements

Values of ellipsoidal harmonic (i.e. Lame) functions and associated normalization constants can be now computed using `ellip_harm`, `ellip_harm_2`, and `ellip_normal`.

New convenience functions `entr`, `rel_entr`, `kl_div`, `huber`, and `pseudo_huber` were added.

scipy.sparse.cgraph improvements

Routines `reverse_cuthill_mckee` and `maximum_bipartite_matching` for computing reorderings of sparse graphs were added.

scipy.stats improvements

Added a Dirichlet multivariate distribution, `scipy.stats.dirichlet`.

The new function `scipy.stats.median_test` computes Mood’s median test.

The new function `scipy.stats.combine_pvalues` implements Fisher’s and Stouffer’s methods for combining p-values.

`scipy.stats.describe` returns a namedtuple rather than a tuple, allowing users to access results by index or by name.
3.14.2 Deprecated features

The `scipy.weave` module is deprecated. It was the only module never ported to Python 3.x, and is not recommended to be used for new code - use Cython instead. In order to support existing code, `scipy.weave` has been packaged separately: https://github.com/scipy/weave. It is a pure Python package, and can easily be installed with `pip install weave`.

`scipy.special.bessel_diff_formula` is deprecated. It is a private function, and therefore will be removed from the public API in a following release.

`scipy.stats.nanmean`, `nanmedian` and `nanstd` functions are deprecated in favor of their numpy equivalents.

3.14.3 Backwards incompatible changes

**scipy.ndimage**

The functions `scipy.ndimage.minimum_positions`, `scipy.ndimage.maximum_positions` and `scipy.ndimage.extrema` return positions as ints instead of floats.

**scipy.integrate**

The format of banded Jacobians in `scipy.integrate.ode` solvers is changed. Note that the previous documentation of this feature was erroneous.

3.14.4 Authors

- Abject +
- Ankit Agrawal +
- Sylvain Bellemare +
- Matthew Brett
- Christian Brodbeck
- Christian Brueffer
- Lars Buitinck
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- Pierre de Buyl +
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- Thomas A Caswell
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- Björn Dahlgren +
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- Jesse Engel +
• Rob Falck +
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• Jaime Fernandez del Rio +
• Clark Fitzgerald +
• Tom Flannaghan +
• Chad Fulton +
• Jochen Garcke +
• François Garillot +
• André Gaul
• Christoph Gohlke
• Ralf Gommers
• Alex Griffing
• Blake Griffith
• Olivier Grisel
• Charles Harris
• Trent Hauck +
• Ian Henriksen +
• Jinhyok Heo +
• Matt Hickford +
• Andreas Hilboll
• Danilo Horta +
• David Menéndez Hurtado +
• Gert-Ludwig Ingold
• Thouis (Ray) Jones
• Chris Kerr +
• Carl Kleffner +
• Andreas Kloeckner
• Thomas Kluyver +
• Adrian Kretz +
• Johannes Kulick +
• Eric Larson
• Brianna Laugher +
• Denis Laxalde
• Antony Lee +
• Gregory R. Lee +
• Brandon Liu
• Alex Loew +
• Loïc Estèye +
• Jaakko Luttinen +
• Benny Malengier
• Tobias Megies +
• Sturla Molden
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• Brett R. Murphy +
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• Maximilian Singh +
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• Benda Xu +
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• Tiziano Zito +

A total of 99 people contributed to this release. People with a “+” by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed

• #1431: ellipk(x) extending its domain for x<0 (Trac #904)
• #1727: consistency of std interface (Trac #1200)
• #1851: Shape parameter negated in genextreme (relative to R, MATLAB,...
• #1889: interp2d is weird (Trac #1364)
• #2188: splev gives wrong values or crashes outside of support when der...
• #2343: scipy.interpolate’s splrep function fails with certain combinations...
• #2669: .signal.lti.sys.ss2tf should only apply to MISO systems in current...
• #2911: interpolate.splder() failure on Fedora
• #3171: future of weave in scipy
• #3176: Suggestion to improve error message in scipy.integrate.odeint
• #3198: pdf() and logpdf() methods for scipy.stats.gaussian_kde
• #3318: Travis CI is breaking on test(“full”)
• #3329: scipy.stats.scoreatpercentile backward-incompatible change not...
• #3362: Reference cycle in scipy.sparse.linalg.eigs with shift-invert...
• #3364: BUG: linalg.hessenberg broken (wrong results)
• #3376: stats f_oneway needs floats
• #3379: Installation of scipy 0.13.3 via zc.buildout fails
• #3403: hierarchy.linkage raises an ugly exception for a compressed 2x2...
• #3422: optimize.curve_fit() handles NaN by returning all parameters...
• #3457: linalg.fractional_matrix_power has no docstring
• #3469: DOC: ndimage.find_object ignores zero-values
• #3491: optimize.leastsq() documentation should mention it does not work...
• #3499: cluster.vq.whiten return nan for all zeros column in observations
• #3503: minimize attempts to do vector addition when numpy arrays are...
• #3508: exponweib.logpdf fails for valid parameters
• #3509: libatlas3-base-dev does not exist
• #3550: BUG: anomalous values computed by special.ellipkinc
• #3555: scipy.ndimage positions are float instead of int
• #3557: UnivariateSpline.__call__ should pass all relevant args through...
• #3569: No license statement for test data imported from boost?
• #3576: mstats test failure (too sensitive?)
• #3579: Errors on scipy 0.14.x branch using MKL, Ubuntu 14.04 x86_64
• #3580: Operator overloading with sparse matrices
• #3587: Wrong alphabetical order in continuous statistical distribution...
• #3596: scipy.signal.fftconvolve no longer threadsafe
• #3623: BUG: signal.convolve takes longer than it needs to
• #3655: Integer returned from integer data in scipy.signal.periodogram...
• #3662: Travis failure on Numpy 1.5.1 (not reproducible?)
• #3668: dendogram(orientation='foo')
• #3669: KroghInterpolator doesn’t pass through points
• #3672: Inserting a knot in a spline
• #3682: misleading documentation of scipy.optimize.curve_fit
• #3699: BUG?: minor problem with scipy.signal.lfilter w/initial conditions
• #3700: Inconsistent exceptions raised by scipy.io.loadmat
• #3703: TypeError for RegularGridInterpolator with big-endian data
• #3714: Misleading error message in eigsh: k must be between 1 and rank(A)-1
• #3720: coo_matrix.setdiag() fails
• #3740: Scipy.Spatial.KdTree (Query) Return Type?
• #3761: Invalid result from scipy.special.btdtri
• #3784: DOC - Special Functions - Drum example fix for higher modes
• #3785: minimize() should have friendlier args=
• #3787: BUG: signal: Division by zero in lombscargle
• #3800: BUG: scipy.sparse.csgraph.shortest_path overwrites input matrix
• #3817: Warning in calculating moments from Binomial distribution for...
• #3821: review scipy usage of np.ma.is_masked
• #3829: Linear algebra function documentation doesn’t mention default...
• #3830: A bug in Docstring of scipy.linalg.eig
• #3844: Issue with shape parameter returned by genextreme
• #3858: “ImportError: No module named Cython.Compiler.Main” on install
• #3876: savgol_filter not in release notes and has no versionadded
• #3884: scipy.stats.kendalltau empty array error
• #3895: ValueError: illegal value in 12-th argument of internal gesdd...
Pull requests

- #3109: ENH Added Fisher’s method and Stouffer’s Z-score method
- #3225: Add the limiting distributions to generalized Pareto distribution...
- #3262: Implement back end of faster multivariate integration
- #3266: ENH: signal: add type=False as parameter for periodogram and...
- #3273: Add PEP8 check to Travis-CI
- #3342: ENH: scipy.special information theory functions
- #3396: ENH: improve stats.nanmedian more by assuming nans are rare
- #3398: Added two wrappers to the gaussian_kde class.
- #3405: BUG: cluster linkage array conversion to double dtype
- #3407: MAINT: use assert_warns instead of a more complicated mechanism
- #3409: ENH: change to use array view in signal/__peak_finding.py
- #3416: Issue 3376 : stats f_oneway needs floats
- #3419: BUG: tools: Fix list of FMA instructions in detect_cpu_extensions_wine.py
- #3420: DOC: stats: Add ‘entropy’ to the stats package-level documentation.
- #3429: BUG: close intermediate file descriptor right after it is used...
- #3430: MAINT: Fix some cython variable declarations to avoid warnings...
- #3433: Correcting the normalization of chebwin window function
- #3435: Add more precise link to R’s quantile documentation
- #3446: ENH: scipy.optimize - adding differential_evolution
- #3450: MAINT: remove unused function scipy.stats.mstats_basic._kolmog1
• #3458: Reworked version of PR-3084 (mstats-stats comparison)
• #3462: MAINT: Returning a warning for low attenuation values of chebwin...
• #3463: DOC: linalg: Add examples to functions in matfuncs.py
• #3477: ENH: sparse: release GIL in sparsertools routines
• #3480: DOC: Add more details to deconvolve docstring
• #3484: BLD: fix Qhull build issue with MinGW-w64. Closes gh-3237.
• #3498: MAINT: io: remove old warnings from idl.py
• #3504: BUG: cluster.vq.whiten returns nan or inf when std==0
• #3510: MAINT: stats: Reimplement the pdf and logpdf methods of exponweib.
• #3512: Fix PEP8 errors showing up on TravisCI after pep8 1.5 release
• #3514: DOC: libatlas3-base-dev seems to have never been a thing
• #3516: DOC improve scipy.sparse docstrings
• #3517: ENH: speed-up ndimage.filters.min(max)imum_filter1d
• #3518: Issues in scipy.misc.logsumexp
• #3526: DOC: graphical example for cwt, and use a more interesting signal
• #3527: ENH: Implement min(max)imum_filter1d using the MINLIST algorithm
• #3537: STY: reduce number of C compiler warnings
• #3540: DOC: linalg: add docstring to fractional_matrix_power
• #3542: kde.py Doc Typo
• #3545: BUG: stats: stats.levy.cdf with small arguments loses precision.
• #3547: BUG: special: erfcinv with small arguments loses precision.
• #3553: DOC: Convolve examples
• #3561: FIX: in ndimage.measurements return positions as int instead...
• #3564: Fix test failures with numpy master. Closes gh-3554
• #3565: ENH: make interp2d accept unsorted arrays for interpolation.
• #3566: BLD: add numpy requirement to metadata if it can’t be imported.
• #3567: DOC: move matfuncs docstrings to user-visible functions
• #3574: Fixes multiple bugs in mstats.theilslopes
• #3577: TST: decrease sensitivity of an mstats test
• #3585: Cleanup of code in scipy.constants
• #3589: BUG: sparse: allow operator overloading
• #3594: BUG: lobpcg returned wrong values for small matrices (n < 10)
• #3598: MAINT: fix coverage and coveralls
• #3599: MAINT: symeig – now that’s a name I’ve not heard in a long time
• #3602: MAINT: clean up the new optimize.linprog and add a few more tests
• #3607: BUG: integrate: Fix some bugs and documentation errors in the...
- #3609: MAINT integrate/odepack: kill dead Fortran code
- #3616: FIX: Invalid values
- #3617: Sort netcdf variables in a Python-3 compatible way
- #3622: DOC: Added 0.15.0 release notes entry for linprog function.
- #3625: Fix documentation for cKDTree.sparse_distance_matrix
- #3626: MAINT: linalg.orth memory efficiency
- #3627: MAINT: stats: A bit of clean up
- #3628: MAINT: signal: remove a useless function from wavelets.py
- #3632: ENH: stats: Add Mood’s median test.
- #3636: MAINT: cluster: some clean up
- #3638: DOC: docstring of optimize.basinhopping confuses singular and...
- #3639: BUG: change ddof default to 1 in mstats.sem, consistent with...
- #3640: Weave: deprecate the module and disable slow tests on TravisCI
- #3641: ENH: Added support for date attributes to io.arff.arffread
- #3644: MAINT: stats: remove superfluous alias in mstats_basic.py
- #3646: ENH: adding sum_duplicates method to COO sparse matrix
- #3647: Fix for #3596: Make fftconvolve threadsafe
- #3650: BUG: sparse: smarter random index selection
- #3652: fix wrong option name in power_divergence docsstring example
- #3654: Changing EPD to Canopy
- #3657: BUG: signal.welch: ensure floating point dtype regardless of...
- #3660: TST: mark a test as known fail
- #3661: BLD: ignore pep8 E302 (expected 2 blank lines, found 1)
- #3663: BUG: fix leaking errstate, and ignore invalid= errors in a test
- #3664: BUG: correlate was extremely slow when in2.size > in1.size
- #3667: ENH: Adds default params to pdfs of multivariate_norm
- #3670: ENH: Small speedup of FFT size check
- #3671: DOC: adding differential_evolution function to 0.15 release notes
- #3673: BUG: interpolate/fitpack: arguments to fortran routines may not...
- #3674: Add support for appending to existing netcdf files
- #3681: Speed up test(‘full’), solve Travis CI timeout issues
- #3683: ENH: cluster: rewrite and optimize vq in Cython
- #3684: Update special docs
- #3688: Spacing in special docstrings
- #3692: ENH: scipy.special: Improving sph_harm function
- #3693: Update refguide entries for signal and fftpack
• #3695: Update continuous.rst
• #3696: ENH: check for valid ‘orientation’ kwarg in dendrogram()
• #3701: make ‘a’ and ‘b’ coefficients atleast_1d array in filtfilt
• #3702: BUG: cluster: _vq unable to handle large features
• #3704: BUG: special: ellip(k,e)inc nan and double expected value
• #3707: BUG: handle fill_value dtype checks correctly in RegularGridInterpolator
• #3708: Reraise exception on failure to read mat file.
• #3709: BUG: cast ‘x’ to correct dtype in KroghInterpolator._evaluate
• #3712: ENH: cluster: reimplement the update-step of K-means in Cython
• #3713: FIX: Check type of lfiltic
• #3718: Changed INSTALL file extension to rst
• #3719: address svds returning nans for zero input matrix
• #3722: MAINT: spatial: static, unused code, sqrt(squeuclidean)
• #3725: ENH: use numpys nanmedian if available
• #3727: TST: add a new fixed_point test and change some test function...
• #3731: BUG: fix romb in scipy.integrate.quadrature
• #3734: DOC: simplify examples with semilogx
• #3735: DOC: Add minimal docstrings to lti.impulse/step
• #3736: BUG: cast pchip arguments to floats
• #3744: stub out inherited methods of Akima1DInterpolator
• #3746: DOC: Fix formatting for Raises section
• #3748: ENH: Added discrete Lyapunov transformation solve
• #3750: Enable automated testing with Python 3.4
• #3751: Reverse Cuthill-McKee and Maximum Bipartite Matching reorderings...
• #3759: MAINT: avoid indexing with a float array
• #3762: TST: filter out RuntimeWarning in vq tests
• #3766: TST: cluster: some cleanups in test_hierarchy.py
• #3767: ENH/BUG: support negative m in elliptic integrals
• #3769: ENH: avoid repeated matrix inverse
• #3770: BUG: signal: In lfilter_zi, b was not rescaled correctly when...
• #3772: STY avoid unnecessary transposes in csr_matrix.getcol/row
• #3773: ENH: Add ext parameter to UnivariateSpline call
• #3774: BUG: in integrate/quadpack.h, put all declarations before statements.
• #3779: Incbet fix
• #3788: BUG: Fix lombscargle ZeroDivisionError
• #3791: Some maintenance for doc builds
• #3795: scipy.special.legendre docstring
• #3796: TYPO: sheroidal -> spheroidal
• #3801: BUG: shortest_path overwrite
• #3803: TST: lombscargle regression test related to atan vs atan2
• #3809: ENH: orthogonal procrustes solver
• #3811: ENH: scipy.special, Implemented Ellipsoidal harmonic function:
• #3819: BUG: make a fully connected csgraph from an ndarray with no zeros
• #3820: MAINT: avoid spurious warnings in binom(n, p=0).mean() etc
• #3825: Don’t claim scipy.cluster does distance matrix calculations.
• #3827: get and set diagonal of coo_matrix, and related csgraph laplacian...
• #3832: DOC: Minor additions to integrate/nquad docstring.
• #3845: Bug fix for #3842: Bug in scipy.optimize.line_search
• #3848: BUG: edge case where the covariance matrix is exactly zero
• #3850: DOC: typo
• #3851: DOC: document default argument values for some arpack functions
• #3860: DOC: sparse: add the function ‘find’ to the module-level docstring
• #3861: BUG: Removed unnecessary storage of args as instance variables...
• #3862: BUG: signal: fix handling of multi-output systems in ss2tf.
• #3865: Feature request: ability to read heterogeneous types in FortranFile
• #3866: MAINT: update pip wheelhouse for installs
• #3871: MAINT: linalg: get rid of calc_lwork.f
• #3872: MAINT: use scipy.linalg instead of np.dual
• #3873: BLD: show a more informative message if Cython wasn’t installed.
• #3874: TST: cluster: cleanup the hierarchy test data
• #3877: DOC: Savitzky-Golay filter version added
• #3878: DOC: move versionadded to notes
• #3879: small tweaks to the docs
• #3881: FIX incorrect sorting during fancy assignment
• #3885: kendalltau function now returns a nan tuple if empty arrays used...
• #3886: BUG: fixing linprog’s kwarg order to match docs
• #3888: BUG: optimize: In __linprog_simplex, handle the case where the...
• #3891: BUG: stats: Fix ValueError message in chi2_contingency.
• #3892: DOC: sparse.linalg: Fix lobpcg docstring.
• #3894: DOC: stats: Assorted docstring edits.
• #3896: Fix 2 mistakes in MatrixMarket format parsing
• #3897: BUG: associated Legendre function of second kind for 1<x<1.0001
• #3899: BUG: fix undefined behavior in alngam
• #3906: MAINT/DOC: Whitespace tweaks in several docstrings.
• #3907: TST: relax bounds of interpolate test to accomodate rounding...
• #3909: MAINT: Create a common version of count_nonzero for compatibility...
• #3910: Fix a couple of test errors in master
• #3911: Use MathJax for the html docs
• #3914: Rework the _roots functions and document them.
• #3916: Remove all linpack_lite code and replace with LAPACK routines
• #3917: splines, constant extrapolation
• #3918: DOC: tweak the rv_discrete docstring example
• #3919: Quadrature speed-up: scipy.special.orthogonal.p_roots with cache
• #3920: DOC: Clarify docstring for sigma parameter for curve_fit
• #3922: Fixed Docstring issues in linprog (Fixes #3905).
• #3924: Coerce args into tuple if necessary.
• #3926: DOC: Surround stats class methods in docstrings with backticks.
• #3927: Changed doc for rombs’s dx parameter to int.
• #3928: check FITPACK conditions in LSQUnivariateSpline
• #3929: Added a warning about leastsq using with NaNs.
• #3930: ENH: optimize: curve_fit now warns if pcov is undetermined
• #3932: Clarified the k > n case.
• #3933: DOC: remove import scipy as sp abbreviation here and there
• #3936: Add license and copyright holders to test data imported from...
• #3938: DOC: Corrected documentation for return types.
• #3939: DOC: fitpack: add a note about Sch-W conditions to splrep docstring
• #3940: TST: integrate: Remove an invalid test of odeint.
• #3942: FIX: Corrected error message of eigsh.
• #3943: ENH: release GIL for filter and interpolation of ndimage
• #3944: FIX: Raise value error if window data-type is unsupported
• #3946: Fixed signal.get_window with unicode window name
• #3947: MAINT: some docstring fixes and style cleanups in stats.mstats
• #3949: DOC: fix a couple of issues in stats docstrings.
• #3950: TST: sparse: remove known failure that doesn’t fail
• #3951: TST: switch from Rackspace wheelhouse to numpy/cython source...
• #3952: DOC: stats: Small formatting correction to the ‘chi’ distribution...
• #3953: DOC: stats: Several corrections and small additions to docstrings.
• #3955: signal.__init__.py: remove duplicated get_window entry
• #3959: TST: sparse: more “known failures” for DOK that don’t fail
• #3960: BUG: io.netcdf: do not close mmap if there are references left...
• #3965: DOC: Fix a few more sphinx warnings that occur when building...
• #3966: DOC: add guidelines for using test generators in HACKING
• #3968: BUG: sparse.linalg: make Inv objects in arpack garbage-collectable...
• #3971: Remove all linpack_lite code and replace with LAPACK routines
• #3972: fix typo in error message
• #3973: MAINT: better error message for multivariate normal.
• #3981: turn the cryptically named scipy.special information theory functions...
• #3984: Wrap her, syr, her2, syr2 blas routines
• #3990: improve UnivariateSpline docs
• #3991: ENH: stats: return namedtuple for describe output
• #3993: DOC: stats: percentileofscore references np.percentile
• #3997: BUG: linalg: pascal(35) was incorrect: last element overflowed...
• #3998: MAINT: use isMaskedArray instead of is_masked to check type
• #3999: TST: test against all of boost data files.
• #4000: BUG: stats: Fix edge-case handling in a few distributions.
• #4003: ENH: using python’s warnings instead of prints in fitpack.
• #4004: MAINT: optimize: remove a couple unused variables in zeros.c
• #4006: BUG: Fix C90 compiler warnings in _NI_MinOrMaxFilter1D
• #4007: MAINT/DOC: Fix spelling of ‘decomposition’ in several files.
• #4008: DOC: stats: Split the descriptions of the distributions in the...
• #4015: TST: logsumexp regression test
• #4016: MAINT: remove some inf-related warnings from logsumexp
• #4020: DOC: stats: split the whitespace in docstrings of several distributions
• #4023: Exactly one space required before assignments
• #4024: In dendrogram(): Correct an argument name and a grammar issue...
• #4041: BUG: misc: Ensure that the ‘size’ argument of PIL’s ‘resize’...
• #4049: BUG: Return of _logpmf
• #4051: BUG: expm of integer matrices
• #4052: ENH: integrate: odeint: Handle exceptions in the callback functions.
• #4053: BUG: stats: Refactor argument validation to avoid a unicode issue.
• #4057: Added newline to scipy.sparse.linalg.svds documentation for correct...
• #4058: MAINT: stats: Add note about change to scoreatpercentile in release...
• #4059: ENH: interpolate: Allow splev to accept an n-dimensional array.
• #4064: Documented the return value for scipy.signal.find_peaks_cwt
• #4074: ENH: Support LinearOperator as input to svds
• #4084: BUG: Match exception declarations in scipy/io/matlab/strems.pyx...
• #4091: DOC: special: more clear instructions on how to evaluate polynomials
• #4105: BUG: Workaround for SGEMV segfault in Accelerate
• #4107: DOC: get rid of ‘import *’ in examples
• #4113: DOC: fix typos in distance.yule
• #4114: MAINT C fixes
• #4117: deprecate nanmean, nanmedian and nanstd in favor of their numpy...
• #4126: scipy.io.idl: support description records and fix bug with null...
• #4131: ENH: release GIL in more ndimage functions
• #4132: MAINT: stats: fix a typo [skip ci]
• #4145: DOC: Fix documentation error for nc chi-squared dist
• #4150: Fix _nd_image.geometric_transform endianness bug
• #4153: MAINT: remove use of deprecated numpy API in lib/lapack/ f2py...
• #4156: MAINT: optimize: remove dead code
• #4159: MAINT: optimize: clean up Zeros code
• #4165: DOC: add missing special functions to __doc__
• #4172: DOC: remove misleading procrustes docstring line
• #4175: DOC: sparse: clarify CSC and CSR constructor usage
• #4177: MAINT: enable np.matrix inputs to solve_discrete_lyapunov
• #4179: TST: fix an intermittently failing test case for special.legendre
• #4181: MAINT: remove unnecessary null checks before free
• #4182: Ellipsoidal harmonics
• #4183: Skip Cython build in Travis-CI
• #4184: Pr 4074
• #4187: Pr/3923
• #4190: BUG: special: fix up ellip_harm build
• #4193: BLD: fix msvc compiler errors
• #4194: BUG: fix buffer dtype mismatch on win-amd64
• #4199: ENH: Changed scipy.stats.describe output from datalen to nobs
• #4201: DOC: add blas2 and nan* deprecations to the release notes
• #4243: TST: bump test tolerances

3.15 SciPy 0.14.1 Release Notes

SciPy 0.14.1 is a bug-fix release with no new features compared to 0.14.0.
3.15.1 Issues closed

- #3630: NetCDF reading results in a segfault
- #3631: SuperLU object not working as expected for complex matrices
- #3733: segfault from map_coordinates
- #3780: Segfault when using CSR/CSC matrix and uint32/uint64
- #3781: BUG: sparse: fix omitted types in sparsetools typemaps
- #3802: 0.14.0 API breakage: _gen generators are missing from scipy.stats.distributions API
- #3805: ndimage test failures with numpy 1.10
- #3812: == sometimes wrong on csr_matrix
- #3853: Many scipy.sparse test errors/failures with numpy 1.9.0b2
- #4084: fix exception declarations for Cython 0.21.1 compatibility
- #4093: BUG: fitpack: avoid a memory error in splev(x, tck, der=k)
- #4104: BUG: Workaroud SGEMV segfault in Accelerate (maintenance 0.14.x)
- #4143: BUG: fix ndimage functions for large data
- #4149: Bug in expm for integer arrays
- #4154: Backport gh-4041 for 0.14.1 (Ensure that the ‘size’ argument of PIL’s ‘resize’ method is a tuple)
- #4163: Backport #4142 (ZeroDivisionError in scipy.sparse.linalg.lsqr)
- #4164: Backport gh-4153 (remove use of deprecated numpy API in lib/lapack/ f2py wrapper)
- #4180: backport pil resize support tuple fix
- #4168: Lots of arpack test failures on windows 32 bits with numpy 1.9.1
- #4203: Matrix multiplication in 0.14.x is more than 10x slower compared...
- #4218: attempt to make ndimage interpolation compatible with numpy relaxed...
- #4225: BUG: off-by-one error in PPoly shape checks
- #4248: BUG: optimize: fix issue with incorrect use of closure for slsqp.

3.16 SciPy 0.14.0 Release Notes

Contents

- SciPy 0.14.0 Release Notes
  - New features
    * scipy.interpolate improvements
    * scipy.linalg improvements
    * scipy.optimize improvements
    * scipy.stats improvements
    * scipy.signal improvements
SciPy 0.14.0 is the culmination of 8 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.14.x branch, and on adding new features on the master branch.

This release requires Python 2.6, 2.7 or 3.2-3.4 and NumPy 1.5.1 or greater.

### 3.16.1 New features

**scipy.interpolate improvements**

A new wrapper function `scipy.interpolate.interpn` for interpolation on regular grids has been added. `interpn` supports linear and nearest-neighbor interpolation in arbitrary dimensions and spline interpolation in two dimensions.

Faster implementations of piecewise polynomials in power and Bernstein polynomial bases have been added as `scipy.interpolate.PPoly` and `scipy.interpolate.BPoly`. New users should use these in favor of `scipy.interpolate.PiecewisePolynomial`.

`scipy.interpolate.interp1d` now accepts non-monotonic inputs and sorts them. If performance is critical, sorting can be turned off by using the new `assume_sorted` keyword.

Functionality for evaluation of bivariate spline derivatives in `scipy.interpolate` has been added.

The new class `scipy.interpolate.Akima1DInterpolator` implements the piecewise cubic polynomial interpolation scheme devised by H. Akima.

Functionality for fast interpolation on regular, unevenly spaced grids in arbitrary dimensions has been added as `scipy.interpolate.RegularGridInterpolator`.

**scipy.linalg improvements**

The new function `scipy.linalg.dft` computes the matrix of the discrete Fourier transform.
A condition number estimation function for matrix exponential, `scipy.linalg.expm_cond`, has been added.

**scipy.optimize improvements**

A set of benchmarks for optimize, which can be run with `optimize.bench()`, has been added.

`scipy.optimize.curve_fit` now has more controllable error estimation via the `absolute_sigma` keyword.

Support for passing custom minimization methods to `optimize.minimize()` and `optimize.minimize_scalar()` has been added, currently useful especially for combining `optimize.basinhopping()` with custom local optimizer routines.

**scipy.stats improvements**

A new class `scipy.stats.multivariate_normal` with functionality for multivariate normal random variables has been added.

A lot of work on the `scipy.stats` distribution framework has been done. Moment calculations (skew and kurtosis mainly) are fixed and verified, all examples are now runnable, and many small accuracy and performance improvements for individual distributions were merged.

The new function `scipy.stats.anderson_ksamp` computes the k-sample Anderson-Darling test for the null hypothesis that k samples come from the same parent population.

**scipy.signal improvements**

`scipy.signal.iirfilter` and related functions to design Butterworth, Chebyshev, elliptical and Bessel IIR filters now all use pole-zero (“zpk”) format internally instead of using transformations to numerator/denominator format. The accuracy of the produced filters, especially high-order ones, is improved significantly as a result.

The Savitzky-Golay filter was added with the new functions `scipy.signal.savgol_filter` and `scipy.signal.savgol_coeffs`.

The new function `scipy.signal.vectorstrength` computes the vector strength, a measure of phase synchrony, of a set of events.

**scipy.special improvements**

The functions `scipy.special.boxcox` and `scipy.special.boxcox1p`, which compute the Box-Cox transformation, have been added.

**scipy.sparse improvements**

- Significant performance improvement in CSR, CSC, and DOK indexing speed.
- When using Numpy >= 1.9 (to be released in MM 2014), sparse matrices function correctly when given to arguments of `np.dot`, `np.multiply` and other ufuncs. With earlier Numpy and Scipy versions, the results of such operations are undefined and usually unexpected.
- Sparse matrices are no longer limited to $2^{31}$ nonzero elements. They automatically switch to using 64-bit index data type for matrices containing more elements. User code written assuming the sparse matrices use int32 as the index data type will continue to work, except for such large matrices. Code dealing with larger matrices needs to accept either int32 or int64 indices.

### 3.16.2 Deprecated features
The global minimization function `scipy.optimize.anneal` is deprecated. All users should use the `scipy.optimize.basinhopping` function instead.

`scipy.stats`

`randwcdf` and `randwppf` functions are deprecated. All users should use distribution-specific `rvs` methods instead.

Probability calculation aliases `zprob`, `fprob` and `ksprob` are deprecated. Use instead the `sf` methods of the corresponding distributions or the `special` functions directly.

`scipy.interpolate`

`PiecewisePolynomial` class is deprecated.

### 3.16.3 Backwards incompatible changes

`scipy.special.lpmn`

`lpmn` no longer accepts complex-valued arguments. A new function `clpmn` with uniform complex analytic behavior has been added, and it should be used instead.

`scipy.sparse.linalg`

Eigenvectors in the case of generalized eigenvalue problem are normalized to unit vectors in 2-norm, rather than following the LAPACK normalization convention.

The deprecated UMFPACK wrapper in `scipy.sparse.linalg` has been removed due to license and install issues. If available, `scikits.umfpack` is still used transparently in the `spsolve` and `factorized` functions. Otherwise, SuperLU is used instead in these functions.

`scipy.stats`

The deprecated functions `glm`, `oneway` and `cmedian` have been removed from `scipy.stats`.

`stats.scoreatpercentile` now returns an array instead of a list of percentiles.

`scipy.interpolate`

The API for computing derivatives of a monotone piecewise interpolation has changed: if `p` is a `PchipInterpolator` object, `p.derivative(der)` returns a callable object representing the derivative of `p`. For in-place derivatives use the second argument of the `__call__` method: `p(0.1, der=2)` evaluates the second derivative of `p` at `x=0.1`.

The method `p.derivatives` has been removed.

### 3.16.4 Other changes

### 3.16.5 Authors

- Marc Abramowitz +
- Anders Bache Borchersen +
- Vincent Arel-Bundock +
- Petr Baudis +
- Max Bolingbroke
• François Boulogne
• Matthew Brett
• Lars Buitinck
• Evgeni Burovski
• CJ Carey +
• Thomas A Caswell +
• Pawel Chojnacki +
• Phillip Cloud +
• Stefano Costa +
• David Cournapeau
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• Matthieu Dartiaiilh +
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• Christoph Gohlke
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• Alex Griffing
• Blake Griffith
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• Andreas Hilboll
• Kat Huang
• Gert-Ludwig Ingold
• James T. Webber +
• Dorota Jarecka +
• Todd Jennings +
• Thouis (Ray) Jones
• Juan Luis Cano Rodríguez
• ktritz +
• Jacques Kvam +
• Eric Larson +
• Justin Lavoie +
• Denis Laxalde
• Jussi Leinonen +
• lemonlaug +
• Tim Leslie
• Alain Leufroy +
• George Lewis +
• Max Linke +
• Brandon Liu +
• Benny Malengier +
• Matthias Kümmerer +
• Cimarron Mittelsteadt +
• Eric Moore
• Andrew Nelson +
• Niklas Hambüchen +
• Joel Nothman +
• Clemens Novak
• Emanuele Olivetti +
• Stefan Otte +
• peb +
• Josef Perktold
• pjwerneck
• poolio
• Jérôme Roy +
• Carl Sandrock +
• Andrew Sczesnak +
• Shauna +
• Fabrice Silva
• Daniel B. Smith
• Patrick Snape +
• Thomas Spura +
• Jacob Stevenson
• Julian Taylor
• Tomas Tomecek
• Richard Tsai
• Jacob Vanderplas
A total of 80 people contributed to this release. People with a “+” by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

**Issues closed**

- #1325: add custom axis keyword to dendrogram function in scipy.cluster.hierarchy...
- #1437: Wrong pochhammer symbol for negative integers (Trac #910)
- #1555: scipy.io.netcdf leaks file descriptors (Trac #1028)
- #1569: sparse matrix failed with element-wise multiplication using numpy.multiply()
- #1833: Sparse matrices are limited to 2^32 non-zero elements (Trac #1307)
- #1834: scipy.linalg.eig does not normalize eigenvector if B is given
- #1866: stats for invgamma (Trac #1340)
- #1886: stats.zipf floating point warnings (Trac #1361)
- #1887: Stats continuous distributions - floating point warnings (Trac...)
- #1897: scoreatpercentile() does not handle empty list inputs (Trac #1372)
- #1918: splint returns incorrect results (Trac #1393)
- #1949: kurtosistest fails in mstats with type error (Trac #1424)
- #2092: scipy.test leaves darwin27compiled_catalog, cpp and so files...
- #2106: stats ENH: shape parameters in distribution docstrings (Trac...)
- #2123: Bad behavior of sparse matrices in a binary ufunc (Trac #1598)
- #2152: Fix mmio/fromfile on gzip on Python 3 (Trac #1627)
- #2164: stats.rice.pdf(x, 0) returns nan (Trac #1639)
- #2169: scipy.optimize.fmin_bfgs not handling functions with boundaries...
- #2177: scipy.cluster.hierarchy.ClusterNode.pre_order returns IndexError...
- #2179: coo.todense() segfaults (Trac #1654)
- #2185: Precision of scipy.ndimage.gaussian_filter() limited (Trac #1660)
- #2186: scipy.stats.mstats.kurtosistest crashes on 1d input (Trac #1661)
- #2238: Negative p-value on hypergeom.cdf (Trac #1719)
- #2283: ascending order in interpolation routines (Trac #1764)
- #2288: mstats.kurtosistest is incorrectly converting to float, and fails...
- #2396: lpmn wrong results for |z| > 1 (Trac #1877)
- #2398: ss2tf returns num as 2D array instead of 1D (Trac #1879)
- #2406: linkage does not take Unicode strings as method names (Trac #1887)
- #2443: IIR filter design should not transform to tf representation internally
- #2572: class method solve of splu return object corrupted or falsely...
• #2667: stats endless loop
• #2671: stats.hypergeom documentation error in the note about pmf
• #2691: BUG scipy.linalg.lapack: potrf/ptroi interpret their ‘lower’
• #2721: Allow use of ellipsis in scipy.sparse slicing
• #2741: stats: deprecate and remove alias for special functions
• #2742: stats add rvs to rice distribution
• #2765: bugs stats entropy
• #2832: argrelextrema returns tuple of 2 empty arrays when no peaks found...
• #2861: scipy.stats.scoreatpercentile broken for vector per
• #2891: COBYLA successful termination when constraints violated
• #2919: test failure with the current master
• #2922: ndimage.percentile_filter ignores origin argument for multidimensional...
• #2938: Sparse/dense matrix inplace operations fail due to __numpy_ufunc__
• #2944: MacPorts builds yield 40Mb worth of build warnings
• #2945: FAIL: test_random_complex (test_basic.TestDet)
• #2947: FAIL: Test some trivial edge cases for savgol_filter()
• #2953: Scipy Delaunay triangulation is not oriented
• #2971: scipy.stats.mstats.winsorize documentation error
• #2980: Problems running what seems a perfectly valid example
• #2996: entropy for rv_discrete is incorrect?!
• #2998: Fix numpy version comparisons
• #3002: python setup.py install fails
• #3014: Bug in stats.fisher_exact
• #3037: scipy.optimize.curve_fit leads to unexpected behavior when input...
• #3047: mstats.ttest_rel axis=None, requires masked array
• #3059: BUG: Slices of sparse matrices return incorrect dtype
• #3063: range keyword in binned_statistics incorrect
• #3069: sinc
• #3086: standard error calculation inconsistent between ‘stats’ and ‘mstats’
• #3094: Add a perm function into scipy.misc and an enhancement of...
• #3111: scipy.sparse.[hv]stack don’t respect anymore the dtype parameter
• #3172: optimize.curve_fit uses different nomenclature from optimize.leastsq
• #3196: scipy.stats.mstats.gmean does not actually take dtype
• #3212: Dot product of csr_matrix causes segmentation fault
- #3227: ZeroDivisionError in broyden1 when initial guess is the right...
- #3238: lbfgsb output not suppressed by disp=0
- #3249: Sparse matrix min/max/etc don’t support axis=-1
- #3251: cdist performance issue with ‘sqeuclidean’ metric
- #3279: logm fails for singular matrix
- #3285: signal.chirp(method=’hyp’) disallows hyperbolic upsweep
- #3299: MEMORY LEAK: fmin_tnc
- #3330: test failures with the current master
- #3345: scipy and/or numpy change is causing tests to fail in another...
- #3363: splu does not work for non-vector inputs
- #3385: expit does not handle large arguments well
- #3395: specfun.f doesn’t compile with MinGW
- #3399: Error message bug in scipy.cluster.hierarchy.linkage
- #3404: interpolate._ppoly doesn’t build with MinGW
- #3412: Test failures in signal
- #3466: `scipy.sparse.csgraph.shortest_path` does not work on `scipy.sparse.csr_matrix` or `lil_matrix`

Pull requests

- #442: ENH: sparse: enable 64-bit index arrays & nnz > 2**31
- #2766: DOC: remove doc/seps/technology-preview.rst
- #2772: TST: stats: Added a regression test for stats.wilcoxon. Closes...
- #2778: Clean up stats._support, close statistics review issues
- #2792: BUG io: fix file descriptor closing for netcdf variables
- #2847: Rice distribution: extend to b=0, add an explicit rvs method.
- #2878: [stats] fix formulas for higher moments of dweibull distribution
- #2904: ENH: moments for the zipf distribution
- #2907: ENH: add coverage info with coveralls.io for Travis runs.
- #2932: BUG+TST: setdiag implementation for dia_matrix (Close #2931)...
- #2942: Misc fixes pointed out by Eclipse PyDev static code analysis
- #2946: ENH: allow non-monotonic input in interp1d
- #2986: BUG: runtests: chdir away from root when running tests
- #2987: DOC: linAlg: don’t recommend np.linalg.norm
- #2992: ENH: Add “limit” parameter to dijkstra calculation
- #2995: ENH: Use int shape
- #3006: DOC: stats: add a log base note to the docstring
- #3007: DEP: stats: Deprecate randwppf and randwcdf
• #3008: Fix mstats.kurtosistest, and test coverage for skewtest/normaltest
• #3009: Minor reST typo
• #3010: Add scipy.optimize.Result to API docs
• #3012: Corrects documentation error
• #3052: PEP-8 conformance improvements
• #3064: Binned statistic
• #3068: Fix Issue #3067 fix cumtrapz that was raising an exception when...
• #3073: Arff reader with nominal value of 1 character
• #3074: Some maintenance work
• #3080: Review and clean up all Box-Cox functions
• #3083: Bug: should return 0 if no regions found
• #3085: BUG: Use zpk in IIR filter design to improve accuracy
• #3101: refactor stats tests a bit
• #3112: ENH: implement Akima interpolation in 1D
• #3123: MAINT: an easier way to make ranges from slices
• #3124: File object support for imread and imsave
• #3126: pep8ify stats/distributions.py
• #3134: MAINT: split distributions.py into three files
• #3138: clean up tests for discrete distributions
• #3155: special: handle the edge case lambda=0 in pdtr, pdtrc and pdtrik
• #3156: Rename optimize.Result to OptimizeResult
• #3166: BUG: make curve_fit() work with array_like input. Closes gh-3037.
• #3170: Fix numpy version checks
• #3175: use numpy sinc
• #3177: Update numpy version warning, remove oldnumeric import
• #3178: DEP: remove deprecated umfpack wrapper. Closes gh-3002.
• #3179: DOC: add BPoly to the docs
• #3180: Suppress warnings when running stats.test()
• #3181: altered sem func in mstats to match stats
• #3182: Make weave tests behave
• #3183: ENH: Add k-sample Anderson-Darling test to stats module
• #3186: Fix stats.scoreatpercentile
• #3187: DOC: make curve_fit nomenclature same as leastsq
• #3201: Added axis keyword to dendrogram function
• #3207: Make docstring examples in stats.distributions docstrings runnable
• #3218: BUG: integrate: Fix banded jacobian handling in the “vode” and...
3.16. SciPy 0.14.0 Release Notes

- #3222: BUG: limit input ranges in special.nctdtr
- #3223: Fix test errors with numpy master
- #3224: Fix int32 overflows in sparsetools
- #3228: DOC: tf2ss zpk2ss note controller canonical form
- #3234: Add See Also links and Example graphs to filter design *ord functions
- #3235: Updated the buttord function to be consistent with the other...
- #3239: correct doc for pchip interpolation
- #3240: DOC: fix ReST errors in the BPoly docstring
- #3241: RF: check write attr of fileobject without writing
- #3243: a bit of maintanence work in stats
- #3245: BUG/ENH: stats: make frozen distributions hold separate instances
- #3247: ENH function to return nnz per row/column in some sparse matrices
- #3248: ENH much more efficient sparse min/max with axis
- #3252: Fast sqeuclidean
- #3253: FIX support axis=-1 and -2 for sparse reduce methods
- #3254: TST tests for non-canonical input to sparse matrix operations
- #3272: BUG: sparse: fix bugs in dia_matrix.setdiag
- #3278: Also generate a tar.xz when running paver sdist
- #3286: DOC: update 0.14.0 release notes.
- #3289: TST: remove insecure mktemp use in tests
- #3292: MAINT: fix a backwards incompatible change to stats.distributions.__all__
- #3293: ENH: signal: Allow upsweeps of frequency in the ‘hyperbolic’...
- #3302: ENH: add dtype arg to stats.mstats.gmean and stats.mstats.hmean
- #3307: DOC: add note about different ba forms in tf2zpk
- #3309: doc enhancements to scipy.stats.mstats.winsorize
- #3310: DOC: clarify matrix vs array in mmio docstrings
- #3314: BUG: fix scipy.io.mmread() of gzipped files under Python3
- #3323: ENH: Efficient interpolation on regular grids in arbitrary dimensions
- #3332: DOC: clean up scipy.special docs
- #3335: ENH: improve nanmedian performance
- #3347: BUG: fix use of np.max in stats.fisher_exact
- #3356: ENH: sparse: speed up LIL indexing + assignment via Cython
- #3357: Fix “imresize does not work with size = int”
- #3358: MAINT: rename AkimaInterpolator to Akima1DInterpolator
- #3366: WHT: sparse: reindent dsolve/*.c *.h
- #3367: BUG: sparse/dsolve: fix dense matrix fortran order bugs in superlu...
- #3369: ENH minimize, minimize_scalar: Add support for user-provided...
- #3371: scipy.stats.sigmaclip doesn’t appear in the html docs.
- #3373: BUG: sparse/dsolve: detect invalid LAPACK parameters in superlu...
- #3375: ENH: sparse/dsolve: make the L and U factors of splu and spilu...
- #3377: MAINT: make travis build one target against Numpy 1.5
- #3378: MAINT: fftpack: Remove the use of ‘import *’ in a couple test...
- #3381: MAINT: replace np.isinf(x) & (x>0) -> np.isposinf(x) to avoid...
- #3383: MAINT: skip float96 tests on platforms without float96
- #3384: MAINT: add pyflakes to Travis-CI
- #3386: BUG: stable evaluation of expit
- #3388: BUG: SuperLU: fix missing declaration of dlamch
- #3389: BUG: sparse: downcast 64-bit indices safely to intp when required
- #3390: BUG: nonlinear solvers are not confused by lucky guess
- #3391: TST: fix sparse test errors due to axis=-1,-2 usage in np.matrix.sum()
- #3392: BUG: sparse/lil: fix up Cython bugs in fused type lookup
- #3393: BUG: sparse/compressed: work around bug in np.unique in earlier...
- #3394: BUG: allow ClusterNode.pre_order() for non-root nodes
- #3400: BUG: cluster.linkage ValueError typo bug
- #3402: BUG: special: in specfun.f, replace the use of CMPLX with DCMPLX,...
- #3408: MAINT: sparse: Numpy 1.5 compatibility fixes
- #3410: MAINT: interpolate: fix blas defs in __ppoly
- #3411: MAINT: Numpy 1.5 fixes in interpolate
- #3413: Fix more test issues with older numpy versions
- #3414: TST: signal: loosen some error tolerances in the filter tests....
- #3415: MAINT: tools: automated close issue + pr listings for release...
- #3440: MAINT: wrap sparsetools manually instead via SWIG
- #3460: TST: open image file in binary mode
- #3467: BUG: fix validation in csgraph.shortest_path

### 3.17 SciPy 0.13.2 Release Notes

SciPy 0.13.2 is a bug-fix release with no new features compared to 0.13.1.

#### 3.17.1 Issues fixed
- 3096: require Cython 0.19, earlier versions have memory leaks in fused types
- 3079: ndimage.label fix swapped 64-bitness test
- 3108: optimize.fmin_slsqp constraint violation
3.18 SciPy 0.13.1 Release Notes

SciPy 0.13.1 is a bug-fix release with no new features compared to 0.13.0. The only changes are several fixes in ndimage, one of which was a serious regression in ndimage.label (Github issue 3025), which gave incorrect results in 0.13.0.

3.18.1 Issues fixed

- 3025: ndimage.label returns incorrect results in scipy 0.13.0
- 1992: ndimage.label return type changed from int32 to uint32
- 1992: ndimage.find_objects doesn’t work with int32 input in some cases

3.19 SciPy 0.13.0 Release Notes

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- SciPy 0.13.0 Release Notes
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    * scipy.integrate improvements
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      - BLAS level 3 functions
      - Matrix functions
    * scipy.optimize improvements
      - Trust-region unconstrained minimization algorithms
    * scipy.sparse improvements
      - Boolean comparisons and sparse matrices
      - CSR and CSC fancy indexing
    * scipy.sparse.linalg improvements
    * scipy.spatial improvements
    * scipy.signal improvements
    * scipy.special improvements
    * scipy.io improvements
      - Unformatted Fortran file reader
      - scipy.io.wavfile enhancements
    * scipy.interpolate improvements
SciPy 0.13.0 is the culmination of 7 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.13.x branch, and on adding new features on the master branch.

This release requires Python 2.6, 2.7 or 3.1-3.3 and NumPy 1.5.1 or greater. Highlights of this release are:

- support for fancy indexing and boolean comparisons with sparse matrices
- interpolative decompositions and matrix functions in the linalg module
- two new trust-region solvers for unconstrained minimization

### 3.19.1 New features

**scipy.integrate improvements**

**N-dimensional numerical integration**

A new function `scipy.integrate.nquad`, which provides N-dimensional integration functionality with a more flexible interface than `dblquad` and `tplquad`, has been added.

**dopri improvements**

The intermediate results from the `dopri` family of ODE solvers can now be accessed by a `solout` callback function.

**scipy.linalg improvements**

**Interpolative decompositions**

Scipy now includes a new module `scipy.linalg.interpolative` containing routines for computing interpolative matrix decompositions (ID). This feature is based on the ID software package by P.G. Martinsson, V. Rokhlin, Y. Shkolnisky, and M. Tygert, previously adapted for Python in the PymatrixId package by K.L. Ho.

**Polar decomposition**

A new function `scipy.linalg.polar`, to compute the polar decomposition of a matrix, was added.

**BLAS level 3 functions**

The BLAS functions `symm`, `syrk`, `syr2k`, `hemm`, `herk` and `her2k` are now wrapped in `scipy.linalg`.
Matrix functions
Several matrix function algorithms have been implemented or updated following detailed descriptions in recent papers of Nick Higham and his co-authors. These include the matrix square root (`sqrtm`), the matrix logarithm (`logm`), the matrix exponential (`expm`) and its Frechet derivative (`expm_frechet`), and fractional matrix powers (fractional_matrix_power).

scipy.optimize improvements

Trust-region unconstrained minimization algorithms
The `minimize` function gained two trust-region solvers for unconstrained minimization: `dogleg` and `trust-ncg`.

scipy.sparse improvements

Boolean comparisons and sparse matrices
All sparse matrix types now support boolean data, and boolean operations. Two sparse matrices $A$ and $B$ can be compared in all the expected ways $A < B$, $A \geq B$, $A \neq B$, producing similar results as dense NumPy arrays. Comparisons with dense matrices and scalars are also supported.

CSR and CSC fancy indexing
Compressed sparse row and column sparse matrix types now support fancy indexing with boolean matrices, slices, and lists. So where $A$ is a (CSC or CSR) sparse matrix, you can do things like:

```python
>>> A[A > 0.5] = 1  # since Boolean sparse matrices work
>>> A[:,2] = 2
>>> A[[1,2], 2] = 3
```

scipy.sparse.linalg improvements

The new function `onenormest` provides a lower bound of the 1-norm of a linear operator and has been implemented according to Higham and Tisseur (2000). This function is not only useful for sparse matrices, but can also be used to estimate the norm of products or powers of dense matrices without explicitly building the intermediate matrix.

The multiplicative action of the matrix exponential of a linear operator (`expm_multiply`) has been implemented following the description in Al-Mohy and Higham (2011).

Abstract linear operators (scipy.sparse.linalg.LinearOperator) can now be multiplied, added to each other, and exponentiated, producing new linear operators. This enables easier construction of composite linear operations.

scipy.spatial improvements

The vertices of a ConvexHull can now be accessed via the `vertices` attribute, which gives proper orientation in 2-D.

scipy.signal improvements

The cosine window function `scipy.signal.cosine` was added.

scipy.special improvements

New functions `scipy.special.xlogy` and `scipy.special.xlog1py` were added. These functions can simplify and speed up code that has to calculate $x \cdot \log(y)$ and give 0 when $x == 0$. 

3.19. SciPy 0.13.0 Release Notes
scipy.io improvements

Unformatted Fortran file reader
The new class `scipy.io.FortranFile` facilitates reading unformatted sequential files written by Fortran code.

scipy.io.wavfile enhancements
`scipy.io.wavfile.write` now accepts a file buffer. Previously it only accepted a filename.
`scipy.io.wavfile.read` and `scipy.io.wavfile.write` can now handle floating point WAV files.

scipy.interpolate improvements

B-spline derivatives and antiderivatives
`scipy.interpolate.splder` and `scipy.interpolate.splantider` functions for computing B-splines that represent derivatives and antiderivatives of B-splines were added. These functions are also available in the class-based FITPACK interface as `UnivariateSpline.derivative` and `UnivariateSpline.antiderivative`.

scipy.stats improvements

Distributions now allow using keyword parameters in addition to positional parameters in all methods.
The function `scipy.stats.power_divergence` has been added for the Cressie-Read power divergence statistic and goodness of fit test. Included in this family of statistics is the “G-test” (https://en.wikipedia.org/wiki/G-test).
`scipy.stats.mood` now accepts multidimensional input.
An option was added to `scipy.stats.wilcoxon` for continuity correction.
`scipy.stats.chisquare` now has an `axis` argument.
`scipy.stats.mstats.chisquare` now has `axis` and `ddof` arguments.

3.19.2 Deprecated features

expm2 and expm3
The matrix exponential functions `scipy.linalg.expm2` and `scipy.linalg.expm3` are deprecated. All users should use the numerically more robust `scipy.linalg.expm` function instead.

scipy.stats functions

`scipy.stats.oneway` is deprecated; `scipy.stats.f_oneway` should be used instead.

`scipy.stats glm` is deprecated. `scipy.stats.ttest_ind` is an equivalent function; more full-featured general (and generalized) linear model implementations can be found in statsmodels.

`scipy.stats.cmedian` is deprecated; `numpy.median` should be used instead.

3.19.3 Backwards incompatible changes

LIL matrix assignment
Assigning values to LIL matrices with two index arrays now works similarly as assigning into ndarrays:

```python
>>> x = lil_matrix((3, 3))
>>> x[[0,1,2],[0,1,2]] = [0,1,2]
>>> x.todense()
```
matrix([[ 0., 0., 0.],
         [ 0., 1., 0.],
         [ 0., 0., 2.]])

rather than giving the result:

```python
>>> x.todense()
matrix([[ 0., 1., 2.],
         [ 0., 1., 2.],
         [ 0., 1., 2.]])
```

Users relying on the previous behavior will need to revisit their code. The previous behavior is obtained by:

```python
x[numpy.ix_([0,1,2],[0,1,2])] = ....
```

### Deprecated `radon` function removed

The `misc.radon` function, which was deprecated in scipy 0.11.0, has been removed. Users can find a more full-featured `radon` function in scikit-image.

### Removed deprecated keywords `xa` and `xb` from `stats.distributions`

The keywords `xa` and `xb`, which were deprecated since 0.11.0, have been removed from the distributions in `scipy.stats`.

### Changes to MATLAB file readers / writers

The major change is that 1D arrays in numpy now become row vectors (shape 1, N) when saved to a MATLAB 5 format file. Previously 1D arrays saved as column vectors (N, 1). This is to harmonize the behavior of writing MATLAB 4 and 5 formats, and adapt to the defaults of numpy and MATLAB - for example `np.atleast_2d` returns 1D arrays as row vectors.

Trying to save arrays of greater than 2 dimensions in MATLAB 4 format now raises an error instead of silently reshaping the array as 2D.

`scipy.io.loadmat('afile')` used to look for `afile` on the Python system path (`sys.path`); now `loadmat` only looks in the current directory for a relative path filename.

### 3.19.4 Other changes

Security fix: `scipy.weave` previously used temporary directories in an insecure manner under certain circumstances.

Cython is now required to build unreleased versions of scipy. The C files generated from Cython sources are not included in the git repo anymore. They are however still shipped in source releases.

The code base received a fairly large PEP8 cleanup. A `tox pep8` command has been added; new code should pass this test command.

Scipy cannot be compiled with gfortran 4.1 anymore (at least on RH5), likely due to that compiler version not supporting entry constructs well.

### 3.19.5 Authors

This release contains work by the following people (contributed at least one patch to this release, names in alphabetical order):

- Jorge Cañardo Alastuey +
A total of 65 people contributed to this release. People with a “+” by their names contributed a patch for the first time.

3.20 SciPy 0.12.1 Release Notes

SciPy 0.12.1 is a bug-fix release with no new features compared to 0.12.0. The single issue fixed by this release is a security issue in `scipy.weave`, which was previously using temporary directories in an insecure manner under certain circumstances.
3.21 SciPy 0.12.0 Release Notes

SciPy 0.12.0 is the culmination of 7 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.12.x branch, and on adding new features on the master branch.

Some of the highlights of this release are:

- Completed QHull wrappers in scipy.spatial.
- cKDTree now a drop-in replacement for KDTree.
- A new global optimizer, basinhopping.
- Support for Python 2 and Python 3 from the same code base (no more 2to3).
This release requires Python 2.6, 2.7 or 3.1-3.3 and NumPy 1.5.1 or greater. Support for Python 2.4 and 2.5 has been dropped as of this release.

## 3.21.1 New features

**scipy.spatial improvements**

**cKDTree feature-complete**
Cython version of KDTree, cKDTree, is now feature-complete. Most operations (construction, query, query_ball_point, query_pairs, count_neighbors and sparse_distance_matrix) are between 200 and 1000 times faster in cKDTree than in KDTree. With very minor caveats, cKDTree has exactly the same interface as KDTree, and can be used as a drop-in replacement.

**Voronoi diagrams and convex hulls**

scipy.spatial now contains functionality for computing Voronoi diagrams and convex hulls using the Qhull library. (Delaunay triangulation was available since Scipy 0.9.0.)

**Delaunay improvements**
It's now possible to pass in custom Qhull options in Delaunay triangulation. Coplanar points are now also recorded, if present. Incremental construction of Delaunay triangulations is now also possible.

**Spectral estimators (scipy.signal)**

The functions `scipy.signal.periodogram` and `scipy.signal.welch` were added, providing DFT-based spectral estimators.

**scipy.optimize improvements**

**Callback functions in L-BFGS-B and TNC**

A callback mechanism was added to L-BFGS-B and TNC minimization solvers.

**Basin hopping global optimization (scipy.optimize.basinhopping)**

A new global optimization algorithm. Basin hopping is designed to efficiently find the global minimum of a smooth function.

**scipy.special improvements**

**Revised complex error functions**

The computation of special functions related to the error function now uses a new Faddeeva library from MIT which increases their numerical precision. The scaled and imaginary error functions `erfcx` and `erfi` were also added, and the Dawson integral `dawsn` can now be evaluated for a complex argument.

**Faster orthogonal polynomials**

Evaluation of orthogonal polynomials (the `eval_*` routines) in now faster in `scipy.special`, and their `out=` argument functions properly.

**scipy.sparse.linalg features**

- In `scipy.sparse.linalg.spsolve`, the `b` argument can now be either a vector or a matrix.
- `scipy.sparse.linalg.inv` was added. This uses `spsolve` to compute a sparse matrix inverse.
- `scipy.sparse.linalg.expm` was added. This computes the exponential of a sparse matrix using a similar algorithm to the existing dense array implementation in `scipy.linalg.expm`.

**Listing Matlab(R) file contents in scipy.io**

A new function `whosmat` is available in `scipy.io` for inspecting contents of MAT files without reading them to memory.
Documented BLAS and LAPACK low-level interfaces (scipy.linalg)

The modules `scipy.linalg.blas` and `scipy.linalg.lapack` can be used to access low-level BLAS and LAPACK functions.

Polynomial interpolation improvements (scipy.interpolate)

The barycentric, Krogh, piecewise and pchip polynomial interpolators in `scipy.interpolate` accept now an `axis` argument.

3.21.2 Deprecated features

`scipy.lib.lapack`

The module `scipy.lib.lapack` is deprecated. You can use `scipy.linalg.lapack` instead. The module `scipy.lib.blas` was deprecated earlier in Scipy 0.10.0.

`fblas` and `cblas`

Accessing the modules `scipy.linalg.fblas`, `cblas`, `flapack`, `clapack` is deprecated. Instead, use the modules `scipy.linalg.lapack` and `scipy.linalg.blas`.

3.21.3 Backwards incompatible changes

Removal of `scipy.io.save_as_module`

The function `scipy.io.save_as_module` was deprecated in Scipy 0.11.0, and is now removed.

Its private support modules `scipy.io.dumbdbm_patched` and `scipy.io.dumb_shelve` are also removed.

`axis` argument added to `scipy.stats.scoreatpercentile`

The function `scipy.stats.scoreatpercentile` has been given an `axis` argument. The default argument is `axis=None`, which means the calculation is done on the flattened array. Before this change, `scoreatpercentile` would act as if `axis=0` had been given. Code using `scoreatpercentile` with a multidimensional array will need to add `axis=0` to the function call to preserve the old behavior. (This API change was not noticed until long after the release of 0.12.0.)

3.21.4 Authors

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A total of 75 people contributed to this release. People with a “+” by their names contributed a patch for the first time.

3.22 SciPy 0.11.0 Release Notes
SciPy 0.11.0 is the culmination of 8 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. Highlights of this release are:

- A new module has been added which provides a number of common sparse graph algorithms.
- New unified interfaces to the existing optimization and root finding functions have been added.

All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Our development attention will now shift to bug-fix releases on the 0.11.x branch, and on adding new features on the master branch.

This release requires Python 2.4-2.7 or 3.1-3.2 and NumPy 1.5.1 or greater.

### 3.22.1 New features

**Sparse Graph Submodule**

The new submodule `scipy.sparse.csgraph` implements a number of efficient graph algorithms for graphs stored as sparse adjacency matrices. Available routines are:

- `connected_components` - determine connected components of a graph
- `laplacian` - compute the laplacian of a graph
• **shortest_path** - compute the shortest path between points on a positive graph

• **dijkstra** - use Dijkstra’s algorithm for shortest path

• **floyd_warshall** - use the Floyd-Warshall algorithm for shortest path

• **breadth_first_order** - compute a breadth-first order of nodes

• **depth_first_order** - compute a depth-first order of nodes

• **breadth_first_tree** - construct the breadth-first tree from a given node

• **depth_first_tree** - construct a depth-first tree from a given node

• **minimum_spanning_tree** - construct the minimum spanning tree of a graph

**scipy.optimize improvements**

The optimize module has received a lot of attention this release. In addition to added tests, documentation improvements, bug fixes and code clean-up, the following improvements were made:

- A unified interface to minimizers of univariate and multivariate functions has been added.
- A unified interface to root finding algorithms for multivariate functions has been added.
- The L-BFGS-B algorithm has been updated to version 3.0.

**Unified interfaces to minimizers**

Two new functions `scipy.optimize.minimize` and `scipy.optimize.minimize_scalar` were added to provide a common interface to minimizers of multivariate and univariate functions respectively. For multivariate functions, `scipy.optimize.minimize` provides an interface to methods for unconstrained optimization (`fmin`, `fmin_powell`, `fmin_cg`, `fmin_ncg`, `fmin_bfgs` and `anneal`) or constrained optimization (`fmin_l_bfgs_b`, `fmin_tnc`, `fmin_cobyla` and `fmin_slsqp`). For univariate functions, `scipy.optimize.minimize_scalar` provides an interface to methods for unconstrained and bounded optimization (`brent`, `golden`, `fminbound`). This allows for easier comparing and switching between solvers.

**Unified interface to root finding algorithms**

The new function `scipy.optimize.root` provides a common interface to root finding algorithms for multivariate functions, embedding `fsolve`, `leastsq` and `nonlin` solvers.

**scipy.linalg improvements**

**New matrix equation solvers**

Solvers for the Sylvester equation (`.scipy.linalg.solve_sylvester`, discrete and continuous Lyapunov equations (`.scipy.linalg.solve_lyapunov`, `.scipy.linalg.solve_discrete_lyapunov`) and discrete and continuous algebraic Riccati equations (`.scipy.linalg.solve_continuous_are`, `.scipy.linalg.solve_discrete_are`) have been added to `scipy.linalg`. These solvers are often used in the field of linear control theory.

**QZ and QR Decomposition**

It is now possible to calculate the QZ, or Generalized Schur, decomposition using `.scipy.linalg.qz`. This function wraps the LAPACK routines `sgges`, `dgges`, `cgges`, and `zgges`.

The function `.scipy.linalg.qr_multiply`, which allows efficient computation of the matrix product of Q (from a QR decomposition) and a vector, has been added.

**Pascal matrices**

A function for creating Pascal matrices, `.scipy.linalg.pascal`, was added.

**Sparse matrix construction and operations**

Two new functions, `.scipy.sparse.diags` and `.scipy.sparse.block_diag`, were added to easily construct diagonal and block-diagonal sparse matrices respectively.
scipy.sparse.csc_matrix and csr_matrix now support the operations \( \sin, \tan, \arcsin, \arctan, \sinh, \tanh, \arcsinh, \arctanh, \rint, \text{sign}, \expm1, \log1p, \deg2rad, \rad2deg, \text{floor}, \text{ceil} \) and \( \text{trunc} \). Previously, these operations had to be performed by operating on the matrices’ data attribute.

LSMR iterative solver

LSMR, an iterative method for solving (sparse) linear and linear least-squares systems, was added as scipy.sparse.linalg.lsmr.

Discrete Sine Transform

Bindings for the discrete sine transform functions have been added to scipy.fftpack.

scipy.interpolate improvements

For interpolation in spherical coordinates, the three classes scipy.interpolate.SmoothSphereBivariateSpline, scipy.interpolate.LSQSphereBivariateSpline, and scipy.interpolate.RectSphereBivariateSpline have been added.

Binned statistics (scipy.stats)

The stats module has gained functions to do binned statistics, which are a generalization of histograms, in 1-D, 2-D and multiple dimensions: scipy.stats.binned_statistic, scipy.stats.binned_statistic_2d and scipy.stats.binned_statistic_dd.

3.22.2 Deprecated features

scipy.sparse.cs_graph_components has been made a part of the sparse graph submodule, and renamed to scipy.sparse.csgraph.connected_components. Calling the former routine will result in a deprecation warning.

scipy.misc.radon has been deprecated. A more full-featured radon transform can be found in scikits-image.

scipy.io.save_as_module has been deprecated. A better way to save multiple Numpy arrays is the numpy.savez function.

The \( xa \) and \( xb \) parameters for all distributions in scipy.stats.distributions already weren’t used; they have now been deprecated.

3.22.3 Backwards incompatible changes

Removal of scipy.maxentropy

The scipy.maxentropy module, which was deprecated in the 0.10.0 release, has been removed. Logistic regression in scikits.learn is a good and modern alternative for this functionality.

Minor change in behavior of splev

The spline evaluation function now behaves similarly to interp1d for size-1 arrays. Previous behavior:

```python
>>> from scipy.interpolate import splev, splrep, interp1d
>>> x = [1,2,3,4,5]
>>> y = [4,5,6,7,8]
>>> tck = splrep(x, y)
>>> splev([1], tck)
4.
>>> splev(1, tck)
4.
```
Corrected behavior:

```python
>>> splev([1], tck)
array([ 4.1])
>>> splev(1, tck)
array(4.)
```

This affects also the `UnivariateSpline` classes.

**Behavior of `scipy.integrate.complex_ode`**

The behavior of the `y` attribute of `complex_ode` is changed. Previously, it expressed the complex-valued solution in the form:

```
z = ode.y[:2] + 1j * ode.y[1:2]
```

Now, it is directly the complex-valued solution:

```
z = ode.y
```

**Minor change in behavior of T-tests**

The T-tests `scipy.stats.ttest_ind`, `scipy.stats.ttest_rel` and `scipy.stats.ttest_1samp` have been changed so that `0 / 0` now returns NaN instead of 1.

**3.22.4 Other changes**

The SuperLU sources in `scipy.sparse.linalg` have been updated to version 4.3 from upstream.

The function `scipy.signal.bode`, which calculates magnitude and phase data for a continuous-time system, has been added.

The two-sample T-test `scipy.stats.ttest_ind` gained an option to compare samples with unequal variances, i.e. Welch’s T-test.

`scipy.misc.logsumexp` now takes an optional `axis` keyword argument.

**3.22.5 Authors**

This release contains work by the following people (contributed at least one patch to this release, names in alphabetical order):

- Jeff Armstrong
- Chad Baker
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• Martin Teichmann
• Matt Terry +
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• Jacob Vanderplas
• Patrick Varilly +
• Pauli Virtanen
SciPy Reference Guide, Release 1.2.0

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- Darryl Wally +
- Stefan van der Walt
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- David Warde-Farley +
- Warren Weckesser
- Sebastian Werk +
- Mike Wimmer +
- Tony S Yu +

A total of 55 people contributed to this release. People with a “+” by their names contributed a patch for the first time.

3.23 SciPy 0.10.1 Release Notes

Contents

- SciPy 0.10.1 Release Notes
  - Main changes
  - Other issues fixed

SciPy 0.10.1 is a bug-fix release with no new features compared to 0.10.0.

3.23.1 Main changes

The most important changes are:

1. The single precision routines of eigs and eigsh in scipy.sparse.linalg have been disabled (they internally use double precision now).

2. A compatibility issue related to changes in NumPy macros has been fixed, in order to make scipy 0.10.1 compile with the upcoming numpy 1.7.0 release.

3.23.2 Other issues fixed

- #835: stats: nan propagation in stats.distributions
- #1202: io: netcdf segfault
- #1531: optimize: make curve_fit work with method as callable.
- #1560: linalg: fixed mistake in eig_banded documentation.
- #1565: ndimage: bug in ndimage.variance
- #1457: ndimage: standard_deviation does not work with sequence of indexes
- #1562: cluster: segfault in linkage function
- #1568: stats: One-sided fisher_exact() returns $p < 1$ for 0 successful attempts
- #1575: stats: zscore and zmap handle the axis keyword incorrectly
3.24 SciPy 0.10.0 Release Notes

SciPy 0.10.0 is the culmination of 8 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a limited number of deprecations and backwards-incompatible changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.10.x branch, and on adding new features on the development master branch.

Release highlights:

- Support for Bento as optional build system.
- Support for generalized eigenvalue problems, and all shift-invert modes available in ARPACK.

This release requires Python 2.4-2.7 or 3.1- and NumPy 1.5 or greater.

3.24.1 New features

Bento: new optional build system

Scipy can now be built with Bento. Bento has some nice features like parallel builds and partial rebuilds, that are not possible with the default build system (distutils). For usage instructions see BENTO_BUILD.txt in the scipy top-level directory.
Currently Scipy has three build systems, distutils, numscons and bento. Numscons is deprecated and is planned and will likely be removed in the next release.

**Generalized and shift-invert eigenvalue problems in scipy.sparse.linalg**

The sparse eigenvalue problem solver functions `scipy.sparse.eigs/eigh` now support generalized eigenvalue problems, and all shift-invert modes available in ARPACK.

**Discrete-Time Linear Systems (scipy.signal)**

Support for simulating discrete-time linear systems, including `scipy.signal.dlsim`, `scipy.signal.dimpulse`, and `scipy.signal.dstep`, has been added to SciPy. Conversion of linear systems from continuous-time to discrete-time representations is also present via the `scipy.signal.cont2discrete` function.

**Enhancements to scipy.signal**

A Lomb-Scargle periodogram can now be computed with the new function `scipy.signal.lombscargle`. The forward-backward filter function `scipy.signal.filtfilt` can now filter the data in a given axis of an n-dimensional numpy array. (Previously it only handled a 1-dimensional array.) Options have been added to allow more control over how the data is extended before filtering. FIR filter design with `scipy.signal.firwin2` now has options to create filters of type III (zero at zero and Nyquist frequencies) and IV (zero at zero frequency).

**Additional decomposition options (scipy.linalg)**

A sort keyword has been added to the Schur decomposition routine (`scipy.linalg.schur`) to allow the sorting of eigenvalues in the resultant Schur form.

**Additional special matrices (scipy.linalg)**

The functions `hilbert` and `invhilbert` were added to `scipy.linalg`.

**Enhancements to scipy.stats**

- The one-sided form of Fisher’s exact test is now also implemented in `stats.fisher_exact`.
- The function `stats.chi2_contingency` for computing the chi-square test of independence of factors in a contingency table has been added, along with the related utility functions `stats.contingency.margins` and `stats.contingency.expected_freq`.

**Enhancements to scipy.special**

The functions `logit(p) = log(p/(1-p))` and `expit(x) = 1/(1+exp(-x))` have been implemented as `scipy.special.logit` and `scipy.special.expit` respectively.

**Basic support for Harwell-Boeing file format for sparse matrices**

Both read and write are support through a simple function-based API, as well as a more complete API to control number format. The functions may be found in `scipy.sparse.io`.

The following features are supported:

- Read and write sparse matrices in the CSC format
- Only real, symmetric, assembled matrix are supported (RUA format)
3.24.2 Deprecated features

**scipy.maxentropy**

The maxentropy module is unmaintained, rarely used and has not been functioning well for several releases. Therefore it has been deprecated for this release, and will be removed for scipy 0.11. Logistic regression in scikit.learn is a good alternative for this functionality. The `scipy.maxentropy.logsumexp` function has been moved to `scipy.misc`.

**scipy.lib.blas**

There are similar BLAS wrappers in `scipy.linalg` and `scipy.lib`. These have now been consolidated as `scipy.linalg.blas`, and `scipy.lib.blas` is deprecated.

**Numscons build system**

The numscons build system is being replaced by Bento, and will be removed in one of the next scipy releases.

3.24.3 Backwards-incompatible changes

The deprecated name `invnorm` was removed from `scipy.stats.distributions`, this distribution is available as `invgauss`.

The following deprecated nonlinear solvers from `scipy.optimize` have been removed:

- `"broyden_modified"` (bad performance)
- `"broyden1_modified"` (bad performance)
- `"broyden_generalized"` (equivalent to `"anderson"`)
- `"anderson2"` (equivalent to `"anderson"`)
- `"broyden3"` (obsoleted by new limited-memory broyden methods)
- `"vackar"` (renamed to `"diagbroyden"`)

3.24.4 Other changes

**scipy.constants** has been updated with the CODATA 2010 constants.

`__all__` dicts have been added to all modules, which has cleaned up the namespaces (particularly useful for interactive work).

An API section has been added to the documentation, giving recommended import guidelines and specifying which submodules are public and which aren’t.

3.24.5 Authors

This release contains work by the following people (contributed at least one patch to this release, names in alphabetical order):

- Jeff Armstrong +
- Matthew Brett
- Lars Buitinck +
- David Cournapeau
- FI$H 2000 +
- Michael McNeil Forbes +
- Matty G +
A total of 35 people contributed to this release. People with a “+” by their names contributed a patch for the first time.

### 3.25 SciPy 0.9.0 Release Notes

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### SciPy 0.9.0 Release Notes

- **Scipy source code location to be changed**

- **New features**
  - Delaunay tessellations (`scipy.spatial`)
  - N-dimensional interpolation (`scipy.interpolate`)
  - Nonlinear equation solvers (`scipy.optimize`)
  - New linear algebra routines (`scipy.linalg`)
  - Improved FIR filter design functions (`scipy.signal`)
  - Improved statistical tests (`scipy.stats`)

- **Deprecated features**
  - Obsolete nonlinear solvers (in `scipy.optimize`)

- **Removed features**
  - Old correlate/convolve behavior (in `scipy.signal`)
  - `scipy.stats`
  - `scipy.sparse`
  - `scipy.sparse.linalg.arpack.speigs`

- **Other changes**
  - ARPACK interface changes

SciPy 0.9.0 is the culmination of 6 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.9.x branch, and on adding new features on the development trunk.

This release requires Python 2.4 - 2.7 or 3.1 - and NumPy 1.5 or greater.

Please note that SciPy is still considered to have “Beta” status, as we work toward a SciPy 1.0.0 release. The 1.0.0 release will mark a major milestone in the development of SciPy, after which changing the package structure or API will be much more difficult. Whilst these pre-1.0 releases are considered to have “Beta” status, we are committed to making them as bug-free as possible.

However, until the 1.0 release, we are aggressively reviewing and refining the functionality, organization, and interface. This is being done in an effort to make the package as coherent, intuitive, and useful as possible. To achieve this, we need help from the community of users. Specifically, we need feedback regarding all aspects of the project - everything - from which algorithms we implement, to details about our function's call signatures.

#### 3.25.1 Python 3

Scipy 0.9.0 is the first SciPy release to support Python 3. The only module that is not yet ported is `scipy.weave`.

#### 3.25.2 Scipy source code location to be changed

Soon after this release, Scipy will stop using SVN as the version control system, and move to Git. The development source code for Scipy can from then on be found at

https://github.com/scipy/scipy
3.25.3 New features

Delaunay tessellations (scipy.spatial)

Scipy now includes routines for computing Delaunay tessellations in N dimensions, powered by the Qhull computational geometry library. Such calculations can now make use of the new scipy.spatial.Delaunay interface.

N-dimensional interpolation (scipy.interpolate)

Support for scattered data interpolation is now significantly improved. This version includes a scipy.interpolate.griddata function that can perform linear and nearest-neighbour interpolation for N-dimensional scattered data, in addition to cubic spline (C1-smooth) interpolation in 2D and 1D. An object-oriented interface to each interpolator type is also available.

Nonlinear equation solvers (scipy.optimize)

Scipy includes new routines for large-scale nonlinear equation solving in scipy.optimize. The following methods are implemented:

- Newton-Krylov (scipy.optimize.newton_krylov)
- (Generalized) secant methods:
  - Limited-memory Broyden methods (scipy.optimize.broyden1, scipy.optimize.broyden2)
  - Anderson method (scipy.optimize.anderson)
- Simple iterations (scipy.optimize.diagbroyden, scipy.optimize.excitingmixing, scipy.optimize.linearmixing)

The scipy.optimize.nonlin module was completely rewritten, and some of the functions were deprecated (see above).

New linear algebra routines (scipy.linalg)

Scipy now contains routines for effectively solving triangular equation systems (scipy.linalg.solve_triangular).

Improved FIR filter design functions (scipy.signal)

The function scipy.signal.firwin was enhanced to allow the design of highpass, bandpass, bandstop and multi-band FIR filters.

The function scipy.signal.firwin2 was added. This function uses the window method to create a linear phase FIR filter with an arbitrary frequency response.

The functions scipy.signal.kaiser_atten and scipy.signal.kaiser_beta were added.

Improved statistical tests (scipy.stats)

A new function scipy.stats.fisher_exact was added, that provides Fisher’s exact test for 2x2 contingency tables.

The function scipy.stats.kendalltau was rewritten to make it much faster (O(n log(n)) vs O(n^2)).

3.25.4 Deprecated features

Obsolete nonlinear solvers (in scipy.optimize)

The following nonlinear solvers from scipy.optimize are deprecated:
• broyden_modified (bad performance)
• broyden1_modified (bad performance)
• broyden_generalized (equivalent to anderson)
• anderson2 (equivalent to anderson)
• broyden3 (obsoleted by new limited-memory broyden methods)
• vackar (renamed to diagbroyden)

3.25.5 Removed features

The deprecated modules helpmod, pexec and ppimport were removed from scipy.misc.
The output_type keyword in many scipy.ndimage interpolation functions has been removed.
The econ keyword in scipy.linalg.qr has been removed. The same functionality is still available by specifying mode='economic'.

Old correlate/convolve behavior (in scipy.signal)
The old behavior for scipy.signal.convolve, scipy.signal.convolve2d, scipy.signal.correlate and scipy.signal.correlate2d was deprecated in 0.8.0 and has now been removed. Convolve and correlate used to swap their arguments if the second argument has dimensions larger than the first one, and the mode was relative to the input with the largest dimension. The current behavior is to never swap the inputs, which is what most people expect, and is how correlation is usually defined.

scipy.stats

Many functions in scipy.stats that are either available from numpy or have been superseded, and have been deprecated since version 0.7, have been removed: std, var, mean, median, cov, corrcoef, z, zs, stderr, samplestd, samplevar, pdfapprox, pdf_moments and erfc. These changes are mirrored in scipy.stats.mstats.

scipy.sparse

Several methods of the sparse matrix classes in scipy.sparse which had been deprecated since version 0.7 were removed: save, rowcol, getdata, listprint, ensure_sorted_indices, matvec, matmat and rmatvec.
The functions spkron, speye, spidentity, lil_eye and lil_diags were removed from scipy.sparse. The first three functions are still available as scipy.sparse.kron, scipy.sparse.eye and scipy.sparse.identity.
The dims and nzmax keywords were removed from the sparse matrix constructor. The colind and rowind attributes were removed from CSR and CSC matrices respectively.

scipy.sparse.linalg.arpack.speigs

A duplicated interface to the ARPACK library was removed.

3.25.6 Other changes

ARPACK interface changes

The interface to the ARPACK eigenvalue routines in scipy.sparse.linalg was changed for more robustness.
The eigenvalue and SVD routines now raise ArpackNoConvergence if the eigenvalue iteration fails to converge. If partially converged results are desired, they can be accessed as follows:
import numpy as np
from scipy.sparse.linalg import eigs, ArpackNoConvergence

m = np.random.randn(30, 30)
try:
    w, v = eigs(m, 6)
except ArpackNoConvergence, err:
    partially_converged_w = err.eigenvalues
    partially_converged_v = err.eigenvectors

Several bugs were also fixed.

The routines were moreover renamed as follows:

- eigen -> eigs
- eigen_symmetric -> eigsh
- svd -> svds

3.26 SciPy 0.8.0 Release Notes

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    * Correlation functions now implement the usual definition (scipy.signal)
    * Additions and modification to LTI functions (scipy.signal)
    * Improved waveform generators (scipy.signal)
    * New functions and other changes in scipy.linalg
    * New function and changes in scipy.optimize
    * New sparse least squares solver
    * ARPACK-based sparse SVD
    * Alternative behavior available for scipy.constants.find
    * Incomplete sparse LU decompositions
SciPy 0.8.0 is the culmination of 17 months of hard work. It contains many new features, numerous bugfixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.8.x branch, and on adding new features on the development trunk. This release requires Python 2.4 - 2.6 and NumPy 1.4.1 or greater.

Please note that SciPy is still considered to have “Beta” status, as we work toward a SciPy 1.0.0 release. The 1.0.0 release will mark a major milestone in the development of SciPy, after which changing the package structure or API will be much more difficult. Whilst these pre-1.0 releases are considered to have “Beta” status, we are committed to making them as bug-free as possible.

However, until the 1.0 release, we are aggressively reviewing and refining the functionality, organization, and interface. This is being done in an effort to make the package as coherent, intuitive, and useful as possible. To achieve this, we need help from the community of users. Specifically, we need feedback regarding all aspects of the project - everything - from which algorithms we implement, to details about our function’s call signatures.

### 3.26.1 Python 3

Python 3 compatibility is planned and is currently technically feasible, since Numpy has been ported. However, since the Python 3 compatible Numpy 1.5 has not been released yet, support for Python 3 in Scipy is not yet included in Scipy 0.8. SciPy 0.9, planned for fall 2010, will very likely include experimental support for Python 3.

### 3.26.2 Major documentation improvements

SciPy documentation is greatly improved.

### 3.26.3 Deprecated features

**Swapping inputs for correlation functions (scipy.signal)**

Concern correlate, correlate2d, convolve and convolve2d. If the second input is larger than the first input, the inputs are swapped before calling the underlying computation routine. This behavior is deprecated, and will be removed in scipy 0.9.0.

**Obsolete code deprecated (scipy.misc)**

The modules `helpmod`, `ppimport` and `pexec` from `scipy.misc` are deprecated. They will be removed from SciPy in version 0.9.
Additional deprecations

- linalg: The function `solveh_banded` currently returns a tuple containing the Cholesky factorization and the solution to the linear system. In SciPy 0.9, the return value will be just the solution.

- The function `constants.codata.find` will generate a DeprecationWarning. In Scipy version 0.8.0, the keyword argument ‘disp’ was added to the function, with the default value ‘True’. In 0.9.0, the default will be ‘False’.

- The `qshape` keyword argument of `signal.chirp` is deprecated. Use the argument `vertex_zero` instead.

- Passing the coefficients of a polynomial as the argument `f0` to `signal.chirp` is deprecated. Use the function `signal.sweep_poly` instead.

- The `io.recaster` module has been deprecated and will be removed in 0.9.0.

3.26.4 New features

**DCT support (scipy.fftpack)**

New real transforms have been added, namely `dct` and `idct` for Discrete Cosine Transform; type I, II and III are available.

**Single precision support for fft functions (scipy.fftpack)**

fft functions can now handle single precision inputs as well: `fft(x)` will return a single precision array if `x` is single precision.

At the moment, for FFT sizes that are not composites of 2, 3, and 5, the transform is computed internally in double precision to avoid rounding error in FFTPACK.

**Correlation functions now implement the usual definition (scipy.signal)**

The outputs should now correspond to their matlab and R counterparts, and do what most people expect if the `old_behavior=False` argument is passed:

- `correlate`, `convolve` and their 2d counterparts do not swap their inputs depending on their relative shape anymore;

- correlation functions now conjugate their second argument while computing the slided sum-products, which correspond to the usual definition of correlation.

**Additions and modification to LTI functions (scipy.signal)**

- The functions `impulse2` and `step2` were added to `scipy.signal`. They use the function `scipy.signal.lsim2` to compute the impulse and step response of a system, respectively.

- The function `scipy.signal.lsim2` was changed to pass any additional keyword arguments to the ODE solver.

**Improved waveform generators (scipy.signal)**

Several improvements to the `chirp` function in `scipy.signal` were made:

- The waveform generated when `method="logarithmic"` was corrected; it now generates a waveform that is also known as an “exponential” or “geometric” chirp. (See https://en.wikipedia.org/wiki/Chirp.)

- A new `chirp` method, “hyperbolic”, was added.

- Instead of the keyword `qshape`, `chirp` now uses the keyword `vertex_zero`, a boolean.
• *chirp* no longer handles an arbitrary polynomial. This functionality has been moved to a new function, *sweep_poly*.

A new function, *sweep_poly*, was added.

**New functions and other changes in scipy.linalg**

The functions *cho_solve_banded*, *circulant*, *companion*, *hadamard* and *leslie* were added to *scipy.linalg*. The function *block_diag* was enhanced to accept scalar and 1D arguments, along with the usual 2D arguments.

**New function and changes in scipy.optimize**

The *curve_fit* function has been added; it takes a function and uses non-linear least squares to fit that to the provided data.

The *leastsq* and *fsolve* functions now return an array of size one instead of a scalar when solving for a single parameter.

**New sparse least squares solver**

The *lsqr* function was added to *scipy.sparse*. This routine finds a least-squares solution to a large, sparse, linear system of equations.

**ARPACK-based sparse SVD**

A naive implementation of SVD for sparse matrices is available in *scipy.sparse.linalg.eigen.arpack*. It is based on using an symmetric solver on \(<A, A>\), and as such may not be very precise.

**Alternative behavior available for scipy.constants.find**

The keyword argument *disp* was added to the function *scipy.constants.find*, with the default value True. When *disp* is True, the behavior is the same as in Scipy version 0.7. When False, the function returns the list of keys instead of printing them. (In SciPy version 0.9, the default will be reversed.)

**Incomplete sparse LU decompositions**

Scipy now wraps SuperLU version 4.0, which supports incomplete sparse LU decompositions. These can be accessed via *scipy.sparse.linalg.spilu*. Upgrade to SuperLU 4.0 also fixes some known bugs.

**Faster matlab file reader and default behavior change**

We’ve rewritten the matlab file reader in Cython and it should now read matlab files at around the same speed that Matlab does.

The reader reads matlab named and anonymous functions, but it can’t write them.

Until scipy 0.8.0 we have returned arrays of matlab structs as numpy object arrays, where the objects have attributes named for the struct fields. As of 0.8.0, we return matlab structs as numpy structured arrays. You can get the older behavior by using the optional *struct_as_record=False* keyword argument to *scipy.io.loadmat* and friends.

There is an inconsistency in the matlab file writer, in that it writes numpy 1D arrays as column vectors in matlab 5 files, and row vectors in matlab 4 files. We will change this in the next version, so both write row vectors. There is a *FutureWarning* when calling the writer to warn of this change; for now we suggest using the *oned_as=’row’* keyword argument to *scipy.io.savemat* and friends.
Faster evaluation of orthogonal polynomials

Values of orthogonal polynomials can be evaluated with new vectorized functions in `scipy.special`: `eval_legendre`, `eval_chebyt`, `eval_chebyu`, `eval_chebyc`, `eval_chebys`, `eval_jacobi`, `eval_laguerre`, `eval_genlaguerre`, `eval_hermite`, `eval_hermitenorm`, `eval_gegenbauer`, `eval_sh_legendre`, `eval_sh_chebyt`, `eval_sh_chebyu`, `eval_sh_jacobi`. This is faster than constructing the full coefficient representation of the polynomials, which was previously the only available way.

Note that the previous orthogonal polynomial routines will now also invoke this feature, when possible.

Lambert W function

`scipy.special.lambertw` can now be used for evaluating the Lambert W function.

Improved hypergeometric 2F1 function

Implementation of `scipy.special.hyp2f1` for real parameters was revised. The new version should produce accurate values for all real parameters.

More flexible interface for Radial basis function interpolation

The `scipy.interpolate.Rbf` class now accepts a callable as input for the “function” argument, in addition to the built-in radial basis functions which can be selected with a string argument.

3.26.5 Removed features

`scipy.stsci`: the package was removed

The module `scipy.misc_limits` was removed.

`scipy.io`

The IO code in both NumPy and SciPy is being extensively reworked. NumPy will be where basic code for reading and writing NumPy arrays is located, while SciPy will house file readers and writers for various data formats (data, audio, video, images, matlab, etc.).

Several functions in `scipy.io` are removed in the 0.8.0 release including: `npyfile`, `save`, `load`, `create_module`, `create_shelf`, `obload`, `obsave`, `fopen`, `read_array`, `write_array`, `freed`, `fwrite`, `bswap`, `packbits`, `unpackbits`, and `convert_objectarray`. Some of these functions have been replaced by NumPy’s raw reading and writing capabilities, memory-mapping capabilities, or array methods. Others have been moved from SciPy to NumPy, since basic array reading and writing capability is now handled by NumPy.

3.27 SciPy 0.7.2 Release Notes

SciPy 0.7.2 is a bug-fix release with no new features compared to 0.7.1. The only change is that all C sources from Cython code have been regenerated with Cython 0.12.1. This fixes the incompatibility between binaries of SciPy 0.7.1 and NumPy 1.4.
3.28 SciPy 0.7.1 Release Notes

SciPy 0.7.1 is a bug-fix release with no new features compared to 0.7.0.

3.28.1 scipy.io

Bugs fixed:
- Several fixes in Matlab file IO

3.28.2 scipy.odr

Bugs fixed:
- Work around a failure with Python 2.6

3.28.3 scipy.signal

Memory leak in lfilter have been fixed, as well as support for array object

Bugs fixed:
- #880, #925: lfilter fixes
- #871: bicgstab fails on Win32

3.28.4 scipy.sparse

Bugs fixed:
- #883: scipy.io.mmread with scipy.sparse.lil_matrix broken

3.28.5 scipy.special

Several bugs of varying severity were fixed in the special functions:
- #503, #640: iv: problems at large arguments fixed by new implementation
- #623: jv: fix errors at large arguments
• #679: struve: fix wrong output for \( v < 0 \)
• #803: pbdv produces invalid output
• #804: lqmn: fix crashes on some input
• #823: betainc: fix documentation
• #834: exp1 strange behavior near negative integer values
• #852: jn_zeros: more accurate results for large \( s \), also in jnp/yn/ynp_zeros
• #853: jv, yv, iv: invalid results for non-integer \( v < 0 \), complex \( x \)
• #854: jv, yv, iv, kv: return nan more consistently when out-of-domain
• #927: ellipj: fix segfault on Windows
• #946: ellpj: fix segfault on Mac OS X/python 2.6 combination.
• ive, jve, yve, kv, kve: with real-valued input, return nan for out-of-domain instead of returning only the real part of the result.

Also, when `scipy.special.errprint(1)` has been enabled, warning messages are now issued as Python warnings instead of printing them to stderr.

### 3.28.6 scipy.stats

- linregress, mannwhitneyu, describe: errors fixed
- kstwobign, norm, expon, exponweib, exponpow, frechet, genexpon, rdist, truncexpon, planck: improvements to numerical accuracy in distributions

### 3.28.7 Windows binaries for python 2.6

Python 2.6 binaries for windows are now included. The binary for python 2.5 requires numpy 1.2.0 or above, and the one for python 2.6 requires numpy 1.3.0 or above.

### 3.28.8 Universal build for scipy

Mac OS X binary installer is now a proper universal build, and does not depend on gfortran anymore (libgfortran is statically linked). The python 2.5 version of scipy requires numpy 1.2.0 or above, the python 2.6 version requires numpy 1.3.0 or above.

### 3.29 SciPy 0.7.0 Release Notes
SciPy 0.7.0 is the culmination of 16 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.7.x branch, and on adding new features on the development trunk. This release requires Python 2.4 or 2.5 and NumPy 1.2 or greater.

Please note that SciPy is still considered to have “Beta” status, as we work toward a SciPy 1.0.0 release. The 1.0.0 release will mark a major milestone in the development of SciPy, after which changing the package structure or API will be much more difficult. Whilst these pre-1.0 releases are considered to have “Beta” status, we are committed to making them as bug-free as possible. For example, in addition to fixing numerous bugs in this release, we have also doubled the number of unit tests since the last release.

However, until the 1.0 release, we are aggressively reviewing and refining the functionality, organization, and interface. This is being done in an effort to make the package as coherent, intuitive, and useful as possible. To achieve this, we need help from the community of users. Specifically, we need feedback regarding all aspects of the project - everything - from which algorithms we implement, to details about our function’s call signatures.

Over the last year, we have seen a rapid increase in community involvement, and numerous infrastructure improvements to lower the barrier to contributions (e.g., more explicit coding standards, improved testing infrastructure, better documentation tools). Over the next year, we hope to see this trend continue and invite everyone to become more involved.

### 3.29.1 Python 2.6 and 3.0

A significant amount of work has gone into making SciPy compatible with Python 2.6; however, there are still some issues in this regard. The main issue with 2.6 support is NumPy. On UNIX (including Mac OS X), NumPy 1.2.1 mostly works, with a few caveats. On Windows, there are problems related to the compilation process. The upcoming NumPy 1.3 release will fix these problems. Any remaining issues with 2.6 support for SciPy 0.7 will be addressed in a bug-fix release.

Python 3.0 is not supported at all; it requires NumPy to be ported to Python 3.0. This requires immense effort, since a lot of C code has to be ported. The transition to 3.0 is still under consideration; currently, we don’t have any timeline or roadmap for this transition.
3.29.2 Major documentation improvements

SciPy documentation is greatly improved; you can view a HTML reference manual online or download it as a PDF file. The new reference guide was built using the popular Sphinx tool.

This release also includes an updated tutorial, which hadn’t been available since SciPy was ported to NumPy in 2005. Though not comprehensive, the tutorial shows how to use several essential parts of Scipy. It also includes the ndimage documentation from the numarray manual.

Nevertheless, more effort is needed on the documentation front. Luckily, contributing to Scipy documentation is now easier than before: if you find that a part of it requires improvements, and want to help us out, please register a user name in our web-based documentation editor at https://docs.scipy.org/ and correct the issues.

3.29.3 Running Tests

NumPy 1.2 introduced a new testing framework based on nose. Starting with this release, SciPy now uses the new NumPy test framework as well. Taking advantage of the new testing framework requires nose version 0.10, or later. One major advantage of the new framework is that it greatly simplifies writing unit tests - which has already paid off, given the rapid increase in tests. To run the full test suite:

```python
>>> import scipy
>>> scipy.test('full')
```

For more information, please see The NumPy/SciPy Testing Guide.

We have also greatly improved our test coverage. There were just over 2,000 unit tests in the 0.6.0 release; this release nearly doubles that number, with just over 4,000 unit tests.

3.29.4 Building SciPy

Support for NumScons has been added. NumScons is a tentative new build system for NumPy/SciPy, using SCons at its core.

SCons is a next-generation build system, intended to replace the venerable Make with the integrated functionality of autoconf/automake and ccache. Scons is written in Python and its configuration files are Python scripts. NumScons is meant to replace NumPy’s custom version of distutils providing more advanced functionality, such as autoconf, improved fortran support, more tools, and support for numpy.distutils/scons cooperation.

3.29.5 Sandbox Removed

While porting SciPy to NumPy in 2005, several packages and modules were moved into scipy.sandbox. The sandbox was a staging ground for packages that were undergoing rapid development and whose APIs were in flux. It was also a place where broken code could live. The sandbox has served its purpose well, but was starting to create confusion. Thus scipy.sandbox was removed. Most of the code was moved into scipy, some code was made into a scikit, and the remaining code was just deleted, as the functionality had been replaced by other code.

3.29.6 Sparse Matrices

Sparse matrices have seen extensive improvements. There is now support for integer dtypes such int8, uint32, etc. Two new sparse formats were added:

- new class dia_matrix : the sparse DIAgonal format
- new class bsr_matrix : the Block CSR format

Several new sparse matrix construction functions were added:
• `sparse.kron`: sparse Kronecker product
• `sparse.bmat`: sparse version of `numpy.bmat`
• `sparse.vstack`: sparse version of `numpy.vstack`
• `sparse.hstack`: sparse version of `numpy.hstack`

Extraction of submatrices and nonzero values have been added:
• `sparse.tril`: extract lower triangle
• `sparse.triu`: extract upper triangle
• `sparse.find`: nonzero values and their indices

`csr_matrix` and `csc_matrix` now support slicing and fancy indexing (e.g., `A[1:3, 4:7]` and `A[[3,2,6,8], :]`). Conversions among all sparse formats are now possible:
• using member functions such as `.tocsr()` and `.tolil()`
• using the `.asformat()` member function, e.g. `A.asformat('csr')`
• using constructors `A = lil_matrix([[1,2]])`; `B = csr_matrix(A)`

All sparse constructors now accept dense matrices and lists of lists. For example:
• `A = csr_matrix( rand(3,3) )` and `B = lil_matrix( [[1,2],[3,4]] )`

The handling of diagonals in the `spdiags` function has been changed. It now agrees with the MATLAB(TM) function of the same name.

Numerous efficiency improvements to format conversions and sparse matrix arithmetic have been made. Finally, this release contains numerous bugfixes.

### 3.29.7 Statistics package

Statistical functions for masked arrays have been added, and are accessible through `scipy.stats.mstats`. The functions are similar to their counterparts in `scipy.stats` but they have not yet been verified for identical interfaces and algorithms.

Several bugs were fixed for statistical functions, of those, `kstest` and `percentileofscore` gained new keyword arguments.

Added deprecation warning for `mean, median, var, std, cov, and corrcoef`. These functions should be replaced by their numpy counterparts. Note, however, that some of the default options differ between the `scipy.stats` and numpy versions of these functions.

Numerous bug fixes to `stats.distributions`: all generic methods now work correctly, several methods in individual distributions were corrected. However, a few issues remain with higher moments (`skew, kurtosis`) and entropy. The maximum likelihood estimator, `fit`, does not work out-of-the-box for some distributions - in some cases, starting values have to be carefully chosen, in other cases, the generic implementation of the maximum likelihood method might not be the numerically appropriate estimation method.

We expect more bugfixes, increases in numerical precision and enhancements in the next release of scipy.

### 3.29.8 Reworking of IO package

The IO code in both NumPy and SciPy is being extensively reworked. NumPy will be where basic code for reading and writing NumPy arrays is located, while SciPy will house file readers and writers for various data formats (data, audio, video, images, matlab, etc.).

Several functions in `scipy.io` have been deprecated and will be removed in the 0.8.0 release including `npfile, save, load, create_module, create_shelf, objload, objsave, fopen, read_array, write_array`,...
fread, fwrite, bswap, packbits, unpackbits, and convert_objectarray. Some of these functions have been replaced by NumPy's raw reading and writing capabilities, memory-mapping capabilities, or array methods. Others have been moved from SciPy to NumPy, since basic array reading and writing capability is now handled by NumPy.

The Matlab (TM) file readers/writers have a number of improvements:

- default version 5
- v5 writers for structures, cell arrays, and objects
- v5 readers/writers for function handles and 64-bit integers
- new struct_as_record keyword argument to loadmat, which loads struct arrays in matlab as record arrays in numpy
- string arrays have dtype='U...' instead of dtype=object
- loadmat no longer squeezes singleton dimensions, i.e. squeeze_me=False by default

### 3.29.9 New Hierarchical Clustering module

This module adds new hierarchical clustering functionality to the scipy.cluster package. The function interfaces are similar to the functions provided MATLAB(TM)'s Statistics Toolbox to help facilitate easier migration to the NumPy/SciPy framework. Linkage methods implemented include single, complete, average, weighted, centroid, median, and ward.

In addition, several functions are provided for computing inconsistency statistics, cophenetic distance, and maximum distance between descendants. The fcluster and fclusterdata functions transform a hierarchical clustering into a set of flat clusters. Since these flat clusters are generated by cutting the tree into a forest of trees, the leaders function takes a linkage and a flat clustering, and finds the root of each tree in the forest. The ClusterNode class represents a hierarchical clusterings as a field-navigable tree object. to_tree converts a matrix-encoded hierarchical clustering to a ClusterNode object. Routines for converting between MATLAB and SciPy linkage encodings are provided. Finally, a dendrogram function plots hierarchical clusterings as a dendrogram, using matplotlib.

### 3.29.10 New Spatial package

The new spatial package contains a collection of spatial algorithms and data structures, useful for spatial statistics and clustering applications. It includes rapidly compiled code for computing exact and approximate nearest neighbors, as well as a pure-python kd-tree with the same interface, but that supports annotation and a variety of other algorithms. The API for both modules may change somewhat, as user requirements become clearer.

It also includes a distance module, containing a collection of distance and dissimilarity functions for computing distances between vectors, which is useful for spatial statistics, clustering, and kd-trees. Distance and dissimilarity functions provided include Bray-Curtis, Canberra, Chebyshev, City Block, Cosine, Dice, Euclidean, Hamming, Jaccard, Kulsinski, Mahalanobis, Matching, Minkowski, Rogers-Tanimoto, Russell-Rao, Squared Euclidean, Standardized Euclidean, Sokal-Michener, Sokal-Sneath, and Yule.

The pdist function computes pairwise distance between all unordered pairs of vectors in a set of vectors. The cdist computes the distance on all pairs of vectors in the Cartesian product of two sets of vectors. Pairwise distance matrices are stored in condensed form; only the upper triangular is stored. squareform converts distance matrices between square and condensed forms.

### 3.29.11 Reworked fftpack package

FFTW2, FFTW3, MKL and DJBFFT wrappers have been removed. Only (NETLIB) fftpack remains. By focusing on one backend, we hope to add new features - like float32 support - more easily.
3.29.12 New Constants package

`scipy.constants` provides a collection of physical constants and conversion factors. These constants are taken from CODATA Recommended Values of the Fundamental Physical Constants: 2002. They may be found at physics.nist.gov/constants. The values are stored in the dictionary `physical_constants` as a tuple containing the value, the units, and the relative precision - in that order. All constants are in SI units, unless otherwise stated. Several helper functions are provided.

3.29.13 New Radial Basis Function module

`scipy.interpolate` now contains a Radial Basis Function module. Radial basis functions can be used for smoothing/interpolating scattered data in n-dimensions, but should be used with caution for extrapolation outside of the observed data range.

3.29.14 New complex ODE integrator

`scipy.integrate.ode` now contains a wrapper for the ZVODE complex-valued ordinary differential equation solver (by Peter N. Brown, Alan C. Hindmarsh, and George D. Byrne).

3.29.15 New generalized symmetric and hermitian eigenvalue problem solver

`scipy.linalg.eigh` now contains wrappers for more LAPACK symmetric and hermitian eigenvalue problem solvers. Users can now solve generalized problems, select a range of eigenvalues only, and choose to use a faster algorithm at the expense of increased memory usage. The signature of the `scipy.linalg.eigh` changed accordingly.

3.29.16 Bug fixes in the interpolation package

The shape of return values from `scipy.interpolate.interp1d` used to be incorrect, if interpolated data had more than 2 dimensions and the axis keyword was set to a non-default value. This has been fixed. Moreover, `interp1d` returns now a scalar (0D-array) if the input is a scalar. Users of `scipy.interpolate.interp1d` may need to revise their code if it relies on the previous behavior.

3.29.17 Weave clean up

There were numerous improvements to `scipy.weave`. `blitz++` was relicensed by the author to be compatible with the SciPy license. `wx_spec.py` was removed.

3.29.18 Known problems

Here are known problems with scipy 0.7.0:

- weave test failures on windows: those are known, and are being revised.
- weave test failure with gcc 4.3 (std::labs): this is a gcc 4.3 bug. A workaround is to add `#include <cstdlib>` in scipy/weave/blitz/blitz/funcs.h (line 27). You can make the change in the installed scipy (in site-packages).
Tutorials with worked examples and background information for most SciPy submodules.

## 4.1 SciPy Tutorial

### 4.1.1 Introduction

SciPy is a collection of mathematical algorithms and convenience functions built on the Numpy extension of Python. It adds significant power to the interactive Python session by providing the user with high-level commands and classes for manipulating and visualizing data. With SciPy an interactive Python session becomes a data-processing and system-prototyping environment rivaling systems such as MATLAB, IDL, Octave, R-Lab, and SciLab.

The additional benefit of basing SciPy on Python is that this also makes a powerful programming language available for use in developing sophisticated programs and specialized applications. Scientific applications using SciPy benefit from the development of additional modules in numerous niches of the software landscape by developers across the world. Everything from parallel programming to web and data-base subroutines and classes have been made available to the Python programmer. All of this power is available in addition to the mathematical libraries in SciPy.

This tutorial will acquaint the first-time user of SciPy with some of its most important features. It assumes that the user has already installed the SciPy package. Some general Python facility is also assumed, such as could be acquired by working through the Python distribution’s Tutorial. For further introductory help the user is directed to the Numpy documentation.

For brevity and convenience, we will often assume that the main packages (numpy, scipy, and matplotlib) have been imported as:

```python
>>> import numpy as np
>>> import matplotlib as mpl
>>> import matplotlib.pyplot as plt
```

These are the import conventions that our community has adopted after discussion on public mailing lists. You will see these conventions used throughout NumPy and SciPy source code and documentation. While we obviously don’t require you to follow these conventions in your own code, it is highly recommended.
SciPy Organization

SciPy is organized into subpackages covering different scientific computing domains. These are summarized in the following table:

<table>
<thead>
<tr>
<th>Subpackage</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>cluster</td>
<td>Clustering algorithms</td>
</tr>
<tr>
<td>constants</td>
<td>Physical and mathematical constants</td>
</tr>
<tr>
<td>fftpack</td>
<td>Fast Fourier Transform routines</td>
</tr>
<tr>
<td>integrate</td>
<td>Integration and ordinary differential equation solvers</td>
</tr>
<tr>
<td>interpolate</td>
<td>Interpolation and smoothing splines</td>
</tr>
<tr>
<td>io</td>
<td>Input and Output</td>
</tr>
<tr>
<td>linalg</td>
<td>Linear algebra</td>
</tr>
<tr>
<td>ndimage</td>
<td>N-dimensional image processing</td>
</tr>
<tr>
<td>odr</td>
<td>Orthogonal distance regression</td>
</tr>
<tr>
<td>optimize</td>
<td>Optimization and root-finding routines</td>
</tr>
<tr>
<td>signal</td>
<td>Signal processing</td>
</tr>
<tr>
<td>sparse</td>
<td>Sparse matrices and associated routines</td>
</tr>
<tr>
<td>spatial</td>
<td>Spatial data structures and algorithms</td>
</tr>
<tr>
<td>special</td>
<td>Special functions</td>
</tr>
<tr>
<td>stats</td>
<td>Statistical distributions and functions</td>
</tr>
</tbody>
</table>

Scipy sub-packages need to be imported separately, for example:

```python
>>> from scipy import linalg, optimize
```

Because of their ubiquitousness, some of the functions in these subpackages are also made available in the scipy namespace to ease their use in interactive sessions and programs. In addition, many basic array functions from numpy are also available at the top-level of the scipy package. Before looking at the subpackages individually, we will first look at some of these common functions.

Finding Documentation

SciPy and NumPy have documentation versions in both HTML and PDF format available at https://docs.scipy.org/, that cover nearly all available functionality. However, this documentation is still work-in-progress and some parts may be incomplete or sparse. As we are a volunteer organization and depend on the community for growth, your participation - everything from providing feedback to improving the documentation and code - is welcome and actively encouraged.

Python’s documentation strings are used in SciPy for on-line documentation. There are two methods for reading them and getting help. One is Python’s command help in the pydoc module. Entering this command with no arguments (i.e. ```>>> help ```) launches an interactive help session that allows searching through the keywords and modules available to all of Python. Secondly, running the command ```help(obj) ``` with an object as the argument displays that object’s calling signature, and documentation string.

The pydoc method of help is sophisticated but uses a pager to display the text. Sometimes this can interfere with the terminal you are running the interactive session within. A numpy/scipy-specific help system is also available under the command numpy.info. The signature and documentation string for the object passed to the help command are printed to standard output (or to a writeable object passed as the third argument). The second keyword argument of numpy.info defines the maximum width of the line for printing. If a module is passed as the argument to help then a list of the functions and classes defined in that module is printed. For example:
>>> np.info(optimize.fmin)

.. automodule:: scipy.optimize.fmin
   :members:
   :undoc-members:

fmin(func, x0, args=(), xtol=0.0001, ftol=0.0001, maxiter=None, maxfun=None,
    full_output=0, disp=1, retall=0, callback=None)

Minimize a function using the downhill simplex algorithm.

Parameters
----------
func : callable func(x,*args)
   The objective function to be minimized.
x0 : ndarray
   Initial guess.
args : tuple
   Extra arguments passed to func, i.e. ``f(x,*args)``.
callback : callable
   Called after each iteration, as callback(xk), where xk is the
   current parameter vector.

Returns
-------
xopt : ndarray
   Parameter that minimizes function.
fopt : float
   Value of function at minimum: ``fopt = func(xopt)``.
iter : int
   Number of iterations performed.
funcalls : int
   Number of function calls made.
warnflag : int
   1 : Maximum number of function evaluations made.
   2 : Maximum number of iterations reached.
allvecs : list
   Solution at each iteration.

Other parameters
----------------
xtol : float
   Relative error in xopt acceptable for convergence.
ftol : number
   Relative error in func(xopt) acceptable for convergence.
maxiter : int
   Maximum number of iterations to perform.
maxfun : number
   Maximum number of function evaluations to make.
full_output : bool
   Set to True if fopt and warnflag outputs are desired.
disp : bool
   Set to True to print convergence messages.
retall : bool
   Set to True to return list of solutions at each iteration.

Notes
(continues on next page)
Uses a Nelder-Mead simplex algorithm to find the minimum of function of one or more variables.

Another useful command is `source`. When given a function written in Python as an argument, it prints out a listing of the source code for that function. This can be helpful in learning about an algorithm or understanding exactly what a function is doing with its arguments. Also don’t forget about the Python command `dir` which can be used to look at the namespace of a module or package.

### 4.1.2 Basic functions

#### Interaction with Numpy

Scipy builds on Numpy, and for all basic array handling needs you can use Numpy functions:

```python
>>> import numpy as np
>>> np.some_function()
```

Rather than giving a detailed description of each of these functions (which is available in the Numpy Reference Guide or by using the `help`, `info` and `source` commands), this tutorial will discuss some of the more useful commands which require a little introduction to use to their full potential.

To use functions from some of the Scipy modules, you can do:

```python
>>> from scipy import some_module
>>> some_module.some_function()
```

The top level of `scipy` also contains functions from `numpy` and `numpy.lib.scimath`. However, it is better to use them directly from the `numpy` module instead.

#### Index Tricks

There are some class instances that make special use of the slicing functionality to provide efficient means for array construction. This part will discuss the operation of `np.mgrid`, `np.ogrid`, `np.r_`, and `np.c_` for quickly constructing arrays.

For example, rather than writing something like the following

```python
>>> a = np.concatenate(([3], [0]*5, np.arange(-1, 1.002, 2/9.0)))
```
with the `r_` command one can enter this as

```python
>>> a = np.r_[3, [0]*5, -1:1:10j]
```

which can ease typing and make for more readable code. Notice how objects are concatenated, and the slicing syntax is (ab)used to construct ranges. The other term that deserves a little explanation is the use of the complex number `10j` as the step size in the slicing syntax. This non-standard use allows the number to be interpreted as the number of points to produce in the range rather than as a step size (note we would have used the long integer notation, `10L`, but this notation may go away in Python as the integers become unified). This non-standard usage may be unsightly to some, but it gives the user the ability to quickly construct complicated vectors in a very readable fashion. When the number of points is specified in this way, the end-point is inclusive.

The “r” stands for row concatenation because if the objects between commas are 2 dimensional arrays, they are stacked by rows (and thus must have commensurate columns). There is an equivalent command `c_` that stacks 2d arrays by columns but works identically to `r_` for 1d arrays.

Another very useful class instance which makes use of extended slicing notation is the function `mgrid`. In the simplest case, this function can be used to construct 1d ranges as a convenient substitute for `arange`. It also allows the use of complex-numbers in the step-size to indicate the number of points to place between the (inclusive) end-points. The real purpose of this function however is to produce N, N-d arrays which provide coordinate arrays for an N-dimensional volume. The easiest way to understand this is with an example of its usage:

```python
>>> np.mgrid[0:5, 0:5]
dtype([[[0, 0, 0, 0, 0],
        [1, 1, 1, 1, 1],
        [2, 2, 2, 2, 2],
        [3, 3, 3, 3, 3],
        [4, 4, 4, 4, 4]],
       [[0, 1, 2, 3, 4],
        [0, 1, 2, 3, 4],
        [0, 1, 2, 3, 4],
        [0, 1, 2, 3, 4],
        [0, 1, 2, 3, 4]])
```

```python
>>> np.mgrid[0:5:4j, 0:5:4j]
dtype([[ 0.0 , 1.6667, 3.3333, 5.0 , 6.6667],
        [ 1.6667, 3.3333, 5.0 , 6.6667, 8.3333],
        [ 3.3333, 5.0 , 6.6667, 8.3333, 10.0 ]])
```

Having meshed arrays like this is sometimes very useful. However, it is not always needed just to evaluate some N-dimensional function over a grid due to the array-broadcasting rules of Numpy and SciPy. If this is the only purpose for generating a meshgrid, you should instead use the function `ogrid` which generates an “open” grid using `newaxis` judiciously to create N, N-d arrays where only one dimension in each array has length greater than 1. This will save memory and create the same result if the only purpose for the meshgrid is to generate sample points for evaluation of an N-d function.

**Shape manipulation**

In this category of functions are routines for squeezing out length-one dimensions from N-dimensional arrays, ensuring that an array is at least 1-, 2-, or 3-dimensional, and stacking (concatenating) arrays by rows, columns, and “pages” (in the third dimension). Routines for splitting arrays (roughly the opposite of
Polynomials

There are two (interchangeable) ways to deal with 1-d polynomials in SciPy. The first is to use the `poly1d` class from Numpy. This class accepts coefficients or polynomial roots to initialize a polynomial. The polynomial object can then be manipulated in algebraic expressions, integrated, differentiated, and evaluated. It even prints like a polynomial:

```python
>>> from numpy import poly1d
>>> p = poly1d([3,4,5])
>>> print(p)
  2
3 x + 4 x + 5
>>> print(p*p)
  4      3      2
9 x + 24 x + 46 x + 40 x + 25
>>> print(p.integ(k=6))
  3      2
1 x + 2 x + 5 x + 6
>>> print(p.deriv())
6 x + 4
>>> p([4, 5])
array([69, 100])
```

The other way to handle polynomials is as an array of coefficients with the first element of the array giving the coefficient of the highest power. There are explicit functions to add, subtract, multiply, divide, integrate, differentiate, and evaluate polynomials represented as sequences of coefficients.

Vectorizing functions (vectorize)

One of the features that NumPy provides is a class `vectorize` to convert an ordinary Python function which accepts scalars and returns scalars into a “vectorized-function” with the same broadcasting rules as other Numpy functions (i.e. the Universal functions, or ufuncs). For example, suppose you have a Python function named `addsubtract` defined as:

```python
>>> def addsubtract(a,b):
...     if a > b:
...         return a - b
...     else:
...         return a + b
```

which defines a function of two scalar variables and returns a scalar result. The class `vectorize` can be used to “vectorize” this function so that

```python
>>> vec_addsubtract = np.vectorize(addsubtract)
```

returns a function which takes array arguments and returns an array result:

```python
>>> vec_addsubtract([0,3,6,9],[1,3,5,7])
array([1, 6, 1, 2])
```

This particular function could have been written in vector form without the use of `vectorize`. However, functions that employ optimization or integration routines can likely only be vectorized using `vectorize`.

Type handling

Note the difference between `np.iscomplex`/`np.isreal` and `np.iscomplexobj`/`np.isrealobj`. The former command is array based and returns byte arrays of ones and zeros providing the result of the element-wise
test. The latter command is object based and returns a scalar describing the result of the test on the entire object.

Often it is required to get just the real and/or imaginary part of a complex number. While complex numbers and arrays have attributes that return those values, if one is not sure whether or not the object will be complex-valued, it is better to use the functional forms `np.real` and `np.imag`. These functions succeed for anything that can be turned into a Numpy array. Consider also the function `np.real_if_close` which transforms a complex-valued number with tiny imaginary part into a real number.

Occasionally the need to check whether or not a number is a scalar (Python (long)int, Python float, Python complex, or rank-0 array) occurs in coding. This functionality is provided in the convenient function `np.isscalar` which returns a 1 or a 0.

Finally, ensuring that objects are a certain Numpy type occurs often enough that it has been given a convenient interface in SciPy through the use of the `np.cast` dictionary. The dictionary is keyed by the type it is desired to cast to and the dictionary stores functions to perform the casting. Thus, `np.cast['f'](d)` returns an array of `np.float32` from `d`. This function is also useful as an easy way to get a scalar of a certain type:

```python
>>> np.cast['f'](np.pi)
array(3.1415927410125732, dtype=float32)
```

Other useful functions

There are also several other useful functions which should be mentioned. For doing phase processing, the functions `angle` and `unwrap` are useful. Also, the `linspace` and `logspace` functions return equally spaced samples in a linear or log scale. Finally, it’s useful to be aware of the indexing capabilities of Numpy. Mention should be made of the function `select` which extends the functionality of `where` to include multiple conditions and multiple choices. The calling convention is `select(condlist, choicelist, default=0)`. `select` is a vectorized form of the multiple if-statement. It allows rapid construction of a function which returns an array of results based on a list of conditions. Each element of the return array is taken from the array in a `choicelist` corresponding to the first condition in `condlist` that is true. For example

```python
>>> x = np.r_[-2:3]
>>> x
array([-2, -1,  0,  1,  2])
>>> np.select([x > 3, x >= 0], [0, x+2])
array([0, 0, 2, 3, 4])
```

Some additional useful functions can also be found in the module `scipy.misc`. For example the `factorial` and `comb` functions compute \( n! \) and \( n!/(n-k)! \) using either exact integer arithmetic (thanks to Python’s Long integer object), or by using floating-point precision and the gamma function. Another function returns a common image used in image processing: `lena`.

Finally, two functions are provided that are useful for approximating derivatives of functions using discrete-differences. The function `central_diff_weights` returns weighting coefficients for an equally-spaced \( N \)-point approximation to the derivative of order \( o \). These weights must be multiplied by the function corresponding to these points and the results added to obtain the derivative approximation. This function is intended for use when only samples of the function are available. When the function is an object that can be handed to a routine and evaluated, the function `derivative` can be used to automatically evaluate the object at the correct points to obtain an \( N \)-point approximation to the \( o \)-th derivative at a given point.

### 4.1.3 Special functions (scipy.special)

The main feature of the `scipy.special` package is the definition of numerous special functions of mathematical physics. Available functions include airy, elliptic, bessel, gamma, beta, hypergeometric, parabolic cylinder, mathieu, spheroidal wave, struve, and kelvin. There are also some low-level stats functions that are not intended for general use as an easier interface to these functions is provided by the `stats` module.
Most of these functions can take array arguments and return array results following the same broadcasting rules as other math functions in Numerical Python. Many of these functions also accept complex numbers as input. For a complete list of the available functions with a one-line description type `>>> help(special)`. Each function also has its own documentation accessible using help. If you don’t see a function you need, consider writing it and contributing it to the library. You can write the function in either C, Fortran, or Python. Look in the source code of the library for examples of each of these kinds of functions.

**Bessel functions of real order** (**jn, jn_zeros**)

Bessel functions are a family of solutions to Bessel’s differential equation with real or complex order alpha:

\[
x^2 \frac{d^2 y}{dx^2} + x \frac{dy}{dx} + (x^2 - \alpha^2) y = 0
\]

Among other uses, these functions arise in wave propagation problems such as the vibrational modes of a thin drum head. Here is an example of a circular drum head anchored at the edge:

```python
>>> from scipy import special
>>> def drumhead_height(n, k, distance, angle, t):
...     kth_zero = special.jn_zeros(n, k)[-1]
...     theta = np.cos(t) * np.cos(n*angle) * special.jn(n, distance*kth_zero)
...     return np.cos(t) * np.cos(n*angle) * special.jn(n, distance*kth_zero)

>>> theta = np.linspace(0, 2*np.pi, 50)
>>> radius = np.linspace(0, 1, 50)
>>> x = np.array([r*np.cos(theta) for r in radius])
>>> y = np.array([r*np.sin(theta) for r in radius])
>>> z = np.array([drumhead_height(1, 1, r, theta, 0.5) for r in radius])
```

**Cython Bindings for Special Functions** (**scipy.special.cython_special**)

Scipy also offers Cython bindings for scalar, typed versions of many of the functions in special. The following Cython code gives a simple example of how to use these functions:

```cython
import scipy.special.cython_special as csc
cdef:
    double x = 1
double complex z = 1 + 1j
double si, ci, rgam
double complex cgam
	ron = csc.gamma(x)
print(rgam)
cgam = csc.gamma(z)
```
print(cgam)
csc.sici(x, &si, &ci)
print(si, ci)

(See the Cython documentation for help with compiling Cython.) In the example the function `csc.gamma` works essentially like its ufunc counterpart `gamma`, though it takes C types as arguments instead of NumPy arrays. Note in particular that the function is overloaded to support real and complex arguments; the correct variant is selected at compile time. The function `csc.sici` works slightly differently from `sici`; for the ufunc we could write `ai, bi = sici(x)` whereas in the Cython version multiple return values are passed as pointers. It might help to think of this as analogous to calling a ufunc with an output array: `sici(x, out=(si, ci))`.

There are two potential advantages to using the Cython bindings:

- They avoid Python function overhead
- They do not require the Python Global Interpreter Lock (GIL)

The following sections discuss how to use these advantages to potentially speed up your code, though of course one should always profile the code first to make sure putting in the extra effort will be worth it.

**Avoiding Python Function Overhead**

For the ufuncs in special, Python function overhead is avoided by vectorizing, that is, by passing an array to the function. Typically this approach works quite well, but sometimes it is more convenient to call a special function on scalar inputs inside a loop, for example when implementing your own ufunc. In this case the Python function overhead can become significant. Consider the following example:

```python
import scipy.special as sc
import scipy.special.cython_special as csc

def python_tight_loop():
    cdef:
        int n
double x = 1
```
```python
for n in range(100):
    sc.jv(n, x)

def cython_tight_loop():
    cdef:
        int n
        double x = 1

    for n in range(100):
        csc.jv(n, x)
```

On one computer python_tight_loop took about 131 microseconds to run and cython_tight_loop took about 18.2 microseconds to run. Obviously this example is contrived: one could just call `special.jv(np.arange(100), 1)` and get results just as fast as in cython_tight_loop. The point is that if Python function overhead becomes significant in your code then the Cython bindings might be useful.

### Releasing the GIL

One often needs to evaluate a special function at many points, and typically the evaluations are trivially parallelizable. Since the Cython bindings do not require the GIL, it is easy to run them in parallel using Cython’s `prange` function. For example, suppose that we wanted to compute the fundamental solution to the Helmholtz equation:

\[
\Delta_x G(x, y) + k^2 G(x, y) = \delta(x - y),
\]

where \( k \) is the wavenumber and \( \delta \) is the Dirac delta function. It is known that in two dimensions the unique (radiating) solution is

\[
G(x, y) = \frac{i}{4} H_0^{(1)}(k|x - y|),
\]

where \( H_0^{(1)} \) is the Hankel function of the first kind, i.e. the function `hankel1`. The following example shows how we could compute this function in parallel:

```python
from libc.math cimport fabs
cimport cython
from cython.parallel cimport prange
import numpy as np
import scipy.special as sc
cimport scipy.special.cython_special as csc

def serial_G(k, x, y):
    return 0.25*j*sc.hankel1(0, k*np.abs(x - y))

@cython.boundscheck(False)
@cython.wraparound(False)
cdef void _parallel_G(double k, double[:,,:] x, double[:,,:] y,
                      double complex[:,,:] out) nogil:
    cdef int i, j

    for i in prange(x.shape[0]):
        for j in range(y.shape[0]):
            out[i,j] = 0.25j*csc.hankel1(0, k*fabs(x[i,j] - y[i,j]))
```
def parallel_G(k, x, y):
    out = np.empty_like(x, dtype='complex128')
    _parallel_G(k, x, y, out)
    return out

(For help with compiling parallel code in Cython see here.) If the above Cython code is in a file test.pyx, then we can write an informal benchmark which compares the parallel and serial versions of the function:

```python
import timeit
import numpy as np
from test import serial_G, parallel_G

def main():
    k = 1
    x, y = np.linspace(-100, 100, 1000), np.linspace(-100, 100, 1000)
    x, y = np.meshgrid(x, y)

    def serial():
        serial_G(k, x, y)

    def parallel():
        parallel_G(k, x, y)

    time_serial = timeit.timeit(serial, number=3)
    time_parallel = timeit.timeit(parallel, number=3)
    print("Serial method took {:.3} seconds").format(time_serial)
    print("Parallel method took {:.3} seconds").format(time_parallel)

if __name__ == '__main__':
    main()
```

On one quad-core computer the serial method took 1.29 seconds and the parallel method took 0.29 seconds.

**Functions not in scipy.special**

Some functions are not included in special because they are straightforward to implement with existing functions in NumPy and SciPy. To prevent reinventing the wheel, this section provides implementations of several such functions which hopefully illustrate how to handle similar functions. In all examples NumPy is imported as np and special is imported as sc.

The binary entropy function:

```python
def binary_entropy(x):
    return -(sc.xlogy(x, x) + sc.xlogy(1 - x, -x))/np.log(2)
```

A rectangular step function on [0, 1]:

```python
def step(x):
    return 0.5*(np.sign(x) + np.sign(1 - x))
```

Translating and scaling can be used to get an arbitrary step function.

The ramp function:
```python
def ramp(x):
    return np.maximum(0, x)
```

### 4.1.4 Integration (scipy.integrate)

The `scipy.integrate` sub-package provides several integration techniques including an ordinary differential equation integrator. An overview of the module is provided by the help command:

```python
>>> help(integrate)
Methods for Integrating Functions given function object.

quad -- General purpose integration.
dblquad -- General purpose double integration.
tplquad -- General purpose triple integration.
fixed_quad -- Integrate func(x) using Gaussian quadrature of order n.
quadrature -- Integrate with given tolerance using Gaussian quadrature.
romberg -- Integrate func using Romberg integration.

Methods for Integrating Functions given fixed samples.

trapz -- Use trapezoidal rule to compute integral from samples.
cumtrapz -- Use trapezoidal rule to cumulatively compute integral.
simps -- Use Simpson's rule to compute integral from samples.
romb -- Use Romberg Integration to compute integral from (2**k + 1) evenly-spaced samples.

See the special module's orthogonal polynomials (special) for Gaussian quadrature roots and weights for other weighting factors and regions.

Interface to numerical integrators of ODE systems.

odeint -- General integration of ordinary differential equations.
ode -- Integrate ODE using VODE and ZVODE routines.
```

#### General integration (quad)

The function `quad` is provided to integrate a function of one variable between two points. The points can be $\pm\infty$ ($\pm\text{inf}$) to indicate infinite limits. For example, suppose you wish to integrate a bessel function $jv(2.5, x)$ along the interval $[0, 4.5]$.

$$I = \int_{0}^{4.5} J_{2.5}(x) \, dx.$$ 

This could be computed using `quad`:

```python
>>> import scipy.integrate as integrate
>>> import scipy.special as special
>>> result = integrate.quad(lambda x: special.jv(2.5, x), 0, 4.5)
>>> result
(1.1178179380783249, 7.8663172481899801e-09)
```

```python
>>> from numpy import sqrt, sin, cos, pi
>>> I = sqrt(2/pi)*(18.0/27*sqrt(2)*cos(4.5) - 4.0/27*sqrt(2)*sin(4.5)) +
```

(continues on next page)
\[
I = \sqrt{2} \left( \frac{18}{27} \sqrt{2} \cos(4.5) - \frac{4}{27} \sqrt{2} \sin(4.5) + \sqrt{2\pi} \text{Si} \left( \frac{3}{\sqrt{\pi}} \right) \right),
\]

where
\[
\text{Si}(x) = \int_0^x \sin \left( \frac{\pi}{2} t^2 \right) dt.
\]
is the Fresnel sine integral. Note that the numerically-computed integral is within \(1.04 \times 10^{-11}\) of the exact result — well below the reported error bound.

If the function to integrate takes additional parameters, the can be provided in the \textit{args} argument. Suppose that the following integral shall be calculated:
\[
I(a, b) = \int_0^1 ax^2 + b \, dx.
\]

This integral can be evaluated by using the following code:

```python
>>> from scipy.integrate import quad
>>> def integrand(x, a, b):
...     return a*x**2 + b
...
>>> a = 2
>>> b = 1
>>> I = quad(integrand, 0, 1, args=(a,b))
>>> I
(1.6666666666666667, 1.8503717077085944e-14)
```

Infinite inputs are also allowed in \textit{quad} by using ± \texttt{inf} as one of the arguments. For example, suppose that a numerical value for the exponential integral:
\[
E_n(x) = \int_1^\infty \frac{e^{-xt}}{t^n} \, dt.
\]
is desired (and the fact that this integral can be computed as \texttt{special.expn(n,x)} is forgotten). The functionality of the function \texttt{special.expn} can be replicated by defining a new function \texttt{vec_expint} based on the routine \textit{quad}:

```python
>>> from scipy.integrate import quad
>>> def integrand(t, n, x):
...     return np.exp(-x*t) / t**n
...
```
```python
>>> def expint(n, x):
...     return quad(integrand, 1, np.inf, args=(n, x))[0]
...

>>> vec_expint = np.vectorize(expint)

>>> vec_expint(3, np.arange(1.0, 4.0, 0.5))
array([ 0.1097, 0.0567, 0.0301, 0.0163, 0.0089, 0.0049])
>>> import scipy.special as special
>>> special.expn(3, np.arange(1.0, 4.0, 0.5))
array([ 0.1097, 0.0567, 0.0301, 0.0163, 0.0089, 0.0049])

The function which is integrated can even use the quad argument (though the error bound may underestimate
the error due to possible numerical error in the integrand from the use of quad). The integral in this case is

\[ I_n = \int_0^\infty \int_1^\infty \frac{e^{-xt}}{t^n} dt \, dx = \frac{1}{n} \]

```
As example for non-constant limits consider the integral

\[ I = \int_{y=0}^{1/2} \int_{x=0}^{1-2y} xy \, dx \, dy = \frac{1}{96}. \]

This integral can be evaluated using the expression below (Note the use of the non-constant lambda functions for the upper limit of the inner integral):

```python
>>> from scipy.integrate import dblquad
>>> area = dblquad(lambda x, y: x*y, 0, 0.5, lambda x: 0, lambda x: 1-2*x)
>>> area
(0.010416666666666668, 1.1564823173178715e-16)
```

For n-fold integration, scipy provides the function `nquad`. The integration bounds are an iterable object: either a list of constant bounds, or a list of functions for the non-constant integration bounds. The order of integration (and therefore the bounds) is from the innermost integral to the outermost one.

The integral from above

\[ I_n = \int_0^\infty \int_1^\infty e^{-xt} \, dx \, dt = \frac{1}{n} \]

can be calculated as

```python
>>> from scipy import integrate
>>> N = 5
>>> def f(t, x):
...     return np.exp(-x*t) / t**N
... >>> integrate.nquad(f, [[1, np.inf],[0, np.inf]])
(0.20000000000000002, 1.2239614263187945e-08)
```

Note that the order of arguments for \( f \) must match the order of the integration bounds; i.e. the inner integral with respect to \( t \) is on the interval \([1, \infty]\) and the outer integral with respect to \( x \) is on the interval \([0, \infty]\).

Non-constant integration bounds can be treated in a similar manner; the example from above

\[ I = \int_{y=0}^{1/2} \int_{x=0}^{1-2y} xy \, dx \, dy = \frac{1}{96}. \]

can be evaluated by means of

```python
>>> from scipy import integrate
>>> def f(x, y):
...     return x*y
... >>> def bounds_y():
...     return [0, 0.5]
... >>> def bounds_x(y):
...     return [0, 1-2*y]
... >>> integrate.nquad(f, [bounds_x, bounds_y])
(0.010416666666666668, 4.101620128472366e-16)
```

which is the same result as before.
**Gaussian quadrature**

A few functions are also provided in order to perform simple Gaussian quadrature over a fixed interval. The first is `fixed_quad` which performs fixed-order Gaussian quadrature. The second function is `quadrature` which performs Gaussian quadrature of multiple orders until the difference in the integral estimate is beneath some tolerance supplied by the user. These functions both use the module `special.orthogonal` which can calculate the roots and quadrature weights of a large variety of orthogonal polynomials (the polynomials themselves are available as special functions returning instances of the polynomial class — e.g. `special.legendre`).

**Romberg Integration**

Romberg’s method [WPR] is another method for numerically evaluating an integral. See the help function for `romberg` for further details.

**Integrating using Samples**

If the samples are equally-spaced and the number of samples available is $2^k + 1$ for some integer $k$, then Romberg `romb` integration can be used to obtain high-precision estimates of the integral using the available samples. Romberg integration uses the trapezoid rule at step-sizes related by a power of two and then performs Richardson extrapolation on these estimates to approximate the integral with a higher-degree of accuracy.

In case of arbitrary spaced samples, the two functions `trapz` (defined in numpy [NPT]) and `simps` are available. They are using Newton-Coates formulas of order 1 and 2 respectively to perform integration. The trapezoidal rule approximates the function as a straight line between adjacent points, while Simpson’s rule approximates the function between three adjacent points as a parabola.

For an odd number of samples that are equally spaced Simpson’s rule is exact if the function is a polynomial of order 3 or less. If the samples are not equally spaced, then the result is exact only if the function is a polynomial of order 2 or less.

```python
>>> import numpy as np
>>> def f1(x):
...     return x**2
... >>> def f2(x):
...     return x**3
... >>> x = np.array([1, 3, 4])
>>> y1 = f1(x)
>>> from scipy.integrate import simps
>>> I1 = simps(y1, x)
>>> print(I1)
21.0

This corresponds exactly to

$$\int_1^4 x^2 \, dx = 21,$$

whereas integrating the second function

```
does not correspond to
\[ \int_1^4 x^3 dx = 63.75 \]
because the order of the polynomial in f2 is larger than two.

**Faster integration using low-level callback functions**

A user desiring reduced integration times may pass a C function pointer through `scipy.LowLevelCallable` to `quad`, `dblquad`, `tplquad` or `nquad` and it will be integrated and return a result in Python. The performance increase here arises from two factors. The primary improvement is faster function evaluation, which is provided by compilation of the function itself. Additionally we have a speedup provided by the removal of function calls between C and Python in `quad`. This method may provide a speed improvements of \( \sim 2x \) for trivial functions such as sine but can produce a much more noticeable improvements (10x+) for more complex functions. This feature then, is geared towards a user with numerically intensive integrations willing to write a little C to reduce computation time significantly.

The approach can be used, for example, via `ctypes` in a few simple steps:

1.) Write an integrand function in C with the function signature `double f(int n, double *x, void *user_data)`, where `x` is an array containing the point the function `f` is evaluated at, and `user_data` to arbitrary additional data you want to provide.

```c
/* testlib.c */
double f(int n, double *x, void *user_data) {
    double c = *(double *)user_data;
    return c + x[0] - x[1] * x[2]; /* corresponds to c + z - y * z */
}
```

2.) Now compile this file to a shared/dynamic library (a quick search will help with this as it is OS-dependent). The user must link any math libraries, etc. used. On Linux this looks like:

```
$ gcc -shared -fPIC -o testlib.so testlib.c
```

The output library will be referred to as `testlib.so`, but it may have a different file extension. A library has now been created that can be loaded into Python with `ctypes`.

3.) Load shared library into Python using `ctypes` and set `restypes` and `argtypes` - this allows Scipy to interpret the function correctly:

```python
import os, ctypes
from scipy import integrate,.LowLevelCallable

lib = ctypes.CDLL(os.path.abspath('testlib.so'))
lib.f.restype = ctypes.c_double
lib.f.argtypes = (ctypes.c_int, ctypes.POINTER(ctypes.c_double), ctypes.c_void_p)

c = ctypes.c_double(1.0)
user_data = ctypes.cast(ctypes.pointer(c), ctypes.c_void_p)

func = LowLevelCallable(lib.f, user_data)
```

4.) Now integrate the library function as normally, here using `nquad`:
The Python tuple is returned as expected in a reduced amount of time. All optional parameters can be used with this method including specifying singularities, infinite bounds, etc.

**Ordinary differential equations (odeint)**

Integrating a set of ordinary differential equations (ODEs) given initial conditions is another useful example. The function `odeint` is available in SciPy for integrating a first-order vector differential equation:

\[
\frac{dy}{dt} = f(y, t),
\]

given initial conditions \( y(0) = y_0 \), where \( y \) is a length \( N \) vector and \( f \) is a mapping from \( \mathbb{R}^N \) to \( \mathbb{R}^N \). A higher-order ordinary differential equation can always be reduced to a differential equation of this type by introducing intermediate derivatives into the \( y \) vector.

For example suppose it is desired to find the solution to the following second-order differential equation:

\[
\frac{d^2w}{dz^2} - zw(z) = 0
\]

with initial conditions \( w(0) = \frac{1}{\sqrt{3}} \) and \( \frac{dw}{dz}|_{z=0} = -\frac{1}{\sqrt{3}} \). It is known that the solution to this differential equation with these boundary conditions is the Airy function \( w = \text{Ai}(z) \), which gives a means to check the integrator using `special.airy`.

First, convert this ODE into standard form by setting \( y = \left[ \frac{dw}{dz}, w \right] \) and \( t = z \). Thus, the differential equation becomes

\[
\frac{dy}{dt} = \begin{bmatrix} ty_1 \\ y_0 \end{bmatrix} = \begin{bmatrix} 0 & t \\ 1 & 0 \end{bmatrix} \begin{bmatrix} y_0 \\ y_1 \end{bmatrix} = \begin{bmatrix} 0 & t \\ 1 & 0 \end{bmatrix} y.
\]

In other words,

\[
f(y, t) = A(t) y.
\]

As an interesting reminder, if \( A(t) \) commutes with \( \int_0^t A(\tau) d\tau \) under matrix multiplication, then this linear differential equation has an exact solution using the matrix exponential:

\[
y(t) = \exp \left( \int_0^t A(\tau) d\tau \right) y(0),
\]

However, in this case, \( A(t) \) and its integral do not commute.

There are many optional inputs and outputs available when using `odeint` which can help tune the solver. These additional inputs and outputs are not needed much of the time, however, and the three required input arguments and the output solution suffice. The required inputs are the function defining the derivative, `fprime`, the initial conditions vector, \( y_0 \), and the time points to obtain a solution, \( t \), (with the initial value point as the first element of this sequence). The output to `odeint` is a matrix where each row contains the solution vector at each requested time point (thus, the initial conditions are given in the first output row).

The following example illustrates the use of `odeint` including the usage of the `Dfun` option which allows the user to specify a gradient (with respect to \( y \) ) of the function, \( f(y, t) \).
```python
from scipy.integrate import odeint
from scipy.special import gamma, airy

ty1_0 = 1.0 / 3**2 / gamma(2.0 / 3.0)
y0_0 = -1.0 / 3**2 / gamma(1.0 / 3.0)
y0 = [y0_0, ty1_0]
def func(y, t):
    return [t*y[1], y[0]]

def gradient(y, t):
    return [[0, t], [1, 0]]

x = np.arange(0, 4.0, 0.01)
t = x
ychk = airy(x)[0]
y = odeint(func, y0, t)
y2 = odeint(func, y0, t, Dfun=gradient)

ychk[:36:6]
array([0.355028, 0.339511, 0.324067, 0.308763, 0.293658, 0.278806])
y[:36:6]
array([0.355028, 0.339511, 0.324067, 0.308763, 0.293658, 0.278806])
y2[:36:6]
array([0.355028, 0.339511, 0.324067, 0.308763, 0.293658, 0.278806])
```

**Solving a system with a banded Jacobian matrix**

`odeint` can be told that the Jacobian is banded. For a large system of differential equations that are known to be stiff, this can improve performance significantly.

As an example, we’ll solve the one-dimensional Gray-Scott partial differential equations using the method of lines [MOL]. The Gray-Scott equations for the functions $u(x, t)$ and $v(x, t)$ on the interval $x \in [0, L]$ are

\[
\frac{\partial u}{\partial t} = D_u \frac{\partial^2 u}{\partial x^2} - uv^2 + f(1 - u)
\]

\[
\frac{\partial v}{\partial t} = D_v \frac{\partial^2 v}{\partial x^2} + uv^2 - (f + k)v
\]

where $D_u$ and $D_v$ are the diffusion coefficients of the components $u$ and $v$, respectively, and $f$ and $k$ are constants. (For more information about the system, see [http://groups.csail.mit.edu/mac/projects/amorphous/GrayScott/](http://groups.csail.mit.edu/mac/projects/amorphous/GrayScott/))

We’ll assume Neumann (i.e. “no flux”) boundary conditions:

\[
\frac{\partial u}{\partial x}(0, t) = 0, \quad \frac{\partial v}{\partial x}(0, t) = 0, \quad \frac{\partial u}{\partial x}(L, t) = 0, \quad \frac{\partial v}{\partial x}(L, t) = 0
\]

To apply the method of lines, we discretize the $x$ variable by defining the uniformly spaced grid of $N$ points \{x_0, x_1, \ldots, x_{N-1}\}, with x_0 = 0 and x_{N-1} = L. We define u_j(t) \equiv u(x_k, t) and v_j(t) \equiv v(x_k, t), and replace the $x$ derivatives with finite differences. That is,

\[
\frac{\partial^2 u}{\partial x^2}(x_j, t) \to \frac{u_{j-1}(t) - 2u_j(t) + u_{j+1}(t)}{(\Delta x)^2}
\]
We then have a system of $2N$ ordinary differential equations:

$$
\frac{du_j}{dt} = \frac{D_u}{(\Delta x)^2} (u_{j-1} - 2u_j + u_{j+1}) - u_j v_j^2 + f(1 - u_j)
$$

$$
\frac{dv_j}{dt} = \frac{D_v}{(\Delta x)^2} (v_{j-1} - 2v_j + v_{j+1}) + u_j v_j^2 - (f + k)v_j
$$

(4.1)

For convenience, the $(t)$ arguments have been dropped.

To enforce the boundary conditions, we introduce “ghost” points $x_{-1}$ and $x_N$, and define $u_{-1}(t) \equiv u_1(t)$, $u_N(t) \equiv u_{N-2}(t)$; $v_{-1}(t)$ and $v_N(t)$ are defined analogously.

Then

$$
\frac{du_0}{dt} = \frac{D_u}{(\Delta x)^2} (2u_1 - 2u_0) - u_0 v_0^2 + f(1 - u_0)
$$

$$
\frac{dv_0}{dt} = \frac{D_v}{(\Delta x)^2} (2v_1 - 2v_0) + u_0 v_0^2 - (f + k)v_0
$$

(4.2)

and

$$
\frac{du_{N-1}}{dt} = \frac{D_u}{(\Delta x)^2} (2u_{N-2} - 2u_{N-1}) - u_{N-1} v_{N-1}^2 + f(1 - u_{N-1})
$$

$$
\frac{dv_{N-1}}{dt} = \frac{D_v}{(\Delta x)^2} (2v_{N-2} - 2v_{N-1}) + u_{N-1} v_{N-1}^2 - (f + k)v_{N-1}
$$

(4.3)

Our complete system of $2N$ ordinary differential equations is (4.1) for $k = 1, 2, \ldots, N - 2$, along with (4.2) and (4.3).

We can now starting implementing this system in code. We must combine $\{u_k\}$ and $\{v_k\}$ into a single vector of length $2N$. The two obvious choices are $\{u_0, u_1, \ldots, u_{N-1}, v_0, v_1, \ldots, v_{N-1}\}$ and $\{u_0, v_0, u_1, v_1, \ldots, u_{N-1}, v_{N-1}\}$. Mathematically, it does not matter, but the choice affects how efficiently odeint can solve the system. The reason is how the order affects the pattern of the nonzero elements of the Jacobian matrix.

When the variables are ordered as $\{u_0, u_1, \ldots, u_{N-1}, v_0, v_1, \ldots, v_{N-1}\}$, the pattern of nonzero elements of the Jacobian matrix is

```
* * 0 0 0 0 * 0 0 0 0 0 0
* * 0 0 0 0 * 0 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0 0
```

The Jacobian pattern with variables interleaved as $\{u_0, v_0, u_1, v_1, \ldots, u_{N-1}, v_{N-1}\}$ is

```
* * 0 0 0 0 * 0 0 0 0 0
* * 0 0 0 0 * 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0
0 0 0 0 0 0 * 0 0 0 0 0
```

In both cases, there are just five nontrivial diagonals, but when the variables are interleaved, the bandwidth is much smaller. That is, the main diagonal and the two diagonals immediately above and the two immediately
below the main diagonal are the nonzero diagonals. This is important, because the inputs \texttt{mu} and \texttt{ml} of \texttt{odeint} are the upper and lower bandwidths of the Jacobian matrix. When the variables are interleaved, \texttt{mu} and \texttt{ml} are 2. When the variables are stacked with \{\texttt{v}\} following \{\texttt{u}\}, the upper and lower bandwidths are \texttt{N}.

With that decision made, we can write the function that implements the system of differential equations.

First, we define the functions for the source and reaction terms of the system:

```python
def G(u, v, f, k):
    return f * (1 - u) - u * v ** 2

def H(u, v, f, k):
    return -(f + k) * v + u * v ** 2
```

Next we define the function that computes the right-hand-side of the system of differential equations:

```python
def grayscott1d(y, t, f, k, Du, Dv, dx):
    
    """
    Differential equations for the 1D Gray-Scott equations.
    
    The ODEs are derived using the method of lines.
    """
    # The vectors \texttt{u} and \texttt{v} are interleaved in \texttt{y}. We define
    # views of \texttt{u} and \texttt{v} by slicing \texttt{y}.
    u = y[::2]
    v = y[1::2]

    # \texttt{dydt} is the return value of this function.
    dydt = np.empty_like(y)

    # Just like \texttt{u} and \texttt{v} are views of the interleaved vectors
    # in \texttt{y}, \texttt{dudt} and \texttt{dvdt} are views of the interleaved output
    # vectors in \texttt{dydt}.
    dudt = dydt[::2]
    dvdt = dydt[1::2]

    # Compute \texttt{du/dt} and \texttt{dv/dt}. The end points and the interior points
    # are handled separately.
    dudt[0] = G(u[0], v[0], f, k) + Du * (-2.0 * u[0] + 2.0 * u[1]) / dx ** 2
    dudt[1:-1] = G(u[1:-1], v[1:-1], f, k) + Du * np.diff(u, 2) / dx ** 2
    dudt[-1] = G(u[-1], v[-1], f, k) + Du * (-2.0 * u[-1] + 2.0 * u[-2]) / dx ** 2
    dvdt[0] = H(u[0], v[0], f, k) + Dv * (-2.0 * v[0] + 2.0 * v[1]) / dx ** 2
    dvdt[1:-1] = H(u[1:-1], v[1:-1], f, k) + Dv * np.diff(v, 2) / dx ** 2
    dvdt[-1] = H(u[-1], v[-1], f, k) + Dv * (-2.0 * v[-1] + 2.0 * v[-2]) / dx ** 2

    return dydt
```

We won’t implement a function to compute the Jacobian, but we will tell \texttt{odeint} that the Jacobian matrix is banded. This allows the underlying solver (LSODA) to avoid computing values that it knows are zero. For a large system, this improves the performance significantly, as demonstrated in the following ipython session.

First, we define the required inputs:
In [31]: y0 = np.random.randn(5000)
In [32]: t = np.linspace(0, 50, 11)
In [33]: f = 0.024
In [34]: k = 0.055
In [35]: Du = 0.01
In [36]: Dv = 0.005
In [37]: dx = 0.025

Time the computation without taking advantage of the banded structure of the Jacobian matrix:

In [38]: %timeit sola = odeint(grayscott1d, y0, t, args=(f, k, Du, Dv, dx))
    ...: 1 loop, best of 3: 25.2 s per loop

Now set ml=2 and mu=2, so odeint knows that the Jacobian matrix is banded:

In [39]: %timeit solb = odeint(grayscott1d, y0, t, args=(f, k, Du, Dv, dx), ml=2, mu=2)
    ...: 10 loops, best of 3: 191 ms per loop

That is quite a bit faster!

Let’s ensure that they have computed the same result:

In [41]: np.allclose(sola, solb)
Out[41]: True

References

4.1.5 Optimization (scipy.optimize)

The scipy.optimize package provides several commonly used optimization algorithms. A detailed listing is available: scipy.optimize (can also be found by help(scipy.optimize)).

The module contains:

1. Unconstrained and constrained minimization of multivariate scalar functions (minimize) using a variety of algorithms (e.g. BFGS, Nelder-Mead simplex, Newton Conjugate Gradient, COBYLA or SLSQP)
2. Global (brute-force) optimization routines (e.g. basinhopping, differential_evolution)
3. Least-squares minimization (least_squares) and curve fitting (curve_fit) algorithms
4. Scalar univariate functions minimizers (minimize_scalar) and root finders (root_scalar)
5. Multivariate equation system solvers (root) using a variety of algorithms (e.g. hybrid Powell, Levenberg-Marquardt or large-scale methods such as Newton-Krylov).

Below, several examples demonstrate their basic usage.

Unconstrained minimization of multivariate scalar functions (minimize)

The minimize function provides a common interface to unconstrained and constrained minimization algorithms for multivariate scalar functions in scipy.optimize. To demonstrate the minimization function
consider the problem of minimizing the Rosenbrock function of $N$ variables:

$$f(x) = \sum_{i=2}^{N} 100 \left[(x_{i+1} - x_i^2)^2 + (1 - x_i)^2\right].$$

The minimum value of this function is 0 which is achieved when $x_i = 1$.

Note that the Rosenbrock function and its derivatives are included in `scipy.optimize`. The implementations shown in the following sections provide examples of how to define an objective function as well as its jacobian and hessian functions.

**Nelder-Mead Simplex algorithm (method='Nelder-Mead')**

In the example below, the `minimize` routine is used with the Nelder-Mead simplex algorithm (selected through the `method` parameter):

```python
>>> import numpy as np
>>> from scipy.optimize import minimize

>>> def rosen(x):
...    """The Rosenbrock function""
...    return sum(100.0*(x[1:]-x[:-1]**2.0)**2.0 + (1-x[:-1])**2.0)

>>> x0 = np.array([1.3, 0.7, 0.8, 1.9, 1.2])
>>> res = minimize(rosen, x0, method='nelder-mead',
...              options={'xtol': 1e-8, 'disp': True})
Optimization terminated successfully.
Current function value: 0.000000
Iterations: 339
Function evaluations: 571

>>> print(res.x)
[1. 1. 1. 1. 1.]
```

The simplex algorithm is probably the simplest way to minimize a fairly well-behaved function. It requires only function evaluations and is a good choice for simple minimization problems. However, because it does not use any gradient evaluations, it may take longer to find the minimum.

Another optimization algorithm that needs only function calls to find the minimum is Powell’s method available by setting `method='powell'` in `minimize`.

**Broyden-Fletcher-Goldfarb-Shanno algorithm (method='BFGS')**

In order to converge more quickly to the solution, this routine uses the gradient of the objective function. If the gradient is not given by the user, then it is estimated using first-differences. The Broyden-Fletcher-Goldfarb-Shanno (BFGS) method typically requires fewer function calls than the simplex algorithm even when the gradient must be estimated.

To demonstrate this algorithm, the Rosenbrock function is again used. The gradient of the Rosenbrock function is the vector:

$$\frac{\partial f}{\partial x_j} = \sum_{i=1}^{N} 200 (x_i - x_{i-1}^2) \delta_{i,j} - 2x_{i-1} \delta_{i-1,j} - 2 (1 - x_i-1) \delta_{i-1,j} = 200 (x_j - x_{j-1}^2) - 400x_j (x_{j+1} - x_j^2) - 2 (1 - x_j).$$
This expression is valid for the interior derivatives. Special cases are
\[
\frac{\partial f}{\partial x_0} = -400x_0 \left( x_1 - x_0^2 \right) - 2 \left( 1 - x_0 \right), \\
\frac{\partial f}{\partial x_{N-1}} = 200 \left( x_{N-1} - x_{N-2}^2 \right).
\]

A Python function which computes this gradient is constructed by the code-segment:

```python
def rosen_der(x):
    xm = x[1:-1]
    xm_m1 = x[:-2]
    xm_p1 = x[2:]
    der = np.zeros_like(x)
    der[1:-1] = 200 * (xm - xm_m1 * 2) - 400 * (xm_p1 - xm * 2) * xm - 2 * (1 - x_m)
    der[0] = -400 * x[0] * (x[1] - x[0] * 2) + 2 * (1 - x[0] - 2 * (1 - x[0]))
    der[-1] = 200 * (x[-1] - x[-2] * 2)
    return der
```

This gradient information is specified in the `minimize` function through the `jac` parameter as illustrated below.

```python
res = minimize(rosen, x0, method='BFGS', jac=rosen_der, 
                options={'disp': True})
```

Optimization terminated successfully.
Current function value: 0.000000
Iterations: 51
Function evaluations: 63
Gradient evaluations: 63

```python
array([1.0, 1.0, 1.0, 1.0, 1.0])
```

**Newton-Conjugate-Gradient algorithm (method='Newton-CG')**

Newton-Conjugate Gradient algorithm is a modified Newton’s method and uses a conjugate gradient algorithm to (approximately) invert the local Hessian \( H_{NW} \). Newton’s method is based on fitting the function locally to a quadratic form:

\[
f(x) \approx f(x_0) + \nabla f(x_0) \cdot (x - x_0) + \frac{1}{2} (x - x_0)^T H(x_0) (x - x_0).
\]

where \( H(x_0) \) is a matrix of second-derivatives (the Hessian). If the Hessian is positive definite then the local minimum of this function can be found by setting the gradient of the quadratic form to zero, resulting in

\[
x_{opt} = x_0 - H^{-1} \nabla f.
\]

The inverse of the Hessian is evaluated using the conjugate-gradient method. An example of employing this method to minimizing the Rosenbrock function is given below. To take full advantage of the Newton-CG method, a function which computes the Hessian must be provided. The Hessian matrix itself does not need to be constructed, only a vector which is the product of the Hessian with an arbitrary vector needs to be available to the minimization routine. As a result, the user can provide either a function to compute the Hessian matrix, or a function to compute the product of the Hessian with an arbitrary vector.

**Full Hessian example:**

The Hessian of the Rosenbrock function is

\[
H_{ij} = \frac{\partial^2 f}{\partial x_i \partial x_j} = 200 (\delta_{i,j} - 2x_{i-1} \delta_{i-1,j}) - 400x_i (\delta_{i+1,j} - 2x_i \delta_{i,j}) - 400 \delta_{i,j} (x_{i+1} - x_i^2) + 2 \delta_{i,j},
\]

\[
= (202 + 1200x_i^2 - 400x_{i+1}) \delta_{i,j} - 400x_i \delta_{i+1,j} - 400x_{i-1} \delta_{i-1,j},
\]
if $i, j \in [1, N - 2]$ with $i, j \in [0, N - 1]$ defining the $N \times N$ matrix. Other non-zero entries of the matrix are

\[
\frac{\partial^2 f}{\partial x_0 \partial x_1} = \frac{\partial^2 f}{\partial x_1 \partial x_0} = -400 x_0,
\]

\[
\frac{\partial^2 f}{\partial x_{N-1} \partial x_{N-2}} = \frac{\partial^2 f}{\partial x_{N-2} \partial x_{N-1}} = -400 x_{N-2},
\]

\[
\frac{\partial^2 f}{\partial x_{k-1} \partial x_k} = 200.
\]

For example, the Hessian when $N = 5$ is

\[
H = \begin{bmatrix}
1200x_0^2 - 400x_1 + 2 & -400x_0 & 0 & 0 & 0 \\
-400x_0 & 202 + 1200x_1^2 - 400x_2 & -400x_1 & 0 & 0 \\
0 & -400x_1 & 202 + 1200x_2^2 - 400x_3 & -400x_2 & 0 \\
0 & 0 & -400x_2 & 202 + 1200x_3^2 - 400x_4 & -400x_3 \\
0 & 0 & 0 & 0 & 200
\end{bmatrix}.
\]

The code which computes this Hessian along with the code to minimize the function using Newton-CG method is shown in the following example:

```python
>>> def rosen_hess(x):
...     x = np.asarray(x)
...     H = np.diag(-400*x[:-1], 1) - np.diag(400*x[:-1], -1)
...     diagonal = np.zeros_like(x)
...     diagonal[0] = 1200*x[0]**2 - 400*x[1] + 2
...     diagonal[-1] = 200
...     diagonal[1:-1] = 202 + 1200*x[1]**2 - 400*x[2] - 400*x[1]**2
...     H = H + np.diag(diagonal)
...     return H
```

```python
>>> res = minimize(rosen, x0, method='Newton-CG',
...                 jac=rosen_der, hess=rosen_hess,
...                 options={'xtol': 1e-8, 'disp': True})
Optimization terminated successfully.
Current function value: 0.000000
Iterations: 19  # may vary
Function evaluations: 22
Gradient evaluations: 19
Hessian evaluations: 19
```

```python
>>> res.x
array([1., 1., 1., 1., 1.])
```

**Hessian product example:**

For larger minimization problems, storing the entire Hessian matrix can consume considerable time and memory. The Newton-CG algorithm only needs the product of the Hessian times an arbitrary vector. As a result, the user can supply code to compute this product rather than the full Hessian by giving a hess function which take the minimization vector as the first argument and the arbitrary vector as the second argument (along with extra arguments passed to the function to be minimized). If possible, using Newton-CG with the Hessian product option is probably the fastest way to minimize the function.
In this case, the product of the Rosenbrock Hessian with an arbitrary vector is not difficult to compute. If \( p \) is the arbitrary vector, then \( H(x)p \) has elements:

\[
H(x)p = \begin{bmatrix}
(1200x_0^2 - 400x_1 + 2)p_0 - 400x_0p_1 \\
-400x_{i-1}p_{i-1} + (202 + 1200x_i^2 - 400x_{i+1})p_i - 400x_ip_{i+1} \\
\vdots \\
-400x_{N-2}p_{N-2} + 200p_{N-1}
\end{bmatrix}.
\]

Code which makes use of this Hessian product to minimize the Rosenbrock function using \texttt{minimize} follows:

```python
>>> def rosen_hess_p(x, p):
...     x = np.asarray(x)
...     Hp = np.zeros_like(x)
...     Hp[0] = (1200*x[0]**2 - 400*x[1] + 2)*p[0] - 400*x[0]*p[1]
...     Hp[1:-1] = -400*x[1:-2]*p[1:-2] + (202+1200*x[1:-1]**2-400*x[2:])*p[1:-1] \
...               -400*x[1:-1]*p[2:] 
...     Hp[-1] = -400*x[-2]*p[-2] + 200*p[-1]
...     return Hp
```

According to [NW] p. 170 the \texttt{Newton-CG} algorithm can be inefficient when the Hessian is ill-conditioned because of the poor quality search directions provided by the method in those situations. The method \texttt{trust-ncg}, according to the authors, deals more effectively with this problematic situation and will be described next.

**Trust-Region Newton-Conjugate-Gradient Algorithm (method='trust-ncg')**

The Newton-CG method is a line search method: it finds a direction of search minimizing a quadratic approximation of the function and then uses a line search algorithm to find the (nearly) optimal step size in that direction. An alternative approach is to, first, fix the step size limit \( \Delta \) and then find the optimal step \( p \) inside the given trust-radius by solving the following quadratic subproblem:

\[
\min_p f(x_k) + \nabla f(x_k) \cdot p + \frac{1}{2}p^T H(x_k) p; \\
\text{subject to: } \|p\| \leq \Delta.
\]

The solution is then updated \( x_{k+1} = x_k + p \) and the trust-radius \( \Delta \) is adjusted according to the degree of agreement of the quadratic model with the real function. This family of methods is known as trust-region methods. The \texttt{trust-ncg} algorithm is a trust-region method that uses a conjugate gradient algorithm to solve the trust-region subproblem [NW].
Full Hessian example:

```python
code
>>> res = minimize(rosen, x0, method='trust-nck',
...                         jac=rosen_der, hess=rosen_hess,
...                         options={'gtol': 1e-8, 'disp': True})
Optimization terminated successfully.
   Current function value: 0.000000
   Iterations: 20  # may vary
   Function evaluations: 21
   Gradient evaluations: 20
   Hessian evaluations: 19

>>> res.x
array([1., 1., 1., 1., 1.])
```

Hessian product example:

```python
code
>>> res = minimize(rosen, x0, method='trust-nck',
...                         jac=rosen_der, hess=rosen_hess,
...                         options={'gtol': 1e-8, 'disp': True})
Optimization terminated successfully.
   Current function value: 0.000000
   Iterations: 20  # may vary
   Function evaluations: 21
   Gradient evaluations: 20
   Hessian evaluations: 0

>>> res.x
array([1., 1., 1., 1., 1.])
```

**Trust-Region Truncated Generalized Lanczos / Conjugate Gradient Algorithm (method='trust-krylov')**

Similar to the trust-nck method, the trust-krylov method is a method suitable for large-scale problems as it uses the hessian only as linear operator by means of matrix-vector products. It solves the quadratic subproblem more accurately than the trust-nck method.

\[
\min_B f(x_k) + \nabla f(x_k) \cdot p + \frac{1}{2} p^T H(x_k) p,
\]

subject to: \( \|p\| \leq \Delta \).

This method wraps the [TRLIB](https://github.com/PyTrILIB/TrILIB) implementation of the [GLTR](https://github.com/PyTrILIB/TrILIB) method solving exactly a trust-region subproblem restricted to a truncated Krylov subspace. For indefinite problems it is usually better to use this method as it reduces the number of nonlinear iterations at the expense of few more matrix-vector products per subproblem solve in comparison to the trust-nck method.

Full Hessian example:

```python
code
>>> res = minimize(rosen, x0, method='trust-krylov',
...                         jac=rosen_der, hess=rosen_hess,
...                         options={'gtol': 1e-8, 'disp': True})
Optimization terminated successfully.
   Current function value: 0.000000
   Iterations: 19  # may vary
   Function evaluations: 20
   Gradient evaluations: 20
   Hessian evaluations: 18
```

(continues on next page)
Hessian product example:

```python
>>> res = minimize(rosen, x0, method='trust-krylov',
...                  jac=rosen_der, hess=rosen_hess_p,
...                  options={'gtol': 1e-8, 'disp': True})
Optimization terminated successfully.
Current function value: 0.000000
Iterations: 19 # may vary
Function evaluations: 20
Gradient evaluations: 20
Hessian evaluations: 0
```

```python
>>> res.x
array([1., 1., 1., 1., 1.])
```

Trust-Region Nearly Exact Algorithm (method='trust-exact')

All methods Newton-CG, trust-ncg and trust-krylov are suitable for dealing with large-scale problems (problems with thousands of variables). That is because the conjugate gradient algorithm approximately solve the trust-region subproblem (or invert the Hessian) by iterations without the explicit Hessian factorization. Since only the product of the Hessian with an arbitrary vector is needed, the algorithm is specially suited for dealing with sparse Hessians, allowing low storage requirements and significant time savings for those sparse problems.

For medium-size problems, for which the storage and factorization cost of the Hessian are not critical, it is possible to obtain a solution within fewer iteration by solving the trust-region subproblems almost exactly. To achieve that, a certain nonlinear equations is solved iteratively for each quadratic subproblem \([CGT]\). This solution requires usually 3 or 4 Cholesky factorizations of the Hessian matrix. As the result, the method converges in fewer number of iterations and takes fewer evaluations of the objective function than the other implemented trust-region methods. The Hessian product option is not supported by this algorithm. An example using the Rosenbrock function follows:

```python
>>> res = minimize(rosen, x0, method='trust-exact',
...                  jac=rosen_der, hess=rosen_hess,
...                  options={'gtol': 1e-8, 'disp': True})
Optimization terminated successfully.
Current function value: 0.000000
Iterations: 13 # may vary
Function evaluations: 14
Gradient evaluations: 13
Hessian evaluations: 14
```

```python
>>> res.x
array([1., 1., 1., 1., 1.])
```

Constrained minimization of multivariate scalar functions (minimize)

The minimize function provides algorithms for constrained minimization, namely 'trust-constr', 'SLSQP' and 'COBYLA'. They require the constraints to be defined using slightly different structures. The method 'trust-constr' requires the constraints to be defined as a sequence of objects LinearConstraint and NonlinearConstraint. Methods 'SLSQP' and 'COBYLA', on the other hand, require constraints to be defined as a sequence of dictionaries, with keys type, fun and jac.
As an example let us consider the constrained minimization of the Rosenbrock function:

\[
\begin{align*}
\text{min} & \quad 100 (x_1 - x_0^2)^2 + (1 - x_0)^2 \\
\text{subject to:} & \quad x_0 + 2x_1 \leq 1 \\
& \quad x_0^2 + x_1 \leq 1 \\
& \quad x_0^2 - x_1 \leq 1 \\
& \quad 2x_0 + x_1 = 1 \\
& \quad 0 \leq x_0 \leq 1 \\
& \quad -0.5 \leq x_1 \leq 2.0.
\end{align*}
\]

This optimization problem has the unique solution \([x_0, x_1] = [0.4149, 0.1701]\), for which only the first and fourth constraints are active.

**Trust-Region Constrained Algorithm (method=’trust-constr’)**

The trust-region constrained method deals with constrained minimization problems of the form:

\[
\begin{align*}
\text{min} & \quad f(x) \\
\text{subject to:} & \quad c^j \leq c(x) \leq c^u, \\
& \quad x^l \leq x \leq x^u.
\end{align*}
\]

When \(c^j \leq c^u\) the method reads the \(j\)-th constraint as an equality constraint and deals with it accordingly. Besides that, one-sided constraint can be specified by setting the upper or lower bound to \(np.inf\) with the appropriate sign.

The implementation is based on [EQSQP] for equality constraint problems and on [TRIP] for problems with inequality constraints. Both are trust-region type algorithms suitable for large-scale problems.

### Defining Bounds Constraints:

The bound constraints \(0 \leq x_0 \leq 1\) and \(-0.5 \leq x_1 \leq 2.0\) are defined using a *Bounds* object.

```python
>>> from scipy.optimize import Bounds
>>> bounds = Bounds([0, -0.5], [1.0, 2.0])
```

### Defining Linear Constraints:

The constraints \(x_0 + 2x_1 \leq 1\) and \(2x_0 + x_1 = 1\) can be written in the linear constraint standard format:

\[
\begin{pmatrix}
-\infty \\
1
\end{pmatrix} \leq \begin{bmatrix} 1 & 2 \\ 2 & 1 \end{bmatrix} \begin{bmatrix} x_0 \\ x_1 \end{bmatrix} \leq \begin{bmatrix} 1 \\ 1 \end{bmatrix},
\]

and defined using a *LinearConstraint* object.

```python
>>> from scipy.optimize import LinearConstraint
>>> linear_constraint = LinearConstraint([[1, 2], [2, 1]], [-np.inf, 1], [1, 1])
```

### Defining Nonlinear Constraints:

The nonlinear constraint:

\[
c(x) = \begin{bmatrix} x_0^2 + x_1 \\ x_0^2 - x_1 \end{bmatrix} \leq \begin{bmatrix} 1 \\ 1 \end{bmatrix},
\]

with Jacobian matrix:

\[
J(x) = \begin{bmatrix} 2x_0 & 1 \\ 2x_0 & -1 \end{bmatrix}.
\]
and linear combination of the Hessians:

\[ H(x, v) = \sum_{i=0}^{1} v_i \nabla^2 c_i(x) = v_0 \begin{bmatrix} 2 & 0 \\ 0 & 0 \end{bmatrix} + v_1 \begin{bmatrix} 2 & 0 \\ 0 & 0 \end{bmatrix}, \]

is defined using a `NonlinearConstraint` object.

```python
>>> def cons_f(x):
...     return [x[0]**2 + x[1], x[0]**2 - x[1]]
>>> def cons_J(x):
...     return [[2*x[0], 1], [2*x[0], -1]]
>>> def cons_H(x, v):
...     return v[0] * np.array([[2, 0], [0, 0]]) + v[1] * np.array([[2, 0], [0, 0]])
>>> from scipy.optimize import NonlinearConstraint
>>> nonlinear_constraint = NonlinearConstraint(cons_f, -np.inf, 1, jac=cons_J, hess=cons_H)
```

Alternatively, it is also possible to define the Hessian \( H(x, v) \) as a sparse matrix,

```python
>>> from scipy.sparse import csc_matrix
>>> def cons_H_sparse(x, v):
...     return v[0] * csc_matrix([[2, 0], [0, 0]]) + v[1] * csc_matrix([[2, 0], [0, 0]])
>>> nonlinear_constraint = NonlinearConstraint(cons_f, -np.inf, 1, jac=cons_J, hess=cons_H_sparse)
```

or as a `LinearOperator` object.

```python
>>> from scipy.sparse.linalg import LinearOperator
>>> def cons_H_linear_operator(x, v):
...     def matvec(p):
...         return np.array([p[0]*2*(v[0]+v[1]), 0])
...     return LinearOperator((2, 2), matvec=matvec)
>>> nonlinear_constraint = NonlinearConstraint(cons_f, -np.inf, 1, jac=cons_J, hess=cons_H_linear_operator)
```

When the evaluation of the Hessian \( H(x, v) \) is difficult to implement or computationally infeasible, one may use `HessianUpdateStrategy`. Currently available strategies are `BFGS` and `SR1`.

```python
>>> from scipy.optimize import BFGS
>>> nonlinear_constraint = NonlinearConstraint(cons_f, -np.inf, 1, jac=cons_J, hess=BFGS())
```

Alternatively, the Hessian may be approximated using finite differences.

```python
>>> nonlinear_constraint = NonlinearConstraint(cons_f, -np.inf, 1, jac=cons_J, hess='2-point')
```

The Jacobian of the constraints can be approximated by finite differences as well. In this case, however, the Hessian cannot be computed with finite differences and needs to be provided by the user or defined using `HessianUpdateStrategy`.

```python
>>> nonlinear_constraint = NonlinearConstraint(cons_f, -np.inf, 1, jac='2-point', hess=BFGS())
```
Solving the Optimization Problem:

The optimization problem is solved using:

```python
>>> x0 = np.array([0.5, 0])
>>> res = minimize(rosen, x0, method='trust-constr', jac=rosen_der, hess=rosen_hess,
...                 constraints=[linear_constraint, nonlinear_constraint],
...                 options={'verbose': 1}, bounds=bounds)
# may vary
`gtol` termination condition is satisfied.
Number of iterations: 12, function evaluations: 8, CG iterations: 7, optimality: 2.99e-09, constraint violation: 1.11e-16, execution time: 0.016 s.
>>> print(res.x)
[0.41494531 0.17010937]
```

When needed, the objective function Hessian can be defined using a `LinearOperator` object,

```python
>>> def rosen_hess_linop(x):
...     def matvec(p):
...         return rosen_hess_p(x, p)
...     return LinearOperator((2, 2), matvec=matvec)
>>> res = minimize(rosen, x0, method='trust-constr', jac=rosen_der, hess=rosen_hess_linop,
...                 constraints=[linear_constraint, nonlinear_constraint],
...                 options={'verbose': 1}, bounds=bounds)
# may vary
`gtol` termination condition is satisfied.
Number of iterations: 12, function evaluations: 8, CG iterations: 7, optimality: 2.99e-09, constraint violation: 1.11e-16, execution time: 0.018 s.
>>> print(res.x)
[0.41494531 0.17010937]
```

or a Hessian-vector product through the parameter `hessp`.

```python
>>> res = minimize(rosen, x0, method='trust-constr', jac=rosen_der, hess=rosen_hess_p,
...                 constraints=[linear_constraint, nonlinear_constraint],
...                 options={'verbose': 1}, bounds=bounds)
# may vary
`gtol` termination condition is satisfied.
Number of iterations: 12, function evaluations: 8, CG iterations: 7, optimality: 2.99e-09, constraint violation: 1.11e-16, execution time: 0.018 s.
>>> print(res.x)
[0.41494531 0.17010937]
```

Alternatively, the first and second derivatives of the objective function can be approximated. For instance, the Hessian can be approximated with `SR1` quasi-Newton approximation and the gradient with finite differences.

```python
>>> from scipy.optimize import SR1
>>> res = minimize(rosen, x0, method='trust-constr', jac="2-point", hess=SR1(),
...                 constraints=[linear_constraint, nonlinear_constraint],
...                 options={'verbose': 1}, bounds=bounds)
# may vary
`gtol` termination condition is satisfied.
Number of iterations: 12, function evaluations: 24, CG iterations: 7, optimality: 4.48e-09, constraint violation: 0.00e+00, execution time: 0.016 s.
```

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Sequential Least SQuares Programming (SLSQP) Algorithm (method='SLSQP')

The SLSQP method deals with constrained minimization problems of the form:

\[
\min_x f(x)
\]

subject to:

\[
c_j(x) = 0, \quad j \in \mathcal{E}
\]
\[
c_j(x) \geq 0, \quad j \in \mathcal{I}
\]
\[
l_i \leq x_i \leq u_i, \quad i = 1, \ldots, N.
\]

Where \(\mathcal{E}\) or \(\mathcal{I}\) are sets of indices containing equality and inequality constraints.

Both linear and nonlinear constraints are defined as dictionaries with keys type, fun and jac.

```python
>>> ineq_cons = {'type': 'ineq',
...               'fun': lambda x: np.array([1 - x[0] - 2*x[1],
...                                         1 - x[0]**2 - x[1],
...                                         1 - x[0]**2 + x[1]]),
...               'jac': lambda x: np.array([[-1.0, -2.0],
...                                           [-2*x[0], -1.0],
...                                           [-2*x[0], 1.0]])
...}
>>> eq_cons = {'type': 'eq',
...             'fun': lambda x: np.array([2*x[0] + x[1] - 1]),
...             'jac': lambda x: np.array([2.0, 1.0])}
```

And the optimization problem is solved with:

```python
>>> x0 = np.array([0.5, 0])
>>> res = minimize(rosen, x0, method='SLSQP', jac=rosen_der,
...                 constraints=[eq_cons, ineq_cons], options={'ftol': 1e-9, 'disp': True})
...# may vary
Optimization terminated successfully.  (Exit mode 0)
Current function value: 0.342717574857755
Iterations: 5
Function evaluations: 6
Gradient evaluations: 5
```

Most of the options available for the method 'trust-constr' are not available for 'SLSQP'.

Least-squares minimization (least_squares)

SciPy is capable of solving robustified bound constrained nonlinear least-squares problems:

\[
\min_x \frac{1}{2} \sum_{i=1}^{m} \rho (f_i(x))^2
\]

subject to \(lb \leq x \leq ub\)

Here \(f_i(x)\) are smooth functions from \(\mathbb{R}^n\) to \(\mathbb{R}\), we refer to them as residuals. The purpose of a scalar valued function \(\rho(\cdot)\) is to reduce the influence of outlier residuals and contribute to robustness of the solution, we
refer to it as a loss function. A linear loss function gives a standard least-squares problem. Additionally, constraints in a form of lower and upper bounds on some of $x_j$ are allowed.

All methods specific to least-squares minimization utilize a $m \times n$ matrix of partial derivatives called Jacobian and defined as $J_{ij} = \partial f_i / \partial x_j$. It is highly recommended to compute this matrix analytically and pass it to \texttt{least\_squares}, otherwise it will be estimated by finite differences which takes a lot of additional time and can be very inaccurate in hard cases.

Function \texttt{least\_squares} can be used for fitting a function $\varphi(t; \mathbf{x})$ to empirical data $\{(t_i, y_i), i = 0, \ldots, m-1\}$. To do this one should simply precompute residuals as $f_i(\mathbf{x}) = w_i(\varphi(t_i; \mathbf{x}) - y_i)$, where $w_i$ are weights assigned to each observation.

**Example of solving a fitting problem**

Here we consider “Analysis of an Enzyme Reaction” problem formulated in\(^1\). There are 11 residuals defined as

$$f_i(x) = \frac{x_0(u_i^3 + u_i x_1)}{u_i^2 + u_i x_2 + x_3} - y_i, \quad i = 0, \ldots, 10,$$

where $y_i$ are measurement values and $u_i$ are values of the independent variable. The unknown vector of parameters is $\mathbf{x} = (x_0, x_1, x_2, x_3)^T$. As was said previously, it is recommended to compute Jacobian matrix in a closed form:

$$J_{ij} = \frac{\partial f_i}{\partial x_j} = \begin{cases} \frac{u_i^2 + u_i x_1}{u_i^2 + u_i x_2 + x_3} & i = j = 0 \\ \frac{u_i x_0}{u_i^2 + u_i x_2 + x_3} & i = j = 1 \\ -\frac{x_0(u_i^2 + u_i x_1)u_i}{(u_i^2 + u_i x_2 + x_3)^2} & i = j = 2 \\ -\frac{x_0(u_i^2 + u_i x_1)}{(u_i^2 + u_i x_2 + x_3)^2} & i = j = 3 \end{cases} \quad (4.6, 4.7, 4.8, 4.9)$$

We are going to use the “hard” starting point defined in\(^1\). To find a physically meaningful solution, avoid potential division by zero and assure convergence to the global minimum we impose constraints $0 \leq x_j \leq 100, j = 0, 1, 2, 3$.

The code below implements least-squares estimation of $\mathbf{x}$ and finally plots the original data and the fitted model function:

```python
>>> from scipy.optimize import least_squares

>>> def model(x, u):
...     return x[0] * (u ** 2 + x[1] * u) / (u ** 2 + x[2] * u + x[3])

>>> def fun(x, u, y):
...     return model(x, u) - y

>>> def jac(x, u, y):
...     J = np.empty((u.size, x.size))
...     den = u ** 2 + x[2] * u + x[3]
...     num = u ** 2 + x[1] * u
...     J[: , 0] = num / den
...     J[: , 1] = x[0] * u / den

(continues on next page)

\(^1\) Brett M. Averick et al., “The MINPACK-2 Test Problem Collection”.

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Further examples
Three interactive examples below illustrate usage of least_squares in greater detail.

1. **Large-scale bundle adjustment in scipy** demonstrates large-scale capabilities of least_squares and how to efficiently compute finite difference approximation of sparse Jacobian.

2. **Robust nonlinear regression in scipy** shows how to handle outliers with a robust loss function in a nonlinear regression.
3. **Solving a discrete boundary-value problem in scipy** examines how to solve a large system of equations and use bounds to achieve desired properties of the solution.

For the details about mathematical algorithms behind the implementation refer to documentation of `least_squares`.

**Univariate function minimizers (minimize_scalar)**

Often only the minimum of an univariate function (i.e. a function that takes a scalar as input) is needed. In these circumstances, other optimization techniques have been developed that can work faster. These are accessible from the `minimize_scalar` function which proposes several algorithms.

**Unconstrained minimization (method='brent')**

There are actually two methods that can be used to minimize an univariate function: `brent` and `golden`, but `golden` is included only for academic purposes and should rarely be used. These can be respectively selected through the `method` parameter in `minimize_scalar`. The `brent` method uses Brent’s algorithm for locating a minimum. Optimally a bracket (the `bracket` parameter) should be given which contains the minimum desired. A bracket is a triple \((a; b; c)\) such that \(f(a) > f(b) < f(c)\) and \(a < b < c\). If this is not given, then alternatively two starting points can be chosen and a bracket will be found from these points using a simple marching algorithm. If these two starting points are not provided 0 and 1 will be used (this may not be the right choice for your function and result in an unexpected minimum being returned).

Here is an example:

```python
>>> from scipy.optimize import minimize_scalar
>>> f = lambda x: (x - 2) * (x + 1)**2
>>> res = minimize_scalar(f, method='brent')
>>> print(res.x)
1.0
```

**Bounded minimization (method='bounded')**

Very often, there are constraints that can be placed on the solution space before minimization occurs. The `bounded` method in `minimize_scalar` is an example of a constrained minimization procedure that provides a rudimentary interval constraint for scalar functions. The interval constraint allows the minimization to occur only between two fixed endpoints, specified using the mandatory `bounds` parameter.

For example, to find the minimum of \(J_1(x)\) near \(x = 5\), `minimize_scalar` can be called using the interval \([4, 7]\) as a constraint. The result is \(x_{\text{min}} = 5.3314\):

```python
>>> from scipy.special import j1
>>> res = minimize_scalar(j1, bounds=(4, 7), method='bounded')
>>> res.x
5.33144184241
```

**Custom minimizers**

Sometimes, it may be useful to use a custom method as a (multivariate or univariate) minimizer, for example when using some library wrappers of `minimize` (e.g. `basinhopping`).

We can achieve that by, instead of passing a method name, we pass a callable (either a function or an object implementing a \(\_\_\_\text{call}\_\_\) method) as the `method` parameter.

Let us consider an (admittedly rather virtual) need to use a trivial custom multivariate minimization method that will just search the neighborhood in each dimension independently with a fixed step size:

```python
>>> from scipy.optimize import OptimizeResult
>>> def custmin(fun, x0, args=(), maxfev=None, stepsize=0.1,
```

(continues on next page)
... maxiter=100, callback=None, **options):
... bestx = x0
... besty = fun(x0)
... funcalls = 1
... niter = 0
... improved = True
... stop = False
...
... while improved and not stop and niter < maxiter:
...     improved = False
...     niter += 1
...     for dim in range(np.size(x0)):
...         for s in [bestx[dim] - stepsize, bestx[dim] + stepsize]:
...             testx = np.copy(bestx)
...             testx[dim] = s
...             testy = fun(testx, *args)
...             funcalls += 1
...             if testy < besty:
...                 besty = testy
...                 bestx = testx
...                 improved = True
...             if callback is not None:
...                 callback(bestx)
...             if maxfev is not None and funcalls >= maxfev:
...                 stop = True
...                 break
... ...
... return OptimizeResult(fun=besty, x=bestx, nit=niter,
...                         nfev=funcalls, success=(niter > 1))

>>> x0 = [1.35, 0.9, 0.8, 1.1, 1.2]
>>> res = minimize(rosen, x0, method='custmin', options=dict(stepsize=0.05))
>>> res.x
array([1., 1., 1., 1., 1.])

This will work just as well in case of univariate optimization:

>>> def custmin(fun, bracket, args=(), maxfev=None, stepsize=0.1,
...     maxiter=100, callback=None, **options):
...     bestx = (bracket[1] + bracket[0]) / 2.0
...     besty = fun(bestx)
...     funcalls = 1
...     niter = 0
...     improved = True
...     stop = False
...
...     while improved and not stop and niter < maxiter:
...         improved = False
...         niter += 1
...         for testx in [bestx - stepsize, bestx + stepsize]:
...             testy = fun(testx, *args)
...             funcalls += 1
...             if testy < besty:

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Root finding

Scalar functions

If one has a single-variable equation, there are multiple different root finding algorithms that can be tried. Most of these algorithms require the endpoints of an interval in which a root is expected (because the function changes signs). In general, brentq is the best choice, but the other methods may be useful in certain circumstances or for academic purposes. When a bracket is not available, but one or more derivatives are available, then newton (or halley, secant) may be applicable. This is especially the case if the function is defined on a subset of the complex plane, and the bracketing methods cannot be used.

Fixed-point solving

A problem closely related to finding the zeros of a function is the problem of finding a fixed-point of a function. A fixed point of a function is the point at which evaluation of the function returns the point:

\[ g(x) = x \]

Clearly the fixed point of \( g \) is the root of \( f(x) = g(x) - x \). Equivalently, the root of \( f \) is the fixed_point of \( g(x) = f(x) + x \). The routine fixed_point provides a simple iterative method using Aitkens sequence acceleration to estimate the fixed point of \( g \) given a starting point.

Sets of equations

Finding a root of a set of non-linear equations can be achieve using the root function. Several methods are available, amongst which hybr (the default) and lm which respectively use the hybrid method of Powell and the Levenberg-Marquardt method from MINPACK.

The following example considers the single-variable transcendental equation

\[ x + 2 \cos(x) = 0, \]

a root of which can be found as follows:

```python
>>> import numpy as np
>>> from scipy.optimize import root
>>> def func(x):
...     return x + 2 * np.cos(x)
>>> sol = root(func, 0.3)
>>> sol.x
array([-1.02986653])
>>> sol.fun
array([-6.66133815e-16])
```
Consider now a set of non-linear equations

\[ \begin{align*}
    x_0 \cos(x_1) &= 4, \\
    x_0 x_1 - x_1 &= 5.
\end{align*} \]

We define the objective function so that it also returns the Jacobian and indicate this by setting the `jac` parameter to `True`. Also, the Levenberg-Marquardt solver is used here.

```python
>>> def func2(x):
    ... f = [x[0] * np.cos(x[1]) - 4,
    ... x[1] * x[0] - x[1] - 5]
    ... df = np.array([[np.cos(x[1]), -x[0] * np.sin(x[1])],
                     [x[1], x[0] - 1]])
    ... return f, df

>>> sol = root(func2, [1, 1], jac=True, method='lm')

>>> sol.x
array([ 6.50409711, 0.90841421])
```

### Root finding for large problems

Methods `hybr` and `lm` in `root` cannot deal with a very large number of variables \((N)\), as they need to calculate and invert a dense \(N \times N\) Jacobian matrix on every Newton step. This becomes rather inefficient when \(N\) grows.

Consider for instance the following problem: we need to solve the following integrodifferential equation on the square \([0,1] \times [0,1]\):

\[
(\partial_x^2 + \partial_y^2)P + 5 \left( \int_0^1 \int_0^1 \cosh(P) \, dx \, dy \right)^2 = 0
\]

with the boundary condition \(P(x,1) = 1\) on the upper edge and \(P = 0\) elsewhere on the boundary of the square. This can be done by approximating the continuous function \(P\) by its values on a grid, \(P_{n,m} = P(nh, mh)\), with a small grid spacing \(h\). The derivatives and integrals can then be approximated; for instance \(\partial_x^2 P(n,m) \approx (P(n+h,m) - 2P(n,m) + P(n-h,m))/h^2\). The problem is then equivalent to finding the root of some function `residual(P)`, where \(P\) is a vector of length \(N_x N_y\).

Now, because \(N_x N_y\) can be large, methods `hybr` or `lm` in `root` will take a long time to solve this problem. The solution can however be found using one of the large-scale solvers, for example `krylov`, `broyden2`, or `anderson`. These use what is known as the inexact Newton method, which instead of computing the Jacobian matrix exactly, forms an approximation for it.

The problem we have can now be solved as follows:

```python
import numpy as np
from scipy.optimize import root
from numpy import cosh, zeros_like, mgrid, zeros

# parameters
nx, ny = 75, 75
hx, hy = 1. / (nx-1), 1. / (ny-1)

P_left, P_right = 0, 0
P_top, P_bottom = 1, 0

def residual(P):
    d2x = zeros_like(P)
    d2y = zeros_like(P)
```
\[
\begin{align*}
\text{d2x}[1:] &= (P[2:] - 2*P[1:] + P[0]) / \text{hx}/\text{hx} \\
\text{d2x}[0] &= (P[1] - 2*P[0] + P_{\text{left}}) / \text{hx}/\text{hx} \\
\text{d2x}[-1] &= (P_{\text{right}} - 2*P[-1] + P[-2]) / \text{hx}/\text{hx} \\
\text{d2y}[:,1:] &= (P[:,2:] - 2*P[:,1:] + P[:,0]) / \text{hy}/\text{hy} \\
\text{d2y}[:,0] &= (P[:,1] - 2*P[:,0] + P_{\text{bottom}}) / \text{hy}/\text{hy} \\
\text{d2y}[:,-1] &= (P_right - 2*P[:,-1] + P[:,-2]) / \text{hy}/\text{hy} \\
\text{return} & d2x + d2y + 5*\text{cosh}(P).\text{mean()}**2 \\
\end{align*}
\]

# solve
guess = zeros((nx, ny), float())
sol = root(residual, guess, method='krylov', options={'disp': True})
# sol = root(residual, guess, method='broyden2', options={'disp': True, 'max_rank': 50})
# sol = root(residual, guess, method='anderson', options={'disp': True, 'M': 10})
print('Residual: %g abs(residual(sol.x)).max()')

# visualize
import matplotlib.pyplot as plt
x, y = mgrid[0:1:(nx*1j), 0:1:(ny*1j)]
plt.pcolor(x, y, sol.x)
plt.colorbar()
plt.show()

---

Still too slow? Preconditioning.

When looking for the zero of the functions \( f_i(x) = 0, \ i = 1, 2, \ldots, N \), the krylov solver spends most of its time inverting the Jacobian matrix,

\[
J_{ij} = \frac{\partial f_i}{\partial x_j}.
\]

If you have an approximation for the inverse matrix \( M \approx J^{-1} \), you can use it for preconditioning the linear inversion problem. The idea is that instead of solving \( Jx = y \) one solves \( MJx = My \); since matrix \( MJ \) is “closer” to the identity matrix than \( J \) is, the equation should be easier for the Krylov method to deal with.
The matrix $M$ can be passed to `root` with method `krylov` as an option `options[\textcolor{red}{\texttt{\textquoteleft\textquoteleft\texttt{\textbackslash {}\textbackslash \texttt{\textbackslash {}jac_options\textbackslash \textbackslash \texttt{\textbackslash \textbackslash {}inner\_M}}}]}`. It can be a (sparse) matrix or a `scipy.sparse.linalg.LinearOperator` instance.

For the problem in the previous section, we note that the function to solve consists of two parts: the first one is application of the Laplace operator, $[\partial_x^2 + \partial_y^2]P$, and the second is the integral. We can actually easily compute the Jacobian corresponding to the Laplace operator part: we know that in one dimension

\[
\partial_x^2 \approx \frac{1}{h_x^2} \begin{pmatrix}
-2 & 1 & 0 & 0 & \cdots \\
1 & -2 & 1 & 0 & \cdots \\
0 & 1 & -2 & 1 & \cdots \\
\vdots & \ddots & \ddots & \ddots & \ddots \\
0 & & 0 & \ddots & -2 & 1 & 0 & 0 & \cdots
\end{pmatrix} = h_x^{-2}L
\]

so that the whole 2-D operator is represented by

\[
J_1 = \partial_x^2 + \partial_y^2 \simeq h_x^{-2}L \otimes I + h_y^{-2}I \otimes L
\]

The matrix $J_2$ of the Jacobian corresponding to the integral is more difficult to calculate, and since all of its entries are nonzero, it will be difficult to invert. $J_1$ on the other hand is a relatively simple matrix, and can be inverted by `scipy.sparse.linalg.splu` (or the inverse can be approximated by `scipy.sparse.linalg.spilu`). So we are content to take $M \approx J_1^{-1}$ and hope for the best.

In the example below, we use the preconditioner $M = J_1^{-1}$.

```python
import numpy as np
from scipy.optimize import root
from scipy.sparse import spdiags, kron
from scipy.sparse.linalg import spilu, LinearOperator
from numpy import cosh, zeros_like, mgrid, zeros, eye

# parameters
nx, ny = 75, 75
hx, hy = 1. / (nx - 1), 1. / (ny - 1)

P_left, P_right = 0, 0
P_top, P_bottom = 1, 0

def get_preconditioner():
    
    """Compute the preconditioner M"
    
    diags_x = zeros((3, nx))
    diags_x[0, :] = 1 / hx / hx
    diags_x[1, :] = -2 / hx / hx
    diags_x[2, :] = 1 / hx / hx
    Lx = spdiags(diags_x, [-1, 0, 1], nx, nx)

    diags_y = zeros((3, ny))
    diags_y[0, :] = 1 / hy / hy
    diags_y[1, :] = -2 / hy / hy
    diags_y[2, :] = 1 / hy / hy
    Ly = spdiags(diags_y, [-1, 0, 1], ny, ny)

    J1 = kron(Lx, eye(ny)) + kron(eye(nx), Ly)

    # Now we have the matrix J_1. We need to find its inverse \( M \) --
    # however, since an approximate inverse is enough, we can use
```

(continues on next page)
# the *incomplete LU* decomposition

J1_ilu = spilu(J1)

# This returns an object with a method .solve() that evaluates
# the corresponding matrix-vector product. We need to wrap it into
# a LinearOperator before it can be passed to the Krylov methods:

M = LinearOperator(shape=(nx*ny, nx*ny), matvec=J1_ilu.solve)
return M

def solve(preconditioning=True):
    """Compute the solution""
    count = [0]

    def residual(P):
        count[0] += 1

        d2x = zeros_like(P)
        d2y = zeros_like(P)

        d2x[1:-1] = (P[2:] - 2*P[1:-1] + P[:2])/hx/hx
        d2x[0]   = (P[1]  - 2*P[0]   + P_left)/hx/hx
        d2x[-1]  = (P_right - 2*P[-1] + P[-2])/hx/hx

        d2y[:,1:-1] = (P[:,2:] - 2*P[:,1:-1] + P[:,-2])/hy/hy
        d2y[:,0]   = (P[:,1]  - 2*P[:,0]   + P_bottom)/hy/hy
        d2y[:,0]   = (P[:,1]  - 2*P[:,0]   + P_bottom)/hy/hy

        return d2x + d2y + 5*cosh(P).mean()**2

    # preconditioner
    if preconditioning:
        M = get_preconditioner()
    else:
        M = None

    # solve
guess = zeros((nx, ny), float)

    sol = root(residual, guess, method='krylov',
               options={'disp': True,
                        'jac_options': {'inner_M': M}})
    print('Residual', abs(residual(sol.x)).max())
    print('Evaluations', count[0])

    return sol.x

def main():
    sol = solve(preconditioning=True)

    # visualize
import matplotlib.pyplot as plt
x, y = mgrid[0:1:(nx+1j), 0:1:(ny+1j)]
plt.clf()
plt.pcolor(x, y, sol)
plt.clim(0, 1)
plt.colorbar()
plt.show()

if __name__ == "__main__":
    main()

Resulting run, first without preconditioning:

0: |F(x)| = 803.614; step 1; tol 0.000257947
1: |F(x)| = 345.912; step 1; tol 0.166755
2: |F(x)| = 139.159; step 1; tol 0.145657
3: |F(x)| = 27.3682; step 1; tol 0.0348109
4: |F(x)| = 1.03303; step 1; tol 0.00128227
5: |F(x)| = 0.0406634; step 1; tol 0.00139451
6: |F(x)| = 0.00344341; step 1; tol 0.00645373
7: |F(x)| = 0.000153671; step 1; tol 0.00179246
8: |F(x)| = 6.7424e-06; step 1; tol 0.00173256
Residual 3.57078908664e-07
Evaluations 317

and then with preconditioning:

0: |F(x)| = 136.993; step 1; tol 7.49599e-06
1: |F(x)| = 4.80983; step 1; tol 0.00110945
2: |F(x)| = 0.195942; step 1; tol 0.00149362
3: |F(x)| = 0.000563597; step 1; tol 7.44604e-06
4: |F(x)| = 1.00698e-09; step 1; tol 2.87308e-12
Residual 9.29603061195e-11
Evaluations 77

Using a preconditioner reduced the number of evaluations of the residual function by a factor of 4. For problems where the residual is expensive to compute, good preconditioning can be crucial — it can even decide whether the problem is solvable in practice or not.

Preconditioning is an art, science, and industry. Here, we were lucky in making a simple choice that worked reasonably well, but there is a lot more depth to this topic than is shown here.

**References**

Some further reading and related software:

### 4.1.6 Interpolation (scipy.interpolate)

**Contents**

- Interpolation (scipy.interpolate)
  - 1-D interpolation (interp1d)
There are several general interpolation facilities available in SciPy, for data in 1, 2, and higher dimensions:

- A class representing an interpolant \( \texttt{interp1d} \) in 1-D, offering several interpolation methods.
- Convenience function \( \texttt{griddata} \) offering a simple interface to interpolation in N dimensions \( (N = 1, 2, 3, 4, \ldots) \). Object-oriented interface for the underlying routines is also available.
- Functions for 1- and 2-dimensional (smoothed) cubic-spline interpolation, based on the FORTRAN library FITPACK. There are both procedural and object-oriented interfaces for the FITPACK library.
- Interpolation using Radial Basis Functions.

### 1-D interpolation (\texttt{interp1d})

The \texttt{interp1d} class in \texttt{scipy.interpolate} is a convenient method to create a function based on fixed data points which can be evaluated anywhere within the domain defined by the given data using linear interpolation. An instance of this class is created by passing the 1-d vectors comprising the data. The instance of this class defines a \_\_call\_\_ method and can therefore by treated like a function which interpolates between known data values to obtain unknown values (it also has a docstring for help). Behavior at the boundary can be specified at instantiation time. The following example demonstrates its use, for linear and cubic spline interpolation:

```python
>>> from scipy.interpolate import interp1d

>>> x = np.linspace(0, 10, num=11, endpoint=True)
>>> y = np.cos(-x**2 / 9.0)
>>> f = interp1d(x, y)
>>> f2 = interp1d(x, y, kind='cubic')

>>> xnew = np.linspace(0, 10, num=41, endpoint=True)

>>> import matplotlib.pyplot as plt
>>> plt.plot(x, y, 'o', xnew, f(xnew), '-', xnew, f2(xnew), '--')
>>> plt.legend(['data', 'linear', 'cubic'], loc='best')
>>> plt.show()
```

Another set of interpolations in \texttt{interp1d} is \texttt{nearest}, \texttt{previous}, and \texttt{next}, where they return the nearest, previous, or next point along the x-axis. Nearest and next can be thought of as a special case of a causal interpolating filter. The following example demonstrates their use, using the same data as in the previous example:
Multivariate data interpolation (griddata)

Suppose you have multidimensional data, for instance for an underlying function \( f(x, y) \) you only know the values at points \((x[i], y[j])\) that do not form a regular grid.

Suppose we want to interpolate the 2-D function

```python
>>> def func(x, y):
...     return x*(1-x)*np.cos(4*np.pi*x) * np.sin(4*np.pi*y**2)**2
```

on a grid in \([0, 1] \times [0, 1]\)

```python
>>> grid_x, grid_y = np.mgrid[0:1:100j, 0:1:200j]
```

but we only know its values at 1000 data points:

```python
>>> points = np.random.rand(1000, 2)
>>> values = func(points[:,0], points[:,1])
```
This can be done with `griddata`—below we try out all of the interpolation methods:

```python
>>> from scipy.interpolate import griddata
>>> grid_z0 = griddata(points, values, (grid_x, grid_y), method='nearest')
>>> grid_z1 = griddata(points, values, (grid_x, grid_y), method='linear')
>>> grid_z2 = griddata(points, values, (grid_x, grid_y), method='cubic')
```

One can see that the exact result is reproduced by all of the methods to some degree, but for this smooth function the piecewise cubic interpolant gives the best results:

```python
>>> import matplotlib.pyplot as plt
>>> plt.subplot(221)
>>> plt.imshow(func(grid_x, grid_y).T, extent=(0,1,0,1), origin='lower')
>>> plt.plot(points[:,0], points[:,1], 'k.', ms=1)
>>> plt.title('Original')
>>> plt.subplot(222)
>>> plt.imshow(grid_z0.T, extent=(0,1,0,1), origin='lower')
>>> plt.title('Nearest')
>>> plt.subplot(223)
>>> plt.imshow(grid_z1.T, extent=(0,1,0,1), origin='lower')
>>> plt.title('Linear')
>>> plt.subplot(224)
>>> plt.imshow(grid_z2.T, extent=(0,1,0,1), origin='lower')
>>> plt.title('Cubic')
>>> plt.gcf().set_size_inches(6, 6)
>>> plt.show()
```

**Spline interpolation**

**Spline interpolation in 1-d: Procedural (interpolate.splXXX)**

Spline interpolation requires two essential steps: (1) a spline representation of the curve is computed, and (2) the spline is evaluated at the desired points. In order to find the spline representation, there are two different ways to represent a curve and obtain (smoothing) spline coefficients: directly and parametrically. The direct method finds the spline representation of a curve in a two-dimensional plane using the function `splrep`. The first two arguments are the only ones required, and these provide the $x$ and $y$ components of...
the curve. The normal output is a 3-tuple, \((t, c, k)\), containing the knot-points, \(t\), the coefficients \(c\) and the order \(k\) of the spline. The default spline order is cubic, but this can be changed with the input keyword, \(k\).

For curves in \(N\)-dimensional space the function \texttt{splprep} allows defining the curve parametrically. For this function only 1 input argument is required. This input is a list of \(N\)-arrays representing the curve in \(N\)-dimensional space. The length of each array is the number of curve points, and each array provides one component of the \(N\)-dimensional data point. The parameter variable is given with the keyword argument, \(u\), which defaults to an equally-spaced monotonic sequence between 0 and 1. The default output consists of two objects: a 3-tuple, \((t, c, k)\), containing the spline representation and the parameter variable \(u\):

The keyword argument, \(s\), is used to specify the amount of smoothing to perform during the spline fit. The default value of \(s\) is \(s = m - \sqrt{2m}\) where \(m\) is the number of data-points being fit. Therefore, if no smoothing is desired a value of \(s = 0\) should be passed to the routines.

Once the spline representation of the data has been determined, functions are available for evaluating the spline (\texttt{splev}) and its derivatives (\texttt{splev}, \texttt{spalde}) at any point and the integral of the spline between any two points (\texttt{splint}). In addition, for cubic splines (\(k = 3\)) with 8 or more knots, the roots of the spline can be estimated (\texttt{sproot}). These functions are demonstrated in the example that follows.

```python
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> from scipy import interpolate

Cubic-spline
```

```python
>>> x = np.arange(0, 2*np.pi+np.pi/4, 2*np.pi/8)
>>> y = np.sin(x)
>>> tck = interpolate.splrep(x, y, s=0)
>>> xnew = np.arange(0, 2*np.pi, np.pi/50)
>>> ynew = interpolate.splev(xnew, tck, der=0)
```

```python
>>> plt.figure()
>>> plt.plot(x, y, 'x', xnew, ynew, np.sin(xnew), x, y, 'b')
>>> plt.legend(['Linear', 'Cubic Spline', 'True'])
>>> plt.axis([-0.05, 6.33, -1.05, 1.05])
>>> plt.title('Cubic-spline interpolation')
>>> plt.show()
```

Derivative of spline

```python
>>> yder = interpolate.splev(xnew, tck, der=1)
>>> plt.figure()
>>> plt.plot(xnew, yder, xnew, np.cos(xnew), '--')
>>> plt.legend(['Cubic Spline', 'True'])
>>> plt.axis([-0.05, 6.33, -1.05, 1.05])
>>> plt.title('Derivative estimation from spline')
>>> plt.show()
```

Integral of spline

```python
>>> def integ(x, tck, constant=-1):
...     x = np.atleast_1d(x)
...     out = np.zeros(x.shape, dtype=x.dtype)
...     for n in range(len(out)):
...         out[n] = interpolate.splint(0, x[n], tck)
```

(continues on next page)
Cubic-spline interpolation

Derivative estimation from spline
... out += constant
... return out

```python
>>> yint = integ(xnew, tck)
>>> plt.figure()
>>> plt.plot(xnew, yint, xnew, -np.cos(xnew), '--')
>>> plt.legend(['Cubic Spline', 'True'])
>>> plt.axis([-0.05, 6.33, -1.05, 1.05])
>>> plt.title('Integral estimation from spline')
>>> plt.show()
```

![Integral estimation from spline](image)

Roots of spline

```python
>>> interpolate.sproot(tck)
array([3.1416])
```

Notice that `sproot` failed to find an obvious solution at the edge of the approximation interval, $x = 0$. If we define the spline on a slightly larger interval, we recover both roots $x = 0$ and $x = 2\pi$:

```python
>>> x = np.linspace(-np.pi/4, 2.*np.pi + np.pi/4, 21)
>>> y = np.sin(x)
>>> tck = interpolate.splrep(x, y, s=0)
>>> interpolate.sproot(tck)
array([0., 3.1416])
```

Parametric spline

```python
>>> t = np.arange(0, 1.1, .1)
>>> x = np.sin(2*np.pi*t)
>>> y = np.cos(2*np.pi*t)
>>> tck, u = interpolate.splprep([x, y], s=0)
>>> unew = np.arange(0, 1.01, 0.01)
>>> out = interpolate.splev(unew, tck)
```
Spline interpolation in 1-d: Object-oriented (UnivariateSpline)

The spline-fitting capabilities described above are also available via an object-oriented interface. The one dimensional splines are objects of the `UnivariateSpline` class, and are created with the x and y components of the curve provided as arguments to the constructor. The class defines `__call__`, allowing the object to be called with the x-axis values at which the spline should be evaluated, returning the interpolated y-values. This is shown in the example below for the subclass `InterpolatedUnivariateSpline`. The integral, derivatives, and roots methods are also available on `UnivariateSpline` objects, allowing definite integrals, derivatives, and roots to be computed for the spline.

The `UnivariateSpline` class can also be used to smooth data by providing a non-zero value of the smoothing parameter `s`, with the same meaning as the `s` keyword of the `splrep` function described above. This results in a spline that has fewer knots than the number of data points, and hence is no longer strictly an interpolating spline, but rather a smoothing spline. If this is not desired, the `InterpolatedUnivariateSpline` class is available. It is a subclass of `UnivariateSpline` that always passes through all points (equivalent to forcing the smoothing parameter to 0). This class is demonstrated in the example below.

The `LSQUnivariateSpline` class is the other subclass of `UnivariateSpline`. It allows the user to specify the number and location of internal knots explicitly with the parameter `t`. This allows creation of customized splines with non-linear spacing, to interpolate in some domains and smooth in others, or change the character of the spline.

```python
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> from scipy import interpolate
```

InterpolatedUnivariateSpline
```python
>>> x = np.arange(0, 2*np.pi*np.pi/4, 2*np.pi/8)
>>> y = np.sin(x)
>>> s = interpolate.InterpolatedUnivariateSpline(x, y)
>>> xnew = np.arange(0, 2*np.pi, np.pi/50)
>>> ynew = s(xnew)

>>> plt.figure()
>>> plt.plot(x, y, 'x', xnew, ynew, xnew, np.sin(xnew), x, y, 'b')
>>> plt.legend(['Linear', 'InterpolatedUnivariateSpline', 'True'])
>>> plt.axis([-0.05, 6.33, -1.05, 1.05])
>>> plt.title('InterpolatedUnivariateSpline')
>>> plt.show()

LSQUnivariateSpline with non-uniform knots

>>> t = [np.pi/2-.1, np.pi/2+.1, 3*np.pi/2-.1, 3*np.pi/2+.1]
>>> s = interpolate.LSQUnivariateSpline(x, y, t, k=2)
>>> ynew = s(xnew)

>>> plt.figure()
>>> plt.plot(x, y, 'x', xnew, ynew, xnew, np.sin(xnew), x, y, 'b')
>>> plt.legend(['Linear', 'LSQUnivariateSpline', 'True'])
>>> plt.axis([-0.05, 6.33, -1.05, 1.05])
>>> plt.title('Spline with Specified Interior Knots')
>>> plt.show()
```

**Two-dimensional spline representation: Procedural (bisplrep)**

For (smooth) spline-fitting to a two dimensional surface, the function `bisplrep` is available. This function takes as required inputs the 1-D arrays `x`, `y`, and `z` which represent points on the surface `z = f(x, y)`. The default output is a list `[tx, ty, c, kx, ky]` whose entries represent respectively, the components of the knot positions, the coefficients of the spline, and the order of the spline in each coordinate. It is convenient to hold this list in a single object, `tck`, so that it can be passed easily to the function `bisplev`. The keyword, `s`, can be used to change the amount of smoothing performed on the data while determining the appropriate spline. The default value is `s = m - \sqrt{2m}` where `m` is the number of data points in the `x`, `y`, and `z` vectors.
As a result, if no smoothing is desired, then \( s = 0 \) should be passed to `bisplrep`.

To evaluate the two-dimensional spline and its partial derivatives (up to the order of the spline), the function `bisplev` is required. This function takes as the first two arguments two 1-D arrays whose cross-product specifies the domain over which to evaluate the spline. The third argument is the `tck` list returned from `bisplrep`. If desired, the fourth and fifth arguments provide the orders of the partial derivative in the \( x \) and \( y \) direction respectively.

It is important to note that two dimensional interpolation should not be used to find the spline representation of images. The algorithm used is not amenable to large numbers of input points. The signal processing toolbox contains more appropriate algorithms for finding the spline representation of an image. The two dimensional interpolation commands are intended for use when interpolating a two dimensional function as shown in the example that follows. This example uses the `mgrid` command in NumPy which is useful for defining a “mesh-grid” in many dimensions. (See also the `ogrid` command if the full-mesh is not needed). The number of output arguments and the number of dimensions of each argument is determined by the number of indexing objects passed in `mgrid`.

```python
>>> import numpy as np
>>> from scipy import interpolate
>>> import matplotlib.pyplot as plt

Define function over sparse 20x20 grid

```python
>>> x, y = np.mgrid[-1:1:20j, -1:1:20j]
>>> z = (x+y) * np.exp(-6.0*(x*x+y*y))
```  
Interpolate function over new 70x70 grid

```python
>>> plt.figure()
>>> plt.pcolor(x, y, z)
>>> plt.colorbar()
>>> plt.title("Sparsely sampled function.")
>>> plt.show()
```
Two-dimensional spline representation: Object-oriented (BivariateSpline)
The `BivariateSpline` class is the 2-dimensional analog of the `UnivariateSpline` class. It and its subclasses implement the FITPACK functions described above in an object oriented fashion, allowing objects to be instantiated that can be called to compute the spline value by passing in the two coordinates as the two
arguments.

Using radial basis functions for smoothing/interpolation

Radial basis functions can be used for smoothing/interpolating scattered data in n-dimensions, but should be used with caution for extrapolation outside of the observed data range.

1-d Example

This example compares the usage of the Rbf and UnivariateSpline classes from the scipy.interpolate module.

```python
>>> import numpy as np
>>> from scipy.interpolate import Rbf, InterpolatedUnivariateSpline
>>> import matplotlib.pyplot as plt

>>> # setup data
>>> x = np.linspace(0, 10, 9)
>>> y = np.sin(x)
>>> xi = np.linspace(0, 10, 101)

>>> # use fitpack2 method
>>> ius = InterpolatedUnivariateSpline(x, y)
>>> yi = ius(xi)

>>> plt.subplot(2, 1, 1)
>>> plt.plot(x, y, 'bo')
>>> plt.plot(xi, yi, 'g')
>>> plt.plot(xi, np.sin(xi), 'r')
>>> plt.title('Interpolation using univariate spline')

>>> # use RBF method
>>> rbf = Rbf(x, y)
>>> fi = rbf(xi)

>>> plt.subplot(2, 1, 2)
>>> plt.plot(x, y, 'bo')
>>> plt.plot(xi, fi, 'g')
>>> plt.plot(xi, np.sin(xi), 'r')
>>> plt.title('Interpolation using RBF - multiquadrics')
>>> plt.show()
```

2-d Example

This example shows how to interpolate scattered 2d data.

```python
>>> import numpy as np
>>> from scipy.interpolate import Rbf
>>> import matplotlib.pyplot as plt
>>> from matplotlib import cm

>>> # 2-d tests - setup scattered data
>>> x = np.random.rand(100)*4.0-2.0
>>> y = np.random.rand(100)*4.0-2.0
>>> z = x*np.exp(-x**2-y**2)
```

(continues on next page)
Interpolation using univariate spline

Interpolation using RBF - multiquadrics

(continued from previous page)

```python
>>> ti = np.linspace(-2.0, 2.0, 100)
>>> XI, YI = np.meshgrid(ti, ti)

>>> # use RBF
>>> rbf = Rbf(x, y, z, epsilon=2)
>>> ZI = rbf(XI, YI)

>>> # plot the result
>>> plt.subplot(1, 1, 1)
>>> plt.pcolor(XI, YI, ZI, cmap=cm.jet)
>>> plt.scatter(x, y, 100, z, cmap=cm.jet)
>>> plt.title('RBF interpolation - multiquadrics')
>>> plt.xlim(-2.0, 2.0)
>>> plt.ylim(-2.0, 2.0)
>>> plt.colorbar()
```

4.1.7 Fourier Transforms (scipy.fftpack)

Contents

- Fourier Transforms (scipy.fftpack)
  - Fast Fourier transforms
    * One dimensional discrete Fourier transforms
    * Two and n-dimensional discrete Fourier transforms
    * FFT convolution
  - Discrete Cosine Transforms
    * Type I DCT
Fourier analysis is a method for expressing a function as a sum of periodic components, and for recovering the signal from those components. When both the function and its Fourier transform are replaced with discretized counterparts, it is called the discrete Fourier transform (DFT). The DFT has become a mainstay of numerical computing in part because of a very fast algorithm for computing it, called the Fast Fourier Transform (FFT), which was known to Gauss (1805) and was brought to light in its current form by Cooley and Tukey [CT65]. Press et al. [NR07] provide an accessible introduction to Fourier analysis and its applications.

Note: PyFFTW provides a way to replace a number of functions in scipy.fftpack with its own functions, which are usually significantly faster, via pyfftw.interfaces. Because PyFFTW relies on the GPL-licensed FFTW it cannot be included in Scipy. Users for whom the speed of FFT routines is critical should consider installing PyFFTW.
One dimensional discrete Fourier transforms

The FFT $y[k]$ of length $N$ of the length-$N$ sequence $x[n]$ is defined as

$$y[k] = \sum_{n=0}^{N-1} e^{-2\pi j \frac{kn}{N}} x[n],$$

and the inverse transform is defined as follows

$$x[n] = \frac{1}{N} \sum_{k=0}^{N-1} e^{2\pi j \frac{kn}{N}} y[k].$$

These transforms can be calculated by means of `fft` and `ifft`, respectively as shown in the following example.

```python
>>> from scipy.fftpack import fft, ifft
>>> x = np.array([1.0, 2.0, 1.0, -1.0, 1.5])
>>> y = fft(x)
>>> y
array([ 4.5+0.j , 2.08155948-1.65109876j,
       -1.83155948+1.60822041j, -1.83155948-1.60822041j,
       2.08155948+1.65109876j])
>>> yinv = ifft(y)
>>> yinv
array([ 1.0+0.j , 2.0+0.j, 1.0+0.j, -1.0+0.j, 1.5+0.j])
```

From the definition of the FFT it can be seen that

$$y[0] = \sum_{n=0}^{N-1} x[n].$$

In the example

```python
>>> np.sum(x)
4.5
```

which corresponds to $y[0]$. For $N$ even, the elements $y[1]...y[N/2-1]$ contain the positive-frequency terms, and the elements $y[N/2]...y[N-1]$ contain the negative-frequency terms, in order of decreasingly negative frequency. For $N$ odd, the elements $y[1]...y[(N-1)/2]$ contain the positive-frequency terms, and the elements $y[(N+1)/2]...y[N-1]$ contain the negative-frequency terms, in order of decreasingly negative frequency.

In case the sequence $x$ is real-valued, the values of $y[n]$ for positive frequencies is the conjugate of the values $y[n]$ for negative frequencies (because the spectrum is symmetric). Typically, only the FFT corresponding to positive frequencies is plotted.

The example plots the FFT of the sum of two sines.

```python
>>> from scipy.fftpack import fft
>>> # Number of sample points
>>> N = 600
>>> # sample spacing
>>> T = 1.0 / 800.0
>>> x = np.linspace(0.0, N*T, N)
>>> y = np.sin(50.0 * 2.0*np.pi*x) + 0.5*np.sin(80.0 * 2.0*np.pi*x)
>>> yf = fft(y)
>>> xf = np.linspace(0.0, 1.0/(2.0*T), N//2)
>>> import matplotlib.pyplot as plt
```

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The FFT input signal is inherently truncated. This truncation can be modelled as multiplication of an infinite signal with a rectangular window function. In the spectral domain this multiplication becomes convolution of the signal spectrum with the window function spectrum, being of form \( \sin(x)/x \). This convolution is the cause of an effect called spectral leakage (see [WPW]). Windowing the signal with a dedicated window function helps mitigate spectral leakage. The example below uses a Blackman window from scipy.signal and shows the effect of windowing (the zero component of the FFT has been truncated for illustrative purposes).

```python
>>> from scipy.fftpack import fft
>>> # Number of sample points
>>> N = 600
>>> # sample spacing
>>> T = 1.0 / 800.0
>>> x = np.linspace(0.0, N*T, N)
>>> y = np.sin(50.0 * 2.0*np.pi*x) + 0.5*np.sin(80.0 * 2.0*np.pi*x)
>>> yf = fft(y)
>>> from scipy.signal import blackman
>>> w = blackman(N)
>>> ywf = fft(y*w)
>>> xf = np.linspace(0.0, 1.0/(2.0*T), N/2)
>>> import matplotlib.pyplot as plt
>>> plt.semilogy(xf[1:N//2], 2.0/N * np.abs(yf[0:N//2]), '-b')
>>> plt.semilogy(xf[1:N//2], 2.0/N * np.abs(ywf[0:N//2]), '-r')
>>> plt.legend(['FFT', 'FFT w. window'])
>>> plt.grid()
>>> plt.show()```

In case the sequence \( x \) is complex-valued, the spectrum is no longer symmetric. To simplify working with the FFT functions, scipy provides the following two helper functions.

The function `fftfreq` returns the FFT sample frequency points.
In a similar spirit, the function `fftshift` allows swapping the lower and upper halves of a vector, so that it becomes suitable for display.

The example below plots the FFT of two complex exponentials; note the asymmetric spectrum.

The function `rfft` calculates the FFT of a real sequence and outputs the FFT coefficients $y[n]$ with separate real and imaginary parts. In case of $N$ being even: $[y[0], Re(y[1]), Im(y[1]), ..., Re(y[N/2])]$; in case $N$ being odd $[y[0], Re(y[1]), Im(y[1]), ..., Re(y[N/2]), Im(y[N/2])]$. 

```python
from scipy.fft import fft, fftfreq, fftshift
>>> yf = fft(y)
>>> xf = fftfreq(N, T)
>>> yplot = fftshift(yf)
>>> plt.plot(xf, 1.0/N * np.abs(yplot))
>>> plt.grid()
>>> plt.show()
```
The corresponding function *irfft* calculates the IFFT of the FFT coefficients with this special ordering.

```python
>>> from scipy.fftpack import fft, rfft, irfft
>>> x = np.array([1.0, 2.0, 1.0, -1.0, 1.5, 1.0])
>>> fft(x)
array([ 5.5 +0.j , 2.25-0.4330127j , -2.75-1.29903811j,
       1.5 +0.j , -2.75+1.29903811j, 2.25+0.4330127j ])
>>> yr = rfft(x)
>>> yr
array([ 5.5 , 2.25 , -0.4330127 , -2.75 , -1.29903811, 1.5 ])
>>> irfft(yr)
array([ 1. , 2. , 1. , -1. , 1.5, 1. ])
>>> x = np.array([1.0, 2.0, 1.0, -1.0, 1.5, 1.0])
>>> fft(x)
array([ 4.5 +0.j , 2.08155948-1.65109876j, -1.83155948+1.60822041j,
       -1.83155948-1.60822041j, 2.08155948+1.65109876j])
>>> yr = rfft(x)
>>> yr
array([ 4.5 , 2.08155948, -1.65109876, -1.83155948, 1.60822041])
```

**Two and n-dimensional discrete Fourier transforms**

The functions *fft2* and *ifft2* provide 2-dimensional FFT, and IFFT, respectively. Similar, *fftn* and *ifftn* provide n-dimensional FFT, and IFFT, respectively.

The example below demonstrates a 2-dimensional IFFT and plots the resulting (2-dimensional) time-domain signals.

```python
>>> from scipy.fftpack import ifftn
>>> import matplotlib.pyplot as plt
>>> import matplotlib.cm as cm
>>> N = 30
>>> f, ((ax1, ax2, ax3), (ax4, ax5, ax6)) = plt.subplots(2, 3, sharex='col', sharey='row')
(continues on next page)```
```python
>>> xf = np.zeros((N,N))
>>> xf[0, 5] = 1
>>> xf[0, N-5] = 1
>>> Z = ifftn(xf)
>>> ax1.imshow(xf, cmap=cm.Reds)
>>> ax4.imshow(np.real(Z), cmap=cm.gray)
>>> xf = np.zeros((N, N))
>>> xf[5, 0] = 1
>>> xf[N-5, 0] = 1
>>> Z = ifftn(xf)
>>> ax2.imshow(xf, cmap=cm.Reds)
>>> ax5.imshow(np.real(Z), cmap=cm.gray)
>>> xf = np.zeros((N, N))
>>> xf[5, 10] = 1
>>> xf[N-5, N-10] = 1
>>> Z = ifftn(xf)
>>> ax3.imshow(xf, cmap=cm.Reds)
>>> ax6.imshow(np.real(Z), cmap=cm.gray)
>>> plt.show()
```

### FFT convolution

`scipy.fftpack.convolve` performs a convolution of two one-dimensional arrays in frequency domain.

### Discrete Cosine Transforms

Scipy provides a DCT with the function `dct` and a corresponding IDCT with the function `idct`. There are 8 types of the DCT [WPC], [Mak]; however, only the first 3 types are implemented in scipy. “The” DCT generally refers to DCT type 2, and “the” Inverse DCT generally refers to DCT type 3. In addition, the DCT coefficients can be normalized differently (for most types, scipy provides `None` and `ortho`). Two parameters of the `dct/idct` function calls allow setting the DCT type and coefficient normalization.

For a single dimension array `x`, `dct(x, norm='ortho')` is equal to MATLAB `dct(x)`. 
**Type I DCT**

SciPy uses the following definition of the unnormalized DCT-I (norm='None'):

\[ y[k] = x_0 + (-1)^k x_{N-1} + 2 \sum_{n=1}^{N-2} x[n] \cos \left( \frac{\pi nk}{N-1} \right), \quad 0 \leq k < N. \]

Only None is supported as normalization mode for DCT-I. Note also that the DCT-I is only supported for input size > 1.

**Type II DCT**

SciPy uses the following definition of the unnormalized DCT-II (norm='None'):

\[ y[k] = 2 \sum_{n=0}^{N-1} x[n] \cos \left( \frac{\pi(2n+1)k}{2N} \right) \quad 0 \leq k < N. \]

In case of the normalized DCT (norm='ortho'), the DCT coefficients \( y[k] \) are multiplied by a scaling factor \( f \):

\[ f = \begin{cases} \sqrt{1/(4N)}, & \text{if } k = 0 \\ \sqrt{1/(2N)}, & \text{otherwise} \end{cases}. \]

In this case, the DCT “base functions” \( \phi_k[n] = 2f \cos \left( \frac{\pi(2n+1)k}{2N} \right) \) become orthonormal:

\[ \sum_{n=0}^{N-1} \phi_k[n]\phi_l[n] = \delta_{lk} \]

**Type III DCT**

SciPy uses the following definition of the unnormalized DCT-III (norm='None'):

\[ y[k] = x_0 + 2 \sum_{n=1}^{N-1} x[n] \cos \left( \frac{\pi n(2k+1)}{2N} \right) \quad 0 \leq k < N, \]

or, for norm='ortho':

\[ y[k] = \frac{x_0}{\sqrt{N}} + 2 \sum_{n=1}^{N-1} x[n] \cos \left( \frac{\pi n(2k+1)}{2N} \right) \quad 0 \leq k < N. \]

**DCT and IDCT**

The (unnormalized) DCT-III is the inverse of the (unnormalized) DCT-II, up to a factor 2N. The orthonormalized DCT-III is exactly the inverse of the orthonormalized DCT-II. The function `idct` performs the mappings between the DCT and IDCT types.

The example below shows the relation between DCT and IDCT for different types and normalizations.

```python
>>> from scipy.fftpack import dct, idct
>>> x = np.array([1.0, 2.0, 1.0, -1.0, 1.5])
>>> dct(dct(x, type=2, norm='ortho'), type=3, norm='ortho')
array([ 1.0,  2.0,  1.0, -1.0,  1.5])
>>> # scaling factor 2*N = 10
>>> idct(dct(x, type=2), type=2)
array([ 10.,  20.,  10., -10.,  15.])
>>> # no scaling factor
```

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Discrete Cosine Transforms

The DCT exhibits the "energy compaction property", meaning that for many signals only the first few DCT coefficients have significant magnitude. Zeroing out the other coefficients leads to a small reconstruction error, a fact which is exploited in lossy signal compression (e.g. JPEG compression).

The example below shows a signal $x$ and two reconstructions ($x_{20}$ and $x_{15}$) from the signal's DCT coefficients. The signal $x_{20}$ is reconstructed from the first 20 DCT coefficients, $x_{15}$ is reconstructed from the first 15 DCT coefficients. It can be seen that the relative error of using 20 coefficients is still very small (~0.1%), but provides a five-fold compression rate.

```plaintext
>>> from scipy.fftpack import dct, idct
>>> import matplotlib.pyplot as plt
>>> N = 100
>>> t = np.linspace(0,20,N)
>>> x = np.exp(-t/3)*np.cos(2*t)
>>> y = dct(x, norm='ortho')
>>> window = np.zeros(N)
>>> window[:20] = 1
>>> yr = idct(y*window, norm='ortho')
>>> sum(abs(x-yr)**2) / sum(abs(x)**2)
0.00109014022575
>>> plt.plot(t, x, '-bx')
>>> plt.plot(t, yr, 'ro')
>>> window = np.zeros(N)
>>> window[:15] = 1
>>> yr = idct(y*window, norm='ortho')
>>> sum(abs(x-yr)**2) / sum(abs(x)**2)
0.07188180650083
>>> plt.plot(t, yr, 'g+')
>>> plt.legend(['x', '$x_{20}$', '$x_{15}$'])
>>> plt.grid()
>>> plt.show()
```

Discrete Sine Transforms

SciPy provides a DST [Mak] with the function `dst` and a corresponding IDST with the function `idst`.

There are theoretically 8 types of the DST for different combinations of even/odd boundary conditions and boundary offset sets [WPS], only the first 3 types are implemented in scipy.
Type I DST
DST-I assumes the input is odd around \( n = -1 \) and \( n = N \). Scipy uses the following definition of the unnormalized DST-I (\texttt{norm='None'}):

\[
y[k] = 2 \sum_{n=0}^{N-1} x[n] \sin \left( \frac{\pi(n+1)(k+1)}{N+1} \right), \quad 0 \leq k < N.
\]

Only \texttt{None} is supported as normalization mode for DST-I. Note also that the DST-I is only supported for input size > 1. The (unnormalized) DST-I is its own inverse, up to a factor \( 2(N+1) \).

Type II DST
DST-II assumes the input is odd around \( n = -1/2 \) and even around \( n = N \). Scipy uses the following definition of the unnormalized DST-II (\texttt{norm='None'}):

\[
y[k] = 2 \sum_{n=0}^{N-1} x[n] \sin \left( \frac{\pi(n+1/2)(k+1)}{N} \right), \quad 0 \leq k < N.
\]

Type III DST
DST-III assumes the input is odd around \( n = -1 \) and even around \( n = N - 1 \). Scipy uses the following definition of the unnormalized DST-III (\texttt{norm='None'}):

\[
y[k] = (-1)^k x[N - 1] + 2 \sum_{n=0}^{N-2} x[n] \sin \left( \frac{\pi(n+1)(k+1/2)}{N} \right), \quad 0 \leq k < N.
\]

DST and IDST
The example below shows the relation between DST and IDST for different types and normalizations.

```python
>>> from scipy.fftpack import dst, idst
>>> x = np.array([1.0, 2.0, 1.0, -1.0, 1.5])
>>> # scaling factor 2*N = 10
>>> idst(dst(x, type=2), type=2)
array([ 10., 20., 10., -10., 15.])
>>> # no scaling factor
```
Cache Destruction

To accelerate repeat transforms on arrays of the same shape and dtype, scipy.fftpack keeps a cache of the prime factorization of length of the array and pre-computed trigonometric functions. These caches can be destroyed by calling the appropriate function in scipy.fftpack._fftpack. dst(type=1) and idst(type=1) share a cache (*dst1_cache). As do dst(type=2), dst(type=3), idst(type=3), and idst(type=3) (*dst2_cache).

References

4.1.8 Signal Processing (scipy.signal)

The signal processing toolbox currently contains some filtering functions, a limited set of filter design tools, and a few B-spline interpolation algorithms for one- and two-dimensional data. While the B-spline algorithms could technically be placed under the interpolation category, they are included here because they only work with equally-spaced data and make heavy use of filter-theory and transfer-function formalism to provide a fast B-spline transform. To understand this section you will need to understand that a signal in SciPy is an array of real or complex numbers.

B-splines

A B-spline is an approximation of a continuous function over a finite-domain in terms of B-spline coefficients and knot points. If the knot-points are equally spaced with spacing \( \Delta x \), then the B-spline approximation to a 1-dimensional function is the finite-basis expansion.

\[
y(x) \approx \sum_j c_j \beta^o \left( \frac{x}{\Delta x} - j \right).
\]

In two dimensions with knot-spacing \( \Delta x \) and \( \Delta y \), the function representation is

\[
z(x, y) \approx \sum_j \sum_k c_{jk} \beta^o \left( \frac{x}{\Delta x} - j \right) \beta^o \left( \frac{y}{\Delta y} - k \right).
\]

In these expressions, \( \beta^o(\cdot) \) is the space-limited B-spline basis function of order, \( o \). The requirement of equally-spaced knot-points and equally-spaced data points, allows the development of fast (inverse-filtering) algorithms for determining the coefficients, \( c_j \), from sample-values, \( y_n \). Unlike the general spline interpolation algorithms, these algorithms can quickly find the spline coefficients for large images.

The advantage of representing a set of samples via B-spline basis functions is that continuous-domain operators (derivatives, re-sampling, integral, etc.) which assume that the data samples are drawn from an underlying continuous function can be computed with relative ease from the spline coefficients. For example,
the second-derivative of a spline is

\[ y''(x) = \frac{1}{\Delta x^2} \sum_j c_j \beta''(x - j) . \]

Using the property of B-splines that

\[ \frac{d^2 \beta^o(w)}{dw^2} = \beta^{o-2}(w+1) - 2\beta^{o-2}(w) + \beta^{o-2}(w-1) \]

it can be seen that

\[ y''(x) = \frac{1}{\Delta x^2} \sum_j c_j \left[ \beta^{o-2}\left(\frac{x}{\Delta x} - j + 1\right) - 2\beta^{o-2}\left(\frac{x}{\Delta x} - j\right) + \beta^{o-2}\left(\frac{x}{\Delta x} - j - 1\right) \right] . \]

If \( o = 3 \), then at the sample points,

\[ \Delta x^2 y'(x)|_{x=n\Delta x} = \sum_j c_j \delta_{n-j+1} - 2c_j \delta_{n-j} + c_j \delta_{n-j-1} , \]

\[ = c_{n+1} - 2c_n + c_{n-1} . \]

Thus, the second-derivative signal can be easily calculated from the spline fit. If desired, smoothing splines can be found to make the second-derivative less sensitive to random-errors.

The savvy reader will have already noticed that the data samples are related to the knot coefficients via a convolution operator, so that simple convolution with the sampled B-spline function recovers the original data from the spline coefficients. The output of convolutions can change depending on how boundaries are handled (this becomes increasingly more important as the number of dimensions in the data-set increases). The algorithms relating to B-splines in the signal-processing sub package assume mirror-symmetric boundary conditions. Thus, spline coefficients are computed based on that assumption, and data-samples can be recovered exactly from the spline coefficients by assuming them to be mirror-symmetric also.

Currently the package provides functions for determining second- and third-order cubic spline coefficients from equally spaced samples in one- and two-dimensions (\texttt{qspline1d}, \texttt{qspline2d}, \texttt{cspline1d}, \texttt{cspline2d}). The package also supplies a function (\texttt{bspline}) for evaluating the \( \beta \)-basis function for arbitrary order and \( x \): For large \( o \), the \( \beta \)-basis function can be approximated well by a zero-mean Gaussian function with standard-deviation equal to \( \sigma_o = (o+1)/12 \):

\[ \beta^o(x) \approx \frac{1}{\sqrt{2\pi\sigma_o^2}} \exp\left( -\frac{x^2}{2\sigma_o^2} \right) . \]

A function to compute this Gaussian for arbitrary \( x \) and \( o \) is also available (\texttt{gauss_spline}). The following code and Figure uses spline-filtering to compute an edge-image (the second-derivative of a smoothed spline) of a raccoon’s face which is an array returned by the command \texttt{misc.face}. The command \texttt{sepfir2d} was used to apply a separable two-dimensional FIR filter with mirror-symmetric boundary conditions to the spline coefficients. This function is ideally suited for reconstructing samples from spline coefficients and is faster than \texttt{convolve2d} which convolves arbitrary two-dimensional filters and allows for choosing mirror-symmetric boundary conditions.

```python
>>> import numpy as np
>>> from scipy import signal, misc
>>> import matplotlib.pyplot as plt

>>> image = misc.face(gray=True).astype(np.float32)
>>> derfilt = np.array([1.0, -2, 1.0], dtype=np.float32)
>>> ck = signal.cspline2d(image, 8.0)
>>> deriv = (signal.sepfir2d(ck, derfilt, [1]) + ...
          signal.sepfir2d(ck, [1], derfilt))
```
Alternatively we could have done:

```python
laplacian = np.array([[0,1,0], [1,-4,1], [0,1,0]], dtype=np.float32)
deriv2 = signal.convolve2d(ck,laplacian,mode='same',boundary='symm')
```

```python
>>> plt.figure()
>>> plt.imshow(image)
>>> plt.gray()
>>> plt.title('Original image')
>>> plt.show()
```

```python
>>> plt.figure()
>>> plt.imshow(deriv)
>>> plt.gray()
>>> plt.title('Output of spline edge filter')
>>> plt.show()
```

**Filtering**

Filtering is a generic name for any system that modifies an input signal in some way. In SciPy a signal can be thought of as a Numpy array. There are different kinds of filters for different kinds of operations. There are two broad kinds of filtering operations: linear and non-linear. Linear filters can always be reduced to multiplication of the flattened Numpy array by an appropriate matrix resulting in another flattened Numpy array. Of course, this is not usually the best way to compute the filter as the matrices and vectors involved may be huge. For example filtering a 512 x 512 image with this method would require multiplication of a 512 x 512 x 512 x 512 matrix with a 512 x 512 x 512 vector. Just trying to store the 512 x 512 x 512 x 512 matrix using a standard Numpy array would require 68,719,476,736 elements. At 4 bytes per element this would require 256GB of memory. In most applications most of the elements of this matrix are zero and a different method for computing the output of the filter is employed.

**Convolution/Correlation**

Many linear filters also have the property of shift-invariance. This means that the filtering operation is the same at different locations in the signal and it implies that the filtering matrix can be constructed from knowledge of one row (or column) of the matrix alone. In this case, the matrix multiplication can be accomplished using Fourier transforms.
Let $x[n]$ define a one-dimensional signal indexed by the integer $n$. Full convolution of two one-dimensional signals can be expressed as

$$y[n] = \sum_{k=-\infty}^{\infty} x[k] h[n-k].$$

This equation can only be implemented directly if we limit the sequences to finite support sequences that can be stored in a computer, choose $n = 0$ to be the starting point of both sequences, let $K+1$ be that value for which $x[n] = 0$ for all $n \geq K + 1$ and $M+1$ be that value for which $h[n] = 0$ for all $n \geq M + 1$, then the discrete convolution expression is

$$y[n] = \sum_{k=\max(n-M,0)}^{\min(n,K)} x[k] h[n-k].$$

For convenience assume $K \geq M$. Then, more explicitly the output of this operation is

\[
\begin{align*}
    y[0] &= x[0] h[0] \\
        &\vdots \\
        &\vdots \\
        &\vdots \\
    y[K+M] &= x[K] h[M].
\end{align*}
\]

Thus, the full discrete convolution of two finite sequences of lengths $K+1$ and $M+1$ respectively results in a finite sequence of length $K + M + 1 = (K + 1) + (M + 1) - 1$. 

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One dimensional convolution is implemented in SciPy with the function `convolve`. This function takes as inputs the signals \( x, h \), and two optional flags ‘mode’ and ‘method’ and returns the signal \( y \).

The first optional flag ‘mode’ allows for specification of which part of the output signal to return. The default value of ‘full’ returns the entire signal. If the flag has a value of ‘same’ then only the middle \( K \) values are returned starting at \( y \left[ \left\lfloor \frac{M+1}{2} \right\rfloor \right] \) so that the output has the same length as the first input. If the flag has a value of ‘valid’ then only the middle \( K = M + 1 = (K + 1) - (M + 1) + 1 \) output values are returned where \( z \) depends on all of the values of the smallest input from \( h[0] \) to \( h[M] \). In other words only the values \( y[M] \) to \( y[K] \) inclusive are returned.

The second optional flag ‘method’ determines how the convolution is computed, either through the Fourier transform approach with `fftconvolve` or through the direct method. By default, it selects the expected faster method. The Fourier transform method has order \( O(N \log N) \) while the direct method has order \( O(N^2) \). Depending on the big O constant and the value of \( N \), one of these two methods may be faster. The default value ‘auto’ performs a rough calculation and chooses the expected faster method, while the values ‘direct’ and ‘fft’ force computation with the other two methods.

The code below shows a simple example for convolution of 2 sequences

```python
>>> x = np.array([1.0, 2.0, 3.0])
>>> h = np.array([0.0, 1.0, 0.0, 0.0, 0.0])
>>> signal.convolve(x, h)
array([0., 1., 2., 3., 0., 0., 0.])
```

This same function `convolve` can actually take \( N \)-dimensional arrays as inputs and will return the \( N \)-dimensional convolution of the two arrays as is shown in the code example below. The same input flags are available for that case as well.

```python
>>> x = np.array([[[1., 1., 0., 0.], [1., 1., 0., 0.], [0., 0., 0., 0.], [0., 0., 0., 0.]]])
>>> h = np.array([[[1., 0., 0., 0.], [0., 0., 0., 0.], [0., 0., 1., 0.], [0., 0., 0., 0.]]])
>>> signal.convolve(x, h)
array([[[1., 1., 0., 0., 0., 0., 0., 0.],
        [1., 1., 0., 0., 0., 0., 0., 0.],
        [0., 0., 1., 1., 0., 0., 0., 0.],
        [0., 0., 1., 1., 0., 0., 0., 0.],
        [0., 0., 0., 0., 0., 0., 0., 0.],
        [0., 0., 0., 0., 0., 0., 0., 0.]]])
```

Correlation is very similar to convolution except for the minus sign becomes a plus sign. Thus

\[
 w[n] = \sum_{k=-\infty}^{\infty} y[k] x[n+k]
\]

is the (cross) correlation of the signals \( y \) and \( x \). For finite-length signals with \( y[n] = 0 \) outside of the range \([0, K]\) and \( x[n] = 0 \) outside of the range \([0, M]\), the summation can simplify to

\[
 w[n] = \sum_{k=\max(0,-n)}^{\min(K-M-n)} y[k] x[n+k].
\]
Assuming again that $K \geq M$ this is

\[
\begin{align*}
  w[-K] &= y[K] x[0] \\
  & \vdots \\
  & \vdots \\
  & \vdots \\
  w[M] &= y[0] x[M].
\end{align*}
\]

The SciPy function `correlate` implements this operation. Equivalent flags are available for this operation to return the full $K + M + 1$ length sequence (‘full’) or a sequence with the same size as the largest sequence starting at $w[-K + \lfloor \frac{M-1}{2} \rfloor]$ (‘same’) or a sequence where the values depend on all the values of the smallest sequence (‘valid’). This final option returns the $K - M + 1$ values $w[M-K]$ to $w[0]$ inclusive.

The function `correlate` can also take arbitrary $N$-dimensional arrays as input and return the $N$-dimensional convolution of the two arrays on output.

When $N = 2$, `correlate` and/or `convolve` can be used to construct arbitrary image filters to perform actions such as blurring, enhancing, and edge-detection for an image.

```python
>>> import numpy as np
>>> from scipy import signal, misc
>>> import matplotlib.pyplot as plt

>>> image = misc.face(gray=True)
>>> w = np.zeros((50, 50))
>>> w[0][0] = 1.0
>>> w[49][25] = 1.0
>>> image_new = signal.fftconvolve(image, w)

>>> plt.figure()
>>> plt.imshow(image)
>>> plt.gray()
>>> plt.title('Original image')
>>> plt.show()

>>> plt.figure()
>>> plt.imshow(image_new)
>>> plt.gray()
>>> plt.title('Filtered image')
>>> plt.show()
```

Calculating the convolution in the time domain as above is mainly used for filtering when one of the signals is much smaller than the other ($K \gg M$), otherwise linear filtering is more efficiently calculated in the...
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frequency domain provided by the function \texttt{fftconvolve}. By default, \texttt{convolve} estimates the fastest method using \texttt{choose_conv_method}.

If the filter function $w[n,m]$ can be factored according to

$$h[n,m] = h_1[n]h_2[m],$$

convolution can be calculated by means of the function \texttt{sepfir2d}. As an example we consider a Gaussian filter \texttt{gaussian}

$$h[n,m] \propto e^{-x^2-y^2} = e^{-x^2}e^{-y^2}$$

which is often used for blurring.

```python
>>> import numpy as np
>>> from scipy import signal, misc
>>> import matplotlib.pyplot as plt

>>> image = misc.ascent()
>>> w = signal.gaussian(50, 10.0)
>>> image_new = signal.sepfir2d(image, w, w)

>>> plt.figure()
>>> plt.imshow(image)
>>> plt.gray()
>>> plt.title('Original image')
>>> plt.show()

Original image
```

```python
>>> plt.figure()
>>> plt.imshow(image_new)
>>> plt.gray()
>>> plt.title('Filtered image')
>>> plt.show()
```

```python
```
**Difference-equation filtering**

A general class of linear one-dimensional filters (that includes convolution filters) are filters described by the difference equation

\[ \sum_{k=0}^{N} a_k y[n-k] = \sum_{k=0}^{M} b_k x[n-k] \]

where \( x[n] \) is the input sequence and \( y[n] \) is the output sequence. If we assume initial rest so that \( y[n] = 0 \) for \( n < 0 \), then this kind of filter can be implemented using convolution. However, the convolution filter sequence \( h[n] \) could be infinite if \( a_k \neq 0 \) for \( k \geq 1 \). In addition, this general class of linear filter allows initial conditions to be placed on \( y[n] \) for \( n < 0 \) resulting in a filter that cannot be expressed using convolution.

The difference equation filter can be thought of as finding \( y[n] \) recursively in terms of its previous values

\[ a_0 y[n] = -a_1 y[n-1] - \cdots - a_N y[n-N] + \cdots + b_0 x[n] + \cdots + b_M x[n-M] \]

Often \( a_0 = 1 \) is chosen for normalization. The implementation in SciPy of this general difference equation filter is a little more complicated than would be implied by the previous equation. It is implemented so that only one signal needs to be delayed. The actual implementation equations are (assuming \( a_0 = 1 \)).

\[
\begin{align*}
  y[n] &= b_0 x[n] + z_0[n-1] \\
  z_0[n] &= b_1 x[n] + z_1[n-1] - a_1 y[n] \\
  z_1[n] &= b_2 x[n] + z_2[n-1] - a_2 y[n] \\
  &\vdots \\
  z_{K-2}[n] &= b_{K-1} x[n] + z_{K-1}[n-1] - a_{K-1} y[n] \\
  z_{K-1}[n] &= b_K x[n] - a_K y[n],
\end{align*}
\]

where \( K = \max(N, M) \). Note that \( b_K = 0 \) if \( K > M \) and \( a_K = 0 \) if \( K > N \). In this way, the output at time \( n \) depends only on the input at time \( n \) and the value of \( z_0 \) at the previous time. This can always be calculated as long as the \( K \) values \( z_0[n-1] \ldots z_{K-1}[n-1] \) are computed and stored at each time step.

The difference-equation filter is called using the command `lfilter` in SciPy. This command takes as inputs the vector \( b \), the vector \( a \), a signal \( x \) and returns the vector \( y \) (the same length as \( x \)) computed using the equation given above. If \( x \) is \( N \)-dimensional, then the filter is computed along the axis provided. If, desired,
initial conditions providing the values of \( z_0 [-1] \) to \( z_{K-1} [-1] \) can be provided or else it will be assumed that they are all zero. If initial conditions are provided, then the final conditions on the intermediate variables are also returned. These could be used, for example, to restart the calculation in the same state.

Sometimes it is more convenient to express the initial conditions in terms of the signals \( x[n] \) and \( y[n] \). In other words, perhaps you have the values of \( x[-M] \) to \( x[-1] \) and the values of \( y[-N] \) to \( y[-1] \) and would like to determine what values of \( z_m [-1] \) should be delivered as initial conditions to the difference-equation filter. It is not difficult to show that for \( 0 \leq m < K \),

\[
z_m[n] = \sum_{p=0}^{K-m-1} (b_{m+p+1} x[n-p] - a_{m+p+1} y[n-p]) .
\]

Using this formula we can find the initial condition vector \( z_0 [-1] \) to \( z_{K-1} [-1] \) given initial conditions on \( y \) (and \( x \)). The command \texttt{lfiltic} performs this function.

As an example consider the following system:

\[
y[n] = \frac{1}{2} x[n] + \frac{1}{4} x[n-1] + \frac{1}{3} y[n-1]
\]

The code calculates the signal \( y[n] \) for a given signal \( x[n] \); first for initial conditions \( y[-1] = 0 \) (default case), then for \( y[-1] = 2 \) by means of \texttt{lfiltic}.

```python
>>> import numpy as np
>>> from scipy import signal

>>> x = np.array([1., 0., 0., 0.])
>>> b = np.array([1.0/2, 1.0/4])
>>> a = np.array([1.0, -1.0/3])
>>> signal.lfilter(b, a, x)
array([0.5, 0.41666667, 0.13888889, 0.0462963])
>>> zi = signal.lfiltic(b, a, y=[2.])
>>> signal.lfilter(b, a, x, zi=zi)
(array([ 1.16666667, 0.63888889, 0.21296296, 0.07098765]), array([0.02366]))
```

Note that the output signal \( y[n] \) has the same length as the length as the input signal \( x[n] \).

### Analysis of Linear Systems

Linear system described a linear difference equation can be fully described by the coefficient vectors \( a \) and \( b \) as was done above; an alternative representation is to provide a factor \( k \), \( N_z \) zeros \( z_k \) and \( N_p \) poles \( p_k \), respectively, to describe the system by means of its transfer function \( H(z) \) according to

\[
H(z) = k \frac{(z - z_1)(z - z_2)...(z - z_{N_z})}{(z - p_1)(z - p_2)...(z - p_{N_p})}
\]

This alternative representation can be obtain with the scipy function \texttt{tf2zpk}; the inverse is provided by \texttt{zpk2tf}.

For the example from above we have

```python
>>> b = np.array([1.0/2, 1.0/4])
>>> a = np.array([1.0, -1.0/3])
>>> signal.tf2zpk(b, a)
(array([-0.5]), array([ 0.33333333]), 0.5)
```
i.e. the system has a zero at $z = -1/2$ and a pole at $z = 1/3$.

The scipy function \textit{freqz} allows calculation of the frequency response of a system described by the coefficients $a_k$ and $b_k$. See the help of the \textit{freqz} function of a comprehensive example.

\textbf{Filter Design}

Time-discrete filters can be classified into finite response (FIR) filters and infinite response (IIR) filters. FIR filters can provide a linear phase response, whereas IIR filters cannot. Scipy provides functions for designing both types of filters.

\textbf{FIR Filter}

The function \textit{firwin} designs filters according to the window method. Depending on the provided arguments, the function returns different filter types (e.g. low-pass, band-pass...).

The example below designs a low-pass and a band-stop filter, respectively.

```python
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt

>>> b1 = signal.firwin(40, 0.5)
>>> b2 = signal.firwin(41, [0.3, 0.8])
>>> w1, h1 = signal.freqz(b1)
>>> w2, h2 = signal.freqz(b2)

>>> plt.title('Digital filter frequency response')
>>> plt.plot(w1, 20*np.log10(np.abs(h1)), 'b')
>>> plt.plot(w2, 20*np.log10(np.abs(h2)), 'r')
>>> plt.ylabel('Amplitude Response (dB)')
>>> plt.xlabel('Frequency (rad/sample)')
>>> plt.grid()
>>> plt.show()
```

Note that \textit{firwin} uses per default a normalized frequency defined such that the value 1 corresponds to the Nyquist frequency, whereas the function \textit{freqz} is defined such that the value $\pi$ corresponds to the Nyquist frequency.
The function \texttt{firwin2} allows design of almost arbitrary frequency responses by specifying an array of corner frequencies and corresponding gains, respectively.

The example below designs a filter with such an arbitrary amplitude response.

```python
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt

>>> b = signal.firwin2(150, [0.0, 0.3, 0.6, 1.0], [1.0, 2.0, 0.5, 0.0])
>>> w, h = signal.freqz(b)
>>> plt.title('Digital filter frequency response')
>>> plt.plot(w, np.abs(h))
>>> plt.title('Digital filter frequency response')
>>> plt.ylabel('Amplitude Response')
>>> plt.xlabel('Frequency (rad/sample)')
>>> plt.grid()
>>> plt.show()
```

Note the linear scaling of the y-axis and the different definition of the Nyquist frequency in \texttt{firwin2} and \texttt{freqz} (as explained above).

### IIR Filter

SciPy provides two functions to directly design IIR \texttt{iirdesign} and \texttt{iirfilter} where the filter type (e.g. elliptic) is passed as an argument and several more filter design functions for specific filter types; e.g. \texttt{ellip}.

The example below designs an elliptic low-pass filter with defined passband and stopband ripple, respectively. Note the much lower filter order (order 4) compared with the FIR filters from the examples above in order to reach the same stop-band attenuation of $\approx 60$ dB.
```python
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt

>>> b, a = signal.iirfilter(4, Wn=0.2, rp=5, rs=60, btype='lowpass', ftype='ellip')

>>> w, h = signal.freqz(b, a)

>>> plt.title('Digital filter frequency response')
>>> plt.plot(w, 20 * np.log10(np.abs(h)))
>>> plt.title('Digital filter frequency response')
>>> plt.ylabel('Amplitude Response [dB]')
>>> plt.xlabel('Frequency (rad/sample)')
>>> plt.grid()
>>> plt.show()
```

**Filter Coefficients**

Filter coefficients can be stored in several different formats:

- ‘ba’ or ‘tf’ = transfer function coefficients
- ‘zpk’ = zeros, poles, and overall gain
- ‘ss’ = state-space system representation
- ‘sos’ = transfer function coefficients of second-order sections

Functions such as `tf2zpk` and `zpk2ss` can convert between them.

**Transfer function representation**

The `ba` or `tf` format is a 2-tuple `(b, a)` representing a transfer function, where `b` is a length M+1 array of coefficients of the M-order numerator polynomial, and `a` is a length N+1 array of coefficients of the N-order denominator, as positive, descending powers of the transfer function variable. So the tuple of
b = [b₀, b₁, ..., b_M] and a = [a₀, a₁, ..., a_N] can represent an analog filter of the form:

\[ H(s) = \frac{b₀s^M + b₁s^{(M-1)} + \cdots + b_M}{a₀s^N + a₁s^{(N-1)} + \cdots + a_N} = \frac{\sum_{i=0}^{M} b_is^{(M-i)}}{\sum_{i=0}^{N} a_is^{(N-i)}} \]

or a discrete-time filter of the form:

\[ H(z) = \frac{b₀ + b₁z^{-1} + \cdots + b_Mz^{-M}}{a₀ + a₁z^{-1} + \cdots + a_Nz^{-N}} = \frac{\sum_{i=0}^{M} b_iz^{-i}}{\sum_{i=0}^{N} a_iz^{-i}} \]

This “positive powers” form is found more commonly in controls engineering. If M and N are equal (which is true for all filters generated by the bilinear transform), then this happens to be equivalent to the “negative powers” discrete-time form preferred in DSP:

\[ H(z) = \frac{b₀ + b₁z^{-1} + \cdots + b_Mz^{-M}}{a₀ + a₁z^{-1} + \cdots + a_Nz^{-N}} = \frac{\sum_{i=0}^{M} b_iz^{-i}}{\sum_{i=0}^{N} a_iz^{-i}} \]

Although this is true for common filters, remember that this is not true in the general case. If M and N are not equal, the discrete-time transfer function coefficients must first be converted to the “positive powers” form before finding the poles and zeros.

This representation suffers from numerical error at higher orders, so other formats are preferred when possible.

**Zeros and poles representation**

The `zpk` format is a 3-tuple \((z, p, k)\), where \(z\) is an \(M\)-length array of the complex zeros of the transfer function \(z = [z₀, z₁, ..., z_{M-1}]\), \(p\) is an \(N\)-length array of the complex poles of the transfer function \(p = [p₀, p₁, ..., p_{N-1}]\), and \(k\) is a scalar gain. These represent the digital transfer function:

\[ H(z) = k \cdot \frac{(z - z₀)(z - z₁) \cdots (z - z_{M-1})}{(z - p₀)(z - p₁) \cdots (z - p_{N-1})} = k \prod_{i=0}^{M-1} \frac{(z - z_i)}{\prod_{i=0}^{N-1} (z - p_i)} \]

or the analog transfer function:

\[ H(s) = k \cdot \frac{(s - z₀)(s - z₁) \cdots (s - z_{M-1})}{(s - p₀)(s - p₁) \cdots (s - p_{N-1})} = k \prod_{i=0}^{M-1} \frac{(s - z_i)}{\prod_{i=0}^{N-1} (s - p_i)} \]

Although the sets of roots are stored as ordered NumPy arrays, their ordering does not matter; \([-1, \ -2, \ [-3, \ -4], \ 1]\) is the same filter as \([-2, \ -1, \ [-4, \ -3], \ 1]\).

**State-space system representation**

The `ss` format is a 4-tuple of arrays \((A, B, C, D)\) representing the state-space of an \(N\)-order digital/discrete-time system of the form:

\[ x[k+1] = Ax[k] + Bu[k] \]
\[ y[k] = Cx[k] + Du[k] \]

or a continuous/analog system of the form:

\[ x(t) = Ax(t) + Bu(t) \]
\[ y(t) = Cx(t) + Du(t) \]

with \(P\) inputs, \(Q\) outputs and \(N\) state variables, where:
• $x$ is the state vector
• $y$ is the output vector of length $Q$
• $u$ is the input vector of length $P$
• $A$ is the state matrix, with shape $(N, N)$
• $B$ is the input matrix with shape $(N, P)$
• $C$ is the output matrix with shape $(Q, N)$
• $D$ is the feedthrough or feedforward matrix with shape $(Q, P)$. (In cases where the system does not have a direct feedthrough, all values in $D$ are zero.)

State-space is the most general representation, and the only one that allows for multiple-input, multiple-output (MIMO) systems. There are multiple state-space representations for a given transfer function. Specifically, the “controllable canonical form” and “observable canonical form” have the same coefficients as the $\text{tf}$ representation, and therefore suffer from the same numerical errors.

### Second-order sections representation

The $\text{sos}$ format is a single 2D array of shape $(\text{n_sections}, 6)$, representing a sequence of second-order transfer functions which, when cascaded in series, realize a higher-order filter with minimal numerical error. Each row corresponds to a second-order $\text{tf}$ representation, with the first three columns providing the numerator coefficients and the last three providing the denominator coefficients:

$$[b_0, b_1, b_2; a_0, a_1, a_2]$$

The coefficients are typically normalized such that $a_0$ is always 1. The section order is usually not important with floating-point computation; the filter output will be the same regardless.

### Filter transformations

The IIR filter design functions first generate a prototype analog lowpass filter with a normalized cutoff frequency of 1 rad/sec. This is then transformed into other frequencies and band types using the following substitutions:

<table>
<thead>
<tr>
<th>Type</th>
<th>Transformation</th>
</tr>
</thead>
<tbody>
<tr>
<td>$lp2lp$</td>
<td>$s \rightarrow \frac{s}{\omega_0}$</td>
</tr>
<tr>
<td>$lp2hp$</td>
<td>$s \rightarrow \frac{s}{\frac{s}{\omega_0}}$</td>
</tr>
<tr>
<td>$lp2bp$</td>
<td>$s \rightarrow \frac{s + \omega_0}{s + \frac{2\omega_0}{\text{BW}}}$</td>
</tr>
<tr>
<td>$lp2bs$</td>
<td>$s \rightarrow \frac{s + j\omega_0}{s^2 + \omega_0^2}$</td>
</tr>
</tbody>
</table>

Here, $\omega_0$ is the new cutoff or center frequency, and $\text{BW}$ is the bandwidth. These preserve symmetry on a logarithmic frequency axis.

To convert the transformed analog filter into a digital filter, the $\text{bilinear}$ transform is used, which makes the following substitution:

$$s \rightarrow \frac{2}{T} \frac{z - 1}{z + 1}$$

where $T$ is the sampling time (the inverse of the sampling frequency).

### Other filters

The signal processing package provides many more filters as well.
Median Filter

A median filter is commonly applied when noise is markedly non-Gaussian or when it is desired to preserve edges. The median filter works by sorting all of the array pixel values in a rectangular region surrounding the point of interest. The sample median of this list of neighborhood pixel values is used as the value for the output array. The sample median is the middle array value in a sorted list of neighborhood values. If there are an even number of elements in the neighborhood, then the average of the middle two values is used as the median. A general purpose median filter that works on N-dimensional arrays is `medfilt`. A specialized version that works only for two-dimensional arrays is available as `medfilt2d`.

Order Filter

A median filter is a specific example of a more general class of filters called order filters. To compute the output at a particular pixel, all order filters use the array values in a region surrounding that pixel. These array values are sorted and then one of them is selected as the output value. For the median filter, the sample median of the list of array values is used as the output. A general order filter allows the user to select which of the sorted values will be used as the output. So, for example one could choose to pick the maximum in the list or the minimum. The order filter takes an additional argument besides the input array and the region mask that specifies which of the elements in the sorted list of neighbor array values should be used as the output. The command to perform an order filter is `order_filter`.

Wiener filter

The Wiener filter is a simple deblurring filter for denoising images. This is not the Wiener filter commonly described in image reconstruction problems but instead it is a simple, local-mean filter. Let \( x \) be the input signal, then the output is

\[
y = \begin{cases} 
\frac{\sigma^2}{\sigma_x^2} m_x + \left(1 - \frac{\sigma^2}{\sigma_x^2}\right) x & \sigma_x^2 \geq \sigma^2, \\
\frac{m_x}{\sigma_x^2} & \sigma_x^2 < \sigma^2,
\end{cases}
\]

where \( m_x \) is the local estimate of the mean and \( \sigma_x^2 \) is the local estimate of the variance. The window for these estimates is an optional input parameter (default is \( 3 \times 3 \)). The parameter \( \sigma^2 \) is a threshold noise parameter. If \( \sigma \) is not given then it is estimated as the average of the local variances.

Hilbert filter

The Hilbert transform constructs the complex-valued analytic signal from a real signal. For example if \( x = \cos \omega n \) then \( y = \text{hilbert}(x) \) would return (except near the edges) \( y = \exp(j\omega n) \). In the frequency domain, the hilbert transform performs

\[
Y = X \cdot H
\]

where \( H \) is 2 for positive frequencies, 0 for negative frequencies and 1 for zero-frequencies.

Analog Filter Design

The functions `iirdesign`, `iirfilter`, and the filter design functions for specific filter types (e.g. `ellip`) all have a flag `analog` which allows design of analog filters as well.

The example below designs an analog (IIR) filter, obtains via `tf2zpk` the poles and zeros and plots them in the complex s-plane. The zeros at \( \omega \approx 150 \) and \( \omega \approx 300 \) can be clearly seen in the amplitude response.

```python
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt
```
>>> b, a = signal.iirdesign(wp=100, ws=200, gpass=2.0, gstop=40., analog=True)
>>> w, h = signal.freqs(b, a)

>>> plt.title('Analog filter frequency response')
>>> plt.plot(w, 20*np.log10(np.abs(h)))
>>> plt.ylabel('Amplitude Response [dB]')
>>> plt.xlabel('Frequency')
>>> plt.grid()
>>> plt.show()

>>> z, p, k = signal.tf2zpk(b, a)

>>> plt.plot(np.real(z), np.imag(z), 'xb')
>>> plt.plot(np.real(p), np.imag(p), 'or')
>>> plt.legend(['Zeros', 'Poles'], loc=2)

>>> plt.title('Pole / Zero Plot')
>>> plt.ylabel('Real')
>>> plt.xlabel('Imaginary')
>>> plt.grid()
>>> plt.show()

### Spectral Analysis

#### Periodogram Measurements

The scipy function `periodogram` provides a method to estimate the spectral density using the periodogram method.

The example below calculates the periodogram of a sine signal in white Gaussian noise.

```python
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt
```
Spectral Analysis using Welch’s Method

An improved method, especially with respect to noise immunity, is Welch’s method which is implemented by the scipy function `welch`.

The example below estimates the spectrum using Welch’s method and uses the same parameters as the example above. Note the much smoother noise floor of the spectrogram.

```python
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt

>>> fs = 10e3
>>> N = 1e5
>>> amp = 2*np.sqrt(2)
>>> freq = 1270.0
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> x = amp*np.sin(2*np.pi*freq*time)
>>> x += np.random.normal(scale=np.sqrt(noise_power), size=time.shape)

>>> f, Pper_spec = signal.periodogram(x, fs, 'flattop', scaling='spectrum')

>>> plt.semilogy(f, Pper_spec)
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('PSD')
>>> plt.grid()
>>> plt.show()
```
```python
>>> time = np.arange(N) / fs
>>> x = amp*np.sin(2*np.pi*freq*time)
>>> x += np.random.normal(scale=np.sqrt(noise_power), size=time.shape)

>>> f, Pwelch_spec = signal.welch(x, fs, scaling='spectrum')

>>> plt.semilogy(f, Pwelch_spec)
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('PSD')
>>> plt.grid()
>>> plt.show()
```
Lomb-Scargle Periodograms (lombscargle)

Least-squares spectral analysis (LSSA) is a method of estimating a frequency spectrum, based on a least squares fit of sinusoids to data samples, similar to Fourier analysis. Fourier analysis, the most used spectral method in science, generally boosts long-periodic noise in long gapped records; LSSA mitigates such problems.

The Lomb-Scargle method performs spectral analysis on unevenly sampled data and is known to be a powerful way to find, and test the significance of, weak periodic signals.

For a time series comprising $N_t$ measurements $X_j \equiv X(t_j)$ sampled at times $t_j$ where $(j = 1, \ldots, N_t)$, assumed to have been scaled and shifted such that its mean is zero and its variance is unity, the normalized Lomb-Scargle periodogram at frequency $f$ is

$$P_n(f) = \frac{1}{2} \left\{ \frac{\left( \sum_{j=1}^{N_t} X_j \cos \omega(t_j - \tau) \right)^2}{\sum_{j=1}^{N_t} \cos^2 \omega(t_j - \tau)} + \frac{\left( \sum_{j=1}^{N_t} X_j \sin \omega(t_j - \tau) \right)^2}{\sum_{j=1}^{N_t} \sin^2 \omega(t_j - \tau)} \right\}.$$ 

Here, $\omega \equiv 2\pi f$ is the angular frequency. The frequency dependent time offset $\tau$ is given by

$$\tan 2\omega \tau = \frac{\sum_{j=1}^{N_t} \sin 2\omega t_j}{\sum_{j=1}^{N_t} \cos 2\omega t_j}.$$ 

The lombscargle function calculates the periodogram using a slightly modified algorithm due to Townsend\(^3\) which allows the periodogram to be calculated using only a single pass through the input arrays for each frequency.

The equation is refactored as:

$$P_n(f) = \frac{1}{2} \left[ \frac{(c_r XC + s_r XS)^2}{c_r^2 CC + 2c_r s_r CS + s_r^2 SS} + \frac{(c_r XS - s_r XC)^2}{c_r^2 SS - 2c_r s_r CS + s_r^2 CC} \right]$$

and

$$\tan 2\omega \tau = \frac{2CS}{CC - SS}.$$ 

Here,

$$c_r = \cos \omega \tau, \quad s_r = \sin \omega \tau$$

while the sums are

$$XC = \sum_{j=1}^{N_t} X_j \cos \omega t_j$$

$$XS = \sum_{j=1}^{N_t} X_j \sin \omega t_j$$

$$CC = \sum_{j=1}^{N_t} \cos^2 \omega t_j$$

$$SS = \sum_{j=1}^{N_t} \sin^2 \omega t_j$$

$$CS = \sum_{j=1}^{N_t} \cos \omega t_j \sin \omega t_j.$$ 

This requires $N_t(2N_t + 3)$ trigonometric function evaluations giving a factor of $\sim 2$ speed increase over the straightforward implementation.

---

Detrend

Scipy provides the function \texttt{detrend} to remove a constant or linear trend in a data series in order to see effect of higher order.

The example below removes the constant and linear trend of a 2-nd order polynomial time series and plots the remaining signal components.

```python
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt

>>> t = np.linspace(-10, 10, 20)
>>> y = 1 + t + 0.01*t**2
>>> yconst = signal.detrend(y, type='constant')
>>> ylin = signal.detrend(y, type='linear')

>>> plt.plot(t, y, '-rx')
>>> plt.plot(t, yconst, '-bo')
>>> plt.plot(t, ylin, '-k+')
>>> plt.grid()
>>> plt.legend(['signal', 'const. detrend', 'linear detrend'])
>>> plt.show()
```

References
Some further reading and related software:

4.1.9 Linear Algebra (scipy.linalg)

When SciPy is built using the optimized ATLAS LAPACK and BLAS libraries, it has very fast linear algebra capabilities. If you dig deep enough, all of the raw lapack and blas libraries are available for your use for even more speed. In this section, some easier-to-use interfaces to these routines are described.

All of these linear algebra routines expect an object that can be converted into a 2-dimensional array. The output of these routines is also a two-dimensional array.
scipy.linalg vs numpy.linalg

scipy.linalg contains all the functions in numpy.linalg. plus some other more advanced ones not contained in numpy.linalg.

Another advantage of using scipy.linalg over numpy.linalg is that it is always compiled with BLAS/LAPACK support, while for numpy this is optional. Therefore, the scipy version might be faster depending on how numpy was installed.

Therefore, unless you don’t want to add scipy as a dependency to your numpy program, use scipy.linalg instead of numpy.linalg.

numpy.matrix vs 2D numpy.ndarray

The classes that represent matrices, and basic operations such as matrix multiplications and transpose are a part of numpy. For convenience, we summarize the differences between numpy.matrix and numpy.ndarray here.

numpy.matrix is matrix class that has a more convenient interface than numpy.ndarray for matrix operations. This class supports for example MATLAB-like creation syntax via the semicolon, has matrix multiplication as default for the * operator, and contains I and T members that serve as shortcuts for inverse and transpose:

```python
>>> import numpy as np
>>> A = np.mat('[1 2;3 4]')
>>> A
matrix([[1, 2],
        [3, 4]]
>>> A.I
matrix([[[-2., 1.],
          [1.5, -0.5]])
>>> b = np.mat('[5 6]')
>>> b
matrix([[5, 6]])
>>> b.T
matrix([[5],
        [6]])
>>> A*b.T
matrix([[17],
        [39]])
```

Despite its convenience, the use of the numpy.matrix class is discouraged, since it adds nothing that cannot be accomplished with 2D numpy.ndarray objects, and may lead to a confusion of which class is being used. For example, the above code can be rewritten as:

```python
>>> import numpy as np
>>> from scipy import linalg
>>> A = np.array([[1,2],[3,4]])
>>> A
array([[1, 2],
       [3, 4]])
>>> linalg.inv(A)
array([[[-2., 1.],
        [1.5, -0.5]])
>>> b = np.array([[5,6]])  #2D array
>>> b
```

(continues on next page)
scipy.linalg operations can be applied equally to numpy.matrix or to 2D numpy.ndarray objects.

**Basic routines**

**Finding Inverse**

The inverse of a matrix \( A \) is the matrix \( B \) such that \( AB = I \) where \( I \) is the identity matrix consisting of ones down the main diagonal. Usually \( B \) is denoted \( B = A^{-1} \). In SciPy, the matrix inverse of the Numpy array, \( A \), is obtained using `linalg.inv (A)` , or using \( A.I \) if \( A \) is a Matrix. For example, let

\[
A = \begin{bmatrix}
1 & 3 & 5 \\
2 & 5 & 1 \\
2 & 3 & 8
\end{bmatrix}
\]

then

\[
A^{-1} = \frac{1}{25} \begin{bmatrix}
-37 & 9 & 22 \\
14 & 2 & -9 \\
4 & -3 & 1
\end{bmatrix} = \begin{bmatrix}
-1.48 & 0.36 & 0.88 \\
0.56 & 0.08 & -0.36 \\
0.16 & -0.12 & 0.04
\end{bmatrix}.
\]

The following example demonstrates this computation in SciPy

```python
g = 5
h = 6
>>> b.T
array([[5],
       [6]])
```

```python
>>> A*b  # not matrix multiplication!
array([[ 5, 12],
       [15, 24]])
```

```python
>>> A.dot(b.T)  # matrix multiplication
array([[17],
       [39]])
```

```python
>>> b = np.array([5, 6])  # 1D array
>>> b
array([5, 6])
>>> b.T  # not matrix transpose!
array([5, 6])
```

```python
>>> A.dot(b)  # does not matter for multiplication
array([17, 39])
```
Solving linear system
Solving linear systems of equations is straightforward using the scipy command `linalg.solve`. This command expects an input matrix and a right-hand-side vector. The solution vector is then computed. An option for entering a symmetric matrix is offered which can speed up the processing when applicable. As an example, suppose it is desired to solve the following simultaneous equations:

\[
\begin{align*}
    x + 3y + 5z &= 10 \\
    2x + 5y + z &= 8 \\
    2x + 3y + 8z &= 3
\end{align*}
\]

We could find the solution vector using a matrix inverse:

\[
\begin{bmatrix}
    x \\
    y \\
    z
\end{bmatrix} = \begin{bmatrix}
    1 & 3 & 5 \\
    2 & 5 & 1 \\
    2 & 3 & 8
\end{bmatrix}^{-1} \begin{bmatrix}
    10 \\
    8 \\
    3
\end{bmatrix} = \frac{1}{25} \begin{bmatrix}
    -232 \\
    129 \\
    19
\end{bmatrix} = \begin{bmatrix}
    -9.28 \\
    5.16 \\
    0.76
\end{bmatrix}.
\]

However, it is better to use the `linalg.solve` command which can be faster and more numerically stable. In this case it however gives the same answer as shown in the following example:

```python
>>> import numpy as np
>>> from scipy import linalg
>>> A = np.array([[1, 2], [3, 4]])
>>> A
array([[1, 2],
       [3, 4]])
>>> b = np.array([[5], [6]])
>>> b
array([[5],
       [6]])
>>> linalg.inv(A).dot(b)  # slow
array([[-4.],
       [ 4.5]])
>>> A.dot(linalg.inv(A).dot(b)) - b  # check
array([[ 8.88178420e-16],
       [ 2.66453526e-15]])
>>> np.linalg.solve(A, b)  # fast
array([[ 0.],
       [ 0.]])
```

Finding Determinant
The determinant of a square matrix \( A \) is often denoted \( |A| \) and is a quantity often used in linear algebra. Suppose \( a_{ij} \) are the elements of the matrix \( A \) and let \( M_{ij} = |A_{ij}| \) be the determinant of the matrix left by removing the \( i \)th row and \( j \)th column from \( A \). Then for any row \( i \),

\[
|A| = \sum_j (-1)^{i+j} a_{ij} M_{ij}.
\]

This is a recursive way to define the determinant where the base case is defined by accepting that the determinant of a \( 1 \times 1 \) matrix is the only matrix element. In SciPy the determinant can be calculated with `linalg.det`. For example, the determinant of

\[
A = \begin{bmatrix}
    1 & 3 & 5 \\
    2 & 5 & 1 \\
    2 & 3 & 8
\end{bmatrix}
\]
is

\[ |A| = 1 \begin{vmatrix} 5 & 1 & -3 \\ 3 & 8 & 2 \\ 2 & 8 & 5 \end{vmatrix} + 5 \begin{vmatrix} 2 & 5 \\ 2 & 3 \end{vmatrix} = 1(5 \cdot 8 - 3 \cdot 1) - 3(2 \cdot 8 - 2 \cdot 1) + 5(2 \cdot 3 - 2 \cdot 5) = -25. \]

In SciPy this is computed as shown in this example:

```python
>>> import numpy as np
>>> from scipy import linalg
>>> A = np.array([[1, 2], [3, 4]])
>>> A
array([[1, 2],
       [3, 4]])
>>> linalg.det(A)
-2.0
```

### Computing norms

Matrix and vector norms can also be computed with SciPy. A wide range of norm definitions are available using different parameters to the order argument of `linalg.norm`. This function takes a rank-1 (vectors) or a rank-2 (matrices) array and an optional order argument (default is 2). Based on these inputs a vector or matrix norm of the requested order is computed.

For vector \( x \), the order parameter can be any real number including \( \text{inf} \) or \( -\text{inf} \). The computed norm is

\[
\|x\| = \begin{cases} 
\max |x_i| & \text{ord} = \text{inf} \\
\min |x_i| & \text{ord} = -\text{inf} \\
\left( \sum |x_i|^{\text{ord}} \right)^{1/\text{ord}} & |\text{ord}| < \infty.
\end{cases}
\]

For matrix \( A \) the only valid values for norm are \( \pm 2, \pm 1, \pm \text{inf} \), and ‘fro’ (or ‘f’). Thus,

\[
\|A\| = \begin{cases} 
\max_i \sum_j |a_{ij}| & \text{ord} = \text{inf} \\
\min_i \sum_j |a_{ij}| & \text{ord} = -\text{inf} \\
\max_j \sum_i |a_{ij}| & \text{ord} = 1 \\
\min_j \sum_i |a_{ij}| & \text{ord} = -1 \\
\max \sigma_i & \text{ord} = 2 \\
\min \sigma_i & \text{ord} = -2 \\
\sqrt{\text{trace}(A^H A)} & \text{ord} = \text{fro'}
\end{cases}
\]

where \( \sigma_i \) are the singular values of \( A \).

Examples:

```python
>>> import numpy as np
>>> from scipy import linalg
>>> A=np.array([[1,2],[3,4]])
>>> A
array([[1, 2],
       [3, 4]])
>>> linalg.norm(A)
5.4772255750516612
>>> linalg.norm(A,'fro') # frobenius norm is the default
5.4772255750516612
>>> linalg.norm(A,1) # L1 norm (max column sum)
6
```

(continues on next page)
Solving linear least-squares problems and pseudo-inverses

Linear least-squares problems occur in many branches of applied mathematics. In this problem a set of linear scaling coefficients is sought that allow a model to fit data. In particular it is assumed that data \( y_i \) is related to data \( x_i \) through a set of coefficients \( c_j \) and model functions \( f_j(x_i) \) via the model

\[
y_i = \sum_j c_j f_j(x_i) + \epsilon_i
\]

where \( \epsilon_i \) represents uncertainty in the data. The strategy of least squares is to pick the coefficients \( c_j \) to minimize

\[
J(c) = \sum_i \left| y_i - \sum_j c_j f_j(x_i) \right|^2.
\]

Theoretically, a global minimum will occur when

\[
\frac{\partial J}{\partial c_n^*} = 0 = \sum_i \left( y_i - \sum_j c_j f_j(x_i) \right) (-f_n^*(x_i))
\]

or

\[
\sum_j c_j \sum_i f_j(x_i) f_n^*(x_i) = \sum_i y_i f_n^*(x_i)
\]

\[
A^H A c = A^H y
\]

where

\[
\{A\}_{ij} = f_j(x_i).
\]

When \( A^H A \) is invertible, then

\[
c = (A^H A)^{-1} A^H y = A^\dagger y
\]

where \( A^\dagger \) is called the pseudo-inverse of \( A \). Notice that using this definition of \( A \) the model can be written

\[
y = A c + \epsilon.
\]

The command \texttt{linalg.lstsq} will solve the linear least squares problem for \( c \) given \( A \) and \( y \). In addition \texttt{linalg.pinv} or \texttt{linalg.pinv2} (uses a different method based on singular value decomposition) will find \( A^\dagger \) given \( A \).

The following example and figure demonstrate the use of \texttt{linalg.lstsq} and \texttt{linalg.pinv} for solving a data-fitting problem. The data shown below were generated using the model:

\[
y_i = c_1 e^{-x_i} + c_2 x_i
\]

where \( x_i = 0.1 i \) for \( i = 1 \ldots 10 \), \( c_1 = 5 \), and \( c_2 = 4 \). Noise is added to \( y_i \) and the coefficients \( c_1 \) and \( c_2 \) are estimated using linear least squares.
```python
>>> import numpy as np
>>> from scipy import linalg
>>> import matplotlib.pyplot as plt

>>> c1, c2 = 5.0, 2.0
>>> i = np.r_[1:11]
>>> xi = 0.1*i
>>> yi = c1*np.exp(-xi) + c2*xi
>>> zi = yi + 0.05 * np.max(yi) * np.random.randn(len(yi))

>>> A = np.c_[np.exp(-xi)[:, np.newaxis], xi[:, np.newaxis]]
>>> c, resid, rank, sigma = linalg.lstsq(A, zi)

>>> xi2 = np.r_[0.1:1.0:100j]
>>> yi2 = c[0]*np.exp(-xi2) + c[1]*xi2

>>> plt.plot(xi,zi,'x',xi2,yi2)
>>> plt.axis([0,1.1,3.0,5.5])
>>> plt.xlabel('$x_i$')
>>> plt.title('Data fitting with linalg.lstsq')
>>> plt.show()
```

**Generalized inverse**

The generalized inverse is calculated using the command `linalg.pinv` or `linalg.pinv2`. These two commands differ in how they compute the generalized inverse. The first uses the `linalg.lstsq` algorithm while the second uses singular value decomposition. Let $A$ be an $M \times N$ matrix, then if $M > N$ the generalized inverse is

$$A^\dagger = (A^H A)^{-1} A^H$$

while if $M < N$ matrix the generalized inverse is

$$A^\# = A^H (A A^H)^{-1} .$$
In both cases for \( M = N \), then
\[
A^\dagger = A^\# = A^{-1}
\]
as long as \( A \) is invertible.

**Decompositions**

In many applications it is useful to decompose a matrix using other representations. There are several decompositions supported by SciPy.

**Eigenvalues and eigenvectors**

The eigenvalue-eigenvector problem is one of the most commonly employed linear algebra operations. In one popular form, the eigenvalue-eigenvector problem is to find for some square matrix \( A \) scalars \( \lambda \) and corresponding vectors \( v \) such that
\[
Av = \lambda v.
\]

For an \( N \times N \) matrix, there are \( N \) (not necessarily distinct) eigenvalues — roots of the (characteristic) polynomial
\[
|A - \lambda I| = 0.
\]
The eigenvectors, \( v \), are also sometimes called right eigenvectors to distinguish them from another set of left eigenvectors that satisfy
\[
v_H^T A = \lambda v_H^T
\]
or
\[
A^H v_L = \lambda^* v_L.
\]

With its default optional arguments, the command \texttt{linalg.eig} returns \( \lambda \) and \( v \). However, it can also return \( v_L \) and just \( \lambda \) by itself (\texttt{linalg.eigvals} returns just \( \lambda \) as well).

In addition, \texttt{linalg.eig} can also solve the more general eigenvalue problem
\[
Av = \lambda Bv
\]
\[
A^H v_L = \lambda^* B^H v_L
\]
for square matrices \( A \) and \( B \). The standard eigenvalue problem is an example of the general eigenvalue problem for \( B = I \). When a generalized eigenvalue problem can be solved, then it provides a decomposition of \( A \) as
\[
A = BVAV^{-1}
\]
where \( V \) is the collection of eigenvectors into columns and \( A \) is a diagonal matrix of eigenvalues.

By definition, eigenvectors are only defined up to a constant scale factor. In SciPy, the scaling factor for the eigenvectors is chosen so that \( ||v||^2 = \sum_i v_i^2 = 1 \).

As an example, consider finding the eigenvalues and eigenvectors of the matrix
\[
A = \begin{bmatrix}
1 & 5 & 2 \\
2 & 4 & 1 \\
3 & 6 & 2
\end{bmatrix}.
\]
The characteristic polynomial is

\[
|A - \lambda I| = (1 - \lambda)[(4 - \lambda)(2 - \lambda) - 6] - 5[2(2 - \lambda) - 3] + 2[12 - 3(4 - \lambda)] = -\lambda^3 + 7\lambda^2 + 8\lambda - 3.
\]

The roots of this polynomial are the eigenvalues of \(A\):

\[
\lambda_1 = 7.9579 \\
\lambda_2 = -1.2577 \\
\lambda_3 = 0.2997.
\]

The eigenvectors corresponding to each eigenvalue can be found using the original equation. The eigenvectors associated with these eigenvalues can then be found.

```python
>>> import numpy as np
>>> from scipy import linalg
>>> A = np.array([[1, 2], [3, 4]])
>>> la, v = linalg.eig(A)
>>> l1, l2 = la
>>> print(l1, l2)  # eigenvalues
(-0.3722813232690143+0j) (5.372281323269014+0j)
>>> print(v[:, 0])  # first eigenvector
[-0.82456484 0.56576746]
>>> print(v[:, 1])  # second eigenvector
[-0.41597356 -0.90937671]
>>> print(np.sum(abs(v**2), axis=0))  # eigenvectors are unitary
[1. 1.]
>>> v1 = np.array(v[:, 0]).T
>>> print(linalg.norm(A.dot(v1) - l1*v1))  # check the computation
3.23682852457e-16
```

**Singular value decomposition**

Singular Value Decomposition (SVD) can be thought of as an extension of the eigenvalue problem to matrices that are not square. Let \(A\) be an \(M \times N\) matrix with \(M\) and \(N\) arbitrary. The matrices \(A^H A\) and \(AA^H\) are square hermitian matrices\(^1\) of size \(N \times N\) and \(M \times M\) respectively. It is known that the eigenvalues of square hermitian matrices are real and non-negative. In addition, there are at most \(\min(M,N)\) identical non-zero eigenvalues of \(A^H A\) and \(AA^H\). Define these positive eigenvalues as \(\sigma_i^2\). The square-root of these are called singular values of \(A\). The eigenvectors of \(A^H A\) are collected by columns into an \(N\times N\) unitary\(^2\) matrix \(V\) while the eigenvectors of \(AA^H\) are collected by columns in the unitary matrix \(U\), the singular values are collected in an \(M \times N\) zero matrix \(\Sigma\) with main diagonal entries set to the singular values. Then

\[
A = U\Sigma V^H
\]

is the singular-value decomposition of \(A\). Every matrix has a singular value decomposition. Sometimes, the singular values are called the spectrum of \(A\). The command `linalg.svd` will return \(U\), \(V^H\), and \(\sigma_i\) as an array of the singular values. To obtain the matrix \(\Sigma\) use `linalg.diagsvd`. The following example illustrates the use of `linalg.svd`.

```python
>>> import numpy as np
>>> from scipy import linalg
>>> A = np.array([[1, 2, 3], [4, 5, 6]])
```

---

\(^1\) A hermitian matrix \(D\) satisfies \(D^H = D\).

\(^2\) A unitary matrix \(D\) satisfies \(D^H D = I = DD^H\) so that \(D^{-1} = D^H\).
LU decomposition

The LU decomposition finds a representation for the $M \times N$ matrix $A$ as

$$A = PLU$$

where $P$ is an $M \times M$ permutation matrix (a permutation of the rows of the identity matrix), $L$ is in $M \times K$ lower triangular or trapezoidal matrix $(K = \min(M,N))$ with unit-diagonal, and $U$ is an upper triangular or trapezoidal matrix. The SciPy command for this decomposition is `linalg.lu`.

Such a decomposition is often useful for solving many simultaneous equations where the left-hand-side does not change but the right hand side does. For example, suppose we are going to solve $Ax_i = b_i$ for many different $b_i$. The LU decomposition allows this to be written as

$$PLUx_i = b_i.$$  

Because $L$ is lower-triangular, the equation can be solved for $Ux_i$ and finally $x_i$ very rapidly using forward- and back-substitution. An initial time spent factoring $A$ allows for very rapid solution of similar systems of equations in the future. If the intent for performing LU decomposition is for solving linear systems then the command `linalg.lu_factor` should be used followed by repeated applications of the command `linalg.lu_solve` to solve the system for each new right-hand-side.

Cholesky decomposition

Cholesky decomposition is a special case of LU decomposition applicable to Hermitian positive definite matrices. When $A = A^H$ and $x^HAx \geq 0$ for all $x$, then decompositions of $A$ can be found so that

$$A = U^H U$$
$$A = LL^H$$

where $L$ is lower-triangular and $U$ is upper triangular. Notice that $L = U^H$. The command `linalg.cholesky` computes the cholesky factorization. For using cholesky factorization to solve systems of equations there are also `linalg.cho_factor` and `linalg.cho_solve` routines that work similarly to their LU decomposition counterparts.
**QR decomposition**

The QR decomposition (sometimes called a polar decomposition) works for any $M \times N$ array and finds an $M \times M$ unitary matrix $Q$ and an $M \times N$ upper-trapezoidal matrix $R$ such that

$$A = QR$$

Notice that if the SVD of $A$ is known then the QR decomposition can be found

$$A = U\Sigma V^H = QR$$

implies that $Q = U$ and $R = \Sigma V^H$. Note, however, that in SciPy independent algorithms are used to find QR and SVD decompositions. The command for QR decomposition is `linalg qr`.

**Schur decomposition**

For a square $N \times N$ matrix, $A$, the Schur decomposition finds (not-necessarily unique) matrices $T$ and $Z$ such that

$$A = ZTZ^H$$

where $Z$ is a unitary matrix and $T$ is either upper-triangular or quasi-upper triangular depending on whether or not a real schur form or complex schur form is requested. For a real schur form both $T$ and $Z$ are real-valued when $A$ is real-valued. When $A$ is a real-valued matrix the real schur form is only quasi-upper triangular because 2 by 2 blocks extrude from the main diagonal corresponding to any complex-valued eigenvalues. The command `linalg schur` finds the Schur decomposition while the command `linalg rsf2csf` converts $T$ and $Z$ from a real Schur form to a complex Schur form. The Schur form is especially useful in calculating functions of matrices.

The following example illustrates the schur decomposition:

```python
>>> from scipy import linalg
>>> A = np.mat('[1 3 2; 1 4 5; 2 3 6]')
>>> T, Z = linalg.schur(A)
>>> T1, Z1 = linalg.schur(A, 'complex')
>>> T2, Z2 = linalg.rsf2csf(T, Z)
>>> T
array([[ 9.90012467,  1.78947961, -0.65498528],
        [ 0.          ,  0.54993766, -1.57754789],
        [ 0.          ,  0.51260928,  0.54993766]])
>>> T2
array([[ 9.90012467+0.00000000e+00j, -0.32436598+1.55463542e+00j,
        -0.88619748+5.69027615e-01j],
        [ 0.          ,  0.54993766+8.99258408e-01j,
        1.06493862+3.05311332e-16j],
        [ 0.          ,  0.00000000e+00j ,  0.54993766-8.99258408e-01j]])
>>> abs(T1 - T2) # different
array([[ 1.06604538e-14,  2.06969555e+00,  1.69375747e+00],
        [ 0.00000000e+00,  1.33688556e-15,  4.74146496e-01],
        [ 0.00000000e+00,  0.00000000e+00,  1.13220977e-15]])
>>> abs(Z1 - Z2) # different
array([[ 0.06833781,  0.88091091,  0.79568503],
        [ 0.11857169,  0.44491892,  0.99594171],
        [ 0.12624999,  0.60264117,  0.77257633]])
>>> abs(A - Z*T*Z.H) # same
```

(continues on next page)
>>> abs(A - Z1*T1*Z1.H)  # same

matrix([[ 4.26993904e-15, 6.21793362e-15, 8.00007092e-15],
        [ 5.77945386e-15, 6.21798014e-15, 1.06653681e-14],
        [ 7.16681444e-15, 8.90271058e-15, 1.77635764e-14]])

>>> abs(A - Z2*T2*Z2.H)  # same

matrix([[ 6.02594127e-16, 1.77648931e-15, 2.22506907e-15],
        [ 2.46275555e-16, 3.99684548e-15, 8.91642616e-16],
        [ 8.88225111e-16, 8.88312432e-16, 4.44104848e-15]])

Interpolative Decomposition

The interpolative decomposition (ID) of a matrix is a factorization

\[ A = \begin{bmatrix} A_{11} & A_{12} \\ \end{bmatrix} = A_{11} \begin{bmatrix} I \\ T \end{bmatrix}, \]

where \( T = \begin{bmatrix} T_1 \\ T_2 \end{bmatrix} \) is a permutation matrix with \( T_1 \in \{0, 1\}^{n \times k} \), i.e., \( A_{12} = A_{11}T \). This can equivalently be written as \( A = BP \), where \( B = A_{11} \) and \( P = \begin{bmatrix} I \\ T \end{bmatrix}T \) are the skeleton and interpolation matrices, respectively.

See also:

scipy.linalg.interpolative — for more information.

Matrix Functions

Consider the function \( f(x) \) with Taylor series expansion

\[ f(x) = \sum_{k=0}^{\infty} \frac{f^{(k)}(0)}{k!} x^k. \]

A matrix function can be defined using this Taylor series for the square matrix \( A \) as

\[ f(A) = \sum_{k=0}^{\infty} \frac{f^{(k)}(0)}{k!} A^k. \]

While, this serves as a useful representation of a matrix function, it is rarely the best way to calculate a matrix function.

Exponential and logarithm functions

The matrix exponential is one of the more common matrix functions. The preferred method for implementing the matrix exponential is to use scaling and a Padé approximation for \( e^x \). This algorithm is implemented as linalg.expm.

The inverse of the matrix exponential is the matrix logarithm defined as the inverse of the matrix exponential.

\[ A = \exp(\log(A)). \]

The matrix logarithm can be obtained with linalg.logm.

Trigonometric functions

The trigonometric functions \( \sin \), \( \cos \), and \( \tan \) are implemented for matrices in linalg.sinm, linalg.cosm, and linalg.tanm respectively. The matrix \( \sin \) and \( \cos \) can be defined using Euler’s identity as

\[ \sin(A) = \frac{e^{jA} - e^{-jA}}{2j}, \quad \cos(A) = \frac{e^{jA} + e^{-jA}}{2}. \]
The tangent is

\[ \tan(x) = \frac{\sin(x)}{\cos(x)} = [\cos(x)]^{-1} \sin(x) \]

and so the matrix tangent is defined as

\[ [\cos(A)]^{-1} \sin(A). \]

**Hyperbolic trigonometric functions**

The hyperbolic trigonometric functions \(\sinh\), \(\cosh\), and \(\tanh\) can also be defined for matrices using the familiar definitions:

\[ \sinh(A) = \frac{e^A - e^{-A}}{2} \]
\[ \cosh(A) = \frac{e^A + e^{-A}}{2} \]
\[ \tanh(A) = [\cosh(A)]^{-1} \sinh(A). \]

These matrix functions can be found using \texttt{linalg.sinhm}, \texttt{linalg.coshm}, and \texttt{linalg.tanhm}.

**Arbitrary function**

Finally, any arbitrary function that takes one complex number and returns a complex number can be called as a matrix function using the command \texttt{linalg.funm}. This command takes the matrix and an arbitrary Python function. It then implements an algorithm from Golub and Van Loan’s book “Matrix Computations” to compute the function applied to the matrix using a Schur decomposition. Note that the function needs to accept complex numbers as input in order to work with this algorithm. For example the following code computes the zeroth-order Bessel function applied to a matrix.

```python
>>> from scipy import special, random, linalg
>>> np.random.seed(1234)
>>> A = random.rand(3, 3)
>>> B = linalg.funm(A, lambda x: special.jv(0, x))
>>> A
array([[ 0.19151945, 0.62210877, 0.43772774],
       [ 0.78535858, 0.77997581, 0.27259261],
       [ 0.27646426, 0.80187218, 0.95813935]])
>>> B
array([[ 0.86511146, -0.19676526, -0.13856748],
       [-0.17479869, 0.7259118 , -0.16606258],
       [-0.19212044, -0.32052767, 0.73590704]])
>>> linalg.eigvals(A)
array([ 1.73881510+0.j,  0.62210877+0.j,  0.37259261+0.j])
>>> linalg.eigvals(B)
array([ 0.37259261+0.j,  0.62210877+0.j,  0.73590704+0.j])
```

Note how, by virtue of how matrix analytic functions are defined, the Bessel function has acted on the matrix eigenvalues.

**Special matrices**

SciPy and NumPy provide several functions for creating special matrices that are frequently used in engineering and science.
<table>
<thead>
<tr>
<th>Type</th>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>block diagonal</td>
<td>scipy.linalg.block_diag</td>
<td>Create a block diagonal matrix from the provided arrays.</td>
</tr>
<tr>
<td>circulant</td>
<td>scipy.linalg.circulant</td>
<td>Construct a circulant matrix.</td>
</tr>
<tr>
<td>companion</td>
<td>scipy.linalg.companion</td>
<td>Create a companion matrix.</td>
</tr>
<tr>
<td>Hadamard</td>
<td>scipy.linalg.hadamard</td>
<td>Construct a Hadamard matrix.</td>
</tr>
<tr>
<td>Hankel</td>
<td>scipy.linalg.hankel</td>
<td>Construct a Hankel matrix.</td>
</tr>
<tr>
<td>Hilbert</td>
<td>scipy.linalg.hilbert</td>
<td>Construct a Hilbert matrix.</td>
</tr>
<tr>
<td>Inverse Hilbert</td>
<td>scipy.linalg.invhilbert</td>
<td>Construct the inverse of a Hilbert matrix.</td>
</tr>
<tr>
<td>Leslie</td>
<td>scipy.linalg.leslie</td>
<td>Create a Leslie matrix.</td>
</tr>
<tr>
<td>Pascal</td>
<td>scipy.linalg.pascal</td>
<td>Create a Pascal matrix.</td>
</tr>
<tr>
<td>Toeplitz</td>
<td>scipy.linalg.toeplitz</td>
<td>Construct a Toeplitz matrix.</td>
</tr>
<tr>
<td>Van der Monde</td>
<td>numpy.vander</td>
<td>Generate a Van der Monde matrix.</td>
</tr>
</tbody>
</table>

For examples of the use of these functions, see their respective docstrings.

### 4.1.10 Sparse Eigenvalue Problems with ARPACK

**Introduction**

ARPACK is a Fortran package which provides routines for quickly finding a few eigenvalues/eigenvectors of large sparse matrices. In order to find these solutions, it requires only left-multiplication by the matrix in question. This operation is performed through a reverse-communication interface. The result of this structure is that ARPACK is able to find eigenvalues and eigenvectors of any linear function mapping a vector to a vector.

All of the functionality provided in ARPACK is contained within the two high-level interfaces scipy.sparse.linalg.eigs and scipy.sparse.linalg.eigsh. eigs provides interfaces to find the eigenvalues/vectors of real or complex nonsymmetric square matrices, while eigsh provides interfaces for real-symmetric or complex-hermitian matrices.

**Basic Functionality**

ARPACK can solve either standard eigenvalue problems of the form

\[ Ax = \lambda x \]

or general eigenvalue problems of the form

\[ Ax = \lambda Mx \]

The power of ARPACK is that it can compute only a specified subset of eigenvalue/eigenvector pairs. This is accomplished through the keyword which. The following values of which are available:

- **which = 'LM'**: Eigenvalues with largest magnitude (eigs, eigsh), that is, largest eigenvalues in the euclidean norm of complex numbers.
- **which = 'SM'**: Eigenvalues with smallest magnitude (eigs, eigsh), that is, smallest eigenvalues in the euclidean norm of complex numbers.
- **which = 'LR'**: Eigenvalues with largest real part (eigs)
- **which = 'SR'**: Eigenvalues with smallest real part (eigs)
- **which = 'LI'**: Eigenvalues with largest imaginary part (eigs)
- **which = 'SI'**: Eigenvalues with smallest imaginary part (eigs)
which = 'LA': Eigenvalues with largest algebraic value (eigsh), that is, largest eigenvalues inclusive of any negative sign.

which = 'SA': Eigenvalues with smallest algebraic value (eigsh), that is, smallest eigenvalues inclusive of any negative sign.

which = 'BE': Eigenvalues from both ends of the spectrum (eigsh)

Note that ARPACK is generally better at finding extremal eigenvalues: that is, eigenvalues with large magnitudes. In particular, using which = 'SM' may lead to slow execution time and/or anomalous results. A better approach is to use shift-invert mode.

Shift-Invert Mode

Shift invert mode relies on the following observation. For the generalized eigenvalue problem

\[ Ax = \lambda Mx \]

it can be shown that

\[ (A - \sigma M)^{-1} Mx = \nu x \]

where

\[ \nu = \frac{1}{\lambda - \sigma} \]

Examples

Imagine you’d like to find the smallest and largest eigenvalues and the corresponding eigenvectors for a large matrix. ARPACK can handle many forms of input: dense matrices such as numpy.ndarray instances, sparse matrices such as scipy.sparse.csr_matrix, or a general linear operator derived from scipy.sparse.linalg.LinearOperator. For this example, for simplicity, we’ll construct a symmetric, positive-definite matrix.

```python
>>> import numpy as np
>>> from scipy.linalg import eigh
>>> from scipy.sparse.linalg import eigsh
>>> np.set_printoptions(suppress=True)
>>> np.random.seed(0)
>>> X = np.random.random((100,100)) - 0.5
>>> X = np.dot(X, X.T) #create a symmetric matrix
```

We now have a symmetric matrix X with which to test the routines. First compute a standard eigenvalue decomposition using eigh:

```python
>>> evals_all, evecs_all = eigh(X)
```

As the dimension of X grows, this routine becomes very slow. Especially if only a few eigenvectors and eigenvalues are needed, ARPACK can be a better option. First let’s compute the largest eigenvalues (which = 'LM') of X and compare them to the known results:

```python
>>> evals_large, evecs_large = eigsh(X, 3, which='LM')
>>> print(evals_all[-3:])
[29.1446102 30.05821805 31.19467646]
>>> print(evals_large)
```

(continues on next page)
[29.1446102 30.05821805 31.19467646]

```python
>>> print(np.dot(evecs_large.T, evecs_all[:, -3:]))
array([[-1.,  0.,  0.],  # may vary (signs)
       [ 0.,  1.,  0.],
       [-0.,  0., -1.])
```

The results are as expected. ARPACK recovers the desired eigenvalues, and they match the previously known results. Furthermore, the eigenvectors are orthogonal, as we’d expect. Now let’s attempt to solve for the eigenvalues with smallest magnitude:

```python
>>> evals_small, evecs_small = eigsh(X, 3, which='SM')
Traceback (most recent call last):  # may vary (convergence)
...
scipy.sparse.linalg.eigen.arpack.arpack.ArpackNoConvergence:
ARPACK error -1: No convergence (1001 iterations, 0/3 eigenvectors converged)
```

Oops. We see that as mentioned above, ARPACK is not quite as adept at finding small eigenvalues. There are a few ways this problem can be addressed. We could increase the tolerance (tol) to lead to faster convergence:

```python
>>> evals_small, evecs_small = eigsh(X, 3, which='SM', tol=1E-2)
>>> evals_all[:3]
array([0.0003783, 0.00122714, 0.00715878])
>>> evals_small
array([0.00037831, 0.00122714, 0.00715881])
>>> np.dot(evecs_small.T, evecs_all[:, :3])
array([[ 1.  0.  0.],  # may vary (signs)
       [-0.  1.  0.],
       [ 0.  0. -1.]])
```

This works, but we lose the precision in the results. Another option is to increase the maximum number of iterations (maxiter) from 1000 to 5000:

```python
>>> evals_small, evecs_small = eigsh(X, 3, which='SM', tol=1E-2, maxiter=5000)
>>> evals_all[:3]
array([0.0003783, 0.00122714, 0.00715878])
>>> evals_small
array([0.0003783, 0.00122714, 0.00715878])
>>> np.dot(evecs_small.T, evecs_all[:, :3])
array([[ 1.  0.  0.],  # may vary (signs)
       [-0.  1.  0.],
       [ 0.  0. -1.]])
```

We get the results we’d hoped for, but the computation time is much longer. Fortunately, ARPACK contains a mode that allows quick determination of non-external eigenvalues: shift-invert mode. As mentioned above, this mode involves transforming the eigenvalue problem to an equivalent problem with different eigenvalues.

In this case, we hope to find eigenvalues near zero, so we’ll choose sigma = 0. The transformed eigenvalues will then satisfy \( \nu = 1/(\lambda - \sigma) = 1/\lambda \), so our small eigenvalues \( \lambda \) become large eigenvalues \( \nu \).

```python
>>> evals_small, evecs_small = eigsh(X, 3, sigma=0, which='LM')
>>> evals_all[:3]
array([0.0003783, 0.00122714, 0.00715878])
>>> evals_small
array([0.0003783, 0.00122714, 0.00715878])
```

(continues on next page)
We get the results we were hoping for, with much less computational time. Note that the transformation from \( \nu \rightarrow \lambda \) takes place entirely in the background. The user need not worry about the details.

The shift-invert mode provides more than just a fast way to obtain a few small eigenvalues. Say you desire to find internal eigenvalues and eigenvectors, e.g. those nearest to \( \lambda = 1 \). Simply set \( \text{sigma} = 1 \) and ARPACK takes care of the rest:

```python
>>> evals_mid, evecs_mid = eigsh(X, 3, sigma=1, which='LM')
>>> i_sort = np.argsort(abs(1. / (1 - evals_all)))[-3:]
>>> evals_all[i_sort]
array([1.16577199, 0.85081388, 1.06642272])
>>> evals_mid
array([0.85081388, 1.06642272, 1.16577199])
>>> print(np.dot(evecs_mid.T, evecs_all[:,i_sort]))
array([[-0. 1. 0.], # may vary (signs)
       [-0. -0. 1.],
       [ 1. 0. 0.]]
```

The eigenvalues come out in a different order, but they’re all there. Note that the shift-invert mode requires the internal solution of a matrix inverse. This is taken care of automatically by \texttt{eigsh} and \texttt{eigs}, but the operation can also be specified by the user. See the docstring of \texttt{scipy.sparse.linalg.eigsh} and \texttt{scipy.sparse.linalg.eigs} for details.

References

4.1.11 Compressed Sparse Graph Routines (\texttt{scipy.sparse.csgraph})

Example: Word Ladders

A Word Ladder is a word game invented by Lewis Carroll in which players find paths between words by switching one letter at a time. For example, one can link “ape” and “man” in the following way:

\[ \text{ape} \rightarrow \text{apt} \rightarrow \text{ait} \rightarrow \text{bit} \rightarrow \text{big} \rightarrow \text{bag} \rightarrow \text{mag} \rightarrow \text{man} \]

Note that each step involves changing just one letter of the word. This is just one possible path from “ape” to “man”, but is it the shortest possible path? If we desire to find the shortest word ladder path between two given words, the sparse graph submodule can help.

First we need a list of valid words. Many operating systems have such a list built-in. For example, on linux, a word list can often be found at one of the following locations:

```
/usr/share/dict
/var/lib/dict
```

Another easy source for words are the scrabble word lists available at various sites around the internet (search with your favorite search engine). We’ll first create this list. The system word lists consist of a file with one word per line. The following should be modified to use the particular word list you have available:

```python
>>> word_list = open('/usr/share/dict/words').readlines()
>>> word_list = map(str.strip, word_list)
```
We want to look at words of length 3, so let’s select just those words of the correct length. We’ll also eliminate words which start with upper-case (proper nouns) or contain non alpha-numeric characters like apostrophes and hyphens. Finally, we’ll make sure everything is lower-case for comparison later:

```python
>>> word_list = [word for word in word_list if len(word) == 3]
>>> word_list = [word for word in word_list if word[0].islower()]
>>> word_list = [word for word in word_list if word.isalpha()]
>>> word_list = list(map(str.lower, word_list))
>>> len(word_list)
586  # may vary
```

Now we have a list of 586 valid three-letter words (the exact number may change depending on the particular list used). Each of these words will become a node in our graph, and we will create edges connecting the nodes associated with each pair of words which differs by only one letter.

There are efficient ways to do this, and inefficient ways to do this. To do this as efficiently as possible, we’re going to use some sophisticated numpy array manipulation:

```python
>>> import numpy as np
>>> word_list = np.asarray(word_list)
>>> word_list.dtype  # these are unicode characters in Python 3
dtype('<U3')
>>> word_list.sort()  # sort for quick searching later
```

We have an array where each entry is three unicode characters long. We’d like to find all pairs where exactly one character is different. We’ll start by converting each word to a three-dimensional vector:

```python
>>> word_bytes = np.ndarray((word_list.size, word_list.itemsize),
...                          dtype='uint8',
...                          buffer=word_list.data)
>>> # each unicode character is four bytes long. We only need first byte
>>> # we know that there are three characters in each word
>>> word_bytes = word_bytes[:, ::word_list.itemsize//3]
>>> word_bytes.shape
(586, 3)  # may vary
```

Now we’ll use the Hamming distance between each point to determine which pairs of words are connected. The Hamming distance measures the fraction of entries between two vectors which differ: any two words with a hamming distance equal to 1/N, where N is the number of letters, are connected in the word ladder:

```python
>>> from scipy.spatial.distance import pdist, squareform
>>> from scipy.sparse import csr_matrix
>>> hamming_dist = pdist(word_bytes, metric='hamming')
>>> graph = csr_matrix(squareform(hamming_dist < 1.5 / 3))
```

When comparing the distances, we don’t use an equality because this can be unstable for floating point values. The inequality produces the desired result as long as no two entries of the word list are identical. Now that our graph is set up, we’ll use a shortest path search to find the path between any two words in the graph:

```python
>>> i1 = word_list.searchsorted('ape')
>>> i2 = word_list.searchsorted('man')
>>> word_list[i1]
'ape'
```
We need to check that these match, because if the words are not in the list that will not be the case. Now all we need is to find the shortest path between these two indices in the graph. We’ll use Dijkstra’s algorithm, because it allows us to find the path for just one node:

```python
>>> from scipy.sparse.csgraph import dijkstra
>>> distances, predecessors = dijkstra(graph, indices=i1, return_predecessors=True)
```

So we see that the shortest path between ‘ape’ and ‘man’ contains only five steps. We can use the predecessors returned by the algorithm to reconstruct this path:

```python
>>> path = []
>>> i = i2
>>> while i != i1:
...     path.append(word_list[i])
...     i = predecessors[i]
>>> path.append(word_list[i1])
>>> print(path[:-1])
['ape', 'apt', 'opt', 'oat', 'mat', 'man'] # may vary
```

This is three fewer links than our initial example: the path from ape to man is only five steps.

Using other tools in the module, we can answer other questions. For example, are there three-letter words which are not linked in a word ladder? This is a question of connected components in the graph:

```python
>>> from scipy.sparse.csgraph import connected_components
>>> N_components, component_list = connected_components(graph)
>>> print(N_components)
15 # may vary
```

In this particular sample of three-letter words, there are 15 connected components: that is, 15 distinct sets of words with no paths between the sets. How many words are in each of these sets? We can learn this from the list of components:

```python
>>> [np.sum(component_list == i) for i in range(N_components)]
[571, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1] # may vary
```

There is one large connected set, and 14 smaller ones. Let’s look at the words in the smaller ones:

```python
>>> [list(word_list[np.nonzero(component_list == i)]) for i in range(1, N_components)]
[['aha'], # may vary
 ['chi'],
 ['ebb'],
 ['ems', 'emu'],
 ['gnu'],
 ['ism'],
 ['khz'],
 ['nth'],
```

(continues on next page)
These are all the three-letter words which do not connect to others via a word ladder.

We might also be curious about which words are maximally separated. Which two words take the most links to connect? We can determine this by computing the matrix of all shortest paths. Note that by convention, the distance between two non-connected points is reported to be infinity, so we’ll need to remove these before finding the maximum:

```python
>>> distances, predecessors = dijkstra(graph, return_predecessors=True)
>>> max_distance = np.max(distances[np.isinf(distances)])
>>> print(max_distance)
13.0 # may vary
```

So there is at least one pair of words which takes 13 steps to get from one to the other! Let’s determine which these are:

```python
>>> i1, i2 = np.nonzero(distances == max_distance)
>>> list(zip(word_list[i1], word_list[i2]))
[('imp', 'ohm'), # may vary
 ('imp', 'ohs'),
 ('ohm', 'imp'),
 ('ohm', 'ump'),
 ('ohs', 'imp'),
 ('ohs', 'ump'),
 ('ump', 'ohm'),
 ('ump', 'ohs')]
```

We see that there are two pairs of words which are maximally separated from each other: ‘imp’ and ‘ump’ on one hand, and ‘ohm’ and ‘ohs’ on the other hand. We can find the connecting list in the same way as above:

```python
>>> path = []
>>> i = i2[0]
>>> while i != i1[0]:
...    path.append(word_list[i])
...    i = predecessors[i1[0], i]
>>> path.append(word_list[i1[0]])
>>> print(path[:])
[ 'imp', 'amp', 'asp', 'ass', 'ads', 'add', 'aid', 'mid', 'mod', 'moo', 'too', 'tho', 'oho -', 'ohm'] # may vary
```

This gives us the path we desired to see.

Word ladders are just one potential application of scipy’s fast graph algorithms for sparse matrices. Graph theory makes appearances in many areas of mathematics, data analysis, and machine learning. The sparse graph tools are flexible enough to handle many of these situations.
4.1.12 Spatial data structures and algorithms (scipy.spatial)

`scipy.spatial` can compute triangulations, Voronoi diagrams, and convex hulls of a set of points, by leveraging the Qhull library.

Moreover, it contains `KDTree` implementations for nearest-neighbor point queries, and utilities for distance computations in various metrics.

Delaunay triangulations

The Delaunay triangulation is a subdivision of a set of points into a non-overlapping set of triangles, such that no point is inside the circumcircle of any triangle. In practice, such triangulations tend to avoid triangles with small angles.

Delaunay triangulation can be computed using `scipy.spatial` as follows:

```python
>>> from scipy.spatial import Delaunay
>>> points = np.array([[0, 0], [0, 1.1], [1, 0], [1, 1]])
>>> tri = Delaunay(points)
```

We can visualize it:

```python
>>> import matplotlib.pyplot as plt
>>> plt.triplot(points[:,0], points[:,1], tri.simplices)
>>> plt.plot(points[:,0], points[:,1], 'o')
```

And add some further decorations:

```python
>>> for j, p in enumerate(points):
...    plt.text(p[0]-0.03, p[1]+0.03, j, ha='right') # label the points
>>> for j, s in enumerate(tri.simplices):
...    p = points[s].mean(axis=0)
...    plt.text(p[0], p[1], '%d' % j, ha='center') # label triangles
>>> plt.xlim(-0.5, 1.5); plt.ylim(-0.5, 1.5)
>>> plt.show()
```
The structure of the triangulation is encoded in the following way: the `simplices` attribute contains the indices of the points in the `points` array that make up the triangle. For instance:

```python
code
>>> i = 1
>>> tri(simplices[i,:]
array([3, 1, 0], dtype=int32)
>>> points[tri(simplices[i,:]
array([[ 1. , 1. ],
    [ 0. , 1.1],
    [ 0. , 0. ]])
```

Moreover, neighboring triangles can also be found out:

```python
code
>>> tri(neighbors[i]
array([-1, 0, -1], dtype=int32)
```

What this tells us is that this triangle has triangle #0 as a neighbor, but no other neighbors. Moreover, it tells us that neighbor 0 is opposite the vertex 1 of the triangle:

```python
code
>>> points[tri(simplices[i, 1]]
array([ 0. , 1.1])
```

Indeed, from the figure we see that this is the case.

Qhull can also perform tessellations to simplices also for higher-dimensional point sets (for instance, subdivision into tetrahedra in 3-D).

**Coplanar points**

It is important to note that not all points necessarily appear as vertices of the triangulation, due to numerical precision issues in forming the triangulation. Consider the above with a duplicated point:

```python
code
>>> points = np.array([[0, 0], [0, 1], [1, 0], [1, 1], [1, 1]])
>>> tri = Delaunay(points)
>>> np.unique(tri(simplices.ravel()))
array([0, 1, 2, 3], dtype=int32)
```

Observe that point #4, which is a duplicate, does not occur as a vertex of the triangulation. That this happened is recorded:

```python
code
>>> tri.coplanar
array([[4, 0, 3]], dtype=int32)
```

This means that point 4 resides near triangle 0 and vertex 3, but is not included in the triangulation.

Note that such degeneracies can occur not only because of duplicated points, but also for more complicated geometrical reasons, even in point sets that at first sight seem well-behaved.

However, Qhull has the “QJ” option, which instructs it to perturb the input data randomly until degeneracies are resolved:

```python
code
>>> tri = Delaunay(points, qhull_options="QJ Pp")
>>> points[tri(simplices]
array([[1, 0],
    [1, 1],
    [0, 0],
    [1, 1],
])
```

(continues on next page)
Two new triangles appeared. However, we see that they are degenerate and have zero area.

**Convex hulls**

Convex hull is the smallest convex object containing all points in a given point set.

These can be computed via the Qhull wrappers in *scipy.spatial* as follows:

```python
>>> from scipy.spatial import ConvexHull
>>> points = np.random.rand(30, 2)  # 30 random points in 2-D
>>> hull = ConvexHull(points)
```

The convex hull is represented as a set of N-1 dimensional simplices, which in 2-D means line segments. The storage scheme is exactly the same as for the simplices in the Delaunay triangulation discussed above.

We can illustrate the above result:

```python
>>> import matplotlib.pyplot as plt
>>> plt.plot(points[:,0], points[:,1], 'o')
>>> for simplex in hull.simplices:
...     plt.plot(points[simplex,0], points[simplex,1], 'k-')
>>> plt.show()
```

The same can be achieved with *scipy.spatial.convex_hull_plot_2d*. 

---

### 4.1. SciPy Tutorial
Voronoi diagrams

A Voronoi diagram is a subdivision of the space into the nearest neighborhoods of a given set of points.

There are two ways to approach this object using `scipy.spatial`. First, one can use the `KDTree` to answer the question “which of the points is closest to this one”, and define the regions that way:

```python
>>> from scipy.spatial import KDTree
>>> points = np.array([[0, 0], [0, 1], [0, 2], [1, 0], [1, 1], [1, 2],
                     [2, 0], [2, 1], [2, 2]])
>>> tree = KDTree(points)
>>> tree.query([0.1, 0.1])
(0.14142135623730953, 0)
```

So the point `(0.1, 0.1)` belongs to region 0. In color:

```python
>>> x = np.linspace(-0.5, 2.5, 31)
>>> y = np.linspace(-0.5, 2.5, 33)
>>> xx, yy = np.meshgrid(x, y)
>>> xy = np.c_[xx.ravel(), yy.ravel()]
>>> import matplotlib.pyplot as plt
>>> plt.pcolor(x, y, tree.query(xy)[1].reshape(33, 31))
>>> plt.plot(points[:,0], points[:,1], 'ko')
>>> plt.show()
```

This does not, however, give the Voronoi diagram as a geometrical object.

The representation in terms of lines and points can be again obtained via the Qhull wrappers in `scipy.spatial`:

```python
>>> from scipy.spatial import Voronoi
>>> vor = Voronoi(points)
>>> vor.vertices
array([[ 0.5, 0.5],
       [ 1.5, 0.5],
       [ 2.5, 0.5],
       [ 0.5, 1.5],
       [ 1.5, 1.5],
       [ 2.5, 1.5],
       [ 0.5, 2.5],
       [ 1.5, 2.5],
       [ 2.5, 2.5]])
```
The Voronoi vertices denote the set of points forming the polygonal edges of the Voronoi regions. In this case, there are 9 different regions:

```
>>> vor.regions
[[], [-1, 0], [-1, 1], [1, -1, 0], [3, -1, 2], [-1, 3], [-1, 2], [3, 2, 0, 1], [2, -1, -0], [3, -1, 1]]
```

Negative value -1 again indicates a point at infinity. Indeed, only one of the regions, [3, 1, 0, 2], is bounded. Note here that due to similar numerical precision issues as in Delaunay triangulation above, there may be fewer Voronoi regions than input points.

The ridges (lines in 2-D) separating the regions are described as a similar collection of simplices as the convex hull pieces:

```
>>> vor.ridge_vertices
[[-1, 0], [-1, 0], [-1, 1], [-1, 1], [0, 1], [-1, 3], [-1, 2], [2, 3], [-1, 3], [-1, 2], [0, 3], [1, 3]]
```

These numbers indicate indices of the Voronoi vertices making up the line segments. -1 is again a point at infinity — only four of the 12 lines is a bounded line segment while the others extend to infinity.

The Voronoi ridges are perpendicular to lines drawn between the input points. Which two points each ridge corresponds to is also recorded:

```
>>> vor.ridge_points
array([[0, 1],
       [0, 3],
       [6, 3],
       [6, 7],
       [3, 4],
       [5, 8],
       [5, 2],
       [5, 4],
       [8, 7],
       [2, 1],
       [4, 1],
       [4, 7]], dtype=int32)
```

This information, taken together, is enough to construct the full diagram.

We can plot it as follows. First the points and the Voronoi vertices:

```
>>> plt.plot(points[:, 0], points[:, 1], 'o')
>>> plt.plot(vor.vertices[:, 0], vor.vertices[:, 1], '*')
>>> plt.xlim(-1, 3); plt.ylim(-1, 3)
```

Plotting the finite line segments goes as for the convex hull, but now we have to guard for the infinite edges:

```
>>> for simplex in vor.ridge_vertices:
...     simplex = np.asarray(simplex)
...     if np.all(simplex >= 0):
...         plt.plot(vor.vertices[simplex, 0], vor.vertices[simplex, 1], 'k-')
```
The ridges extending to infinity require a bit more care:

```python
>>> center = points.mean(axis=0)

>>> for pointidx, simplex in zip(vor.ridge_points, vor.ridge_vertices):
...     simplex = np.asarray(simplex)
...     if np.any(simplex < 0):
...         i = simplex[simplex >= 0][0]  # finite end Voronoi vertex
...         t = points[pointidx[1]] - points[pointidx[0]]  # tangent
...         t = t / np.linalg.norm(t)
...         n = np.array([-t[1], t[0]])  # normal
...         midpoint = points[pointidx].mean(axis=0)
...         far_point = vor.vertices[i] + np.sign(np.dot(midpoint - center, n)) * n * 100
...         plt.plot([vor.vertices[i, 0], far_point[0]], [vor.vertices[i, 1], far_point[1]], 'k--')
```

This plot can also be created using `scipy.spatial.voronoi_plot_2d`.

### 4.1.13 Statistics (scipy.stats)

#### Introduction

In this tutorial we discuss many, but certainly not all, features of `scipy.stats`. The intention here is to provide a user with a working knowledge of this package. We refer to the reference manual for further details.

Note: This documentation is work in progress.

#### Discrete Statistical Distributions

Discrete random variables take on only a countable number of values. The commonly used distributions are included in SciPy and described in this document. Each discrete distribution can take one extra integer parameter: $L$. The relationship between the general distribution $p$ and the standard distribution $p_0$ is

$$p(x) = p_0(x - L)$$

which allows for shifting of the input. When a distribution generator is initialized, the discrete distribution can either specify the beginning and ending (integer) values $a$ and $b$ which must be such that

$$p_0(x) = 0 \text{ if } x < a \text{ or } x > b$$
in which case, it is assumed that the pdf function is specified on the integers \( a + mk \leq b \) where \( k \) is a non-negative integer (\( 0, 1, 2, \ldots \)) and \( m \) is a positive integer multiplier. Alternatively, the two lists \( x_k \) and \( p(x_k) \) can be provided directly in which case a dictionary is set up internally to evaluate probabilities and generate random variates.

**Probability Mass Function (PMF)**

The probability mass function of a random variable \( X \) is defined as the probability that the random variable takes on a particular value.

\[
p(x_k) = P[X = x_k]
\]

This is also sometimes called the probability density function, although technically

\[
f(x) = \sum_k p(x_k) \delta(x - x_k)
\]

is the probability density function for a discrete distribution\(^1\).

**Cumulative Distribution Function (CDF)**

The cumulative distribution function is

\[
F(x) = P[X \leq x] = \sum_{x_k \leq x} p(x_k)
\]

and is also useful to be able to compute. Note that

\[
F(x_k) - F(x_{k-1}) = p(x_k)
\]

**Survival Function**

The survival function is just

\[
S(x) = 1 - F(x) = P[X > k]
\]

the probability that the random variable is strictly larger than \( k \).

**Percent Point Function (Inverse CDF)**

The percent point function is the inverse of the cumulative distribution function and is

\[
G(q) = F^{-1}(q)
\]

for discrete distributions, this must be modified for cases where there is no \( x_k \) such that \( F(x_k) = q \). In these cases we choose \( G(q) \) to be the smallest value \( x_k = G(q) \) for which \( F(x_k) \geq q \). If \( q = 0 \) then we define \( G(0) = a - 1 \). This definition allows random variates to be defined in the same way as with continuous rv’s using the inverse cdf on a uniform distribution to generate random variates.

**Inverse survival function**

The inverse survival function is the inverse of the survival function

\[
Z(\alpha) = S^{-1}(\alpha) = G(1 - \alpha)
\]

and is thus the smallest non-negative integer \( k \) for which \( F(k) \geq 1 - \alpha \) or the smallest non-negative integer \( k \) for which \( S(k) \leq \alpha \).

---

\(^1\) XXX: Unknown layout Plain Layout: Note that we will be using \( p \) to represent the probability mass function and a parameter (a XXX: probability). The usage should be obvious from context.
Hazard functions

If desired, the hazard function and the cumulative hazard function could be defined as

\[
h(x_k) = \frac{p(x_k)}{1 - F(x_k)}
\]

and

\[
H(x) = \sum_{x_k \leq x} h(x_k) = \sum_{x_k \leq x} \frac{F(x_k) - F(x_{k-1})}{1 - F(x_k)}.
\]

Moments

Non-central moments are defined using the PDF

\[
\mu'_m = E[X^m] = \sum_k x_k^m p(x_k).
\]

Central moments are computed similarly \( \mu = \mu'_1 \)

\[
\mu_m = E[(X - \mu)^m] = \sum_k (x_k - \mu)^m p(x_k) \\
= \sum_{k=0}^m (-1)^{m-k} \binom{m}{k} \mu^{m-k} \mu'_k
\]

The mean is the first moment

\[
\mu = \mu'_1 = E[X] = \sum_k x_k p(x_k)
\]

the variance is the second central moment

\[
\mu_2 = E[(X - \mu)^2] = \sum_{x_k} x_k^2 p(x_k) - \mu^2.
\]

Skewness is defined as

\[
\gamma_1 = \frac{\mu_3}{\mu_2^{3/2}}
\]

while (Fisher) kurtosis is

\[
\gamma_2 = \frac{\mu_4}{\mu_2^2} - 3,
\]

so that a normal distribution has a kurtosis of zero.

Moment generating function

The moment generating function is defined as

\[
M_X(t) = E[e^{Xt}] = \sum_{x_k} e^{x_k t} p(x_k)
\]

Moments are found as the derivatives of the moment generating function evaluated at 0.
Fitting data

To fit data to a distribution, maximizing the likelihood function is common. Alternatively, some distributions have well-known minimum variance unbiased estimators. These will be chosen by default, but the likelihood function will always be available for minimizing.

If \( f_i(k; \theta) \) is the PDF of a random-variable where \( \theta \) is a vector of parameters (e.g. \( L \) and \( S \)), then for a collection of \( N \) independent samples from this distribution, the joint distribution the random vector \( k \) is

\[
f(k; \theta) = \prod_{i=1}^{N} f_i(k_i; \theta).
\]

The maximum likelihood estimate of the parameters \( \theta \) are the parameters which maximize this function with \( x \) fixed and given by the data:

\[
\hat{\theta} = \arg \max_{\theta} f(k; \theta) = \arg \min_{\theta} l_k(\theta).
\]

Where

\[
l_k(\theta) = -\sum_{i=1}^{N} \log f(k_i; \theta) = -N \log f(k; \theta)
\]

Standard notation for mean

We will use

\[
\bar{y}(x) = \frac{1}{N} \sum_{i=1}^{N} y(x_i)
\]

where \( N \) should be clear from context.

Combinations

Note that

\[
k! = k \cdot (k-1) \cdot (k-2) \cdots 1 = \Gamma(k+1)
\]

and has special cases of

\[
0! \equiv 1 \quad k! \equiv 0 \quad k < 0
\]

and

\[
\binom{n}{k} = \frac{n!}{(n-k)!k!}
\]

If \( n < 0 \) or \( k < 0 \) or \( k > n \) we define \( \binom{n}{k} = 0 \)
Discrete Distributions in scipy.stats

Bernoulli Distribution
A Bernoulli random variable of parameter $p$ takes one of only two values $X = 0$ or $X = 1$. The probability of success ($X = 1$) is $p$, and the probability of failure ($X = 0$) is $1 - p$. It can be thought of as a binomial random variable with $n = 1$. The PMF is $p(k) = 0$ for $k \neq 0, 1$ and

$$p(k; p) = \begin{cases} 1 - p & k = 0 \\ p & k = 1 \end{cases}$$

$$F(x; p) = \begin{cases} 0 & x < 0 \\ 1 - p & 0 \leq x < 1 \\ 1 & 1 \leq x \end{cases}$$

$$G(q; p) = \begin{cases} 0 & 0 \leq q < 1 - p \\ 1 & 1 - p \leq q \leq 1 \end{cases}$$

$$
\begin{align*}
\mu &= p \\
\mu_2 &= p(1 - p) \\
\gamma_3 &= \frac{1 - 2p}{\sqrt{p(1 - p)}} \\
\gamma_4 &= \frac{1 - 6p(1 - p)}{p(1 - p)} \\
M(t) &= 1 - p \left(1 - e^t\right) \\
\mu'_m &= p \\
h[X] &= p \log p + (1 - p) \log(1 - p)
\end{align*}
$$

Implementation: scipy.stats.bernoulli

Binomial Distribution
A binomial random variable with parameters $(n, p)$ can be described as the sum of $n$ independent Bernoulli random variables of parameter $p$;

$$Y = \sum_{i=1}^{n} X_i.$$

Therefore, this random variable counts the number of successes in $n$ independent trials of a random experiment where the probability of success is $p$.

$$p(k; n, p) = \binom{n}{k} p^k (1 - p)^{n-k} \text{, } k \in \{0, 1, \ldots, n\},$$

$$F(x; n, p) = \sum_{k \leq x} \binom{n}{k} p^k (1 - p)^{n-k} = I_{1-p} \left(n - \lfloor x \rfloor, \lfloor x \rfloor + 1\right) \text{ for } x \geq 0$$

where the incomplete beta integral is

$$I_x(a, b) = \frac{\Gamma(a + b)}{\Gamma(a) \Gamma(b)} \int_0^x t^{a-1} (1 - t)^{b-1} dt.$$
Now
\[
\begin{align*}
\mu &= np \\
\mu_2 &= np(1-p) \\
\gamma_1 &= \frac{1-2p}{\sqrt{np(1-p)}} \\
\gamma_2 &= \frac{1-6p(1-p)}{np(1-p)}.
\end{align*}
\]
\[M(t) = [1 - p (1 - e^t)]^n\]

Implementation: `scipy.stats.binom`

### Boltzmann (truncated Planck) Distribution

\[
p(k; N, \lambda) = \frac{1-e^{-\lambda}}{1-e^{-\lambda N}} \exp(-\lambda k) \quad k \in \{0, 1, \ldots, N-1\}
\]
\[
F(x; N, \lambda) = \begin{cases} 
0 & x < 0 \\
\frac{1-\exp(-\lambda(x+1))}{1-\exp(-\lambda N)} & 0 \leq x \leq N-1 \\
1 & x \geq N-1
\end{cases}
\]
\[
G(q, \lambda) = \left\lfloor \frac{-1}{\lambda} \log\left[1 - q \left(1 - e^{-\lambda N}\right)\right] - 1 \right\rfloor
\]

Define \(z = e^{-\lambda}\)

\[
\begin{align*}
\mu &= \frac{z}{1-z} - \frac{Nz^N}{1-z^N} \\
\mu_2 &= \frac{z}{(1-z)^2} - \frac{N^2z^N}{(1-z^N)^2} \\
\gamma_1 &= \frac{z (1+z) \left(\frac{1-z^N}{1-z}\right)^3 - N^3z^N (1+z^N)}{\left[\frac{z^N}{1-z^N} - Nz^N\right]^{3/2}} \\
\gamma_2 &= \frac{z (1+4z+z^2) \left(\frac{1-z^N}{1-z}\right)^4 - N^4z^N (1+4z^N + z^2N)}{\left[\frac{z^N}{1-z^N} - N^2z^N\right]^2} \\
M(t) &= \frac{1-e^{N(t-\lambda)}}{1 - e^{t-\lambda}} \frac{1-e^{-\lambda}}{1-e^{-\lambda N}}
\end{align*}
\]

Implementation: `scipy.stats.boltzmann`

### Planck (discrete exponential) Distribution

Named Planck because of its relationship to the black-body problem he solved.

\[
p(k; \lambda) = (1 - e^{-\lambda}) e^{-\lambda k} \quad k\lambda \geq 0
\]
\[
F(x; \lambda) = 1 - e^{-\lambda(x+1)} \quad x\lambda \geq 0
\]
\[
G(q; \lambda) = \left\lfloor \frac{1}{\lambda} \log\left[1 - q\right] - 1 \right\rfloor.
\]
\[
\begin{align*}
\mu &= \frac{1}{e^\lambda - 1} \\
\mu_2 &= \frac{e^{-\lambda}}{(1 - e^{-\lambda})^2} \\
\gamma_1 &= 2 \cosh \left( \frac{\lambda}{2} \right) \\
\gamma_2 &= 4 + 2 \cosh (\lambda) \\
M (t) &= \frac{1 - e^{-\lambda}}{1 - e^{t - \lambda}} \\
h [X] &= \frac{\lambda e^{-\lambda}}{1 - e^{-\lambda}} - \log (1 - e^{-\lambda})
\end{align*}
\]

Implementation: \texttt{scipy.stats.planck}

**Poisson Distribution**

The Poisson random variable counts the number of successes in \( n \) independent Bernoulli trials in the limit as \( n \to \infty \) and \( p \to 0 \) where the probability of success in each trial is \( p \) and \( np = \lambda \geq 0 \) is a constant. It can be used to approximate the Binomial random variable or in its own right to count the number of events that occur in the interval \([0, t]\) for a process satisfying certain “sparsity” constraints. The functions are:

\[
\begin{align*}
p (k; \lambda) &= e^{-\lambda} \frac{\lambda^k}{k!} \quad k \geq 0, \\
F (x; \lambda) &= \sum_{n=0}^{[x]} e^{-\lambda} \frac{\lambda^n}{n!} = \frac{1}{\Gamma([x] + 1)} \int_{\lambda}^{\infty} t^{[x]} e^{-t} dt, \\
\mu &= \lambda \\
\mu_2 &= \lambda \\
\gamma_1 &= \frac{1}{\sqrt{\lambda}} \\
\gamma_2 &= \frac{1}{\lambda}.
\end{align*}
\]

Implementation: \texttt{scipy.stats.poisson}

**Geometric Distribution**

The geometric random variable with parameter \( p \in (0, 1) \) can be defined as the number of trials required to obtain a success where the probability of success on each trial is \( p \). Thus,

\[
\begin{align*}
p (k; p) &= (1 - p)^{k-1} p \quad k \geq 1 \\
F (x; p) &= 1 - (1 - p)^{[x]} \quad x \geq 1 \\
G (q; p) &= \left[ \frac{\log (1 - q)}{\log (1 - p)} \right] \\
\mu &= \frac{1}{p} \\
\mu_2 &= \frac{1 - p}{p^2} \\
\gamma_1 &= \frac{2 - p}{\sqrt{1 - p}} \\
\gamma_2 &= \frac{p^2 - 6p + 6}{1 - p}.
\end{align*}
\]
\[ M(t) = \frac{p}{e^{-t} - (1 - p)} \]

Implementation: `scipy.stats.geom`

**Negative Binomial Distribution**

The negative binomial random variable with parameters \( n \) and \( p \in (0, 1) \) can be defined as the number of extra independent trials (beyond \( n \)) required to accumulate a total of \( n \) successes where the probability of a success on each trial is \( p \). Equivalently, this random variable is the number of failures encountered while accumulating \( n \) successes during independent trials of an experiment that succeeds with probability \( p \).

Thus,

\[ p(k; n, p) = \binom{k + n - 1}{n - 1} p^n (1 - p)^k \quad k \geq 0 \]

\[ F(x; n, p) = \sum_{i=0}^{\lfloor x \rfloor} \binom{i + n - 1}{i} p^n (1 - p)^i \quad x \geq 0 \]

\[ = I_p(n, \lfloor x \rfloor + 1) \quad x \geq 0 \]

\[ \mu = \frac{n - 1}{p} \]

\[ \mu_2 = \frac{n - 1}{p^2} \]

\[ \gamma_1 = \frac{2 - p}{\sqrt{n(1 - p)}} \]

\[ \gamma_2 = \frac{p^2 + 6 (1 - p)}{n(1 - p)} \]

Recall that \( I_p(a, b) \) is the incomplete beta integral.

Implementation: `scipy.stats.nbinom`

**Hypergeometric Distribution**

The hypergeometric random variable with parameters \((M, n, N)\) counts the number of “good” objects in a sample of size \(N\) chosen without replacement from a population of \(M\) objects where \(n\) is the number of “good” objects in the total population.

\[ p(k; N, n, M) = \frac{\binom{n}{k} \binom{M - n}{N - k}}{\binom{M}{N}} \quad N - (M - n) \leq k \leq \min(n, N) \]

\[ F(x; N, n, M) = \sum_{k=0}^{\lfloor x \rfloor} \binom{m}{k} \binom{N - m}{n - k}, \]

\[ \mu = \frac{nN}{M} \]

\[ \mu_2 = \frac{nN (M - n) (M - N)}{M^2 (M - 1)} \]

\[ \gamma_1 = \frac{(M - 2n) (M - 2N)}{M - 2} \sqrt{\frac{M - 1}{nN (M - m) (M - n)}} \]

\[ \gamma_2 = \frac{g(N, n, M)}{nN (M - n) (M - 3) (M - 2) (N - M)} \]
where (defining \( m = M - n \))

\[
g(N, n, M) = m^3 - m^5 + 3m^2n - 6m^3n + m^4n + 3mn^2 \\
-12m^2n^2 + 8m^3n^2 + n^3 - 6mn^3 + 8m^2n^3 \\
+mn^4 - n^5 - 6m^3N + 6m^4N + 18m^2nN \\
-6m^3nN + 18mn^2N - 24m^2n^2N - 6n^3N \\
-6mn^3N + 6n^4N + 6m^2N^2 - 6m^3N^2 - 24mnN^2 \\
+12m^2nN^2 + 6n^2N^2 + 12mn^2N^2 - 6n^3N^2.
\]

Implementation: `scipy.stats.hypergeom`

**Zipf (Zeta) Distribution**

A random variable has the zeta distribution (also called the zipf distribution) with parameter \( \alpha > 1 \) if its probability mass function is given by

\[
p(k; \alpha) = \frac{1}{\zeta(\alpha) k^\alpha} \quad k \geq 1
\]

where

\[
\zeta(\alpha) = \sum_{n=1}^{\infty} \frac{1}{n^\alpha}
\]

is the Riemann zeta function. Other functions of this distribution are

\[
F(x; \alpha) = \frac{1}{\zeta(\alpha)} \sum_{k=1}^{\lfloor x \rfloor} \frac{1}{k^\alpha}
\]

\[
\mu = \frac{\zeta_1}{\zeta_0} \quad \alpha > 2
\]

\[
\mu_2 = \frac{\zeta_2 \zeta_0 - \zeta_1^2}{\zeta_0^2} \quad \alpha > 3
\]

\[
\gamma_1 = \frac{\zeta_3 \zeta_0^2 - 3\zeta_0 \zeta_1 \zeta_2 + 2\zeta_1^3}{[\zeta_2 \zeta_0 - \zeta_1^2]^{3/2}} \quad \alpha > 4
\]

\[
\gamma_2 = \frac{\zeta_4 \zeta_0^3 - 4\zeta_3 \zeta_1 \zeta_2^2 + 12\zeta_2 \zeta_1^2 \zeta_0 - 6\zeta_1^4 - 3\zeta_2^2 \zeta_0^2}{(\zeta_2 \zeta_0 - \zeta_1^2)^2}
\]

\[
M(t) = \frac{\text{Li}_n(e^t)}{\zeta(\alpha)}
\]

where \( \zeta_i = \zeta(\alpha - i) \) and \( \text{Li}_n(z) \) is the \( n \)th polylogarithm function of \( z \) defined as

\[
\text{Li}_n(z) = \sum_{k=1}^{\infty} \frac{z^k}{k^n}
\]

\[
\mu'_n = M^{(n)}(t) \bigg|_{t=0} = \frac{\text{Li}_{n-1}(e^t)}{\zeta(\alpha)} \bigg|_{t=0} = \frac{\zeta(\alpha - n)}{\zeta(\alpha)}
\]

Implementation: `scipy.stats.zipf`
Logarithmic (Log-Series, Series) Distribution

The logarithmic distribution with parameter \( p \) has a probability mass function with terms proportional to the Taylor series expansion of \( \log (1 - p) \)

\[
p(k; p) = - \frac{p^k}{k \log (1 - p)} \quad k \geq 1
\]

\[
F(x; p) = - \frac{1}{\log (1 - p)} \sum_{k=1}^{\lfloor x \rfloor} \frac{p^k}{k} = 1 + \frac{p^{1+\lfloor x \rfloor} \Phi(p, 1, 1 + \lfloor x \rfloor)}{\log (1 - p)}
\]

where

\[
\Phi(z, s, a) = \sum_{k=0}^{\infty} \frac{z^k}{(a + k)^s}
\]

is the Lerch Transcendent. Also define \( r = \log (1 - p) \)

\[
\mu = - \frac{p}{(1 - p) r}
\]

\[
\mu_2 = - \frac{p [p + r]}{(1 - p)^2 r^2}
\]

\[
\gamma_1 = - \frac{2p^2 + 3pr + (1 + p) r^2}{r (p + r) \sqrt{-p (p + r)}}
\]

\[
\gamma_2 = - \frac{6p^3 + 12p^2 r + p (4p + 7) r^2 + (p^2 + 4p + 1) r^3}{p (p + r)^2}
\]

\[
M(t) = - \frac{1}{\log (1 - p)} \sum_{k=1}^{\infty} \frac{e^{tk} p^k}{k} = \frac{\log (1 - pe^t)}{\log (1 - p)}
\]

Thus,

\[
\mu'_n = M^{(n)}(t) \bigg|_{t=0} = \frac{\text{Li}_{1-n}(pe^t)}{\log (1 - p)} \bigg|_{t=0} = - \frac{\text{Li}_{1-n}(p)}{\log (1 - p)}.
\]

Implementation: \texttt{scipy.stats.logser}

Discrete Uniform (randint) Distribution

The discrete uniform distribution with parameters \((a, b)\) constructs a random variable that has an equal probability of being any one of the integers in the half-open range \([a, b)\). If \( a \) is not given it is assumed to be zero and the only parameter is \( b \). Therefore,

\[
p(k; a, b) = \frac{1}{b - a} \quad a \leq k < b
\]

\[
F(x; a, b) = \frac{\lfloor x \rfloor - a}{b - a} \quad a \leq x \leq b
\]

\[
G(q; a, b) = \lfloor q (b - a) + a \rfloor
\]

\[
\mu = \frac{b + a - 1}{2}
\]

\[
\mu_2 = \frac{(b - a - 1) (b - a + 1)}{12}
\]

\[
\gamma_1 = 0
\]

\[
\gamma_2 = \frac{6}{5} \frac{(b - a)^2 + 1}{(b - a - 1) (b - a + 1)}.
\]
\[ M(t) = \frac{1}{b-a} \sum_{k=a}^{b-1} e^{tk} = \frac{e^{bt} - e^{at}}{(b-a)(e^t - 1)} \]

Implementation: `scipy.stats.randint`

**Discrete Laplacian Distribution**

Defined over all integers for \( a > 0 \)

\[ p(k) = \tanh \left( \frac{a}{2} \right) e^{-a|k|}, \]

\[ F(x) = \begin{cases} \frac{e^{a(x+1)}}{e^{a(x+1)} - e^{a(x-1)}} & |x| < 0, \\ 1 - \frac{e^{a(x-1)}}{e^{a(x+1)} - e^{a(x-1)}} & |x| \geq 0. \end{cases} \]

\[ G(q) = \begin{cases} \left[ \frac{1}{a} \log \left[ q(e^a + 1) \right] - 1 \right] & q < \frac{1}{e^a - 1} \cdot 1, \\ \left[ \frac{1}{a} \log \left[ (1 - q)(1 + e^a) \right] \right] & q \geq \frac{1}{e^a - 1}. \end{cases} \]

\[ M(t) = \tanh \left( \frac{a}{2} \right) \sum_{k=-\infty}^{\infty} e^{tk} e^{-a|k|} = C \left( 1 + \sum_{k=1}^{\infty} e^{-(t+a)k} + \sum_{k=1}^{\infty} e^{(t-a)k} \right) = \tanh \left( \frac{a}{2} \right) \left( 1 + \frac{e^{-(t+a)}}{1 - e^{-(t+a)}} + \frac{e^{t-a}}{1 - e^{t-a}} \right) = \frac{\tanh \left( \frac{a}{2} \right) \sinh a}{\cosh a - \cosh t}. \]

Thus,

\[ \mu_n = M^{(n)}(0) = [1 + (-1)^n] \text{Li}_{-n} \left( e^{-a} \right) \]

where \( \text{Li}_{-n} \left( z \right) \) is the polylogarithm function of order \( -n \) evaluated at \( z \).

\[ h[X] = -\log \left( \tanh \left( \frac{a}{2} \right) \right) + \frac{a}{\sinh a} \]

Implementation: `scipy.stats.dlaplace`

**Continuous Statistical Distributions**

**Overview**

All distributions will have location (\( L \)) and Scale (\( S \)) parameters along with any shape parameters needed, the names for the shape parameters will vary. Standard form for the distributions will be given where \( L = 0.0 \) and \( S = 1.0 \). The nonstandard forms can be obtained for the various functions using (note \( U \) is a standard uniform random variate).
Note, that these can always be computed using the PPF. Substitute $x = G(q)$ in the above equation and get

$$
\mu'_n = \int_0^1 G^n(q) \, dq
$$

which may be easier to compute numerically. Note that $q = F(x)$ so that $dq = f(x) \, dx$. Central moments are computed similarly $\mu = \mu'_1$

$$
\mu_n = \int_0^\infty (x-\mu)^n f(x) \, dx
= \int_0^1 (G(q) - \mu)^n \, dq
= \sum_{k=0}^n \binom{n}{k} (-\mu)^k \mu'_{n-k}
$$

In particular

$$
\mu_3 = \mu'_3 - 3\mu'_2 + 2\mu^3 = \mu'_3 - 3\mu^2\mu_2 - \mu^3
$$
$$
\mu_4 = \mu'_4 - 4\mu'_3 + 6\mu'_2\mu - 3\mu^4 = \mu'_4 - 4\mu^3 - 6\mu^2\mu_2 - \mu^4
$$

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<td>$F(x; L, S) = F\left(\frac{x-L}{S}\right)$</td>
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<td>Probability Density Function (PDF)</td>
<td>$f(x) = F'(x)$</td>
<td>$f(x; L, S) = \frac{1}{S} f\left(\frac{x-L}{S}\right)$</td>
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<tr>
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<td>$G(q) = F^{-1}(q)$</td>
<td>$G(q; L, S) = L + SG(q)$</td>
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<tr>
<td>Probability Sparsity Function (PSF)</td>
<td>$g(q) = G'(q)$</td>
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<tr>
<td>Hazard Function (HF)</td>
<td>$h_a(x) = \frac{f(x)}{1-F(x)}$</td>
<td>$h_a(x; L, S) = \frac{1}{S} h_a\left(\frac{x-L}{S}\right)$</td>
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<tr>
<td>Cumulative Hazard Function (CHF)</td>
<td>$H_a(x) = \log \frac{1}{1-F(x)}$</td>
<td>$H_a(x; L, S) = H_a\left(\frac{x-L}{S}\right)$</td>
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<tr>
<td>Survival Function (SF)</td>
<td>$S(x) = 1 - F(x)$</td>
<td>$S(x; L, S) = S\left(\frac{x-L}{S}\right)$</td>
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<tr>
<td>Moment Generating Function (MGF)</td>
<td>$M_X(t) = E[e^{tx}]$</td>
<td>$M_X(t) = e^{Lt}M_Y(St)$</td>
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<tr>
<td>Random Variates</td>
<td>$Y = G(U)$</td>
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<td>(Differential) Entropy</td>
<td>$h</td>
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<tr>
<td>(Non-central) Moments</td>
<td>$\mu'_n = E[Y^n]$</td>
<td>$E[X^n] = L^n \sum_{k=0}^n \binom{n}{k} (\frac{S}{2})^k \mu'_k$</td>
</tr>
<tr>
<td>Central Moments</td>
<td>$\mu_n = E[(Y-\mu)^n]$</td>
<td>$E[(X-\mu_X)^n] = S^n\mu_n$</td>
</tr>
<tr>
<td>mean (mode, median), var</td>
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<tr>
<td>skewness, kurtosis</td>
<td>$\gamma_1 = \frac{\mu'_3}{(\mu'_2)^{3/2}}, \gamma_2 = \frac{\mu'_4}{(\mu'_2)^2} - 3$</td>
<td>$\gamma_1, \gamma_2$</td>
</tr>
</tbody>
</table>
Skewness is defined as
\[ \gamma_1 = \sqrt{\beta_1} = \frac{\mu_3}{\mu_2^{3/2}} \]
while (Fisher) kurtosis is
\[ \gamma_2 = \frac{\mu_4}{\mu_2^2} - 3, \]
so that a normal distribution has a kurtosis of zero.

**Median and mode**

The median, \( m_n \) is defined as the point at which half of the density is on one side and half on the other. In other words, \( F(m_n) = \frac{1}{2} \) so that
\[ m_n = G \left( \frac{1}{2} \right). \]
In addition, the mode, \( m_d \), is defined as the value for which the probability density function reaches its peak
\[ m_d = \arg \max_x f(x). \]

**Fitting data**

To fit data to a distribution, maximizing the likelihood function is common. Alternatively, some distributions have well-known minimum variance unbiased estimators. These will be chosen by default, but the likelihood function will always be available for minimizing.

If \( f(x; \theta) \) is the PDF of a random-variable where \( \theta \) is a vector of parameters (e.g. \( L \) and \( S \)), then for a collection of \( N \) independent samples from this distribution, the joint distribution the random vector \( x \) is
\[ f(x; \theta) = \prod_{i=1}^{N} f(x_i; \theta). \]
The maximum likelihood estimate of the parameters \( \theta \) are the parameters which maximize this function with \( x \) fixed and given by the data:
\[ \theta_{\text{es}} = \arg \max_{\theta} f(x; \theta) = \arg \min_{\theta} l_x(\theta). \]
Where
\[ l_x(\theta) = -\sum_{i=1}^{N} \log f(x_i; \theta) = -N \log f(x_i; \theta). \]
Note that if \( \theta \) includes only shape parameters, the location and scale-parameters can be fit by replacing \( x_i \) with \( (x_i - L)/S \) in the log-likelihood function adding \( N \log S \) and minimizing, thus
\[ l_x(L, S; \theta) = N \log S - \sum_{i=1}^{N} \log f \left( \frac{x_i - L}{S}; \theta \right) = N \log S + l_{x,S}(\theta) \]
If desired, sample estimates for \( L \) and \( S \) (not necessarily maximum likelihood estimates) can be obtained from samples estimates of the mean and variance using

\[
\hat{S} = \sqrt{\frac{\hat{\mu}_2}{\mu_2}}
\]

\[
L = \hat{\mu} - \hat{S} \mu
\]

where \( \mu \) and \( \mu_2 \) are assumed known as the mean and variance of the untransformed distribution (when \( L = 0 \) and \( S = 1 \)) and

\[
\hat{\mu} = \frac{1}{N} \sum_{i=1}^{N} x_i = \bar{x}
\]

\[
\hat{\mu}_2 = \frac{1}{N-1} \sum_{i=1}^{N} (x_i - \hat{\mu})^2 = \frac{N}{N-1} (\bar{x} - \bar{x})^2
\]

**Standard notation for mean**

We will use

\[
\bar{y} (\bar{x}) = \frac{1}{N} \sum_{i=1}^{N} y (x_i)
\]

where \( N \) should be clear from context as the number of samples \( x_i \)

**References**

- Documentation for ranlib, rv2, cdflib

**Continuous Distributions in scipy.stats**

**Alpha Distribution**

One shape parameters \( \alpha > 0 \) (parameter \( \beta \) in DATAPLOT is a scale-parameter). Standard form is \( x > 0 \) :

\[
f(x; \alpha) = \frac{1}{x^2 \Phi(\alpha) \sqrt{2\pi}} \exp \left( -\frac{1}{2} \left( \frac{\alpha - \frac{1}{x}}{\bar{x}} \right)^2 \right)
\]

\[
F(x; \alpha) = \Phi \left( \frac{\alpha - \frac{1}{x}}{\bar{x}} \right)
\]

\[
G(q; \alpha) = \left[ \alpha - \Phi^{-1}(q \Phi(\alpha)) \right]^{-1}
\]

\[
M(t) = \frac{1}{\Phi(\alpha) \sqrt{2\pi}} \int_{0}^{\infty} \frac{e^{xt}}{x^2} \exp \left( -\frac{1}{2} \left( \frac{\alpha - \frac{1}{x}}{\bar{x}} \right)^2 \right) dx
\]
No moments?

\[
\lambda_b (\alpha) = N \log \left[ \Phi (\alpha \sqrt{2\pi}) \right] + 2N \log x + \frac{N}{2} \alpha^2 - \alpha^{-1}x + \frac{1}{2}x^{-2}
\]

Implementation: `scipy.stats.alpha`

**Anglit Distribution**

Defined over \( x \in [-\frac{\pi}{4}, \frac{\pi}{4}] \)

\[
\begin{align*}
  f(x) &= \sin \left( 2x + \frac{\pi}{2} \right) = \cos (2x) \\
  F(x) &= \sin^2 \left( x + \frac{\pi}{4} \right) \\
  G(q) &= \arcsin \left( \sqrt{q} \right) - \frac{\pi}{4}
\end{align*}
\]

\[
\begin{align*}
  \mu &= 0 \\
  \mu_2 &= \frac{\pi^2}{16} - \frac{1}{2} \\
  \gamma_1 &= 0 \\
  \gamma_2 &= -2 \frac{\pi^4 - 96}{(\pi^2 - 8)^2}
\end{align*}
\]

\[
\begin{align*}
  h[X] &= 1 - \log 2 \\
  &\approx 0.30685281944005469058
\end{align*}
\]

\[
\begin{align*}
  M(t) &= \int_{-\frac{\pi}{4}}^{\frac{\pi}{4}} \cos (2x)e^{xt} \, dx \\
  &= \frac{4 \cosh \left( \frac{\pi t}{4} \right)}{t^2 + 4} \\
  l_x (\cdot) &= -N \log \left[ \cos (2x) \right]
\end{align*}
\]

Implementation: `scipy.stats.anglit`

**Arcsine Distribution**

Defined over \( x \in (0, 1) \). To get the JKB definition put \( x = \frac{u+1}{2} \), i.e. \( L = -1 \) and \( S = 2 \).

\[
\begin{align*}
  f(x) &= \frac{1}{\pi \sqrt{x(1-x)}} \\
  F(x) &= \frac{2}{\pi} \arcsin \left( \sqrt{x} \right) \\
  G(q) &= \sin^2 \left( \frac{\pi q}{2} \right) \\
  M(t) &= E^{t/2}I_0 \left( \frac{t}{2} \right)
\end{align*}
\]

\[
\begin{align*}
  \mu'_n &= \frac{1}{\pi} \int_0^1 dx \, x^{n-1/2} (1-x)^{-1/2} \\
  &= \frac{1}{\pi} B \left( \frac{1}{2}, n + \frac{1}{2} \right) = \frac{(2n-1)!!}{2^n n!}
\end{align*}
\]
\[ \mu = \frac{1}{2} \]
\[ \mu_2 = \frac{1}{8} \]
\[ \gamma_1 = 0 \]
\[ \gamma_2 = -\frac{3}{2} \]

\[ h[X] \approx -0.24156447527049044468 \]

\[ l_x(\cdot) = N \log \pi + \frac{N}{2} \log x + \frac{N}{2} \log (1 - x) \]

Implementation: \texttt{scipy.stats.arcsine}

**Beta Distribution**

Two shape parameters

\[ a, b > 0 \]

\[ f(x; a, b) = \frac{\Gamma(a + b)}{\Gamma(a) \Gamma(b)} x^{a-1} (1 - x)^{b-1} I_{(0,1)}(x) \]

\[ F(x; a, b) = \int_0^x f(y; a, b) \, dy = I(x, a, b) \]

\[ G(\alpha; a, b) = I^{-1}(\alpha; a, b) \]

\[ M(t) = \frac{\Gamma(a) \Gamma(b)}{\Gamma(a + b)} \, _1F_1(a; a + b; t) \]

\[ \mu = \frac{a}{a + b} \]

\[ \mu_2 = \frac{ab(a + b + 1)}{(a + b)^2} \]

\[ \gamma_1 = 2 \frac{b - a}{a + b + 2} \sqrt{\frac{a + b + 1}{ab}} \]

\[ \gamma_2 = 6 \frac{(a^3 + a^2(1 - 2b) + b^2(b + 1) - 2ab(b + 2))}{ab(a + b + 2)(a + b + 3)} \]

\[ m_d = \frac{(a - 1)}{(a + b - 2)} \frac{a + b}{a + b - 2} \neq 2 \]

\[ f(x; a, 1) \text{ is also called the Power-function distribution.} \]

\[ l_x(a, b) = -N \log \Gamma(a + b) + N \log \Gamma(a) + N \log \Gamma(b) - N(a - 1) \log x - N(b - 1) \log (1 - x) \]

All of the \( x_i \in [0, 1] \)

Implementation: \texttt{scipy.stats.beta}

**Beta Prime Distribution**

Defined over \( 0 < x < \infty. \alpha, \beta > 0 \). (Note the CDF evaluation uses Eq. 3.194.1 on pg. 313 of Gradshteyn & Ryzhik (sixth edition).

\[ f(x; \alpha, \beta) = \frac{\Gamma(\alpha + \beta)}{\Gamma(\alpha) \Gamma(\beta)} x^{\alpha-1} (1 + x)^{-\alpha-\beta} \]

\[ F(x; \alpha, \beta) = \frac{\Gamma(\alpha + \beta)}{\alpha \Gamma(\alpha) \Gamma(\beta)} \, _2F_1(\alpha + \beta, \alpha; 1 + \alpha; -x) \]

\[ G(q; \alpha, \beta) = F^{-1}(x; \alpha, \beta) \]
\[
\mu'_n = \begin{cases} 
{\frac{\Gamma(n+\alpha)\Gamma(\beta-n)}{\Gamma(\alpha)\Gamma(\beta)}} & \beta > n \\
0 & \text{otherwise}
\end{cases}
\]

Therefore,
\[
\mu = \frac{\alpha}{\beta - 1} \quad \beta > 1
\]
\[
\mu_2 = \frac{\alpha(\alpha+1)}{\beta - 2} \quad \beta > 2
\]
\[
\gamma_1 = \frac{\alpha(\alpha+1)(\alpha+2)}{(\beta-3)(\beta-4)(\beta-1)} - 3\mu_2 - \mu^2
\]
\[
\gamma_2 = \frac{\mu_4}{\mu_2^2} - 3
\]
\[
\mu_4 = \frac{\alpha(\alpha+1)(\alpha+2)(\alpha+3)}{(\beta-4)(\beta-3)(\beta-2)(\beta-1)} - 4\mu_3 - 6\mu_2^2 - \mu^4
\]

Implementation: \texttt{scipy.stats.betaprime}

**Bradford Distribution**

\[
f(x; c) = \frac{c}{k(1+cx)} I_{(0,1)}(x)
\]
\[
F(x; c) = \frac{\log(1+cx)}{k}
\]
\[
G(\alpha c) = \frac{(1+c)^\alpha - 1}{c}
\]
\[
M(t) = \frac{1}{k} e^{-t/c} \left[ \text{Ei} \left( \frac{t}{c} \right) - \text{Ei} \left( \frac{t}{c} \right) \right]
\]
\[
\mu = \frac{c-k}{ck}
\]
\[
\mu_2 = \frac{(c+2)k - 2c}{2ck^2}
\]
\[
\gamma_1 = \frac{\sqrt{2} \left( 12c^2 - 9kc(c+2) + 2k^2(c(c+3) + 3) \right)}{\sqrt{c(c(k-2) + 2k)(3c(k-2) + 6k)}}
\]
\[
\gamma_2 = \frac{c^3(k-3)(k(3k-16) + 24) + 12k^2(c(k-4)(k-3) + 6ck^2(3k-14) + 12k^3)}{3c(c(k-2) + 2k)^2}
\]
\[
m_d = 0
\]
\[
m_n = \sqrt{1+c} - 1
\]

where \(\text{Ei}(z)\) is the exponential integral function. Also
\[
h[X] = \frac{1}{2} \log(1+c) - \log \left( \frac{c}{\log(1+c)} \right)
\]

Implementation: \texttt{scipy.stats.bradford}
Burr Distribution

\[ c > 0 \]
\[ d > 0 \]
\[ k = \frac{\Gamma(d)\Gamma\left(\frac{2}{c} + d\right) - \Gamma^2\left(\frac{2}{c} + d\right) \Gamma^2\left(\frac{1}{c} + d\right)}{x^{c+1}(1 + x)^{d+1}} I_{(0,\infty)}(x) \]
\[ f(x; c, d) = \frac{cd}{x^{c+1}(1 + x)^{d+1}} \]
\[ F(x; c, d) = (1 + x^{-c})^{-d} \]
\[ G(\alpha; c, d) = \left(\alpha^{-1/d} - 1\right)^{-1/c} \]
\[ \mu = \frac{\Gamma\left(1 - \frac{1}{c}\right) \Gamma\left(\frac{1}{c} + d\right)}{\Gamma(d)} \]
\[ \mu_2 = \frac{k}{\Gamma^2(d)} \]
\[ \gamma_1 = \frac{1}{\sqrt{k^2}} \left[ 2\Gamma^3\left(\frac{1}{c}\right) \Gamma^3\left(\frac{c + d}{c}\right) + \Gamma^2\left(\frac{1}{c}\right) \Gamma\left(\frac{2}{c}\right) \Gamma^2\left(\frac{c + d}{c}\right) \Gamma\left(\frac{3}{c}\right) \Gamma\left(\frac{3}{c} + d\right) \right. \]
\[ -3\Gamma\left(\frac{3}{c}\right) \Gamma\left(\frac{2}{c}\right) \Gamma\left(\frac{1}{c}\right) \Gamma\left(\frac{c + d}{c}\right) \Gamma\left(\frac{3}{c} + d\right) \]
\[ \gamma_2 = -3 + \frac{1}{k^2} \left[ 6\Gamma\left(\frac{1}{c}\right) \Gamma^2\left(\frac{2}{c} + d\right) \Gamma\left(\frac{1}{c} + d\right) \Gamma\left(\frac{2}{c} + d\right) \Gamma\left(\frac{3}{c} + d\right) \left[ 1 + \frac{1}{\sqrt{k^2}} \left[ 2\Gamma^3\left(\frac{1}{c}\right) \Gamma^3\left(\frac{c + d}{c}\right) + \Gamma^2\left(\frac{1}{c}\right) \Gamma\left(\frac{2}{c}\right) \Gamma^2\left(\frac{c + d}{c}\right) \Gamma\left(\frac{3}{c}\right) \Gamma\left(\frac{3}{c} + d\right) \right. \right. \right. \]
\[ -3\Gamma^4\left(\frac{1}{c}\right) \Gamma^4\left(\frac{c + d}{c}\right) + \Gamma^3\left(\frac{1}{c}\right) \Gamma\left(\frac{2}{c}\right) \Gamma^3\left(\frac{c + d}{c}\right) \Gamma\left(\frac{4}{c} + d\right) \Gamma\left(\frac{3}{c} + d\right) \left. \right. \right. \]
\[ -4\Gamma^2\left(\frac{1}{c}\right) \Gamma^2\left(\frac{2}{c} + d\right) \Gamma\left(\frac{1}{c} + d\right) \Gamma\left(\frac{2}{c} + d\right) \Gamma\left(\frac{3}{c} + d\right) \left. \right. \right. \]
\[ m_d = \left(\frac{cd - 1}{c + 1}\right)^{1/c} \text{ if } cd > 1 \text{ otherwise } 0 \]
\[ m_n = \left(2^{1/d} - 1\right)^{-1/c} \]

Implementation: \texttt{scipy.stats.burr}

Cauchy Distribution

\[ f(x) = \frac{1}{\pi (1 + x^2)} \]
\[ F(x) = \frac{1}{2} + \frac{1}{\pi} \tan^{-1} x \]
\[ G(\alpha) = \tan \left(\pi \alpha - \frac{\pi}{2}\right) \]
\[ m_d = 0 \]
\[ m_n = 0 \]

No finite moments. This is the t distribution with one degree of freedom.
\[ h[X] = \log (4\pi) \approx 2.5310242469692907930. \]

Implementation: \texttt{scipy.stats.cauchy}
Chi Distribution

Generated by taking the (positive) square-root of chi-squared variates.

\[ f(x; \nu) = \frac{x^{\nu-1}e^{-x^2/2}}{2^{\nu/2-1/2} \Gamma(\nu/2)} I(0, \infty) (x) \]

\[ F(x; \nu) = \Gamma\left(\frac{\nu}{2}, \frac{x^2}{2}\right) \]

\[ G(\alpha; \nu) = \sqrt{2}^{-1} \left(\frac{\nu}{2}, \alpha\right) \]

\[ M(t) = \Gamma\left(\frac{\nu}{2}\right) {}_1F_1\left(\frac{\nu}{2}, \frac{1}{2}; \frac{t^2}{2}\right) + \frac{t}{\sqrt{2}} \Gamma\left(\frac{1+\nu}{2}\right) {}_1F_1\left(\frac{1+\nu}{2}; \frac{3}{2}; \frac{t^2}{2}\right) \]

\[ \mu = \frac{\sqrt{2} \Gamma\left(\frac{\nu+1}{2}\right)}{\Gamma\left(\frac{\nu}{2}\right)} \]

\[ \mu_2 = \nu - \mu^2 \]

\[ \gamma_1 = \frac{2\nu^3 + \mu (1 - 2\nu)}{\mu_2^{3/2}} \]

\[ \gamma_2 = \frac{2\nu (1 - \nu) - 6\mu^4 + 4\mu^2 (2\nu - 1)}{\mu_2^2} \]

\[ m_d = \sqrt{\nu - 1}, \quad \nu \geq 1 \]

\[ m_n = \sqrt{2}^{-1} \left(\frac{\nu-1}{2}, \frac{\nu}{2}\right) \]

Implementation: scipy.stats.chi

Chi-squared Distribution

This is the gamma distribution with \( L = 0.0 \) and \( S = 2.0 \) and \( \alpha = \nu/2 \) where \( \nu \) is called the degrees of freedom. If \( Z_1 \ldots Z_n \) are all standard normal distributions, then \( W = \sum_k Z_k^2 \) has (standard) chi-square distribution with \( \nu \) degrees of freedom.

The standard form (most often used in standard form only) is \( x > 0 \)

\[ f(x; \alpha) = \frac{1}{2^{\nu/2} \Gamma(\nu/2)} x^{\nu/2-1} e^{-x/2} \]

\[ F(x; \alpha) = \Gamma\left(\frac{\nu}{2}, \frac{x}{2}\right) \]

\[ G(\nu; \alpha) = 2^{-1} \left(\nu, \frac{1}{2}, \alpha\right) \]

\[ M(t) = \frac{\Gamma\left(\frac{\nu}{2}\right)}{(1 - t)^{\nu/2}} \]

\[ \mu = \nu \]

\[ \mu_2 = 2\nu \]

\[ \gamma_1 = \frac{2\sqrt{2}}{\sqrt{\nu}} \]

\[ \gamma_2 = \frac{12}{\nu} \]

\[ m_d = \frac{\nu}{2} - 1 \]

Implementation: scipy.stats.chi2
Cosine Distribution

Approximation to the normal distribution.

\[ f(x) = \frac{1}{2\pi} [1 + \cos x] I_{[-\pi, \pi]}(x) \]
\[ F(x) = \frac{1}{2\pi} [\pi + x + \sin x] I_{[-\pi, \pi]}(x) + I_{(\pi, \infty)}(x) \]
\[ G(\alpha) = F^{-1}(\alpha) \]
\[ M(t) = \frac{\sinh(\pi t)}{\pi t(1 + t^2)} \]
\[ \mu = m_d = m_n = 0 \]
\[ \mu_2 = \frac{\pi^2}{3} - 2 \]
\[ \gamma_1 = 0 \]
\[ \gamma_2 = -\frac{6(\pi^4 - 90)}{5(\pi^2 - 6)^2} \]
\[ h[X] = \log(4\pi) - 1 \approx 1.5310242469692907930. \]

Implementation: `scipy.stats.cosine`

Double Gamma Distribution

The double gamma is the signed version of the Gamma distribution. For \( \alpha > 0 \):

\[ f(x; \alpha) = \frac{1}{2\Gamma(\alpha)} |x|^{\alpha-1} e^{-|x|} \]
\[ F(x; \alpha) = \begin{cases} 
\frac{1}{2} - \frac{1}{2}\Gamma(\alpha, |x|) & x \leq 0 \\
\frac{1}{2} + \frac{1}{2}\Gamma(\alpha, |x|) & x > 0 
\end{cases} \]
\[ G(q; \alpha) = \begin{cases} 
-\Gamma^{-1}(\alpha, |2q - 1|) & q \leq \frac{1}{2} \\
\Gamma^{-1}(\alpha, |2q - 1|) & q > \frac{1}{2} 
\end{cases} \]
\[ M(t) = \frac{1}{2(1-t)^{\alpha}} + \frac{1}{2(1+t)^{\alpha}} \]
\[ \mu = m_n = 0 \]
\[ \mu_2 = \alpha(\alpha + 1) \]
\[ \gamma_1 = 0 \]
\[ \gamma_2 = \frac{(\alpha + 2)(\alpha + 3)}{\alpha(\alpha + 1)} - 3 \]
\[ m_d = NA \]

Implementation: `scipy.stats.dgamma`
**Double Weibull Distribution**

This is a signed form of the Weibull distribution.

\[
f(x; c) = \frac{c}{2} |x|^{c-1} \exp(-|x|^c)
\]

\[
F(x; c) = \begin{cases} 
\frac{1}{2} \exp(-|x|^c) & x \leq 0 \\
1 - \frac{1}{2} \exp(-|x|^c) & x > 0 
\end{cases}
\]

\[
G(q; c) = \begin{cases} 
-\log^{1/c} \left( \frac{1}{2q} \right) & q \leq \frac{1}{2} \\
\log^{1/c} \left( \frac{1}{2q-1} \right) & q > \frac{1}{2}
\end{cases}
\]

\[
\mu'_n = \mu_n = \begin{cases} 
\Gamma \left( 1 + \frac{n}{2} \right) & \text{neven} \\
0 & \text{nodd}
\end{cases}
\]

\[
m_d = \mu = 0
\]

\[
\mu_2 = \Gamma \left( \frac{c+2}{c} \right)
\]

\[
\gamma_1 = 0
\]

\[
\gamma_2 = \frac{\Gamma(1 + \frac{4}{c})}{\Gamma^2(1 + \frac{2}{c})}
\]

\[
m_d = \text{NAbimodal}
\]

Implementation: `scipy.stats.dweibull`

**Erlang Distribution**

This is just the Gamma distribution with shape parameter \( \alpha = n \) an integer.

Implementation: `scipy.stats.erlang`

**Exponential Distribution**

This is a special case of the Gamma (and Erlang) distributions with shape parameter \( \alpha = 1 \) and the same location and scale parameters. The standard form is therefore \( x \geq 0 \)

\[
f(x) = e^{-x}
\]

\[
F(x) = \Gamma(1, x) = 1 - e^{-x}
\]

\[
G(q) = -\log(1 - q)
\]

\[
\mu'_n = n!
\]

\[
M(t) = \frac{1}{1 - t}
\]

\[
\mu = 1
\]

\[
\mu_2 = 1
\]

\[
\gamma_1 = 2
\]

\[
\gamma_2 = 6
\]

\[
m_d = 0
\]

\[
h[X] = 1.
\]

Implementation: `scipy.stats.expon`
Exponentiated Weibull Distribution

Two positive shape parameters \( a \) and \( c \) and \( x \in (0, \infty) \)

\[
f(x; a, c) = ac[1 - \exp(-x^c)]^{a-1} \exp(-x^c) x^{c-1}
\]

\[
F(x; a, c) = [1 - \exp(-x^c)]^a
\]

\[
G(q; a, c) = \left[- \log \left(1 - q^{1/a}\right)\right]^{1/c}
\]

Implementation: \texttt{scipy.stats.exponweib}

Exponential Power Distribution

One positive shape parameter \( b \). Defined for \( x \geq 0 \).

\[
f(x; b) = ebx^{b-1} \exp\left[\frac{b}{2b} - e^{bx}\right]
\]

\[
F(x; b) = 1 - \exp\left[1 - e^{bx}\right]
\]

\[
G(q; b) = \log^{1/b} [1 - \log (1 - q)]
\]

Implementation: \texttt{scipy.stats.exponpow}

Fatigue Life (Birnbaum-Saunders) Distribution

This distribution's pdf is the average of the inverse-Gaussian (\( \mu = 1 \)) and reciprocal inverse-Gaussian pdf (\( \mu = 1 \)). We follow the notation of JKB here with \( \beta = S \) for \( x > 0 \)

\[
f(x; c) = \frac{x + 1}{2c\sqrt{2\pi}x^3} \exp\left(-\frac{(x-1)^2}{2xc^2}\right)
\]

\[
F(x; c) = \Phi\left(\frac{1}{c}\left(\sqrt{x} - \frac{1}{\sqrt{x}}\right)\right)
\]

\[
G(q; c) = \frac{1}{4} \left[c\Phi^{-1}(q) + \sqrt{c^2 (\Phi^{-1}(q))^2 + 4}\right]^2
\]

\[
M(t) = c\sqrt{2\pi} \exp\left[\frac{1}{c^2} \left(1 - \sqrt{1 - 2c^2t}\right)\right] \left(1 + \frac{1}{\sqrt{1 - 2c^2t}}\right)
\]

\[
\mu = \frac{c^2}{2} + 1
\]

\[
\mu_2 = c^2 \left(\frac{5}{4}c^2 + 1\right)
\]

\[
\gamma_1 = \frac{4c\sqrt{11c^2 + 6}}{(5c^2 + 4)^{3/2}}
\]

\[
\gamma_2 = \frac{6c^2 (93c^2 + 41)}{(5c^2 + 4)^2}
\]

Implementation: \texttt{scipy.stats.fatiguelife}

Fisk (Log Logistic) Distribution

Special case of the Burr distribution with \( d = 1 \)

\[
c > 0
\]

\[
k = \Gamma\left(1 - \frac{2}{c}\right) \Gamma\left(\frac{2}{c} + 1\right) - \Gamma^2\left(1 - \frac{1}{c}\right) \Gamma^2\left(\frac{1}{c} + 1\right)
\]
\[ f(x; c, d) = \frac{cx^{-1}}{(1 + x^2)^{d/2}}I_{(0, \infty)}(x) \]
\[ F(x; c, d) = (1 + x^{-c})^{-1} \]
\[ G(\alpha; c, d) = (\alpha^{-1} - 1)^{-1/c} \]
\[ \mu = \Gamma \left(1 - \frac{1}{c}\right) \Gamma \left(\frac{1}{c} + 1\right) \]
\[ \mu_2 = k \]
\[ \gamma_1 = \frac{1}{\sqrt{k^3}} \left[ 2\Gamma^3 \left(1 - \frac{1}{c}\right) \Gamma^3 \left(\frac{1}{c} + 1\right) + \Gamma \left(1 - \frac{3}{c}\right) \Gamma \left(\frac{3}{c} + 1\right) -3 \Gamma \left(1 - \frac{2}{c}\right) \Gamma \left(1 - \frac{1}{c}\right) \Gamma \left(\frac{1}{c} + 1\right) \Gamma \left(\frac{2}{c} + 1\right) \right] \]
\[ \gamma_2 = -3 + \frac{1}{k^2} \left[ 6\Gamma \left(1 - \frac{2}{c}\right) \Gamma^2 \left(1 - \frac{1}{c}\right) \Gamma \left(\frac{1}{c} + 1\right) \Gamma \left(\frac{2}{c} + 1\right) -3 \Gamma^4 \left(1 - \frac{1}{c}\right) \Gamma^4 \left(\frac{1}{c} + 1\right) + \Gamma \left(1 - \frac{4}{c}\right) \Gamma \left(\frac{4}{c} + 1\right) \right] \]
\[ m_d = \left(\frac{c - 1}{c + 1}\right)^{1/c} \text{ if } c > 1 \text{ otherwise } 0 \]
\[ m_n = 1 \]
\[ h[X] = 2 - \log c. \]

Implementation: \texttt{scipy.stats.fisk}

**Folded Cauchy Distribution**

This formula can be expressed in terms of the standard formulas for the Cauchy distribution (call the cdf \( C(x) \) and the pdf \( d(x) \)). if \( Y \) is cauchy then \(|Y|\) is folded cauchy. Note that \( x \geq 0 \).

\[ f(x; c) = \frac{1}{\pi (1 + (x - c)^2)} + \frac{1}{\pi (1 + (x + c)^2)} \]
\[ F(x; c) = \frac{1}{\pi} \tan^{-1}(x - c) + \frac{1}{\pi} \tan^{-1}(x + c) \]
\[ G(q; c) = F^{-1}(x; c) \]

No moments

Implementation: \texttt{scipy.stats.foldcauchy}

**Folded Normal Distribution**

If \( Z \) is Normal with mean \( L \) and \( \sigma = S \), then \(|Z|\) is a folded normal with shape parameter \( c = |L|/S \), location parameter 0 and scale parameter \( S \). This is a special case of the non-central chi distribution with one- degree of freedom and non-centrality parameter \( c^2 \). Note that \( c \geq 0 \). The standard form of the folded normal is

\[ f(x; c) = \sqrt{\frac{2}{\pi}} \cosh(cx) \exp \left(-\frac{x^2 + c^2}{2}\right) \]
\[ F(x; c) = \Phi(x - c) - \Phi(-x - c) = \Phi(x - c) + \Phi(x + c) - 1 \]
\[ G(\alpha; c) = F^{-1}(x; c) \]
\[ M(t) = \exp \left[ \frac{t}{2} (t - 2c) \right] (1 + e^{2ct}) \]

\[ k = \text{erf} \left( \frac{c}{\sqrt{2}} \right) \]
\[ p = \exp \left( -\frac{c^2}{2} \right) \]
\[ \mu = \sqrt{\frac{2}{\pi}} p + ck \]
\[ \mu_2 = \frac{c^2 + 1 - \mu^2}{\mu^2} \]
\[ \gamma_1 = \frac{\pi \mu_2^{3/2}}{\sqrt{2\pi}} \left( 4 - \frac{3}{\mu_2^2} \right)(2c^2 + 1) + 2c k (6c^2 + 3c^2 + 6) \left( 2c^2 + 2 + \frac{c k}{\mu} (c^2 + 3) \right) \]
\[ \gamma_2 = \frac{\sqrt{2\pi} \left( 4 - \frac{3}{\mu_2^2} \right)(2c^2 + 1) + 2c k (6c^2 + 3c^2 + 6) \left( 2c^2 + 2 + \frac{c k}{\mu} (c^2 + 3) \right)}{\mu^2} \]

Implementation: \textit{scipy.stats.foldnorm}

\section*{Fratio (or F) Distribution}

Defined for \( x > 0 \). The distribution of \( \left( \frac{X_1}{X_2}, \frac{\nu_2}{\nu_1} \right) \) if \( X_1 \) is chi-squared with \( \nu_1 \) degrees of freedom and \( X_2 \) is chi-squared with \( \nu_2 \) degrees of freedom.

\[ f(x; \nu_1, \nu_2) = \frac{\nu_2^{\nu_1/2} \nu_1^{\nu_2/2} x^{\nu_1/2 - 1}}{\left( \nu_2 + \nu_1 x \right)^{(\nu_1 + \nu_2)/2} \beta \left( \frac{\nu_1}{2}, \frac{\nu_2}{2} \right)} \]
\[ F(x; \nu_1, \nu_2) = I \left( \frac{\nu_1}{2}, \frac{\nu_2}{2}, \frac{\nu_2 x}{\nu_2 + \nu_1 x} \right) \]
\[ G(q; \nu_1, \nu_2) = \left[ \frac{\nu_2}{I^{-1} \left( \frac{\nu_1}{2}, \frac{\nu_2}{2}, q \right)} - \frac{\nu_1}{\nu_2} \right]^{-1} \]

\[ \mu = \frac{\nu_2}{\nu_2 - 2}, \quad \nu_2 > 2 \]
\[ \mu_2 = \frac{2\nu_2 (\nu_1 + \nu_2 - 2)}{\nu_1 (\nu_2 - 2)^2 (\nu_2 - 4)}, \quad \nu_2 > 4 \]
\[ \gamma_1 = \frac{2 (2\nu_1 + \nu_2 - 2)}{\nu_2 - 6} \sqrt{\frac{2 (\nu_2 - 4)}{\nu_1 (\nu_1 + \nu_2 - 2)}}, \quad \nu_2 > 6 \]
\[ \gamma_2 = \frac{3 [8 + (\nu_2 - 6) \gamma_1^2]}{2\nu_2 - 16}, \quad \nu_2 > 8 \]

Implementation: \textit{scipy.stats.f}

\section*{Gamma Distribution}

The standard form for the gamma distribution is \( (\alpha > 0) \) valid for \( x \geq 0 \).

\[ f(x; \alpha) = \frac{1}{\Gamma(\alpha)} x^{\alpha-1} e^{-x} \]
\[ F(x; \alpha) = \Gamma(\alpha, x) \]
\[ G(q; \alpha) = \Gamma^{-1}(\alpha, q) \]
\begin{equation}
M(t) = \frac{1}{(1-t)^\alpha}
\end{equation}
\begin{align*}
\mu &= \alpha \\
\mu_2 &= \alpha \\
\gamma_1 &= \frac{2}{\sqrt{\alpha}} \\
\gamma_2 &= \frac{6}{\alpha} \\
m_d &= \alpha - 1
\end{align*}

\begin{equation}
h[X] = \Psi(a) \left[ 1 - a \right] + a + \log \Gamma(a)
\end{equation}

where

\begin{equation}
\Psi(a) = \frac{\Gamma'(a)}{\Gamma(a)}
\end{equation}

Implementation: \texttt{scipy.stats.gamma}

**Generalized Logistic Distribution**

Has been used in the analysis of extreme values. Has one shape parameter \( c > 0 \). And \( x > 0 \)

\begin{align*}
f(x; c) &= \frac{c \exp(-x)}{[1 + \exp(-x)]^{c+1}} \\
F(x; c) &= \frac{1}{[1 + \exp(-x)]^\alpha} \\
G(q; c) &= -\log \left( q^{-1/c} - 1 \right)
\end{align*}

\begin{equation}
M(t) = \frac{c}{1-t} 2F_1 (1+c, 1-t; 2-t; -1)
\end{equation}

\begin{align*}
\mu &= \gamma + \psi_0 (c) \\
\mu_2 &= \frac{\pi^2}{6} + \psi_1 (c) \\
\gamma_1 &= \frac{\psi_2 (c) + 2\zeta (3)}{\mu_2^{3/2}} \\
\gamma_2 &= \frac{\left( \frac{\pi^4}{12} + \psi_3 (c) \right)}{\mu_2^2} \\
m_d &= \log c \\
m_n &= -\log \left( 2^{1/c} - 1 \right)
\end{align*}

Note that the polygamma function is

\begin{equation}
\psi_n (z) = \frac{d^{n+1}}{dz^{n+1}} \log \Gamma(z)
\end{equation}

\begin{align*}
&= (-1)^{n+1} n! \sum_{k=0}^{\infty} \frac{1}{(z+k)^{n+1}} \\
&= (-1)^{n+1} n! \zeta(n+1, z)
\end{align*}

where \( \zeta(k, x) \) is a generalization of the Riemann zeta function called the Hurwitz zeta function. Note that \( \zeta(n) \equiv \zeta(n, 1) \)

Implementation: \texttt{scipy.stats.genlogistic}
Generalized Pareto Distribution

Shape parameter $c \neq 0$ and defined for $x \geq 0$ for all $c$ and $x < \frac{1}{|c|}$ if $c$ is negative.

\[
\begin{align*}
    f(x; c) & = (1 + cx)^{-1 - \frac{1}{c}} \\
    F(x; c) & = 1 - \frac{1}{(1 + cx)^{1/c}} \\
    G(q; c) & = \frac{1}{c} \left[ \left( \frac{1}{1 - q} \right)^{c} - 1 \right]
\end{align*}
\]

\[
M(t) = \begin{cases} 
    (\frac{-1}{c})^\frac{1}{c} e^{-\frac{1}{c}} \Gamma \left( 1 - \frac{1}{c} \right) + \Gamma \left( \frac{1}{c}, -\frac{1}{c} \right) - \pi \csc \left( \frac{\pi}{c} \right) / \Gamma \left( \frac{1}{c} \right) & c > 0 \\
    (\frac{|c|}{c})^{1/|c|} \Gamma \left[ 1, \frac{1}{|c|} \right] & c < 0
\end{cases}
\]

\[
\mu'_n = \frac{(-1)^n}{c^n} \sum_{k=0}^{n} \left( \frac{n}{k} \right) \frac{(-1)^k}{1 - ck} \quad cn < 1
\]

\[
\begin{align*}
    \mu'_1 & = \frac{1}{1 - c} \quad c < 1 \\
    \mu'_2 & = \frac{2}{(1 - 2c)(1 - c)} \quad c < \frac{1}{2} \\
    \mu'_3 & = \frac{6}{(1 - c)(1 - 2c)(1 - 3c)} \quad c < \frac{1}{3} \\
    \mu'_4 & = \frac{24}{(1 - c)(1 - 2c)(1 - 3c)(1 - 4c)} \quad c < \frac{1}{4}
\end{align*}
\]

Thus,

\[
\begin{align*}
    \mu & = \mu'_1 \\
    \mu_2 & = \mu'_2 - \mu^2 \\
    \gamma_1 & = \mu'_3 - 3\mu_2 - \mu^3 \\
    \gamma_2 & = \mu'_4 - 4\mu_3 - 6\mu^2\mu_2 - \mu^4
\end{align*}
\]

\[
h[X] = 1 + c \quad c > 0
\]

Implementation: \texttt{scipy.stats.genpareto}

Generalized Exponential Distribution

Three positive shape parameters for $x \geq 0$. Note that $a$, $b$, and $c$ are all $> 0$.

\[
\begin{align*}
    f(x; a, b, c) & = (a + b (1 - e^{-cx})) \exp \left( ax - bx + \frac{b}{c} (1 - e^{-cx}) \right) \\
    F(x; a, b, c) & = 1 - \exp \left( ax - bx + \frac{b}{c} (1 - e^{-cx}) \right) \\
    G(q; a, b, c) & = F^{-1}
\end{align*}
\]

Implementation: \texttt{scipy.stats.genexpon}
Generalized Extreme Value Distribution

Extreme value distributions with shape parameter \( c \).

For \( c > 0 \) defined on \(-\infty < x \leq 1/c\).

\[
\begin{align*}
    f(x;c) &= \exp \left[ - (1 - cx)^{1/c} \right] (1 - cx)^{1/c - 1} \\
    F(x;c) &= \exp \left[ - (1 - cx)^{1/c} \right] \\
    G(q;c) &= \frac{1}{c} \left[ 1 - (-\log q)^c \right]
\end{align*}
\]

\[
\mu'_n = \frac{1}{cn} \sum_{k=0}^{n} \binom{n}{k} (1 - 1/c) ^ k \Gamma(ck + 1) \quad cn > -1
\]

So,

\[
\begin{align*}
    \mu'_1 &= \frac{1}{c} (1 - \Gamma(1 + c)) \quad c > -1 \\
    \mu'_2 &= \frac{1}{c^2} (1 - 2\Gamma(1 + c) + \Gamma(1 + 2c)) \quad c > -\frac{1}{2} \\
    \mu'_3 &= \frac{1}{c^3} (1 - 3\Gamma(1 + c) + 3\Gamma(1 + 2c) - \Gamma(1 + 3c)) \quad c > -\frac{1}{3} \\
    \mu'_4 &= \frac{1}{c^4} (1 - 4\Gamma(1 + c) + 6\Gamma(1 + 2c) - 4\Gamma(1 + 3c) + \Gamma(1 + 4c)) \quad c > -\frac{1}{4}
\end{align*}
\]

For \( c < 0 \) defined on \( \frac{1}{c} \leq x < \infty \). For \( c = 0 \) defined over all space

\[
\begin{align*}
    f(x;0) &= \exp \left[ -e^{-x} \right] e^{-x} \\
    F(x;0) &= \exp \left[ -e^{-x} \right] \\
    G(q;0) &= -\log (-\log q)
\end{align*}
\]

This is just the (left-skewed) Gumbel distribution for \( c=0 \).

\[
\begin{align*}
    \mu &= \gamma = -\psi_0(1) \\
    \mu_2 &= \frac{\pi^2}{6} \\
    \gamma_1 &= \frac{12\sqrt{6}}{\pi^3} \zeta(3) \\
    \gamma_2 &= \frac{12}{5}
\end{align*}
\]

Implementation: \texttt{scipy.stats.genextreme}

Generalized Gamma Distribution

A general probability form that reduces to many common distributions: \( x > 0 \ a > 0 \) and \( c \neq 0 \).

\[
\begin{align*}
    f(x;a,c) &= \frac{|c| \cdot x^{ca-1}}{\Gamma(a)} \exp (-x^c) \\
    F(x;a,c) &= \frac{\Gamma(a,x^c)}{\Gamma(a)} \quad c > 0 \\
    G(q;a,c) &= \left\{ \Gamma^{-1} [a, \Gamma(a) q] \right\}^{1/c} \quad c > 0 \\
    G(q;a,c) &= \left\{ \Gamma^{-1} [a, \Gamma(a) (1 - q)] \right\}^{1/c} \quad c < 0
\end{align*}
\]
\[ \mu'_{n} = \frac{\Gamma\left(a + \frac{n}{c}\right)}{\Gamma(a)} \]

\[ \mu = \frac{\Gamma\left(a + \frac{1}{c}\right)}{\Gamma(a)} \]

\[ \mu_2 = \frac{\Gamma\left(a + \frac{2}{c}\right)}{\Gamma(a)} - \mu^2 \]

\[ \gamma_1 = \frac{\Gamma\left(a + \frac{3}{c}\right) / \Gamma(a) - 3\mu_2 - \mu^3}{\mu_2^{3/2}} \]

\[ \gamma_2 = \frac{\Gamma\left(a + \frac{4}{c}\right) / \Gamma(a) - 4\mu_3 - 6\mu^2\mu_2 - \mu^4}{\mu_2^2} - 3 \]

\[ m_d = \left( \frac{ac - 1}{c} \right)^{1/c} \]

Special cases are Weibull \((a = 1)\), half-normal \((a = 1/2, c = 2)\) and ordinary gamma distributions \(c = 1\). If \(c = -1\) then it is the inverted gamma distribution.

\[ h[X] = a - a \Psi(a) + \frac{1}{c} \Psi(a) + \log \Gamma(a) - \log |c|. \]

Implementation: \texttt{scipy.stats.gengamma}

**Generalized Half-Logistic Distribution**

For \(x \in [0, 1/c]\) and \(c > 0\) we have

\[ f(x;c) = \frac{2 (1 - cx)^{\frac{1}{c} - 1}}{\left(1 + (1 - cx)^{1/c}\right)^2} \]

\[ F(x;c) = \frac{1 - (1 - cx)^{1/c}}{1 + (1 - cx)^{1/c}} \]

\[ G(q;c) = \frac{1}{c} \left[ 1 - \left( \frac{1 - q}{1 + q} \right)^c \right] \]

\[ h[X] = 2 - (2c + 1) \log 2. \]

Implementation: \texttt{scipy.stats.genhalflogistic}

**Generalized Normal Distribution**

This distribution is also known as the exponential power distribution. It has a single shape parameter \(\beta > 0\). It reduces to a number of common distributions.

**Functions**

\[ f(x;\beta) = \frac{\beta}{2\Gamma(1/\beta)} e^{-|x|^\beta} \]

\[ F(x;\beta) = \frac{1}{2} + \text{sgn}(x) \frac{\gamma\left(1/\beta, x^\beta\right)}{2\Gamma(1/\beta)} \]

\(\gamma\) is the lower incomplete gamma function. \(\gamma(s,x) = \int_0^x t^{s-1} e^{-t} dt\)

\[ h[X;\beta] = \frac{1}{\beta} - \log \left[ \frac{\beta}{2\Gamma(1/\beta)} \right] \]
Moments

\[
\begin{align*}
\mu &= 0 \\
m_n &= 0 \\
m_d &= 0 \\
\mu_2 &= \frac{\Gamma(3/\beta)}{\gamma(1/\beta)} \\
\gamma_1 &= 0 \\
\gamma_2 &= \frac{\Gamma(5/\beta) \Gamma(1/\beta)}{\Gamma(3/\beta)^2} - 3
\end{align*}
\]

Special Cases

- Laplace distribution \((\beta = 1)\)
- Normal distribution with \(\mu_2 = 1/2 \ (\beta = 2)\)
- Uniform distribution over the interval \([-1, 1]\) \((\beta \to \infty)\)

Sources

- https://en.wikipedia.org/wiki/Generalized_normal_distribution#Version_1
- https://en.wikipedia.org/wiki/Incomplete_gamma_function#Lower_incomplete_Gamma_function

Implementation: `scipy.stats.gennorm`

Gilbrat Distribution

Special case of the log-normal with \(\sigma = 1\) and \(S = 1.0\) (typically also \(L = 0.0\))

\[
\begin{align*}
f(x; \sigma) &= \frac{1}{x \sqrt{2\pi}} \exp\left[-\frac{1}{2} (\log x)^2\right] \\
F(x; \sigma) &= \Phi(\log x) = \frac{1}{2} \left[1 + \text{erf}\left(\frac{\log x}{\sqrt{2}}\right)\right] \\
G(q; \sigma) &= \exp\{\Phi^{-1}(q)\} \\
\mu &= \sqrt{e} \\
\mu_2 &= e [e - 1] \\
\gamma_1 &= \sqrt{e} - 1 (2 + e) \\
\gamma_2 &= e^4 + 2e^3 + 3e^2 - 6
\end{align*}
\]

\[
h[X] = \log \left(\sqrt{2\pi e}\right) \\
\approx 1.4189385332046727418
\]

Implementation: `scipy.stats.gilbrat`
**Gompertz (Truncated Gumbel) Distribution**

For $x \geq 0$ and $c > 0$. In JKB the two shape parameters $b, a$ are reduced to the single shape-parameter $c = b/a$. As $a$ is just a scale parameter when $a \neq 0$. If $a = 0$, the distribution reduces to the exponential distribution scaled by $1/b$. Thus, the standard form is given as

$$f(x; c) = ce^x \exp[-c(e^x - 1)]$$

$$F(x; c) = 1 - \exp[-c(e^x - 1)]$$

$$G(q; c) = \log \left[ 1 - \frac{1}{c}\log(1 - q) \right]$$

$$h[X] = 1 - \log(c) - e^{c} \text{Ei}(1, c),$$

where

$$\text{Ei}(n, x) = \int_1^\infty t^{-n} \exp(-xt) \, dt$$

Implementation: `scipy.stats.gompertz`

**Gumbel (LogWeibull, Fisher-Tippetts, Type I Extreme Value) Distribution**

One of a class of extreme value distributions (right-skewed).

$$f(x) = \exp \left( - (x + e^{-x}) \right)$$

$$F(x) = \exp \left( -e^{-x} \right)$$

$$G(q) = -\log(-\log(q))$$

$$M(t) = \Gamma (1 - t)$$

$$\mu = \gamma = -\psi_0(1)$$

$$\mu_2 = \frac{\pi^2}{6}$$

$$\gamma_1 = \frac{12\sqrt{6}}{\pi^3}\zeta(3)$$

$$\gamma_2 = \frac{12}{5}$$

$$m_d = 0$$

$$m_n = -\log(\log 2)$$

$$h[X] \approx 1.0608407169541684911$$

Implementation: `scipy.stats.gumbel_r`

**Gumbel Left-skewed (for minimum order statistic) Distribution**

$$f(x) = \exp(x - e^x)$$

$$F(x) = 1 - \exp(-e^x)$$

$$G(q) = \log(-\log(1 - q))$$

$$M(t) = \Gamma (1 + t)$$

Note, that $\mu$ is negative the mean for the right-skewed distribution. Similar for median and mode. All other moments are the same.

$$h[X] \approx 1.0608407169541684911.$$
HalfCauchy Distribution

If \( Z \) is Hyperbolic Secant distributed then \( e^Z \) is Half-Cauchy distributed. Also, if \( W \) is (standard) Cauchy distributed, then \( |W| \) is Half-Cauchy distributed. Special case of the Folded Cauchy distribution with \( c = 0 \). The standard form is

\[
\begin{align*}
    f(x) &= \frac{2}{\pi (1 + x^2)} I_{[0,\infty)}(x) \\
    F(x) &= \frac{2}{\pi} \arctan(x) I_{[0,\infty]}(x) \\
    G(q) &= \tan\left(\frac{\pi}{2} q\right) \\
    M(t) &= \cos t + \frac{2}{\pi} \left[ \text{Si}(t) \cos t - \text{Ci}(-t) \sin t \right] \\
    m_d &= 0 \\
    m_n &= \tan\left(\frac{\pi}{4}\right)
\end{align*}
\]

No moments, as the integrals diverge.

\[
\begin{align*}
    h[X] &= \log\left(2\pi\right) \\
    &\approx 1.8378770664093454836.
\end{align*}
\]

Implementation: \texttt{scipy.stats.halfcauchy}

HalfNormal Distribution

This is a special case of the chi distribution with \( L = a \) and \( S = b \) and \( \nu = 1 \). This is also a special case of the folded normal with shape parameter \( c = 0 \) and \( S = S \). If \( Z \) is (standard) normally distributed then, \( |Z| \) is half-normal. The standard form is

\[
\begin{align*}
    f(x) &= \sqrt{\frac{2}{\pi}} e^{-x^2/2} I_{[0,\infty)}(x) \\
    F(x) &= 2\Phi(x) - 1 \\
    G(q) &= \Phi^{-1}\left(\frac{1 + q}{2}\right) \\
    M(t) &= \sqrt{2\pi} e^{t^2/2} \Phi(t) \\
    \mu &= \sqrt{\frac{2}{\pi}} \\
    \mu_2 &= 1 - \frac{2}{\pi} \\
    \gamma_1 &= \sqrt{2} \frac{4 - \pi}{(\pi - 2)^{3/2}} \\
    \gamma_2 &= \frac{8 (\pi - 3)}{(\pi - 2)^2} \\
    m_d &= 0 \\
    m_n &= \Phi^{-1}\left(\frac{3}{4}\right)
\end{align*}
\]

\[
\begin{align*}
    h[X] &= \log\left(\sqrt{\frac{\pi e}{2}}\right) \\
    &\approx 0.72579135264472743239.
\end{align*}
\]

Implementation: \texttt{scipy.stats.halfnorm}
Half-Logistic Distribution

In the limit as $c \to \infty$ for the generalized half-logistic we have the half-logistic defined over $x \geq 0$. Also, the distribution of $|X|$ where $X$ has logistic distribution.

$$\begin{align*}
f(x) &= \frac{2e^{-x}}{(1 + e^{-x})^2} = \frac{1}{2} \text{sech}^2 \left( \frac{x}{2} \right) \\
F(x) &= \frac{1 - e^{-x}}{1 + e^{-x}} = \tanh \left( \frac{x}{2} \right) \\
G(q) &= \log \left( \frac{1 + q}{1 - q} \right) = 2 \tanh^{-1}(q) \\
M(t) &= 1 - t \psi_0 \left( \frac{1}{2} - \frac{t}{2} \right) + t \psi_0 \left( 1 - \frac{t}{2} \right) \\
\mu'_n &= 2 \left( 1 - 2^{1-n} \right) n! \zeta(n) \quad n \neq 1 \\
\mu'_1 &= 2 \log(2) \\
\mu'_2 &= 2\zeta(2) = \frac{\pi^2}{3} \\
\mu'_3 &= 9\zeta(3) \\
\mu'_4 &= 42\zeta(4) = \frac{7\pi^4}{15}
\end{align*}$$

$$h[X] = 2 - \log(2) \approx 1.3068528194400546906.$$ 

Implementation: `scipy.stats.halflogistic`

Hyperbolic Secant Distribution

Related to the logistic distribution and used in lifetime analysis. Standard form is (defined over all $x$)

$$\begin{align*}
f(x) &= \frac{1}{\pi} \text{sech}(x) \\
F(x) &= \frac{2}{\pi} \arctan(e^x) \\
G(q) &= \log \left( \tan \left( \frac{\pi}{2} q \right) \right) \\
M(t) &= \sec \left( \frac{\pi t}{2} \right) \\
\mu'_n &= \frac{1 + (-1)^n}{2\pi 2^{2n}} n! \left[ \zeta \left( n + 1, \frac{1}{4} \right) - \zeta \left( n + 1, \frac{3}{4} \right) \right] \\
&= \left\{ \begin{array}{ll}
0 & \text{n odd} \\
C_{n/2} \frac{\pi^{n}}{2^n} & \text{n even}
\end{array} \right.
\end{align*}$$

where $C_m$ is an integer given by

$$C_m = \frac{(2m)! \left[ \zeta \left( 2m + 1, \frac{1}{4} \right) - \zeta \left( 2m + 1, \frac{3}{4} \right) \right]}{\pi^{2m+1} 2^{2m}}$$

$$= 4 (-1)^{m-1} \frac{16^m}{2m + 1} B_{2m+1} \left( \frac{1}{4} \right)$$

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where $B_{2m+1}\left(\frac{1}{4}\right)$ is the Bernoulli polynomial of order $2m + 1$ evaluated at $1/4$. Thus

$$
\mu'_n = \begin{cases} 
0 & \text{nodd} \\
4(-1)^{n/2-1}\left(\frac{\pi}{4}\right)^n B_{n+1}\left(\frac{1}{4}\right) & \text{neven}
\end{cases}
$$

$$m_d = m_n = \mu = 0$$

$$\mu_2 = \frac{\pi^2}{4}$$

$$\gamma_1 = 0$$

$$\gamma_2 = 2$$

$$h[X] = \log(2\pi).$$

Implementation: `scipy.stats.hypsecant`

Gauss Hypergeometric Distribution

$x \in [0, 1], \alpha > 0, \beta > 0$

$$C^{-1} = B(\alpha, \beta) \, _2F_1(\gamma; \alpha + \beta; -z)$$

$$f(x; \alpha, \beta, \gamma, z) = Cx^{a-1}(1-x)^{\beta-1}(1+zx)^{-\gamma}$$

$$\mu'_n = \frac{B(n + \alpha, \beta)}{B(\alpha, \beta)} \, _2F_1(\gamma, \alpha + n; \alpha + \beta + n; -z)$$

Implementation: `scipy.stats.gausshyper`

Inverted Gamma Distribution

Special case of the generalized Gamma distribution with $c = -1$ and $a > 0$, $x > 0$

$$f(x; a) = x^{a-1} \frac{\exp\left(-\frac{1}{x}\right)}{\Gamma(a)}$$

$$F(x; a) = \frac{\Gamma\left(a, \frac{1}{x}\right)}{\Gamma(a)}$$

$$G(q; a) = \left\{\Gamma^{-1}[a, \Gamma(a)q]\right\}^{-1}$$

$$\mu'_n = \frac{\Gamma(a-n)}{\Gamma(a)} \quad a > n$$

$$\mu = \frac{1}{a-1} \quad a > 1$$

$$\mu_2 = \frac{1}{(a-2)(a-1)} - \mu^2 \quad a > 2$$

$$\gamma_1 = \frac{1}{(a-3)(a-2)(a-1)} - 3\mu_2 - \mu^3$$

$$\gamma_2 = \frac{1}{(a-4)(a-3)(a-2)(a-1)} - 4\mu_3 - 6\mu^2\mu_2 - \mu^4 - 3$$

$$m_d = \frac{1}{a+1}$$

$$h[X] = a - (a + 1) \Psi(a) + \log \Gamma(a).$$

Implementation: `scipy.stats.invgamma`
Inverse Normal (Inverse Gaussian) Distribution

The standard form involves the shape parameter $\mu$ (in most definitions, $L = 0$ is used). (In terms of the regress documentation $\mu = A/B$) and $B = S$ and $L$ is not a parameter in that distribution. A standard form is $x > 0$

$$f(x; \mu) = \frac{1}{\sqrt{2\pi}x^3} \exp\left(-\frac{(x - \mu)^2}{2x\mu^2}\right).$$

$$F(x; \mu) = \Phi\left(\frac{1}{\sqrt{x}} - \frac{x}{\mu}\right) + \exp\left(\frac{1}{\mu}\right) \Phi\left(-\frac{1}{\sqrt{x}} + \frac{x}{\mu}\right)$$

$$G(q; \mu) = F^{-1}(q; \mu)$$

$$\mu = \mu$$

$$\mu_2 = \mu^3$$

$$\gamma_1 = 3\sqrt{\mu}$$

$$\gamma_2 = 15\mu$$

$$m_d = \frac{\mu}{2} \left(\sqrt{9\mu^2 + 4} - 3\mu\right)$$

This is related to the canonical form or JKB “two-parameter” inverse Gaussian when written in it’s full form with scale parameter $S$ and location parameter $L$ by taking $L = 0$ and $S = \lambda$, then $\mu S$ is equal to $\mu_2$ where $\mu_2$ is the parameter used by JKB. We prefer this form because of it’s consistent use of the scale parameter. Notice that in JKB the skew $(\sqrt{\beta_1})$ and the kurtosis $(\beta_2 - 3)$ are both functions only of $\mu_2/\lambda = \mu S / S = \mu$ as shown here, while the variance and mean of the standard form here are transformed appropriately.

Implementation: \textit{scipy.stats.invgauss}

Inverted Weibull Distribution

Shape parameter $c > 0$ and $x > 0$. Then

$$f(x; c) = cx^{c-1} \exp(-x^c)$$

$$F(x; c) = \exp(-x^c)$$

$$G(q; c) = (-\log q)^{-1/c}$$

$$h[X] = 1 + \gamma + \frac{\gamma}{c} - \log(c)$$

where $\gamma$ is Euler’s constant.

Implementation: \textit{scipy.stats.invweibull}

Johnson SB Distribution

Defined for $x \in (0, 1)$ with two shape parameters $a$ and $b > 0$.

$$f(x; a, b) = \frac{b}{x(1-x)} \phi\left(a + b \log \frac{x}{1-x}\right)$$

$$F(x; a, b) = \Phi\left(a + b \log \frac{x}{1-x}\right)$$

$$G(q; a, b) = \frac{1}{1 + \exp\left[-\frac{1}{b} (\Phi^{-1}(q) - a)\right]}$$

Implementation: \textit{scipy.stats.johnsonsb}
Johnson SU Distribution

Defined for all $x$ with two shape parameters $a$ and $b > 0$.

$$f(x; a, b) = \frac{b}{\sqrt{x^2 + 1}} \phi \left( a + b \log \left( x + \sqrt{x^2 + 1} \right) \right)$$

$$F(x; a, b) = \Phi \left( a + b \log \left( x + \sqrt{x^2 + 1} \right) \right)$$

$$G(q; a, b) = \sinh \left[ \Phi^{-1} \left( q - a \right) \frac{b}{a} \right]$$

Implementation: `scipy.stats.johnsonsu`

KSone Distribution

This is the distribution of maximum positive differences between an empirical distribution function, computed from $n$ samples or observations, and a comparison (or target) cumulative distribution function. Writing $D^+_n = \sup_t (F_{\text{empirical}, n}(t) - F_{\text{target}}(t))$, `ksone` is the distribution of the $D^+_n$ values. (The distribution of $D^-_n = \sup_t (F_{\text{target}}(t) - F_{\text{empirical}, n}(t))$ differences follows the same distribution, so `ksone` can be used for one-sided tests on either side.)

There is one shape parameter $n$, a positive integer, and the support is $x \in [0, 1]$.

$$F(n, x) = 1 - \sum_{j=0}^{\left\lfloor n(1-x) \right\rfloor} \binom{n}{j} x^j \left( 1 - \frac{j}{n} \right)^{n-j}$$

$$\lim_{n \to \infty} F \left( n, \frac{x}{\sqrt{n}} \right) = e^{-2x^2}$$

References


Implementation: `scipy.stats.ksone`

KStwo Distribution

This is the limiting distribution of the normalized maximum absolute differences between an empirical distribution function, computed from $n$ samples or observations, and a comparison (or target) cumulative distribution function. (`ksone` is the distribution of the unnormalized positive differences, $D^+_n$.)

Writing $D_n = \sup_t |F_{\text{empirical}, n}(t) - F_{\text{target}}(t)|$, the normalization factor is $\sqrt{n}$, and `kstwobign` is the limiting distribution of the $\sqrt{n}D_n$ values as $n \to \infty$.

Note that $D_n = \max(D^+_n, D^-_n)$, but $D^+_n$ and $D^-_n$ are not independent.

`kstwobign` can also be used with the differences between two empirical distribution functions, for sets of observations with $m$ and $n$ samples respectively, where $m$ and $n$ are “big”. Writing $D_{m,n} = \sup_t |F_{1,m}(t) - F_{2,n}(t)|$, where $F_{1,m}$ and $F_{2,n}$ are the two empirical distribution functions, then `kstwobign` is also the limiting distribution of the $\sqrt{\frac{mn}{m+n}}D_{m,n}$ values, as $m, n \to \infty$. 

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There are no shape parameters, and the support is $x \in [0, \infty)$.

\[
F(x) = 1 - 2 \sum_{k=1}^{\infty} (-1)^{k-1} e^{-2k^2 x^2}
\]

\[
= \frac{\sqrt{2\pi}}{x} \sum_{k=1}^{\infty} e^{-(2k-1)^2 x^2/(8x^2)}
\]

\[
= 1 - \text{scipy.special.kolmogorov}(n, x)
\]

\[
f(x) = 8x \sum_{k=1}^{\infty} (-1)^{k-1} k^2 e^{-2k^2 x^2}
\]

References


Implementation: scipy.stats.kstwobign

Laplace (Double Exponential, Bilateral Exponential) Distribution

\[
f(x) = \frac{1}{2} e^{-|x|}
\]

\[
F(x) = \begin{cases} 
\frac{1}{2} e^x & x \leq 0 \\
1 - \frac{1}{2} e^{-x} & x > 0
\end{cases}
\]

\[
G(q) = \begin{cases} 
\log (2q) & q \leq \frac{1}{2} \\
-\log (2-2q) & q > \frac{1}{2}
\end{cases}
\]

\[
m_d = m_n = \mu = 0 \\
\mu_2 = 2 \\
\gamma_1 = 0 \\
\gamma_2 = 3
\]

The ML estimator of the location parameter is

\[
\hat{L} = \text{median} (X_i)
\]

where $X_i$ is a sequence of $N$ mutually independent Laplace RV’s and the median is some number between the $\frac{1}{2}N$th and the $(N/2 + 1)$th order statistic (e.g. take the average of these two) when $N$ is even. Also,

\[
\hat{S} = \frac{1}{N} \sum_{j=1}^{N} |X_j - \hat{L}|
\]

Replace $\hat{L}$ with $L$ if it is known. If $L$ is known then this estimator is distributed as $(2N)^{-1} S \cdot \chi_{2N}^2$.

\[
h(X) = \log (2e) \\
\approx 1.6931471805599453094.
\]

Implementation: scipy.stats.laplace
Left-skewed Lévy Distribution

Special case of Lévy-stable distribution with $\alpha = \frac{1}{2}$ and $\beta = -1$ the support is $x < 0$. In standard form
\[
f(x) = \frac{1}{|x| \sqrt{2\pi |x|}} \exp \left( -\frac{1}{2} \frac{1}{|x|} \right) \\
F(x) = 2\Phi \left( \frac{1}{\sqrt{|x|}} \right) - 1 \\
G(q) = -\left[ \Phi^{-1} \left( \frac{q + 1}{2} \right) \right]^{-2}.
\]
No moments.
Implementation: `scipy.stats.levy_l`

Lévy Distribution

A special case of Lévy-stable distributions with $\alpha = \frac{1}{2}$ and $\beta = 1$. In standard form it is defined for $x > 0$ as
\[
f(x) = \frac{1}{x \sqrt{2\pi x}} \exp \left( -\frac{1}{2} \frac{1}{x} \right) \\
F(x) = 2 \left[ 1 - \Phi \left( \frac{1}{\sqrt{x}} \right) \right] \\
G(q) = \left[ \Phi^{-1} \left( 1 - \frac{q}{2} \right) \right]^{-2}.
\]
It has no finite moments.
Implementation: `scipy.stats.levy`

Logistic (Sech-squared) Distribution

A special case of the Generalized Logistic distribution with $c = 1$. Defined for $x > 0$
\[
f(x) = \frac{\exp(-x)}{[1 + \exp(-x)]^2} \\
F(x) = \frac{1}{1 + \exp(-x)} \\
G(q) = -\log(1/q - 1) \\
\mu = \gamma + \psi_0(1) = 0 \\
\mu_2 = \frac{\pi^2}{6} + \psi_1(1) = \frac{\pi^2}{3} \\
\gamma_1 = \psi_2(c) + 2\zeta(3) = 0 \\
\gamma_2 = \frac{\psi_4(c)}{\mu_2^2} = \frac{6}{5} \\
m_d = \log 1 = 0 \\
m_n = -\log (2 - 1) = 0 \\
h[X] = 1.
\]
Implementation: `scipy.stats.logistic`
Log Double Exponential (Log-Laplace) Distribution

Defined over \( x > 0 \) with \( c > 0 \)

\[
\begin{align*}
    f(x; c) &= \begin{cases} 
        \frac{c}{2} x^{c-1} & 0 < x < 1 \\
        \frac{1}{2} x^{-c} & x \geq 1
    \end{cases} \\
    F(x; c) &= \begin{cases} 
        \frac{c}{2} x^{c} & 0 < x < 1 \\
        1 - \frac{1}{2} x^{-c} & x \geq 1
    \end{cases} \\
    G(q; c) &= \begin{cases} 
        (2q)^{1/c} & 0 \leq q < \frac{1}{2} \\
        (2 - 2q)^{-1/c} & \frac{1}{2} \leq q \leq 1
    \end{cases}
\end{align*}
\]

\[
h[X] = \log \left( \frac{2c}{c} \right)
\]

Implementation: \texttt{scipy.stats.loglaplace}

Log Gamma Distribution

A single shape parameter \( c > 0 \) (Defined for all \( x \))

\[
\begin{align*}
    f(x; c) &= \exp \left( cx - e^x \right) / \Gamma(c) \\
    F(x; c) &= \frac{\Gamma(c, e^x)}{\Gamma(c)} \\
    G(q; c) &= \log \left[ \Gamma^{-1} [c, q\Gamma (c)] \right]
\end{align*}
\]

\[
\begin{align*}
    &\mu_n' = \int_0^\infty [\log y]^n y^{c-1} \exp (-y) dy, \\
    &\mu_1 = \mu_1' \\
    &\mu_2 = \mu_2' - \mu^2 \\
    &\gamma_1 = \frac{\mu_4' - 3\mu_2^2 - \mu^3}{\mu_2^{3/2}} \\
    &\gamma_2 = \frac{\mu_4' - 4\mu_2^2 - 6\mu^2 - \mu^4 - 3}{\mu_2^2}
\end{align*}
\]

Implementation: \texttt{scipy.stats.loggamma}

Log Normal (Cobb-Douglas) Distribution

Has one shape parameter \( \sigma > 0 \). (Notice that the “Regress “\( A = \log S \) where \( S \) is the scale parameter and \( A \) is the mean of the underlying normal distribution). The standard form is \( x > 0 \)

\[
\begin{align*}
    f(x; \sigma) &= \frac{1}{\sigma \sqrt{2\pi}} \exp \left[ -\frac{1}{2} \left( \frac{\log x - \mu}{\sigma} \right)^2 \right] \\
    F(x; \sigma) &= \Phi \left( \frac{\log x}{\sigma} \right) \\
    G(q; \sigma) &= \exp \left\{ \sigma \Phi^{-1} (q) \right\}
\end{align*}
\]

\[
\begin{align*}
    \mu &= \exp (\sigma^2/2) \\
    \mu_2 &= \exp (\sigma^2) \left[ \exp (\sigma^2) - 1 \right] \\
    \gamma_1 &= \sqrt{p - 1} (2 + p) \\
    \gamma_2 &= p^4 + 2p^3 + 3p^2 - 6 \quad p = e^{\sigma^2}
\end{align*}
\]
Notice that using JKB notation we have \( \theta = L, \ \zeta = \log S \) and we have given the so-called antilognormal form of the distribution. This is more consistent with the location, scale parameter description of general probability distributions.

\[
h [X] = \frac{1}{2} [1 + \log (2\pi) + 2 \log (\sigma)].
\]

Also, note that if \( X \) is a log-normally distributed random-variable with \( L = 0 \) and \( S \) and shape parameter \( \sigma \). Then, \( \log X \) is normally distributed with variance \( \sigma^2 \) and mean \( \log S \).

Implementation: `scipy.stats.lognorm`

**Maxwell Distribution**

This is a special case of the Chi distribution with \( L = 0 \) and \( S = S = \frac{1}{\sqrt{\pi}} \) and \( \nu = 3 \).

\[
\begin{align*}
f (x) &= \sqrt{\frac{2}{\pi}} \frac{x^2 e^{-x^2/2}}{I_{(0,\infty)} (x)} \\
F (x) &= \Gamma \left( \frac{3}{2}, \frac{x^2}{2} \right) \\
G (\alpha) &= \sqrt{2 \Gamma^{-1} \left( \frac{3}{2}, \alpha \right)}
\end{align*}
\]

\[
\begin{align*}
\mu &= 2 \sqrt{\frac{2}{\pi}} \\
\mu_2 &= 3 - \frac{8}{\pi} \\
\gamma_1 &= \sqrt{2} \frac{32 - 10\pi}{(3\pi - 8)^{3/2}} \\
\gamma_2 &= - \frac{12\pi^2 + 160\pi - 384}{(3\pi - 8)^2} \\
m_d &= \sqrt{2} \\
m_n &= \sqrt{2 \Gamma^{-1} \left( \frac{3}{2}, \frac{1}{2} \right)}
\end{align*}
\]

\[
h [X] = \log \left( \sqrt{\frac{2\pi}{e}} \right) + \gamma.
\]

Implementation: `scipy.stats.maxwell`

**Mielke’s Beta-Kappa Distribution**

A generalized F distribution. Two shape parameters \( \kappa \) and \( \theta \), and \( x > 0 \). The \( \beta \) in the DATAPLOT reference is a scale parameter.

\[
\begin{align*}
f (x; \kappa, \theta) &= \frac{\kappa x^{\kappa - 1}}{(1 + x^\theta)^{1 + \frac{\kappa}{\theta}}} \\
F (x; \kappa, \theta) &= \frac{x^\kappa}{(1 + x^\theta)^{\kappa/\theta}} \\
G (q; \kappa, \theta) &= \left( \frac{q^{\theta/\kappa}}{1 - q^{\theta/\kappa}} \right)^{1/\theta}
\end{align*}
\]

Implementation: `scipy.stats.mielke`
Nakagami Distribution

Generalization of the chi distribution. Shape parameter is $\nu > 0$. Defined for $x > 0$.

$$f(x; \nu) = \frac{2\nu^\nu}{\Gamma(\nu)} x^{2\nu-1} \exp\left(-\nu x^2\right)$$

$$F(x; \nu) = \left(\nu x^2\right)^{-1}$$

$$G(\nu; \nu) = \sqrt{\frac{1}{\nu}} \Gamma^{-1}(\nu, q)$$

$$\mu = \frac{\Gamma(\nu + \frac{1}{2})}{\sqrt{\pi} \Gamma(\nu)}$$

$$\mu_2 = \left[1 - \mu^2\right]$$

$$\gamma_1 = \frac{\mu(1 - 4\nu\mu_2)}{2\nu\mu_2^{3/2}}$$

$$\gamma_2 = \frac{-6\mu^4\nu + (8\nu - 2)\mu^2 - 2\nu + 1}{\nu\mu_2^2}$$

Implementation: `scipy.stats.nakagami`

Noncentral chi-squared Distribution

The distribution of $\sum_{i=1}^{\nu} (Z_i + \delta_i)^2$ where $Z_i$ are independent standard normal variables and $\delta_i$ are constants. $\lambda = \sum_{i=1}^{\nu} \delta_i^2 > 0$. (In communications it is called the Marcum-Q function). Can be thought of as a Generalized Rayleigh-Rice distribution. For $x > 0$

$$f(x; \nu, \lambda) = e^{-(\lambda+x)/2} \frac{1}{2} \left(\frac{x}{\lambda}\right)^{(\nu-2)/4} I_{(\nu-2)/2}\left(\sqrt{\lambda x}\right)$$

$$F(x; \nu, \lambda) = \sum_{j=0}^{\infty} \left\{\frac{(\lambda/2)^j}{j!} e^{-\lambda/2}\right\} \Pr\left[\chi^2_{\nu+2j} \leq x\right]$$

$$G(q; \nu, \lambda) = F^{-1}(x; \nu, \lambda)$$

$$\mu = \nu + \lambda$$

$$\mu_2 = 2(\nu + 2\lambda)$$

$$\gamma_1 = \frac{\sqrt{8}(\nu + 3\lambda)}{(\nu + 2\lambda)^{3/2}}$$

$$\gamma_2 = \frac{12(\nu + 4\lambda)}{(\nu + 2\lambda)^2}$$

Implementation: `scipy.stats.ncx2`

Noncentral F Distribution

Let $\lambda > 0$ and $\nu_1 > 0$ and $\nu_2 > 0$.

$$f(x; \nu_1, \nu_2) = \exp\left[\frac{\lambda}{2} + \frac{(\lambda\nu_1 x)}{2(\nu_1 x + \nu_2)}\right] \nu_1^{\nu_1/2} \nu_2^{\nu_2/2} x^{\nu_1/2 - 1}$$

$$\times (\nu_2 + \nu_1 x)^{-(\nu_1 + \nu_2)/2}$$

$$B\left(\frac{\nu_1}{2}, \frac{\nu_2}{2}\right) \Gamma\left(1 + \frac{\nu_2}{2}\right) L_{\nu_2/2}^{\nu_1/2 - 1}\left(\frac{-\lambda\nu_1 x}{\nu_1 x + \nu_2}\right)$$

Implementation: `scipy.stats.ncf`
Noncentral t Distribution

The distribution of the ratio

\[ U + \lambda / \chi / \sqrt{\nu} \]

where \( U \) and \( \chi \) are independent and distributed as a standard normal and chi with \( \nu \) degrees of freedom. Note \( \lambda > 0 \) and \( \nu > 0 \).

\[
f(x; \lambda, \nu) = \frac{\nu^{\nu/2} \Gamma(\nu + 1)}{2 \nu^2 \nu^2 (\nu + x^2)^\nu / 2 \Gamma(\nu/2)} \times \left\{ \frac{\sqrt{2} \lambda x _1 F_1 \left( \frac{\nu}{2} + 1, \frac{3}{2}; \frac{\lambda^2 x^2}{2(\nu + x^2)} \right)}{(\nu + x^2) \Gamma \left( \frac{\nu + 1}{2} \right)} \right\} \frac{1}{\sqrt{\nu + x^2} \Gamma \left( \frac{\nu}{2} + 1 \right)}
\]

\[
F(x; \lambda, \nu) = \frac{\Gamma(\nu + 1)}{2(\nu + 1) \sqrt{\pi \nu} \Gamma(\nu/2)} \exp \left[ -\frac{\nu \lambda^2}{\nu + x^2} \right] \times \left( \frac{\nu}{\nu + x^2} \right)^{(\nu - 1)/2} H_{\nu} \left( -\frac{\lambda x}{\sqrt{\nu + x^2}} \right)
\]

Implementation: scipy.stats.nct

Normal Distribution

\[
f(x) = e^{-x^2/2} / \sqrt{2\pi}
\]

\[
F(x) = \Phi(x) = \frac{1}{2} + \frac{1}{2} \text{erf} \left( \frac{x}{\sqrt{2}} \right)
\]

\[
G(q) = \Phi^{-1}(q)
\]

\[
m_d = m_n = \mu = 0
\]

\[
\mu_2 = 1
\]

\[
\gamma_1 = 0
\]

\[
\gamma_2 = 0
\]

\[
h[X] = \log \left( \sqrt{2\pi e} \right)
\]

\[
\approx 1.4189385332046727418
\]

Implementation: scipy.stats.norm

Pareto Distribution

For \( x \geq 1 \) and \( b > 0 \). Standard form is

\[
f(x; b) = \frac{b}{x^{b+1}}
\]

\[
F(x; b) = 1 - \frac{1}{x^b}
\]

\[
G(q; b) = (1 - q)^{-1/b}
\]
\[
\begin{align*}
\mu &= \frac{b}{b-1} \quad b > 1 \\
\mu_2 &= \frac{b}{(b-2)(b-1)^2} \quad b > 2 \\
\gamma_1 &= \frac{2(b+1)\sqrt{b-2}}{(b-3)\sqrt{b}} \quad b > 3 \\
\gamma_2 &= \frac{6(b^3 + b^2 - 6b - 2)}{b(b^2 - 7b + 12)} \quad b > 4 \\
h(X) &= \frac{1}{c} + 1 - \log(c)
\end{align*}
\]

Implementation: `scipy.stats.pareto`

**Pareto Second Kind (Lomax) Distribution**

\( c > 0 \). This is Pareto of the first kind with \( L = -1.0 \) so \( x \geq 0 \)

\[
\begin{align*}
f(x; c) &= \frac{c}{(1+x)^{c+1}} \\
F(x; c) &= 1 - \left(\frac{1}{1+x}\right)^c \\
G(q; c) &= (1-q)^{-1/c} - 1 \\
h[X] &= \frac{1}{c} + 1 - \log(c).
\end{align*}
\]

Implementation: `scipy.stats.lomax`

**Power Log Normal Distribution**

A generalization of the log-normal distribution \( \sigma > 0 \) and \( c > 0 \) and \( x > 0 \)

\[
\begin{align*}
f(x; \sigma, c) &= \frac{c}{x\sigma} \phi\left(\frac{\log x}{\sigma}\right) \left(\Phi\left(-\frac{\log x}{\sigma}\right)\right)^{c-1} \\
F(x; \sigma, c) &= 1 - \left(\Phi\left(-\frac{\log x}{\sigma}\right)\right)^c \\
G(q; \sigma, c) &= \exp\left[-\sigma\Phi^{-1}\left[(1-q)^{1/c}\right]\right] \\
\mu'_n &= \int_0^1 \exp\left[-n\sigma\Phi^{-1}\left(y^{1/c}\right)\right] dy \\
\mu &= \mu'_1 \\
\mu_2 &= \mu'_2 - \mu'^2 \\
\gamma_1 &= \frac{\mu'_3 - 3\mu_2\mu_1 - \mu^3}{\mu_2^{3/2}} \\
\gamma_2 &= \frac{\mu'_4 - 4\mu_2\mu_3 - 6\mu_2^2\mu_2 - \mu^4}{\mu_2^2} - 3
\end{align*}
\]

This distribution reduces to the log-normal distribution when \( c = 1 \).

Implementation: `scipy.stats.powerlognorm`
Power Normal Distribution

A generalization of the normal distribution, \( c > 0 \) for

\[
    f(x; c) = c \phi(x) \left( \Phi(-x) \right)^{c-1}
\]

\[
    F(x; c) = 1 - \left( \Phi(-x) \right)^c
\]

\[
    G(q; c) = -\Phi^{-1} \left( (1 - q)^{1/c} \right)
\]

\[
    \mu'_n = (-1)^n \int_0^1 \left[ \Phi^{-1} \left( y^{1/c} \right) \right]^n dy
\]

\[
    \mu = \mu'_1
\]

\[
    \mu_2 = \mu'_2 - \mu^2
\]

\[
    \gamma_1 = \frac{\mu'_3 - 3\mu\mu_2 - \mu^3}{\mu_2^{3/2}}
\]

\[
    \gamma_2 = \frac{\mu'_4 - 4\mu\mu_3 - 6\mu^2\mu_2 - \mu^4}{\mu_2^2} - 3
\]

For \( c = 1 \) this reduces to the normal distribution.

Implementation: `scipy.stats.powernorm`

Power-function Distribution

A special case of the beta distribution with \( b = 1 \) : defined for \( x \in [0, 1] \)

\( a > 0 \)

\[
    f(x; a) = ax^{a-1}
\]

\[
    F(x; a) = x^a
\]

\[
    G(q; a) = q^{1/a}
\]

\[
    \mu = \frac{a}{a + 1}
\]

\[
    \mu_2 = \frac{a(a + 2)}{(a + 1)^2}
\]

\[
    \gamma_1 = 2(1 - a) \sqrt{\frac{a + 2}{a(a + 3)}}
\]

\[
    \gamma_2 = \frac{6(a^3 - a^2 - 6a + 2)}{a(a + 3)(a + 4)}
\]

\[
    m_d = 1
\]

\[
    h\left[ x \right] = 1 - \frac{1}{a} - \log(a)
\]

Implementation: `scipy.stats.powerlaw`
R-distribution Distribution

A general-purpose distribution with a variety of shapes controlled by $c > 0$. Range of standard distribution is $x \in [-1, 1]$

\[
f(x;c) = \frac{(1-x^2)^{c/2-1}}{B\left(\frac{1}{2}, \frac{c}{2}\right)}
\]

\[
F(x;c) = \frac{1}{2} + \frac{x}{B\left(\frac{1}{2}, \frac{c}{2}\right)} _2F_1\left(\frac{1}{2}, 1 - \frac{c}{2}; \frac{3}{2}; x^2\right)
\]

\[
\mu'_n = \frac{1 + (-1)^n}{2} B\left(\frac{n+1}{2}, \frac{c}{2}\right)
\]

The R-distribution with parameter $n$ is the distribution of the correlation coefficient of a random sample of size $n$ drawn from a bivariate normal distribution with $\rho = 0$. The mean of the standard distribution is always zero and as the sample size grows, the distribution’s mass concentrates more closely about this mean.

Implementation: `scipy.stats.rdist`

Rayleigh Distribution

This is Chi distribution with $L = 0.0$ and $\nu = 2$ and $S = S$ (no location parameter is generally used), the mode of the distribution is $S$.

\[
f(r) = re^{-r^2/2}I_{(0,\infty)}(r)
\]

\[
F(r) = 1 - e^{-r^2/2}I_{(0,\infty)}(r)
\]

\[
G(q) = \sqrt{-2\log(1-q)}
\]

\[
\mu = \sqrt{\frac{\pi}{2}}
\]

\[
\mu_2 = \frac{4 - \pi}{2}
\]

\[
\gamma_1 = \frac{2(\pi - 3)\sqrt{\pi}}{(4 - \pi)^{3/2}}
\]

\[
\gamma_2 = \frac{24\pi - 6\pi^2 - 16}{(4 - \pi)^2}
\]

\[
m_d = 1
\]

\[
m_n = \sqrt{2\log(2)}
\]

\[
h[X] = \frac{\gamma}{2} + \log\left(\frac{e}{\sqrt{2}}\right).
\]

\[
\mu'_n = \sqrt{2\pi} \Gamma\left(\frac{n}{2} + 1\right)
\]

Implementation: `scipy.stats.rayleigh`

Rice Distribution

Defined for $x > 0$ and $b > 0$

\[
f(x; b) = x \exp\left(-\frac{x^2 + b^2}{2}\right) I_0(xb)
\]

\[
F(x; b) = \int_0^x a \exp\left(-\frac{a^2 + b^2}{2}\right) I_0(ab) \, da
\]
\[ \mu_n = \sqrt{2\pi} \Gamma \left( \frac{1 + n}{2} \right) {}_1 F_1 \left( -\frac{n}{2}; 1; -\frac{b^2}{2} \right) \]

Implementation: `scipy.stats.rice`

**Reciprocal Distribution**

Shape parameters \( a, b > 0 \) \( x \in [a, b] \)

\[
\begin{align*}
  f(x; a, b) &= \frac{1}{x \log(b/a)} \\
  F(x; a, b) &= \frac{\log(x/a)}{\log(b/a)} \\
  G(q; a, b) &= a \exp(q \log(b/a)) = a \left( \frac{b}{a} \right)^q
\end{align*}
\]

\[
\begin{align*}
  d &= \log(a/b) \\
  \mu &= \frac{a - b}{d} \\
  \mu_2 &= \mu^2 - \frac{a + b}{2} = \frac{(a - b) \left( a (d - 2) + b (d + 2) \right)}{2d^2} \\
  \gamma_1 &= \frac{\sqrt{2} \left( 12d (a - b)^2 + d^2 (a^2 (2d - 9) + 2abd + b^2 (2d + 9)) \right)}{3d \sqrt{a - b} \left( a (d - 2) + b (d + 2) \right)^{3/2}} \\
  \gamma_2 &= \frac{-36 (a - b)^3 + 36d (a - b)^2 (a + b) - 16d^2 (a^3 - b^3) + 3d^3 (a^2 + b^2) (a + b)}{3 (a - b) \left( a (d - 2) + b (d + 2) \right)^2} - 3 \\
  m_d &= \frac{a}{\sqrt{a-b}} \\
  m_n &= \sqrt{ab}
\end{align*}
\]

\[
h[X] = \frac{1}{2} \log(ab) + \log \left[ \log \left( \frac{b}{a} \right) \right]
\]

Implementation: `scipy.stats.recipinvgauss`

**Reciprocal Inverse Gaussian Distribution**

The pdf is found from the inverse gaussian (IG), \( f_{RIG}(x; \mu) = \frac{1}{x^2} f_{IG} \left( \frac{1}{x}; \mu \right) \) defined for \( x \geq 0 \) as

\[
\begin{align*}
  f_{IG}(x; \mu) &= \frac{1}{\sqrt{2\pi x^3}} \exp \left( -\frac{(x - \mu)^2}{2x\mu^2} \right) \\
  F_{IG}(x; \mu) &= \Phi \left( \frac{1}{\sqrt{x}} \frac{x - \mu}{\mu} \right) + \exp \left( \frac{2}{\mu} \right) \Phi \left( -\frac{1}{\sqrt{x}} \frac{x + \mu}{\mu} \right) \\
  f_{RIG}(x; \mu) &= \frac{1}{\sqrt{2\pi x}} \exp \left( -\frac{(1 - \mu x)^2}{2x\mu^2} \right) \\
  F_{RIG}(x; \mu) &= 1 - F_{IG} \left( \frac{1}{x}, \mu \right) \\
  &= 1 - \Phi \left( \frac{1}{\sqrt{x}} \frac{1 - \mu x}{\mu} \right) - \exp \left( \frac{2}{\mu} \right) \Phi \left( -\frac{1}{\sqrt{x}} \frac{1 + \mu x}{\mu} \right)
\end{align*}
\]

Implementation: `scipy.stats.recipinvgauss`
Semicircular Distribution

Defined on \( x \in [-1, 1] \)

\[
\begin{align*}
f(x) &= \frac{2}{\pi} \sqrt{1 - x^2} \\
F(x) &= \frac{1}{2} + \frac{1}{\pi} \left[ x \sqrt{1 - x^2} + \arcsin x \right] \\
G(q) &= F^{-1}(q)
\end{align*}
\]

\[
m_d = m_n = \mu = 0 \\
\mu_2 = \frac{1}{4} \\
\gamma_1 = 0 \\
\gamma_2 = -1
\]

\[
h[X] = 0.64472988584940017414.
\]

Implementation: \texttt{scipy.stats.semicircular}

Student t Distribution

Shape parameter \( \nu > 0 \). \( I(a, b, x) \) is the incomplete beta integral and \( I^{-1}(a, b, I(a, b, x)) = x \)

\[
\begin{align*}
f(x; \nu) &= \frac{\Gamma \left( \frac{\nu+1}{2} \right)}{\sqrt{\pi \nu} \Gamma \left( \frac{\nu}{2} \right) \left[ 1 + \frac{x^2}{\nu} \right]^{\frac{\nu+1}{2}}} \\
F(x; \nu) &= \begin{cases} \\
\frac{1}{2} I \left( \frac{\nu}{2}, \frac{1}{2}, \frac{\nu}{\nu + x^2} \right) & x \leq 0 \\
1 - \frac{1}{2} I \left( \frac{\nu}{2}, \frac{1}{2}, \frac{\nu}{\nu + x^2} \right) & x \geq 0
\end{cases} \\
G(q; \nu) &= \begin{cases} \\
- \sqrt{I^{-1} \left( \frac{\nu}{2}, \frac{1}{2}, 2q \right) - \nu} & q \leq \frac{1}{2} \\
\sqrt{I^{-1} \left( \frac{\nu}{2}, \frac{1}{2}, 2q \right) - \nu} & q \geq \frac{1}{2}
\end{cases}
\end{align*}
\]

\[
m_n = m_d = \mu = 0 \\
\mu_2 = \frac{\nu}{\nu - 2} \quad \nu > 2 \\
\gamma_1 = 0 \quad \nu > 3 \\
\gamma_2 = \frac{6}{\nu - 4} \quad \nu > 4
\]

As \( \nu \to \infty \), this distribution approaches the standard normal distribution.

\[
h[X] = \frac{1}{4} \log \left( \frac{\pi c \Gamma^2 \left( \frac{3}{2} \right)}{\Gamma^2 \left( \frac{c+1}{2} \right)} \right) - \frac{(c+1)}{4} \left[ \Psi \left( \frac{c}{2} \right) - c Z \left( c \right) + \pi \tan \left( \frac{\pi c}{2} \right) + \gamma + 2 \log 2 \right]
\]

where

\[
Z(c) = _3F_2 \left( 1, 1, 1 + \frac{c}{2}, 3; 2; 1 \right) = \sum_{k=0}^{\infty} \frac{k!}{k+1} \frac{\Gamma \left( \frac{3}{2} + 1 + k \right)}{\Gamma \left( \frac{3}{2} + 1 \right)} \frac{\Gamma \left( \frac{c}{2} + k \right)}{\Gamma \left( \frac{c}{2} + k \right)}
\]

Implementation: \texttt{scipy.stats.t}
Triangular Distribution

One shape parameter $c \in [0, 1]$ giving the distance to the peak as a percentage of the total extent of the non-zero portion. The location parameter is the start of the non-zero portion, and the scale-parameter is the width of the non-zero portion. In standard form we have $x \in [0, 1]$:

$$f(x; c) = \begin{cases} \frac{2x}{c} & x < c \\ \frac{1-c}{1-x} & x \ge c \end{cases}$$

$$F(x; c) = \begin{cases} \frac{c^2}{2} & x < c \\ \frac{c^2}{c-1} & x \ge c \end{cases}$$

$$G(q; c) = \begin{cases} \frac{1 - \sqrt{q}}{(1-(1-c)^{-1})} & q < c \\ q - c & q \ge c \end{cases}$$

$$\mu = \frac{c}{3} + \frac{1}{3}$$

$$\mu_2 = \frac{1-c+c^2}{18}$$

$$\gamma_1 = \frac{\sqrt{2} (2c-1)(c+1)(c-2)}{5(1-c+c^2)^{3/2}}$$

$$\gamma_2 = -\frac{3}{5}$$

$$h(X) = \log\left(\frac{1}{2}\sqrt{e}\right) \approx -0.19314718055994530942.$$ 

Implementation: \texttt{scipy.stats.triang}

Truncated Exponential Distribution

This is an exponential distribution defined only over a certain region $0 < x < B$. In standard form this is

$$f(x; B) = \frac{e^{-x}}{1-e^{-B}}$$

$$F(x; B) = \frac{1-e^{-x}}{1-e^{-B}}$$

$$G(q; B) = -\log(1-q+qe^{-B})$$

$$\mu_n = \Gamma(1+n) - \Gamma(1+n,B)$$

$$h[X] = \log(e^B - 1) + \frac{1+e^B(B-1)}{1-e^B}.$$ 

Implementation: \texttt{scipy.stats.truncexpon}

Truncated Normal Distribution

A normal distribution restricted to lie within a certain range given by two parameters $A$ and $B$. Notice that this $A$ and $B$ correspond to the bounds on $x$ in standard form. For $x \in [A, B]$ we get

$$f(x; A, B) = \frac{\phi(x)}{\Phi(B) - \Phi(A)}$$

$$F(x; A, B) = \frac{\Phi(x) - \Phi(A)}{\Phi(B) - \Phi(A)}$$

$$G(q; A, B) = \Phi^{-1}[q\Phi(B) + \Phi(A)(1-q)]$$
where

\[ \phi(x) = \frac{1}{\sqrt{2\pi}} e^{-x^2/2} \]

\[ \Phi(x) = \int_{-\infty}^{x} \phi(u) du. \]

\[ \mu = \frac{\phi(A) - \phi(B)}{\Phi(B) - \Phi(A)} \]

\[ \mu_2 = 1 + (\Phi(B) - \Phi(A)) \left( \frac{\phi(A) - \phi(B)}{\Phi(B) - \Phi(A)} \right)^2 \]

Implementation: \texttt{scipy.stats.truncnorm}

**Tukey-Lambda Distribution**

\[ f(x; \lambda) = F'(x; \lambda) = \frac{1}{G'(F(x; \lambda); \lambda)} = \frac{1}{F^{\lambda-1}(x; \lambda) + (1 - F(x; \lambda))^{\lambda-1}} \]

\[ F(x; \lambda) = G^{-1}(x; \lambda) \]

\[ G(p; \lambda) = \frac{p^\lambda - (1 - p)^\lambda}{\lambda} \]

\[ \mu = 0 \]

\[ \mu_2 = \int_0^1 G^2(p; \lambda) \, dp \]

\[ = \frac{2\Gamma(\lambda + \frac{3}{2}) - \lambda^{-\lambda} \sqrt{\pi} \Gamma(\lambda)(1 - 2\lambda)}{\lambda^2(1 + 2\lambda) \Gamma(\lambda + \frac{3}{2})} \]

\[ \gamma_1 = 0 \]

\[ \gamma_2 = \frac{\mu_4}{\mu_2^2} - 3 \]

\[ \mu_4 = \frac{3\Gamma(\lambda) \Gamma(\lambda + \frac{1}{2}) 2^{-2\lambda}}{\lambda^3 \Gamma(2\lambda + \frac{3}{2})} + \frac{2}{\lambda^4(1 + 4\lambda)} \]

\[ - \frac{2\sqrt{3}\Gamma(\lambda) 2^{-6\lambda} \Gamma(\lambda + \frac{1}{2}) \Gamma(\lambda + \frac{3}{2})}{\lambda^3 \Gamma(2\lambda + \frac{3}{2}) \Gamma(\lambda + \frac{3}{2})} \]

Notice that the \( \lim_{\lambda \to 0} G(p; \lambda) = \log(p/(1-p)) \)

\[ h[X] = \int_0^1 \log[G'(p)] \, dp \]

\[ = \int_0^1 \log \left[ p^{\lambda-1} + (1 - p)^{\lambda-1} \right] dp. \]

Implementation: \texttt{scipy.stats.tukeylambda}

**Uniform Distribution**

Standard form \( x \in (0, 1) \). In general form, the lower limit is \( L \), the upper limit is \( S + L \).

\[ f(x) = 1 \]

\[ F(x) = x \]

\[ G(q) = q \]
\[ \mu = \frac{1}{2} \]
\[ \mu_2 = \frac{1}{12} \]
\[ \gamma_1 = 0 \]
\[ \gamma_2 = -\frac{6}{5} \]
\[ h[X] = 0 \]

Implementation: \texttt{scipy.stats.uniform}

**Von Mises Distribution**

Defined for \( x \in [-\pi, \pi] \) with shape parameter \( \kappa > 0 \). Note, the PDF and CDF functions are periodic and are always defined over \( x \in [-\pi, \pi] \) regardless of the location parameter. Thus, if an input beyond this range is given, it is converted to the equivalent angle in this range. For values of \( \kappa < 100 \) the PDF and CDF formulas below are used. Otherwise, a normal approximation with variance \( 1/\kappa \) is used.

\[
\begin{align*}
  f(x; \kappa) & = \frac{e^{\kappa \cos x}}{2\pi I_0(\kappa)} \\
  F(x; \kappa) & = \frac{1}{2} + \frac{x}{2\pi} + \sum_{k=1}^{\infty} \frac{I_k(\kappa) \sin(kx)}{I_0(\kappa) \pi k} \\
  G(q; \kappa) & = F^{-1}(x; \kappa)
\end{align*}
\]

\[ \mu = 0 \]
\[ \mu_2 = \int_{-\pi}^{\pi} x^2 f(x; \kappa) \, dx \]
\[ \gamma_1 = 0 \]
\[ \gamma_2 = \frac{\int_{-\pi}^{\pi} x^4 f(x; \kappa) \, dx}{\mu_2} - 3 \]

This can be used for defining circular variance.

Implementation: \texttt{scipy.stats.vonmises}

**Wald Distribution**

Special case of the Inverse Normal with shape parameter set to 1.0. Defined for \( x > 0 \).

\[
\begin{align*}
  f(x) & = \frac{1}{\sqrt{2\pi x^3}} \exp\left(-\frac{(x-1)^2}{2x}\right) \\
  F(x) & = \Phi\left(\frac{x-1}{\sqrt{x}}\right) + \exp(2) \Phi\left(\frac{x+1}{\sqrt{x}}\right) \\
  G(q; \mu) & = F^{-1}(q; \mu)
\end{align*}
\]

\[ \mu = 1 \]
\[ \mu_2 = 1 \]
\[ \gamma_1 = 3 \]
\[ \gamma_2 = 15 \]
\[ m_d = \frac{1}{2} \left(\sqrt{13} - 3\right) \]

Implementation: \texttt{scipy.stats.wald}
Weibull Maximum Extreme Value Distribution

Defined for \( x < 0 \) and \( c > 0 \).

\[
\begin{align*}
\frac{\partial}{\partial c} & = c (x)^{c-1} \exp(-x^c) \\
F(x; c) & = \exp(-x^c) \\
G(q; c) & = (-\log(q))^{1/c}
\end{align*}
\]

The mean is the negative of the right-skewed Frechet distribution given above, and the other statistical parameters can be computed from

\[
\begin{align*}
\mu' & = (-1)^n \Gamma \left(1 + \frac{n}{c}\right) \\
\mu & = -\Gamma \left(1 + \frac{1}{c}\right) \\
\gamma_1 & = \frac{\Gamma (1 + \frac{3}{c}) - \Gamma^2 (1 + \frac{1}{c})}{\mu_2^{3/2}} - 3 \\
\gamma_2 & = \frac{\Gamma (1 + \frac{2}{c}) - 4\Gamma (1 + \frac{1}{c}) \Gamma (1 + \frac{3}{c}) + 6\Gamma^2 (1 + \frac{1}{c}) \Gamma (1 + \frac{2}{c}) - 3\Gamma^4 (1 + \frac{1}{c})}{\mu_2^2} - 3 \\
m_d & = \begin{cases} 
\left(\frac{c-1}{c}\right)^{1/2} & \text{if } c > 1 \\
0 & \text{if } c \leq 1
\end{cases} \\
m_n & = -\ln(2)^{1/2} \\
\frac{\partial}{\partial x} & = -\frac{\gamma}{c} - \ln(c) + \gamma + 1
\end{align*}
\]

where \( \gamma \) is Euler’s constant and equal to

\[
\gamma \approx 0.57721566490153286061.
\]

Implementation: scipy.stats.weibull_max

Weibull Minimum Extreme Value Distribution

A type of extreme-value distribution with a lower bound. Defined for \( x > 0 \) and \( c > 0 \)

\[
\begin{align*}
\frac{\partial}{\partial c} & = cx^{c-1} \exp(-x^c) \\
F(x; c) & = 1 - \exp(-x^c) \\
G(q; c) & = [-\log(1 - q)]^{1/c}
\end{align*}
\]

\[
\begin{align*}
\mu' & = \Gamma \left(1 + \frac{n}{c}\right) \\
\mu & = -\Gamma \left(1 + \frac{1}{c}\right)
\end{align*}
\]
\[ \mu = \Gamma \left( 1 + \frac{1}{c} \right) \]
\[ \mu_2 = \Gamma \left( 1 + \frac{2}{c} \right) - \Gamma^2 \left( 1 + \frac{1}{c} \right) \]
\[ \gamma_1 = \frac{\Gamma \left( 1 + \frac{2}{c} \right) - 3 \Gamma \left( 1 + \frac{1}{c} \right) \Gamma \left( 1 + \frac{1}{c} \right) + 2 \Gamma^3 \left( 1 + \frac{1}{c} \right)}{\mu_2^{3/2}} \]
\[ \gamma_2 = \frac{\Gamma \left( 1 + \frac{3}{c} \right) - 4 \Gamma \left( 1 + \frac{1}{c} \right) \Gamma \left( 1 + \frac{1}{c} \right) + 6 \Gamma^2 \left( 1 + \frac{1}{c} \right) \Gamma \left( 1 + \frac{1}{c} \right) - 3 \Gamma^4 \left( 1 + \frac{1}{c} \right)}{\mu_2^2} - 3 \]
\[ m = \begin{cases} \left( \frac{c-1}{c} \right)^{\frac{1}{2}} & \text{if } c > 1 \\ 0 & \text{if } c \leq 1 \end{cases} \]
\[ m_n = \ln \left( 2^{\frac{1}{2}} \right) \]

where \( \gamma \) is Euler’s constant and equal to \( \gamma \approx 0.57721566490153286061 \).

Implementation: \texttt{scipy.stats.weibull_min}

**Wrapped Cauchy Distribution**

For \( x \in [0, 2\pi] \) \( c \in (0, 1) \)
\[ f(x; c) = \frac{1 - c^2}{2\pi (1 + c^2 - 2c \cos x)} \]
\[ g_c(x) = \frac{1}{\pi} \arctan \left[ \frac{1 + c}{1 - c} \tan \left( \frac{x}{2} \right) \right] \]
\[ r_c(q) = 2 \arctan \left[ \frac{1 - c}{1 + c} \tan (\pi q) \right] \]
\[ F(x; c) = \begin{cases} g_c(x) & 0 \leq x < \pi \\ 1 - g_c(2\pi - x) & \pi \leq x \leq 2\pi \end{cases} \]
\[ G(q; c) = \begin{cases} r_c(q) & 0 \leq q < \frac{1}{2} \\ 2\pi - r_c(1 - q) & \frac{1}{2} \leq q \leq 1 \end{cases} \]
\[ h[X] = \log \left( 2\pi (1 - c^2) \right) \]

Implementation: \texttt{scipy.stats.wrapcauchy}

**Random Variables**

There are two general distribution classes that have been implemented for encapsulating \textit{continuous random variables} and \textit{discrete random variables}. Over 80 continuous random variables (RVs) and 10 discrete random variables have been implemented using these classes. Besides this, new routines and distributions can easily be added by the end user. (If you create one, please contribute it).

All of the statistics functions are located in the sub-package \texttt{scipy.stats} and a fairly complete listing of these functions can be obtained using \texttt{info(stats)}. The list of the random variables available can also be obtained from the docstring for the stats sub-package.

In the discussion below we mostly focus on continuous RVs. Nearly all applies to discrete variables also, but we point out some differences here: \textit{Specific Points for Discrete Distributions}.

In the code samples below we assume that the \texttt{scipy.stats} package is imported as

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---
>>> from scipy import stats

and in some cases we assume that individual objects are imported as

>>> from scipy.stats import norm

For consistency between Python 2 and Python 3, we'll also ensure that print is a function:

>>> from __future__ import print_function

Getting Help

First of all, all distributions are accompanied with help functions. To obtain just some basic information we print the relevant docstring: `print(stats.norm.__doc__)`.

To find the support, i.e., upper and lower bound of the distribution, call:

```python
>>> print('bounds of distribution lower: %s, upper: %s' % (norm.a, norm.b))
bounds of distribution lower: -inf, upper: inf
```

We can list all methods and properties of the distribution with `dir(norm)`. As it turns out, some of the methods are private methods although they are not named as such (their name does not start with a leading underscore), for example `veccdf`, are only available for internal calculation (those methods will give warnings when one tries to use them, and will be removed at some point).

To obtain the real main methods, we list the methods of the frozen distribution. (We explain the meaning of a frozen distribution below).

```python
>>> rv = norm()
>>> dir(rv)  # reformatted
['__class__', '__delattr__', '__dict__', '__dir__', '__doc__', '__eq__',
 '__format__', '__ge__', '__getattribute__', '__gt__', '__hash__',
 '__init__', '__le__', '__lt__', '__module__', '__ne__', '__new__',
 '__reduce__', '__reduce_ex__', '__repr__', '__setattr__', '__sizeof__',
 '__str__', '__subclasshook__', '__weakref__', 'a', 'args', 'b', 'cdf',
 'dist', 'entropy', 'expect', 'interval', 'isf', 'kwds', 'logcdf',
 'logpdf', 'logpmf', 'logsf', 'mean', 'median', 'moment', 'pdf', 'pmf',
 'ppf', 'random_state', 'rvs', 'sf', 'stats', 'std', 'var']
```

Finally, we can obtain the list of available distribution through introspection:

```python
>>> dist_continu = [d for d in dir(stats) if...
...   isinstance(getattr(stats, d), stats.rv_continuous)]
>>> dist_discrete = [d for d in dir(stats) if...
...   isinstance(getattr(stats, d), stats.rv_discrete)]
>>> print('number of continuous distributions: %d' % len(dist_continu))
number of continuous distributions: 98
>>> print('number of discrete distributions: %d' % len(dist_discrete))
number of discrete distributions: 14
```

Common Methods

The main public methods for continuous RVs are:

- `rvs`: Random Variates
- `pdf`: Probability Density Function
- `cdf`: Cumulative Distribution Function
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- `sf`: Survival Function (1-CDF)
- `ppf`: Percent Point Function (Inverse of CDF)
- `isf`: Inverse Survival Function (Inverse of SF)
- `stats`: Return mean, variance, (Fisher’s) skew, or (Fisher’s) kurtosis
- `moment`: non-central moments of the distribution

Let’s take a normal RV as an example.

```python
>>> norm.cdf(0)
0.5
```

To compute the `cdf` at a number of points, we can pass a list or a numpy array.

```python
>>> norm.cdf([-1., 0, 1])
array([ 0.15865525, 0.5, 0.84134475])
>>> import numpy as np
>>> norm.cdf(np.array([-1., 0, 1]))
array([ 0.15865525, 0.5, 0.84134475])
```

Thus, the basic methods such as `pdf`, `cdf`, and so on are vectorized.

Other generally useful methods are supported too:

```python
>>> norm.mean(), norm.std(), norm.var()
(0.0, 1.0, 1.0)
>>> norm.stats(moments="mv")
(array(0.0), array(1.0))
```

To find the median of a distribution we can use the percent point function `ppf`, which is the inverse of the `cdf`:

```python
>>> norm.ppf(0.5)
0.0
```

To generate a sequence of random variates, use the `size` keyword argument:

```python
>>> norm.rvs(size=3)
array([-0.35687759, 1.34347647, -0.11710531]) # random
```

Note that drawing random numbers relies on generators from `numpy.random` package. In the example above, the specific stream of random numbers is not reproducible across runs. To achieve reproducibility, you can explicitly seed a global variable

```python
>>> np.random.seed(1234)
```

Relying on a global state is not recommended though. A better way is to use the `random_state` parameter which accepts an instance of `numpy.random.RandomState` class, or an integer which is then used to seed an internal `RandomState` object:

```python
>>> norm.rvs(size=5, random_state=1234)
array([0.47143516, -1.19097569, 1.43270697, -0.31265190, -0.72058873])
```

Don’t think that `norm.rvs(5)` generates 5 variates:
Here, 5 with no keyword is being interpreted as the first possible keyword argument, `loc`, which is the first of a pair of keyword arguments taken by all continuous distributions. This brings us to the topic of the next subsection.

**Shifting and Scaling**

All continuous distributions take `loc` and `scale` as keyword parameters to adjust the location and scale of the distribution, e.g., for the standard normal distribution the location is the mean and the scale is the standard deviation.

```python
>>> norm.stats(loc=3, scale=4, moments='mv')
(array(3.0), array(16.0))
```

In many cases the standardized distribution for a random variable $X$ is obtained through the transformation $(X - \text{loc}) / \text{scale}$. The default values are $\text{loc} = 0$ and $\text{scale} = 1$.

Smart use of `loc` and `scale` can help modify the standard distributions in many ways. To illustrate the scaling further, the cdf of an exponentially distributed RV with mean $1/\lambda$ is given by

$$F(x) = 1 - \exp(-\lambda x)$$

By applying the scaling rule above, it can be seen that by taking $\text{scale} = 1./\lambda$ we get the proper scale.

```python
>>> from scipy.stats import expon
>>> expon.mean(scale=3.)
3.0
```

**Note:** Distributions that take shape parameters may require more than simple application of `loc` and/or `scale` to achieve the desired form. For example, the distribution of 2-D vector lengths given a constant vector of length $R$ perturbed by independent $N(0, \sigma^2)$ deviations in each component is `rice(R/\sigma, \text{scale} = \sigma)`. The first argument is a shape parameter that needs to be scaled along with $x$.

The uniform distribution is also interesting:

```python
>>> from scipy.stats import uniform
>>> uniform.cdf([0, 1, 2, 3, 4, 5], loc=1, scale=4)
array([ 0. ,  0. ,  0.25,  0.5 ,  0.75,  1. ])
```

Finally, recall from the previous paragraph that we are left with the problem of the meaning of `norm.rvs(5)`. As it turns out, calling a distribution like this, the first argument, i.e., the 5, gets passed to set the `loc` parameter. Let’s see:

```python
>>> np.mean(norm.rvs(5, size=500))
5.0098355106969992
```

Thus, to explain the output of the example of the last section: `norm.rvs(5)` generates a single normally distributed random variate with mean $\text{loc}=5$, because of the default $\text{size}=1$.

We recommend that you set `loc` and `scale` parameters explicitly, by passing the values as keywords rather than as arguments. Repetition can be minimized when calling more than one method of a given RV by using the technique of `Freezing a Distribution`, as explained below.
Shape Parameters
While a general continuous random variable can be shifted and scaled with the loc and scale parameters, some distributions require additional shape parameters. For instance, the gamma distribution, with density

\[ \gamma(x, a) = \frac{\lambda^a x^{a-1}}{\Gamma(a)} e^{-\lambda x}, \]

requires the shape parameter \( a \). Observe that setting \( \lambda \) can be obtained by setting the scale keyword to \( 1/\lambda \).

Let’s check the number and name of the shape parameters of the gamma distribution. (We know from the above that this should be 1.)

```python
>>> from scipy.stats import gamma
>>> gamma.numargs
1
>>> gamma.shapes
'a'
```

Now we set the value of the shape variable to 1 to obtain the exponential distribution, so that we compare easily whether we get the results we expect.

```python
>>> gamma(1, scale=2.).stats(moments="mv")
(array(2.0), array(4.0))
```

Notice that we can also specify shape parameters as keywords:

```python
>>> gamma(a=1, scale=2.).stats(moments="mv")
(array(2.0), array(4.0))
```

Freezing a Distribution
Passing the loc and scale keywords time and again can become quite bothersome. The concept of freezing a RV is used to solve such problems.

```python
>>> rv = gamma(1, scale=2.)
```

By using rv we no longer have to include the scale or the shape parameters anymore. Thus, distributions can be used in one of two ways, either by passing all distribution parameters to each method call (such as we did earlier) or by freezing the parameters for the instance of the distribution. Let us check this:

```python
>>> rv.mean(), rv.std()
(2.0, 2.0)
```

This is indeed what we should get.

Broadcasting
The basic methods pdf and so on satisfy the usual numpy broadcasting rules. For example, we can calculate the critical values for the upper tail of the t distribution for different probabilities and degrees of freedom.

```python
>>> stats.t.isf([0.1, 0.05, 0.01], [[10], [11]])
array([[ 1.37218364, 1.81246112, 2.76376946],
       [ 1.36343032, 1.79588482, 2.71807918]])
```

Here, the first row are the critical values for 10 degrees of freedom and the second row for 11 degrees of freedom (d.o.f.). Thus, the broadcasting rules give the same result of calling isf twice:
>>> stats.t.isf([0.1, 0.05, 0.01], 10)
array([ 1.37218364, 1.81246112, 2.76376946])
>>> stats.t.isf([0.1, 0.05, 0.01], 11)
array([ 1.36343032, 1.79588482, 2.71807918])

If the array with probabilities, i.e., [0.1, 0.05, 0.01] and the array of degrees of freedom i.e., [10, 11, 12], have the same array shape, then element wise matching is used. As an example, we can obtain the 10% tail for 10 d.o.f., the 5% tail for 11 d.o.f. and the 1% tail for 12 d.o.f. by calling

>>> stats.t.isf([0.1, 0.05, 0.01], [10, 11, 12])
array([ 1.37218364, 1.79588482, 2.68099799])

Specific Points for Discrete Distributions
Discrete distribution have mostly the same basic methods as the continuous distributions. However pdf is replaced the probability mass function pmf, no estimation methods, such as fit, are available, and scale is not a valid keyword parameter. The location parameter, keyword loc can still be used to shift the distribution.

The computation of the cdf requires some extra attention. In the case of continuous distribution the cumulative distribution function is in most standard cases strictly monotonic increasing in the bounds (a,b) and has therefore a unique inverse. The cdf of a discrete distribution, however, is a step function, hence the inverse cdf, i.e., the percent point function, requires a different definition:

\[ \text{ppf}(q) = \min \{ x : \text{cdf}(x) \geq q, x \text{ integer} \} \]

For further info, see the docs [here](#).

We can look at the hypergeometric distribution as an example

```python
>>> from scipy.stats import hypergeom
>>> [M, n, N] = [20, 7, 12]
```

If we use the cdf at some integer points and then evaluate the ppf at those cdf values, we get the initial integers back, for example

```python
>>> x = np.arange(4)*2
>>> x
array([0, 2, 4, 6])
>>> prb = hypergeom.cdf(x, M, n, N)
>>> prb
array([ 1.03199174e-04, 5.21155831e-02, 6.08359133e-01,
         9.89783282e-01])
>>> hypergeom.ppf(prb, M, n, N)
array([ 0., 2., 4., 6.])
```

If we use values that are not at the kinks of the cdf step function, we get the next higher integer back:

```python
>>> hypergeom.ppf(prb + 1e-8, M, n, N)
array([ 1., 3., 5., 7.])
>>> hypergeom.ppf(prb - 1e-8, M, n, N)
array([ 0., 2., 4., 6.])
```

Fitting Distributions
The main additional methods of the not frozen distribution are related to the estimation of distribution parameters:

- **fit**: maximum likelihood estimation of distribution parameters, including location
and scale

- `fit_loc_scale`: estimation of location and scale when shape parameters are given
- `nnlf`: negative log likelihood function
- `expect`: Calculate the expectation of a function against the pdf or pmf

Performance Issues and Cautionary Remarks

The performance of the individual methods, in terms of speed, varies widely by distribution and method. The results of a method are obtained in one of two ways: either by explicit calculation, or by a generic algorithm that is independent of the specific distribution.

Explicit calculation, on the one hand, requires that the method is directly specified for the given distribution, either through analytic formulas or through special functions in `scipy.special` or `numpy.random` for `rvs`. These are usually relatively fast calculations.

The generic methods, on the other hand, are used if the distribution does not specify any explicit calculation. To define a distribution, only one of pdf or cdf is necessary; all other methods can be derived using numeric integration and root finding. However, these indirect methods can be very slow. As an example, `rgh = stats.gausshyper.rvs(0.5, 2, 2, 2, size=100)` creates random variables in a very indirect way and takes about 19 seconds for 100 random variables on my computer, while one million random variables from the standard normal or from the t distribution take just above one second.

Remaining Issues

The distributions in `scipy.stats` have recently been corrected and improved and gained a considerable test suite, however a few issues remain:

- the distributions have been tested over some range of parameters, however in some corner ranges, a few incorrect results may remain.
- the maximum likelihood estimation in `fit` does not work with default starting parameters for all distributions and the user needs to supply good starting parameters. Also, for some distribution using a maximum likelihood estimator might inherently not be the best choice.

Building Specific Distributions

The next examples shows how to build your own distributions. Further examples show the usage of the distributions and some statistical tests.

Making a Continuous Distribution, i.e., Subclassing `rv_continuous`

Making continuous distributions is fairly simple.

```python
>>> from scipy import stats
>>> class deterministic_gen(stats.rv_continuous):
...    def _cdf(self, x):
...        return np.where(x < 0, 0., 1.)
...    def _stats(self):
...        return 0., 0., 0., 0.

>>> deterministic = deterministic_gen(name="deterministic")
>>> deterministic.pdf(np.arange(-3, 3, 0.5))
array([ 0., 0., 0., 0., 0., 1., 1., 1., 1., 1.])
```

Interestingly, the `pdf` is now computed automatically:

```python
>>> deterministic.pdf(np.arange(-3, 3, 0.5))
array([ 0.00000000e+00, 0.00000000e+00, 0.00000000e+00, 0.00000000e+00, 0.00000000e+00, 0.00000000e+00, 0.00000000e+00, 0.00000000e+00, 0.00000000e+00,])
```
Be aware of the performance issues mentioned in *Performance Issues and Cautionary Remarks*. The computation of unspecified common methods can become very slow, since only general methods are called which, by their very nature, cannot use any specific information about the distribution. Thus, as a cautionary example:

```python
from scipy.integrate import quad

quad(deterministic.pdf, -1e-1, 1e-1)
```

But this is not correct: the integral over this pdf should be 1. Let’s make the integration interval smaller:

```python
quad(deterministic.pdf, -1e-3, 1e-3)  # warning removed
```

This looks better. However, the problem originated from the fact that the pdf is not specified in the class definition of the deterministic distribution.

**Subclassing `rv_discrete`**

In the following we use `stats.rv_discrete` to generate a discrete distribution that has the probabilities of the truncated normal for the intervals centered around the integers.

**General Info**

From the docstring of `rv_discrete`, `help(stats.rv_discrete),`

```
"You can construct an arbitrary discrete rv where P{X=xk} = pk by passing to the rv_discrete initialization method (through the values= keyword) a tuple of sequences (xk, pk) which describes only those values of X (xk) that occur with nonzero probability (pk)."
```

Next to this, there are some further requirements for this approach to work:

- The keyword `name` is required.
- The support points of the distribution xk have to be integers.
- The number of significant digits (decimals) needs to be specified.

In fact, if the last two requirements are not satisfied an exception may be raised or the resulting numbers may be incorrect.

**An Example**

Let’s do the work. First:

```python
>>> npoints = 20  # number of integer support points of the distribution minus 1
>>> npointsh = npoints // 2
>>> npointssf = float(npointsh)
>>> nbound = 4  # bounds for the truncated normal
>>> normbound = (1+1/npointssf) * nbound  # actual bounds of truncated normal
>>> grid = np.arange(-npointsh, npointsh+2, 1)  # integer grid
>>> gridlimitsnorm = (grid-0.5) / npointsh * nbound  # bin limits for the truncnorm
>>> gridlimits = grid - 0.5  # used later in the analysis
>>> grid = grid[:-1]
>>> probs = np.diff(stats.truncnorm.cdf(gridlimitsnorm, -normbound, normbound))
>>> gridint = grid
```
And finally we can subclass `rv_discrete`:

```python
def normdiscrete = stats.rv_discrete(values=(gridint, ...
    np.round(probs, decimals=7)), name='normdiscrete')
```

Now that we have defined the distribution, we have access to all common methods of discrete distributions.

```python
mean = -0.0000, variance = 6.3302, skew = 0.0000, kurtosis = -0.0076
```

### Testing the Implementation

Let’s generate a random sample and compare observed frequencies with the probabilities.

```python
f2 = np.hstack([f[:5].sum(), f[5:]].sum())
p2 = np.hstack([probs[:5].sum(), probs[5:].sum()])
ch2, pval = stats.chisquare(f2, p2 * n_sample)
```
Frequency and Probability of normdiscrete

Cumulative Frequency and CDF of normdiscrete
The p-value in this case is high, so we can be quite confident that our random sample was actually generated by the distribution.

### Analysing One Sample

First, we create some random variables. We set a seed so that in each run we get identical results to look at. As an example we take a sample from the Student t distribution:

```python
>>> np.random.seed(282629734)
>>> x = stats.t.rvs(10, size=1000)
```

Here, we set the required shape parameter of the t distribution, which in statistics corresponds to the degrees of freedom, to 10. Using size=1000 means that our sample consists of 1000 independently drawn (pseudo) random numbers. Since we did not specify the keyword arguments `loc` and `scale`, those are set to their default values zero and one.

### Descriptive Statistics

$x$ is a numpy array, and we have direct access to all array methods, e.g.

```python
>>> print(x.min())  # equivalent to np.min(x)
-3.78975572422
>>> print(x.max())  # equivalent to np.max(x)
5.26327732981
>>> print(x.mean()) # equivalent to np.mean(x)
0.0140610663985
>>> print(x.var())  # equivalent to np.var(x))
1.28899386208
```

How do the some sample properties compare to their theoretical counterparts?

```python
>>> m, v, s, k = stats.t.stats(10, moments='mvsk')
>>> n, (smin, smax), sm, sv, ss, sk = stats.describe(x)
```

```python
>>> sstr = '%-14s mean = %.6f, variance = %.6f, skew = %.6f, kurtosis = %.6f'
>>> print(sstr % ('distribution:', m, v, s, k))
distribution: mean = 0.0000, variance = 1.2500, skew = 0.0000, kurtosis = 1.0000
>>> print(sstr % ('sample:', sm, sv, ss, sk))
sample: mean = 0.0141, variance = 1.2903, skew = 0.2165, kurtosis = 1.0556
```

Note: `stats.describe` uses the unbiased estimator for the variance, while `np.var` is the biased estimator.

For our sample the sample statistics differ a by a small amount from their theoretical counterparts.

### T-test and KS-test

We can use the t-test to test whether the mean of our sample differs in a statistically significant way from the theoretical expectation.

```python
>>> print('t-statistic = %.6f pvalue = %.6f' % stats.ttest_1samp(x, m))
t-statistic = 0.391 pvalue = 0.6955
```

The p-value is 0.7, this means that with an alpha error of, for example, 10%, we cannot reject the hypothesis that the sample mean is equal to zero, the expectation of the standard t-distribution.
As an exercise, we can calculate our t-test also directly without using the provided function, which should give us the same answer, and so it does:

```python
>>> tt = (sm-m)/np.sqrt(sv/float(n))  # t-statistic for mean
>>> pval = stats.t.sf(np.abs(tt), n-1)*2  # two-sided pvalue = Prob(abs(t)>tt)
>>> print('t-statistic = %6.3f pvalue = %6.4f' % (tt, pval))
t-statistic = 0.391 pvalue = 0.6955
```

The Kolmogorov-Smirnov test can be used to test the hypothesis that the sample comes from the standard t-distribution

```python
>>> print('KS-statistic D = %6.3f pvalue = %6.4f' % stats.kstest(x, 't', (10,)))
KS-statistic D = 0.016 pvalue = 0.9606
```

Again the p-value is high enough that we cannot reject the hypothesis that the random sample really is distributed according to the t-distribution. In real applications, we don’t know what the underlying distribution is. If we perform the Kolmogorov-Smirnov test of our sample against the standard normal distribution, then we also cannot reject the hypothesis that our sample was generated by the normal distribution given that in this example the p-value is almost 40%.

```python
>>> print('KS-statistic D = %6.3f pvalue = %6.4f' % stats.kstest(x, 'norm'))
KS-statistic D = 0.028 pvalue = 0.3949
```

However, the standard normal distribution has a variance of 1, while our sample has a variance of 1.29. If we standardize our sample and test it against the normal distribution, then the p-value is again large enough that we cannot reject the hypothesis that the sample came form the normal distribution.

```python
>>> d, pval = stats.kstest((x-x.mean())/x.std(), 'norm')
>>> print('KS-statistic D = %6.3f pvalue = %6.4f' % (d, pval))
KS-statistic D = 0.032 pvalue = 0.2402
```

Note: The Kolmogorov-Smirnov test assumes that we test against a distribution with given parameters, since in the last case we estimated mean and variance, this assumption is violated, and the distribution of the test statistic on which the p-value is based, is not correct.

**Tails of the distribution**

Finally, we can check the upper tail of the distribution. We can use the percent point function ppf, which is the inverse of the cdf function, to obtain the critical values, or, more directly, we can use the inverse of the survival function

```python
>>> crit01, crit05, crit10 = stats.t.ppf([1-0.01, 1-0.05, 1-0.10], 10)
>>> print('critical values from ppf at 1%, 5% and 10% \%s\%s\%s' % (crit01, crit05, crit10))
critical values from ppf at 1%, 5% and 10% 2.7638 1.8125 1.3722
>>> print('critical values from isf at 1%, 5% and 10% \%s\%s\%s' % (stats.t.isf([0.01,0.05,0.10]),10)))
critical values from isf at 1%, 5% and 10% 2.7638 1.8125 1.3722
```

```python
>>> freq01 = np.sum(x>crit01) / float(n) * 100
>>> freq05 = np.sum(x>crit05) / float(n) * 100
>>> freq10 = np.sum(x>crit10) / float(n) * 100
>>> print('sample %%-frequency at 1%, 5% and 10% tail \%s\%s\%s' % (freq01, freq05, freq10))
sample %-frequency at 1%, 5% and 10% tail 1.4000 5.8000 10.5000
```
In all three cases, our sample has more weight in the top tail than the underlying distribution. We can briefly check a larger sample to see if we get a closer match. In this case the empirical frequency is quite close to the theoretical probability, but if we repeat this several times the fluctuations are still pretty large.

```python
>>> freq05l = np.sum(stats.t.rvs(10, size=10000) > crit05) / 10000.0 * 100
>>> print('larger sample %%-frequency at 5% tail %8.4f' % freq05l)
larger sample %-frequency at 5% tail 4.8000
```

We can also compare it with the tail of the normal distribution, which has less weight in the tails:

```python
>>> print('tail prob. of normal at 1%, 5% and 10% %8.4f %8.4f %8.4f' %
      ... tuple(stats.norm.sf([crit01, crit05, crit10])*100))
tail prob. of normal at 1%, 5% and 10% 0.2857 3.4957 8.5003
```

The chisquare test can be used to test, whether for a finite number of bins, the observed frequencies differ significantly from the probabilities of the hypothesized distribution.

```python
>>> quantiles = [0.0, 0.01, 0.05, 0.1, 1-0.10, 1-0.05, 1-0.01, 1.0]
>>> crit = stats.t.ppf(quantiles, 10)
>>> crit
array([-inf, -2.76376946, -1.81246112, -1.37218364, 1.37218364,
       1.81246112, 2.76376946, inf])
>>> n_sample = x.size
>>> freqcount = np.histogram(x, bins=crit)[0]
>>> tprob = np.diff(quantiles)
>>> nprob = np.diff(stats.norm.cdf(crit))
>>> tch, tpval = stats.chisquare(freqcount, tprob*n_sample)
>>> nch, npval = stats.chisquare(freqcount, nprob*n_sample)
>>> print('chisquare for t: chi2 = %6.2f pvalue = %6.4f' % (tch, tpval))
chisquare for t: chi2 = 2.30 pvalue = 0.8901
>>> print('chisquare for normal: chi2 = %6.2f pvalue = %6.4f' % (nch, npval))
chisquare for normal: chi2 = 64.60 pvalue = 0.0000
```

We see that the standard normal distribution is clearly rejected while the standard t-distribution cannot be rejected. Since the variance of our sample differs from both standard distribution, we can again redo the test taking the estimate for scale and location into account.

The fit method of the distributions can be used to estimate the parameters of the distribution, and the test is repeated using probabilities of the estimated distribution.

```python
>>> tdf0, tloc, tscale = stats.t.fit(x)
>>> nloc, nscale = stats.norm.fit(x)
>>> tprob = np.diff(stats.t.cdf(crit, tdf0, loc=tloc, scale=tscale))
>>> nprob = np.diff(stats.norm.cdf(crit, loc=nloc, scale=nscale))
>>> tch, tpval = stats.chisquare(freqcount, tprob*n_sample)
>>> nch, npval = stats.chisquare(freqcount, nprob*n_sample)
>>> print('chisquare for t: chi2 = %6.2f pvalue = %6.4f' % (tch, tpval))
chisquare for t: chi2 = 1.58 pvalue = 0.9542
>>> print('chisquare for normal: chi2 = %6.2f pvalue = %6.4f' % (nch, npval))
chisquare for normal: chi2 = 11.08 pvalue = 0.0858
```

Taking account of the estimated parameters, we can still reject the hypothesis that our sample came from a normal distribution (at the 5% level), but again, with a p-value of 0.95, we cannot reject the t distribution.
Special tests for normal distributions
Since the normal distribution is the most common distribution in statistics, there are several additional
functions available to test whether a sample could have been drawn from a normal distribution

First we can test if skew and kurtosis of our sample differ significantly from those of a normal distribution:

```python
>>> print('normal skewtest teststat = %.6f pvalue = %.6f' % stats.skewtest(x))
normal skewtest teststat = 2.785 pvalue = 0.0054
>>> print('normal kurtosistest teststat = %.6f pvalue = %.6f' % stats.kurtosistest(x))
normal kurtosistest teststat = 4.757 pvalue = 0.0000
```

These two tests are combined in the normality test

```python
>>> print('normaltest teststat = %.6f pvalue = %.6f' % stats.normaltest(x))
normaltest teststat = 30.379 pvalue = 0.0000
```

In all three tests the p-values are very low and we can reject the hypothesis that the our sample has skew
and kurtosis of the normal distribution.

Since skew and kurtosis of our sample are based on central moments, we get exactly the same results if we
test the standardized sample:

```python
>>> print('normaltest teststat = %.6f pvalue = %.6f' %
...       stats.normaltest((x-x.mean())/x.std()))
normaltest teststat = 30.379 pvalue = 0.0000
```

Because normality is rejected so strongly, we can check whether the normaltest gives reasonable results for
other cases:

```python
>>> print('normaltest teststat = %.6f pvalue = %.6f' %
...       stats.normaltest(stats.t.rvs(10, size=100)))
normaltest teststat = 4.698 pvalue = 0.0955
>>> print('normaltest teststat = %.6f pvalue = %.6f' %
...       stats.normaltest(stats.norm.rvs(size=1000)))
normaltest teststat = 0.613 pvalue = 0.7361
```

When testing for normality of a small sample of t-distributed observations and a large sample of normal
distributed observation, then in neither case can we reject the null hypothesis that the sample comes from
a normal distribution. In the first case this is because the test is not powerful enough to distinguish a t and
a normally distributed random variable in a small sample.

Comparing two samples
In the following, we are given two samples, which can come either from the same or from different distribution,
and we want to test whether these samples have the same statistical properties.

Comparing means
Test with sample with identical means:

```python
>>> rvs1 = stats.norm.rvs(loc=5, scale=10, size=500)
>>> rvs2 = stats.norm.rvs(loc=5, scale=10, size=500)
>>> stats.ttest_ind(rvs1, rvs2)
Ttest_indResult(statistic=-0.5489036175088705, pvalue=0.5831943748663959)
```

Test with sample with different means:
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```python
>>> rvs3 = stats.norm.rvs(loc=8, scale=10, size=500)
>>> stats.ttest_ind(rvs1, rvs3)
Ttest_indResult(statistic=-4.533414290175026, pvalue=6.507128186389019e-06)
```

Kolmogorov-Smirnov test for two samples `ks_2samp`

For the example where both samples are drawn from the same distribution, we cannot reject the null hypothesis since the pvalue is high.

```python
>>> stats.ks_2samp(rvs1, rvs2)
Ks_2sampResult(statistic=0.025999999999999995, pvalue=0.9954119517306488)
```

In the second example, with different location, i.e. means, we can reject the null hypothesis since the pvalue is below 1%

```python
>>> stats.ks_2samp(rvs1, rvs3)
Ks_2sampResult(statistic=0.11399999999999999, pvalue=0.002713210366128314)
```

Kernel Density Estimation

A common task in statistics is to estimate the probability density function (PDF) of a random variable from a set of data samples. This task is called density estimation. The most well-known tool to do this is the histogram. A histogram is a useful tool for visualization (mainly because everyone understands it), but doesn’t use the available data very efficiently. Kernel density estimation (KDE) is a more efficient tool for the same task. The `gaussian_kde` estimator can be used to estimate the PDF of univariate as well as multivariate data. It works best if the data is unimodal.

Univariate estimation

We start with a minimal amount of data in order to see how `gaussian_kde` works, and what the different options for bandwidth selection do. The data sampled from the PDF is show as blue dashes at the bottom of the figure (this is called a rug plot):

```python
>>> from scipy import stats
>>> import matplotlib.pyplot as plt

>>> x1 = np.array([-7, -5, 1, 4, 5], dtype=np.float)
>>> kde1 = stats.gaussian_kde(x1)
>>> kde2 = stats.gaussian_kde(x1, bw_method='silverman')

>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)

>>> ax.plot(x1, np.zeros(x1.shape), 'b+', ms=20)  # rug plot
>>> x_eval = np.linspace(-10, 10, num=200)
>>> ax.plot(x_eval, kde1(x_eval), 'k-', label="Scott's Rule")
>>> ax.plot(x_eval, kde2(x_eval), 'r-', label="Silverman's Rule")

>>> plt.show()
```

We see that there is very little difference between Scott’s Rule and Silverman’s Rule, and that the bandwidth selection with a limited amount of data is probably a bit too wide. We can define our own bandwidth function to get a less smoothed out result.
We see that if we set bandwidth to be very narrow, the obtained estimate for the probability density function
SciPy Reference Guide, Release 1.2.0

(PDF) is simply the sum of Gaussians around each data point.

We now take a more realistic example, and look at the difference between the two available bandwidth selection rules. Those rules are known to work well for (close to) normal distributions, but even for unimodal distributions that are quite strongly non-normal they work reasonably well. As a non-normal distribution we take a Student's T distribution with 5 degrees of freedom.

```python
import numpy as np
import matplotlib.pyplot as plt
from scipy import stats

np.random.seed(12456)
x1 = np.random.normal(size=200)  # random data, normal distribution
xs = np.linspace(x1.min()-1, x1.max()+1, 200)

kde1 = stats.gaussian_kde(x1)
kde2 = stats.gaussian_kde(x1, bw_method='silverman')

fig = plt.figure(figsize=(8, 6))
ax1 = fig.add_subplot(211)
ax1.plot(x1, np.zeros(x1.shape), 'b+', ms=12)  # rug plot
ax1.plot(xs, kde1(xs), 'k-', label="Scott's Rule")
ax1.plot(xs, kde2(xs), 'b-', label="Silverman's Rule")
ax1.plot(xs, stats.norm.pdf(xs), 'r--', label="True PDF")

ax1.set_xlabel('x')
ax1.set_ylabel('Density')
ax1.set_title("Normal (top) and Student's T$_{df=5}$ (bottom) distributions")
ax1.legend(loc=1)

x2 = stats.t.rvs(5, size=200)  # random data, T distribution
xs = np.linspace(x2.min()-1, x2.max()+1, 200)

kde3 = stats.gaussian_kde(x2)
kde4 = stats.gaussian_kde(x2, bw_method='silverman')

ax2 = fig.add_subplot(212)
ax2.plot(x2, np.zeros(x2.shape), 'b+', ms=12)  # rug plot
ax2.plot(xs, kde3(xs), 'k-', label="Scott's Rule")
ax2.plot(xs, kde4(xs), 'b-', label="Silverman's Rule")
ax2.plot(xs, stats.t.pdf(xs, 5), 'r--', label="True PDF")

ax2.set_xlabel('x')
ax2.set_ylabel('Density')

plt.show()
```

We now take a look at a bimodal distribution with one wider and one narrower Gaussian feature. We expect that this will be a more difficult density to approximate, due to the different bandwidths required to accurately resolve each feature.

```python
>>> from functools import partial
```
Normal (top) and Student's T\(_{\sigma=5}\) (bottom) distributions

- Scott's Rule
- Silverman's Rule
- True PDF
```python
>>> loc1, scale1, size1 = (-2, 1, 175)
>>> loc2, scale2, size2 = (2, 0.2, 50)
>>> x2 = np.concatenate([np.random.normal(loc=loc1, scale=scale1, size=size1),
...                       np.random.normal(loc=loc2, scale=scale2, size=size2)])

>>> x_eval = np.linspace(x2.min() - 1, x2.max() + 1, 500)

>>> kde = stats.gaussian_kde(x2)
>>> kde2 = stats.gaussian_kde(x2, bw_method='silverman')
>>> kde3 = stats.gaussian_kde(x2, bw_method=partial(my_kde_bandwidth, fac=0.2))
>>> kde4 = stats.gaussian_kde(x2, bw_method=partial(my_kde_bandwidth, fac=0.5))

>>> pdf = stats.norm.pdf
>>> bimodal_pdf = pdf(x_eval, loc=loc1, scale=scale1) * float(size1) / x2.size + 
...               pdf(x_eval, loc=loc2, scale=scale2) * float(size2) / x2.size

>>> fig = plt.figure(figsize=(8, 6))
>>> ax = fig.add_subplot(111)

>>> ax.plot(x2, np.zeros(x2.shape), 'b+', ms=12)
>>> ax.plot(x_eval, kde(x_eval), 'k-', label="Scott's Rule")
>>> ax.plot(x_eval, kde2(x_eval), 'b-', label="Silverman's Rule")
>>> ax.plot(x_eval, kde3(x_eval), 'g-', label="Scott * 0.2")
>>> ax.plot(x_eval, kde4(x_eval), 'c-', label="Scott * 0.5")
>>> ax.plot(x_eval, bimodal_pdf, 'r--', label="Actual PDF")

>>> ax.set_xlim([x_eval.min(), x_eval.max()])
>>> ax.legend(loc=2)
>>> ax.set_xlabel('x')
>>> ax.set_ylabel('Density')
>>> plt.show()
```

As expected, the KDE is not as close to the true PDF as we would like due to the different characteristic size of the two features of the bimodal distribution. By halving the default bandwidth (Scott ∗ 0.5) we can do somewhat better, while using a factor 5 smaller bandwidth than the default doesn’t smooth enough. What we really need though in this case is a non-uniform (adaptive) bandwidth.

**Multivariate estimation**

With `gaussian_kde` we can perform multivariate as well as univariate estimation. We demonstrate the bivariate case. First we generate some random data with a model in which the two variates are correlated.

```python
>>> def measure(n):
...     """Measurement model, return two coupled measurements."""
...     m1 = np.random.normal(size=n)
...     m2 = np.random.normal(scale=0.5, size=n)
...     return m1+m2, m1-m2

>>> m1, m2 = measure(2000)
>>> xmin = m1.min()
>>> xmax = m1.max()
>>> ymin = m2.min()
>>> ymax = m2.max()
```
Then we apply the KDE to the data:

```python
>>> X, Y = np.mgrid[xmin:xmax:100j, ymin:ymax:100j]
>>> positions = np.vstack([X.ravel(), Y.ravel()])
>>> values = np.vstack([m1, m2])
>>> kernel = stats.gaussian_kde(values)
>>> Z = np.reshape(kernel.evaluate(positions).T, X.shape)
```

Finally we plot the estimated bivariate distribution as a colormap, and plot the individual data points on top.

```python
>>> fig = plt.figure(figsize=(8, 6))
>>> ax = fig.add_subplot(111)

>>> ax.imshow(np.rot90(Z), cmap=plt.cm.gist_earth_r, 
... extent=[xmin, xmax, ymin, ymax])
>>> ax.plot(m1, m2, 'k.', markersize=2)

>>> ax.set_xlim([xmin, xmax])
>>> ax.set_ylim([ymin, ymax])

>>> plt.show()
```
4.1.14 Multidimensional image processing (scipy.ndimage)

Introduction

Image processing and analysis are generally seen as operations on two-dimensional arrays of values. There are however a number of fields where images of higher dimensionality must be analyzed. Good examples of these are medical imaging and biological imaging. numpy is suited very well for this type of applications due its inherent multidimensional nature. The scipy.ndimage packages provides a number of general image processing and analysis functions that are designed to operate with arrays of arbitrary dimensionality. The packages currently includes functions for linear and non-linear filtering, binary morphology, B-spline interpolation, and object measurements.

Properties shared by all functions

All functions share some common properties. Notably, all functions allow the specification of an output array with the output argument. With this argument you can specify an array that will be changed in-place with the result with the operation. In this case the result is not returned. Usually, using the output argument is more efficient, since an existing array is used to store the result.

The type of arrays returned is dependent on the type of operation, but it is in most cases equal to the type of the input. If, however, the output argument is used, the type of the result is equal to the type of the specified output argument. If no output argument is given, it is still possible to specify what the result of the output should be. This is done by simply assigning the desired numpy type object to the output argument. For example:

```python
>>> from scipy.ndimage import correlate
>>> correlate(np.arange(10), [1, 2.5])
array([ 0, 2, 6, 9, 13, 16, 20, 23, 27, 30])
>>> correlate(np.arange(10), [1, 2.5], output=np.float64)
array([ 0. , 2.5, 6. , 9.5, 13. , 16.5, 20. , 23.5, 27. , 30.5])
```

Filter functions

The functions described in this section all perform some type of spatial filtering of the input array: the elements in the output are some function of the values in the neighborhood of the corresponding input element. We refer to this neighborhood of elements as the filter kernel, which is often rectangular in shape but may also have an arbitrary footprint. Many of the functions described below allow you to define the footprint of the kernel, by passing a mask through the footprint parameter. For example a cross shaped kernel can be defined as follows:

```python
>>> footprint = np.array([[0, 1, 0], [1, 1, 1], [0, 1, 0]])
```

Usually the origin of the kernel is at the center calculated by dividing the dimensions of the kernel shape by two. For instance, the origin of a one-dimensional kernel of length three is at the second element. Take for example the correlation of a one-dimensional array with a filter of length 3 consisting of ones:

```python
>>> from scipy.ndimage import correlate1d
>>> a = [0, 0, 0, 1, 0, 0, 0]
>>> correlate1d(a, [1, 1, 1])
array([0, 0, 1, 1, 1, 0, 0])
```
Sometimes it is convenient to choose a different origin for the kernel. For this reason most functions support the `origin` parameter which gives the origin of the filter relative to its center. For example:

```python
>>> a = [0, 0, 0, 1, 0, 0]
>>> correlate1d(a, [1, 1, 1], origin = -1)
array([0, 1, 1, 1, 0, 0, 0])
```

The effect is a shift of the result towards the left. This feature will not be needed very often, but it may be useful especially for filters that have an even size. A good example is the calculation of backward and forward differences:

```python
>>> a = [0, 0, 1, 1, 1, 0, 0]
>>> correlate1d(a, [-1, 1])  # backward difference
array([0, 0, 1, 0, 0, -1, 0])
>>> correlate1d(a, [-1, 1], origin = -1)  # forward difference
array([0, 1, 0, 0, -1, 0, 0])
```

We could also have calculated the forward difference as follows:

```python
>>> correlate1d(a, [0, -1, 1])
array([0, 1, 0, 0, -1, 0, 0])
```

However, using the origin parameter instead of a larger kernel is more efficient. For multidimensional kernels `origin` can be a number, in which case the origin is assumed to be equal along all axes, or a sequence giving the origin along each axis.

Since the output elements are a function of elements in the neighborhood of the input elements, the borders of the array need to be dealt with appropriately by providing the values outside the borders. This is done by assuming that the arrays are extended beyond their boundaries according certain boundary conditions. In the functions described below, the boundary conditions can be selected using the `mode` parameter which must be a string with the name of the boundary condition. The following boundary conditions are currently supported:

<table>
<thead>
<tr>
<th>Mode</th>
<th>Description</th>
<th>Example</th>
</tr>
</thead>
<tbody>
<tr>
<td>&quot;nearest&quot;</td>
<td>Use the value at the boundary</td>
<td>[1 2 3] -&gt; [1 1 2 3 3]</td>
</tr>
<tr>
<td>&quot;wrap&quot;</td>
<td>Periodically replicate the array</td>
<td>[1 2 3] -&gt; [3 1 2 3 1]</td>
</tr>
<tr>
<td>&quot;reflect&quot;</td>
<td>Reflect the array at the boundary</td>
<td>[1 2 3] -&gt; [1 1 2 3 3]</td>
</tr>
<tr>
<td>&quot;constant&quot;</td>
<td>Use a constant value, default is 0.0</td>
<td>[1 2 3] -&gt; [0 1 2 3 0]</td>
</tr>
</tbody>
</table>

The “constant” mode is special since it needs an additional parameter to specify the constant value that should be used.

**Note:** The easiest way to implement such boundary conditions would be to copy the data to a larger array and extend the data at the borders according to the boundary conditions. For large arrays and large filter kernels, this would be very memory consuming, and the functions described below therefore use a different approach that does not require allocating large temporary buffers.

**Correlation and convolution**

- The `correlate1d` function calculates a one-dimensional correlation along the given axis. The lines of the array along the given axis are correlated with the given `weights`. The `weights` parameter must be a one-dimensional sequences of numbers.
- The function `correlate` implements multidimensional correlation of the input array with a given kernel.
• The `convolve1d` function calculates a one-dimensional convolution along the given axis. The lines of the array along the given axis are convoluted with the given `weights`. The `weights` parameter must be a one-dimensional sequences of numbers.

**Note:** A convolution is essentially a correlation after mirroring the kernel. As a result, the `origin` parameter behaves differently than in the case of a correlation: the result is shifted in the opposite directions.

• The function `convolve` implements multidimensional convolution of the input array with a given kernel.

**Note:** A convolution is essentially a correlation after mirroring the kernel. As a result, the `origin` parameter behaves differently than in the case of a correlation: the result is shifted in the opposite direction.

### Smoothing filters

• The `gaussian_filter1d` function implements a one-dimensional Gaussian filter. The standard-deviation of the Gaussian filter is passed through the parameter `sigma`. Setting `order = 0` corresponds to convolution with a Gaussian kernel. An order of 1, 2, or 3 corresponds to convolution with the first, second or third derivatives of a Gaussian. Higher order derivatives are not implemented.

• The `gaussian_filter` function implements a multidimensional Gaussian filter. The standard-deviations of the Gaussian filter along each axis are passed through the parameter `sigma` as a sequence or numbers. If `sigma` is not a sequence but a single number, the standard deviation of the filter is equal along all directions. The order of the filter can be specified separately for each axis. An order of 0 corresponds to convolution with a Gaussian kernel. An order of 1, 2, or 3 corresponds to convolution with the first, second or third derivatives of a Gaussian. Higher order derivatives are not implemented. The `order` parameter must be a number, to specify the same order for all axes, or a sequence of numbers to specify a different order for each axis.

**Note:** The multidimensional filter is implemented as a sequence of one-dimensional Gaussian filters. The intermediate arrays are stored in the same data type as the output. Therefore, for output types with a lower precision, the results may be imprecise because intermediate results may be stored with insufficient precision. This can be prevented by specifying a more precise output type.

• The `uniform_filter1d` function calculates a one-dimensional uniform filter of the given `size` along the given axis.

• The `uniform_filter` implements a multidimensional uniform filter. The sizes of the uniform filter are given for each axis as a sequence of integers by the `size` parameter. If `size` is not a sequence, but a single number, the sizes along all axis are assumed to be equal.

**Note:** The multidimensional filter is implemented as a sequence of one-dimensional uniform filters. The intermediate arrays are stored in the same data type as the output. Therefore, for output types with a lower precision, the results may be imprecise because intermediate results may be stored with insufficient precision. This can be prevented by specifying a more precise output type.

### Filters based on order statistics

• The `minimum_filter1d` function calculates a one-dimensional minimum filter of given `size` along the given axis.

• The `maximum_filter1d` function calculates a one-dimensional maximum filter of given `size` along the given axis.
The `minimum_filter` function calculates a multidimensional minimum filter. Either the sizes of a rectangular kernel or the footprint of the kernel must be provided. The `size` parameter, if provided, must be a sequence of sizes or a single number in which case the size of the filter is assumed to be equal along each axis. The `footprint`, if provided, must be an array that defines the shape of the kernel by its non-zero elements.

The `maximum_filter` function calculates a multidimensional maximum filter. Either the sizes of a rectangular kernel or the footprint of the kernel must be provided. The `size` parameter, if provided, must be a sequence of sizes or a single number in which case the size of the filter is assumed to be equal along each axis. The `footprint`, if provided, must be an array that defines the shape of the kernel by its non-zero elements.

The `rank_filter` function calculates a multidimensional rank filter. The `rank` may be less than zero, i.e., `rank = -1` indicates the largest element. Either the sizes of a rectangular kernel or the footprint of the kernel must be provided. The `size` parameter, if provided, must be a sequence of sizes or a single number in which case the size of the filter is assumed to be equal along each axis. The `footprint`, if provided, must be an array that defines the shape of the kernel by its non-zero elements.

The `percentile_filter` function calculates a multidimensional percentile filter. The `percentile` may be less than zero, i.e., `percentile = -20` equals `percentile = 80`. Either the sizes of a rectangular kernel or the footprint of the kernel must be provided. The `size` parameter, if provided, must be a sequence of sizes or a single number in which case the size of the filter is assumed to be equal along each axis. The `footprint`, if provided, must be an array that defines the shape of the kernel by its non-zero elements.

The `median_filter` function calculates a multidimensional median filter. Either the sizes of a rectangular kernel or the footprint of the kernel must be provided. The `size` parameter, if provided, must be a sequence of sizes or a single number in which case the size of the filter is assumed to be equal along each axis. The `footprint` if provided, must be an array that defines the shape of the kernel by its non-zero elements.

**Derivatives**

Derivative filters can be constructed in several ways. The function `gaussian_filter1d` described in *Smoothing filters* can be used to calculate derivatives along a given axis using the `order` parameter. Other derivative filters are the Prewitt and Sobel filters:

- The `prewitt` function calculates a derivative along the given axis.
- The `sobel` function calculates a derivative along the given axis.

The Laplace filter is calculated by the sum of the second derivatives along all axes. Thus, different Laplace filters can be constructed using different second derivative functions. Therefore we provide a general function that takes a function argument to calculate the second derivative along a given direction.

- The function `generic_laplace` calculates a laplace filter using the function passed through `derivative2` to calculate second derivatives. The function `derivative2` should have the following signature

\[
\text{derivative2}(\text{input}, \text{axis}, \text{output}, \text{mode}, \text{cval}, \ast\ast\ast\text{extra_arguments}, \ast\ast\ast\text{extra_keywords})
\]

It should calculate the second derivative along the dimension `axis`. If `output` is not `None` it should use that for the output and return `None`, otherwise it should return the result. `mode`, `cval` have the usual meaning.

The `extra_arguments` and `extra_keywords` arguments can be used to pass a tuple of extra arguments and a dictionary of named arguments that are passed to `derivative2` at each call.

For example
To demonstrate the use of the `extra_arguments` argument we could do

```python
>>> def d2(input, axis, output, mode, cval, weights):
...     return correlate1d(input, weights, axis, output, mode, cval, 0)
...
>>> a = np.zeros((5, 5))
>>> a[2, 2] = 1
>>> from scipy.ndimage import generic_laplace
>>> generic_laplace(a, d2, extra_arguments = ([1, -2, 1],))
array([[ 0., 0., 0., 0., 0.],
       [ 0., 0., 1., 0., 0.],
       [ 0., 1., -4., 1., 0.],
       [ 0., 0., 1., 0., 0.],
       [ 0., 0., 0., 0., 0.]]
```

or

```python
>>> generic_laplace(a, d2, extra_keywords = {'weights': [1, -2, 1]})
array([[ 0., 0., 0., 0., 0.],
       [ 0., 0., 1., 0., 0.],
       [ 0., 1., -4., 1., 0.],
       [ 0., 0., 1., 0., 0.],
       [ 0., 0., 0., 0., 0.]]
```

The following two functions are implemented using `generic_laplace` by providing appropriate functions for the second derivative function:

- The function `laplace` calculates the Laplace using discrete differentiation for the second derivative (i.e. convolution with `[1, -2, 1]`).
- The function `gaussian_laplace` calculates the Laplace filter using `gaussian_filter` to calculate the second derivatives. The standard-deviations of the Gaussian filter along each axis are passed through the parameter `sigma` as a sequence or numbers. If `sigma` is not a sequence but a single number, the standard deviation of the filter is equal along all directions.

The gradient magnitude is defined as the square root of the sum of the squares of the gradients in all directions. Similar to the generic Laplace function there is a `generic_gradient_magnitude` function that calculates the gradient magnitude of an array.

- The function `generic_gradient_magnitude` calculates a gradient magnitude using the function passed through `derivative` to calculate first derivatives. The function `derivative` should have the following signature...
derivative(input, axis, output, mode, cval, *extra_arguments, **extra_keywords)

It should calculate the derivative along the dimension axis. If output is not None it should use that for
the output and return None, otherwise it should return the result. mode, cval have the usual meaning.

The extra_arguments and extra_keywords arguments can be used to pass a tuple of extra arguments
and a dictionary of named arguments that are passed to derivative at each call.

For example, the sobel function fits the required signature

```python
>>> a = np.zeros((5, 5))
>>> a[2, 2] = 1
>>> from scipy.ndimage import sobel, generic_gradient_magnitude

>>> generic_gradient_magnitude(a, sobel)
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0., 1.41421356, 2., 1.41421356, 0.],
       [ 0.,  2.,  0.,  2.,  0.],
       [ 0., 1.41421356, 2., 1.41421356, 0.],
       [ 0.,  0.,  0.,  0.,  0.]]))
```

See the documentation of generic_laplace for examples of using the extra_arguments and extra_keywords arguments.

The sobel and prewitt functions fit the required signature and can therefore directly be used with

```
generic_gradient_magnitude
```

- The function gaussian_gradient_magnitude calculates the gradient magnitude using
gaussian_filter to calculate the first derivatives. The standard-deviations of the Gaussian
filter along each axis are passed through the parameter sigma as a sequence or numbers. If sigma is
not a sequence but a single number, the standard deviation of the filter is equal along all directions.

**Generic filter functions**

To implement filter functions, generic functions can be used that accept a callable object that implements the
filtering operation. The iteration over the input and output arrays is handled by these generic functions, along
with such details as the implementation of the boundary conditions. Only a callable object implementing a
callback function that does the actual filtering work must be provided. The callback function can also be
written in C and passed using a PyCapsule (see Extending scipy.ndimage in C for more information).

- The generic_filter1d function implements a generic one-dimensional filter function, where the
actual filtering operation must be supplied as a python function (or other callable object). The
generic_filter1d function iterates over the lines of an array and calls function at each line. The
arguments that are passed to function are one-dimensional arrays of the np.float64 type. The first
contains the values of the current line. It is extended at the beginning end the end, according to the
filter_size and origin arguments. The second array should be modified in-place to provide the output
values of the line. For example consider a correlation along one dimension:

```python
>>> a = np.arange(12).reshape(3,4)
>>> correlate1d(a, [1, 2, 3])
array([[ 3, 8, 14, 17],
       [27, 32, 38, 41],
       [51, 56, 62, 65]])
```

The same operation can be implemented using generic_filter1d as follows:

```python
>>> def fnc(iline, oline):
...     oline[:] = iline[-2:] + 2 * iline[1:-1] + 3 * iline[2:]
(continues on next page)```
Here the origin of the kernel was (by default) assumed to be in the middle of the filter of length 3. Therefore, each input line was extended by one value at the beginning and at the end, before the function was called.

Optionally extra arguments can be defined and passed to the filter function. The `extra_arguments` and `extra_keywords` arguments can be used to pass a tuple of extra arguments and/or a dictionary of named arguments that are passed to derivative at each call. For example, we can pass the parameters of our filter as an argument

```python
>>> def fnc(iline, oline, a, b):
...     oline[...] = iline[:-2] + a * iline[1:-1] + b * iline[2:]
... >>> generic_filter1d(a, fnc, 3, extra_arguments = (2, 3))
array([[ 3,  8, 14, 17],
       [27, 32, 38, 41],
       [51, 56, 62, 65]])
```

or

```python
>>> generic_filter1d(a, fnc, 3, extra_keywords = {'a':2, 'b':3})
array([[ 3,  8, 14, 17],
       [27, 32, 38, 41],
       [51, 56, 62, 65]])
```

- The `generic_filter` function implements a generic filter function, where the actual filtering operation must be supplied as a python function (or other callable object). The `generic_filter` function iterates over the array and calls `function` at each element. The argument of `function` is a one-dimensional array of the `np.float64` type, that contains the values around the current element that are within the footprint of the filter. The function should return a single value that can be converted to a double precision number. For example consider a correlation:

```python
>>> a = np.arange(12).reshape(3,4)
>>> correlate(a, [[1, 0], [0, 3]])
array([[ 0,  3,  7, 11],
       [12, 15, 19, 23],
       [28, 31, 35, 39]])
```

The same operation can be implemented using `generic_filter` as follows:

```python
>>> def fnc(buffer):
...     return (buffer * np.array([1, 3])).sum()
... >>> from scipy.ndimage import generic_filter
>>> generic_filter(a, fnc, footprint = [[1, 0], [0, 1]])
array([[ 0,  3,  7, 11],
       [12, 15, 19, 23],
       [28, 31, 35, 39]])
```
Here a kernel footprint was specified that contains only two elements. Therefore the filter function
receives a buffer of length equal to two, which was multiplied with the proper weights and the result
summed.

When calling \texttt{generic\_filter}, either the sizes of a rectangular kernel or the footprint of the kernel
must be provided. The \texttt{size} parameter, if provided, must be a sequence of sizes or a single number in
which case the size of the filter is assumed to be equal along each axis. The \texttt{footprint}, if provided, must
be an array that defines the shape of the kernel by its non-zero elements.

Optionally extra arguments can be defined and passed to the filter function. The \texttt{extra\_arguments}
and \texttt{extra\_keywords} arguments can be used to pass a tuple of extra arguments and/or a dictionary of
named arguments that are passed to derivative at each call. For example, we can pass the parameters
of our filter as an argument

\begin{verbatim}
>>> def fnc(buffer, weights):
...     weights = np.asarray(weights)
...     return (buffer * weights).sum()
...
>>> generic_filter(a, fnc, footprint = [[1, 0], [0, 1]], extra_arguments = ([1, 3],))
array([[ 0,  3,  7, 11],
       [12, 15, 19, 23],
       [28, 31, 35, 39]])

either

>>> generic_filter(a, fnc, footprint = [[1, 0], [0, 1]], extra_keywords= {'weights': [1, 3]})
array([[ 0,  3,  7, 11],
       [12, 15, 19, 23],
       [28, 31, 35, 39]])
\end{verbatim}

These functions iterate over the lines or elements starting at the last axis, i.e. the last index changes the
fastest. This order of iteration is guaranteed for the case that it is important to adapt the filter depending on
spatial location. Here is an example of using a class that implements the filter and keeps track of the current
coordinates while iterating. It performs the same filter operation as described above for \texttt{generic\_filter},
but additionally prints the current coordinates:

\begin{verbatim}
>>> a = np.arange(12).reshape(3,4)
>>> class fnc_class:
...     def __init__(self, shape):
...         # store the shape:
...         self.shape = shape
...         # initialize the coordinates:
...         self.coordinates = [0] * len(shape)
...
...     def filter(self, buffer):
...         result = (buffer * np.array([1, 3])).sum()
...         print(self.coordinates)
...         # calculate the next coordinates:
...         axes = list(range(len(self.shape)))
...         axes.reverse()
...         for jj in axes:
...             if self.coordinates[jj] < self.shape[jj] - 1:
...                 (continues on next page)
\end{verbatim}
... self.coordinates[jj] += 1
... break
... else:
...     self.coordinates[jj] = 0
... return result
...

>>> fnc = fnc_class(shape = (3,4))
>>> generic_filter(a, fnc.filter, footprint = [[1, 0], [0, 1]])

[[ 0, 0],
[0, 1]
[0, 2]
[0, 3]
[1, 0]
[1, 1]
[1, 2]
[1, 3]
[2, 0]
[2, 1]
[2, 2]
[2, 3]
array([[ 0, 3, 7, 11],
       [12, 15, 19, 23],
       [28, 31, 35, 39]])

For the generic_filter1d function the same approach works, except that this function does not iterate over the axis that is being filtered. The example for generic_filter1d then becomes this:

>>> a = np.arange(12).reshape(3,4)

>>> class fncld_class:
...     def __init__(self, shape, axis = -1):
...         # store the filter axis:
...         self.axis = axis
...         # store the shape:
...         self.shape = shape
...         # initialize the coordinates:
...         self.coordinates = [0] * len(shape)
...     
...     def filter(self, iline, oline):
...         oline[:] = iline[:-2] + 2 * iline[1:-1] + 3 * iline[2:]
...         print(self.coordinates)
...         # calculate the next coordinates:
...         axes = list(range(len(self.shape)))
...         # skip the filter axis:
...         del axes[self.axis]
...         axes.reverse()
...         for jj in axes:
...             if self.coordinates[jj] < self.shape[jj] - 1:
...                 self.coordinates[jj] += 1
...             break
...         else:
...             self.coordinates[jj] = 0
Fourier domain filters
The functions described in this section perform filtering operations in the Fourier domain. Thus, the input array of such a function should be compatible with an inverse Fourier transform function, such as the functions from the `numpy.fft` module. We therefore have to deal with arrays that may be the result of a real or a complex Fourier transform. In the case of a real Fourier transform only half of the of the symmetric complex transform is stored. Additionally, it needs to be known what the length of the axis was that was transformed by the real fft. The functions described here provide a parameter `n` that in the case of a real transform must be equal to the length of the real transform axis before transformation. If this parameter is less than zero, it is assumed that the input array was the result of a complex Fourier transform. The parameter `axis` can be used to indicate along which axis the real transform was executed.

- The `fourier_shift` function multiplies the input array with the multidimensional Fourier transform of a shift operation for the given shift. The `shift` parameter is a sequences of shifts for each dimension, or a single value for all dimensions.

- The `fourier_gaussian` function multiplies the input array with the multidimensional Fourier transform of a Gaussian filter with given standard-deviations `sigma`. The `sigma` parameter is a sequences of values for each dimension, or a single value for all dimensions.

- The `fourier_uniform` function multiplies the input array with the multidimensional Fourier transform of a uniform filter with given sizes `size`. The `size` parameter is a sequences of values for each dimension, or a single value for all dimensions.

- The `fourier_ellipsoid` function multiplies the input array with the multidimensional Fourier transform of an elliptically shaped filter with given sizes `size`. The `size` parameter is a sequences of values for each dimension, or a single value for all dimensions. This function is only implemented for dimensions 1, 2, and 3.

Interpolation functions
This section describes various interpolation functions that are based on B-spline theory. A good introduction to B-splines can be found in¹.

Spline pre-filters
Interpolation using splines of an order larger than 1 requires a pre-filtering step. The interpolation functions described in section Interpolation functions apply pre-filtering by calling `spline_filter`, but they can be instructed not to do this by setting the `prefilter` keyword equal to False. This is useful if more than one interpolation operation is done on the same array. In this case it is more efficient to do the pre-filtering only once and use a prefiltered array as the input of the interpolation functions. The following two functions implement the pre-filtering:

- The `spline_filter1d` function calculates a one-dimensional spline filter along the given axis. An output array can optionally be provided. The order of the spline must be larger than 1 and less than 6.

• The \texttt{spline\_filter} function calculates a multidimensional spline filter.

\textbf{Note:} The multidimensional filter is implemented as a sequence of one-dimensional spline filters. The intermediate arrays are stored in the same data type as the output. Therefore, if an output with a limited precision is requested, the results may be imprecise because intermediate results may be stored with insufficient precision. This can be prevented by specifying a output type of high precision.

\textbf{Interpolation functions}

Following functions all employ spline interpolation to effect some type of geometric transformation of the input array. This requires a mapping of the output coordinates to the input coordinates, and therefore the possibility arises that input values outside the boundaries are needed. This problem is solved in the same way as described in \texttt{Filter functions} for the multidimensional filter functions. Therefore these functions all support a \texttt{mode} parameter that determines how the boundaries are handled, and a \texttt{cval} parameter that gives a constant value in case that the ‘constant’ mode is used.

• The \texttt{geometric\_transform} function applies an arbitrary geometric transform to the input. The given \texttt{mapping} function is called at each point in the output to find the corresponding coordinates in the input. \texttt{mapping} must be a callable object that accepts a tuple of length equal to the output array rank and returns the corresponding input coordinates as a tuple of length equal to the input array rank. The output shape and output type can optionally be provided. If not given they are equal to the input shape and type.

For example:

```python
>>> a = np.arange(12).reshape(4,3).astype(np.float64)
>>> def shift_func(output_coordinates):
...     return (output_coordinates[0] - 0.5, output_coordinates[1] - 0.5)
...
>>> from scipy.ndimage import geometric_transform
>>> geometric_transform(a, shift_func)
array([[ 0. , 0. , 0. ],
       [ 0. , 1.3625, 2.7375],
       [ 0. , 4.8125, 6.1875],
       [ 0. , 8.2625, 9.6375]])
```

Optionally extra arguments can be defined and passed to the filter function. The \texttt{extra\_arguments} and \texttt{extra\_keywords} arguments can be used to pass a tuple of extra arguments and/or a dictionary of named arguments that are passed to derivative at each call. For example, we can pass the shifts in our example as arguments

```python
>>> def shift_func(output_coordinates, s0, s1):
...     return (output_coordinates[0] - s0, output_coordinates[1] - s1)
...
>>> geometric_transform(a, shift_func, extra_arguments = (0.5, 0.5))
array([[ 0. , 0. , 0. ],
       [ 0. , 1.3625, 2.7375],
       [ 0. , 4.8125, 6.1875],
       [ 0. , 8.2625, 9.6375]])
```

or

```python
>>> geometric_transform(a, shift_func, extra_keywords = {'s0': 0.5, 's1': 0.5})
array([[ 0. , 0. , 0. ],
       [ 0. , 1.3625, 2.7375],
       ...]
```

(continues on next page)
The mapping function can also be written in C and passed using a `scipy.LowLevelCallable`. See `Extending scipy.ndimage in C` for more information.

- The function `map_coordinates` applies an arbitrary coordinate transformation using the given array of coordinates. The shape of the output is derived from that of the coordinate array by dropping the first axis. The parameter `coordinates` is used to find for each point in the output the corresponding coordinates in the input. The values of `coordinates` along the first axis are the coordinates in the input array at which the output value is found. (See also the numarray `coordinates` function.) Since the coordinates may be non-integer coordinates, the value of the input at these coordinates is determined by spline interpolation of the requested order.

Here is an example that interpolates a 2D array at (0.5, 0.5) and (1, 2):

```python
>>> a = np.arange(12).reshape(4,3).astype(np.float64)
>>> a
array([[ 0.,  1.,  2.],
       [ 3.,  4.,  5.],
       [ 6.,  7.,  8.],
       [ 9., 10., 11.]]
>>> from scipy.ndimage import map_coordinates
>>> map_coordinates(a, [[0.5, 2], [0.5, 1]])
array([ 1.3625,  7.0])
```

- The `affine_transform` function applies an affine transformation to the input array. The given transformation `matrix` and `offset` are used to find for each point in the output the corresponding coordinates in the input. The value of the input at the calculated coordinates is determined by spline interpolation of the requested order. The transformation `matrix` must be two-dimensional or can also be given as a one-dimensional sequence or array. In the latter case, it is assumed that the matrix is diagonal. A more efficient interpolation algorithm is then applied that exploits the separability of the problem. The output shape and output type can optionally be provided. If not given they are equal to the input shape and type.

- The `shift` function returns a shifted version of the input, using spline interpolation of the requested `order`.

- The `zoom` function returns a rescaled version of the input, using spline interpolation of the requested `order`.

- The `rotate` function returns the input array rotated in the plane defined by the two axes given by the parameter `axes`, using spline interpolation of the requested `order`. The angle must be given in degrees. If `reshape` is true, then the size of the output array is adapted to contain the rotated input.

**Morphology**

**Binary morphology**

- The `generate_binary_structure` functions generates a binary structuring element for use in binary morphology operations. The `rank` of the structure must be provided. The size of the structure that is returned is equal to three in each direction. The value of each element is equal to one if the square of the Euclidean distance from the element to the center is less or equal to `connectivity`. For instance, two dimensional 4-connected and 8-connected structures are generated as follows:
Most binary morphology functions can be expressed in terms of the basic operations erosion and dilation.

- The `binary_erosion` function implements binary erosion of arrays of arbitrary rank with the given structuring element. The origin parameter controls the placement of the structuring element as described in Filter functions. If no structuring element is provided, an element with connectivity equal to one is generated using `generate_binary_structure`. The `border_value` parameter gives the value of the array outside boundaries. The erosion is repeated `iterations` times. If `iterations` is less than one, the erosion is repeated until the result does not change anymore. If a `mask` array is given, only those elements with a true value at the corresponding mask element are modified at each iteration.

- The `binary_dilation` function implements binary dilation of arrays of arbitrary rank with the given structuring element. The origin parameter controls the placement of the structuring element as described in Filter functions. If no structuring element is provided, an element with connectivity equal to one is generated using `generate_binary_structure`. The `border_value` parameter gives the value of the array outside boundaries. The dilation is repeated `iterations` times. If `iterations` is less than one, the dilation is repeated until the result does not change anymore. If a `mask` array is given, only those elements with a true value at the corresponding mask element are modified at each iteration.

Here is an example of using `binary_dilation` to find all elements that touch the border, by repeatedly dilating an empty array from the border using the data array as the mask:

```python
>>> struct = np.array([[0, 1, 0], [1, 1, 1], [0, 1, 0]])
>>> a = np.array([[1,0,0,0,0], [1,1,0,1,0], [0,0,1,1,0], [0,0,0,0,0]])
>>> a
array([[1, 0, 0, 0, 0],
       [1, 1, 0, 1, 0],
       [0, 0, 1, 1, 0],
       [0, 0, 0, 0, 0]])
>>> from scipy.ndimage import binary_dilation
>>> binary_dilation(np.zeros(a.shape), struct, -1, a, border_value=1)
array([[ True, False, False, False, False],
       [ True, True, False, False, False],
       [False, False, False, False, False],
       [False, False, False, False, False]], dtype=bool)
```

The `binary_erosion` and `binary_dilation` functions both have an `iterations` parameter which allows the erosion or dilation to be repeated a number of times. Repeating an erosion or a dilation with a given structure \( n \) times is equivalent to an erosion or a dilation with a structure that is \( n-1 \) times dilated with itself. A function is provided that allows the calculation of a structure that is dilated a number of times with itself:

- The `iterate_structure` function returns a structure by dilation of the input structure \( iteration - 1 \) times with itself.

For instance:

```python
```
```python
>>> struct = generate_binary_structure(2, 1)

>>> struct
array([[False,  True, False],
       [ True,  True,  True],
       [False,  True, False]], dtype=bool)

>>> from scipy.ndimage import iterate_structure

>>> iterate_structure(struct, 2)
array([[False, False, True, False, False],
       [False, True, True, True, False],
       [ True, True, True, True, True],
       [False, True, True, True, False],
       [False, False, True, False, False]], dtype=bool)
```

If the origin of the original structure is equal to 0, then it is also equal to 0 for the iterated structure. If not, the origin must also be adapted if the equivalent of the *iterations* erosions or dilations must be achieved with the iterated structure. The adapted origin is simply obtained by multiplying with the number of iterations. For convenience the :func:`iterate_structure` also returns the adapted origin if the *origin* parameter is not ``None``:

```python
>>> iterate_structure(struct, 2, -1)
(array([[False, False, True, False, False],
       [False, True, True, True, False],
       [ True, True, True, True, True],
       [False, True, True, True, False],
       [False, False, True, False, False]], dtype=bool), [-2, -2])
```

Other morphology operations can be defined in terms of erosion and dilation. The following functions provide a few of these operations for convenience:

- **The binary_opening function** implements binary opening of arrays of arbitrary rank with the given structuring element. Binary opening is equivalent to a binary erosion followed by a binary dilation with the same structuring element. The origin parameter controls the placement of the structuring element as described in Filter functions. If no structuring element is provided, an element with connectivity equal to one is generated using `generate_binary_structure`. The iterations parameter gives the number of erosions that is performed followed by the same number of dilations.

- **The binary_closing function** implements binary closing of arrays of arbitrary rank with the given structuring element. Binary closing is equivalent to a binary dilation followed by a binary erosion with the same structuring element. The origin parameter controls the placement of the structuring element as described in Filter functions. If no structuring element is provided, an element with connectivity equal to one is generated using `generate_binary_structure`. The iterations parameter gives the number of dilations that is performed followed by the same number of erosions.

- **The binary_fill_holes function** is used to close holes in objects in a binary image, where the structure defines the connectivity of the holes. The origin parameter controls the placement of the structuring element as described in Filter functions. If no structuring element is provided, an element with connectivity equal to one is generated using `generate_binary_structure`.

- **The binary_hit_or_miss function** implements a binary hit-or-miss transform of arrays of arbitrary rank with the given structuring elements. The hit-or-miss transform is calculated by erosion of the
input with the first structure, erosion of the logical not of the input with the second structure, followed by the logical and of these two erosions. The origin parameters control the placement of the structuring elements as described in Filter functions. If origin2 equals None it is set equal to the origin1 parameter. If the first structuring element is not provided, a structuring element with connectivity equal to one is generated using generate_binary_structure, if structure2 is not provided, it is set equal to the logical not of structure1.

Grey-scale morphology
Grey-scale morphology operations are the equivalents of binary morphology operations that operate on arrays with arbitrary values. Below we describe the grey-scale equivalents of erosion, dilation, opening and closing. These operations are implemented in a similar fashion as the filters described in Filter functions, and we refer to this section for the description of filter kernels and footprints, and the handling of array borders. The grey-scale morphology operations optionally take a structure parameter that gives the values of the structuring element. If this parameter is not given the structuring element is assumed to be flat with a value equal to zero. The shape of the structure can optionally be defined by the footprint parameter. If this parameter is not given, the structure is assumed to be rectangular, with sizes equal to the dimensions of the structure array, or by the size parameter if structure is not given. The size parameter is only used if both structure and footprint are not given, in which case the structuring element is assumed to be rectangular and flat with the dimensions given by size. The size parameter, if provided, must be a sequence of sizes or a single number in which case the size of the filter is assumed to be equal along each axis. The footprint parameter, if provided, must be an array that defines the shape of the kernel by its non-zero elements.

Grey-scale opening and dilation there are operations for grey-scale erosion and dilation:

- The grey_erosion function calculates a multidimensional grey-scale erosion.
- The grey_dilation function calculates a multidimensional grey-scale dilation.

Grey-scale opening and closing operations can be defined similar to their binary counterparts:

- The grey_opening function implements grey-scale opening of arrays of arbitrary rank. Grey-scale opening is equivalent to a grey-scale erosion followed by a grey-scale dilation.
- The grey_closing function implements grey-scale closing of arrays of arbitrary rank. Grey-scale opening is equivalent to a grey-scale dilation followed by a grey-scale erosion.
- The morphological_gradient function implements a grey-scale morphological gradient of arrays of arbitrary rank. The grey-scale morphological gradient is equal to the difference of a grey-scale dilation and a grey-scale erosion.
- The morphological_laplace function implements a grey-scale morphological laplace of arrays of arbitrary rank. The grey-scale morphological laplace is equal to the sum of a grey-scale dilation and a grey-scale erosion minus twice the input.
- The white_tophat function implements a white top-hat filter of arrays of arbitrary rank. The white top-hat is equal to the difference of the input and a grey-scale opening.
- The black_tophat function implements a black top-hat filter of arrays of arbitrary rank. The black top-hat is equal to the difference of a grey-scale closing and the input.

Distance transforms
Distance transforms are used to calculate the minimum distance from each element of an object to the background. The following functions implement distance transforms for three different distance metrics: Euclidean, City Block, and Chessboard distances.

- The function distance_transform_cdt uses a chamfer type algorithm to calculate the distance transform of the input, by replacing each object element (defined by values larger than zero) with the shortest distance to the background (all non-object elements). The structure determines the type of chamfering that is done. If the structure is equal to ‘cityblock’ a structure is generated using
generate_binary_structure with a squared distance equal to 1. If the structure is equal to ‘chessboard’, a structure is generated using generate_binary_structure with a squared distance equal to the rank of the array. These choices correspond to the common interpretations of the cityblock and the chessboard distance metrics in two dimensions.

In addition to the distance transform, the feature transform can be calculated. In this case the index of the closest background element is returned along the first axis of the result. The return_distances, and return_indices flags can be used to indicate if the distance transform, the feature transform, or both must be returned.

The distances and indices arguments can be used to give optional output arrays that must be of the correct size and type (both np.int32). The basics of the algorithm used to implement this function is described in\(^2\).

- The function distance_transform_edt calculates the exact euclidean distance transform of the input, by replacing each object element (defined by values larger than zero) with the shortest euclidean distance to the background (all non-object elements).

In addition to the distance transform, the feature transform can be calculated. In this case the index of the closest background element is returned along the first axis of the result. The return_distances, and return_indices flags can be used to indicate if the distance transform, the feature transform, or both must be returned.

Optionally the sampling along each axis can be given by the sampling parameter which should be a sequence of length equal to the input rank, or a single number in which the sampling is assumed to be equal along all axes.

The distances and indices arguments can be used to give optional output arrays that must be of the correct size and type (np.float64 and np.int32). The algorithm used to implement this function is described in\(^3\).

- The function distance_transform_bf uses a brute-force algorithm to calculate the distance transform of the input, by replacing each object element (defined by values larger than zero) with the shortest distance to the background (all non-object elements). The metric must be one of “euclidean”, “cityblock”, or “chessboard”.

In addition to the distance transform, the feature transform can be calculated. In this case the index of the closest background element is returned along the first axis of the result. The return_distances, and return_indices flags can be used to indicate if the distance transform, the feature transform, or both must be returned.

Optionally the sampling along each axis can be given by the sampling parameter which should be a sequence of length equal to the input rank, or a single number in which the sampling is assumed to be equal along all axes. This parameter is only used in the case of the euclidean distance transform.

The distances and indices arguments can be used to give optional output arrays that must be of the correct size and type (np.float64 and np.int32).

**Note:** This function uses a slow brute-force algorithm, the function distance_transform_cdt can be used to more efficiently calculate cityblock and chessboard distance transforms. The function distance_transform_edt can be used to more efficiently calculate the exact euclidean distance transform.


Segmentation and labeling

Segmentation is the process of separating objects of interest from the background. The most simple approach is probably intensity thresholding, which is easily done with numpy functions:

```python
g = np.array([[1,2,2,1,1,0],
              ...  [0,2,3,1,2,0],
              ...  [1,1,1,3,3,2],
              ...  [1,1,1,1,2,1]])
g = np.where(g > 1, 1, 0)
```

The result is a binary image, in which the individual objects still need to be identified and labeled. The function `label` generates an array where each object is assigned a unique number:

- The `label` function generates an array where the objects in the input are labeled with an integer index. It returns a tuple consisting of the array of object labels and the number of objects found, unless the `output` parameter is given, in which case only the number of objects is returned. The connectivity of the objects is defined by a structuring element. For instance, in two dimensions using a four-connected structuring element gives:

```python
g = np.array([[0,1,1,0,0,0],[0,1,0,1,1,1],[0,0,0,0,1,0]])
s = [[0, 1, 0], [1,1,1], [0,1,0]]
from scipy.ndimage import label
label(g, s)[0]
```

These two objects are not connected because there is no way in which we can place the structuring element such that it overlaps with both objects. However, an 8-connected structuring element results in only a single object:

```python
g = np.array([[0,1,1,0,0,0],[0,1,1,0,1,0],[0,0,0,1,1,1],[0,0,0,0,1,0]])
s = [[1,1,1], [1,1,1], [1,1,1]]
label(g, s)[0]
```

If no structuring element is provided, one is generated by calling `generate_binary_structure` (see Binary morphology) using a connectivity of one (which in 2D is the 4-connected structure of the first example). The input can be of any type, any value not equal to zero is taken to be part of an object. This is useful if you need to ‘re-label’ an array of object indices, for instance after removing unwanted objects. Just apply the label function again to the index array. For instance:

```python
l, n = label([1, 0, 1, 0, 1])
l = np.where(l != 2, 1, 0)
```
>>> 1
array([1, 0, 0, 0, 3])
>>> label(1)[0]
array([1, 0, 0, 0, 2])

Note: The structuring element used by label is assumed to be symmetric.

There is a large number of other approaches for segmentation, for instance from an estimation of the borders of the objects that can be obtained for instance by derivative filters. One such an approach is watershed segmentation. The function watershed_ift generates an array where each object is assigned a unique label, from an array that localizes the object borders, generated for instance by a gradient magnitude filter. It uses an array containing initial markers for the objects:

- The watershed_ift function applies a watershed from markers algorithm, using an Iterative Forest Transform, as described in

- The inputs of this function are the array to which the transform is applied, and an array of markers that designate the objects by a unique label, where any non-zero value is a marker. For instance:

```python
>>> input = np.array([[0, 0, 0, 0, 0, 0, 0],
                    ... [0, 1, 1, 1, 1, 1, 1],
                    ... [0, 1, 0, 0, 0, 1, 1],
                    ... [0, 1, 0, 0, 0, 1, 1],
                    ... [0, 1, 0, 0, 0, 1, 1],
                    ... [0, 1, 1, 1, 1, 1, 1],
                    ... [0, 0, 0, 0, 0, 0, 0]], np.uint8)
>>> markers = np.array([[1, 0, 0, 0, 0, 0, 0],
                      ... [0, 0, 0, 0, 0, 0, 0],
                      ... [0, 0, 0, 0, 0, 0, 0],
                      ... [0, 0, 0, 2, 0, 0, 0],
                      ... [0, 0, 0, 0, 0, 0, 0],
                      ... [0, 0, 0, 0, 0, 0, 0],
                      ... [0, 0, 0, 0, 0, 0, 0]], np.int8)
>>> from scipy.ndimage import watershed_ift
```

```python
>>> watershed_ift(input, markers)
array([[1, 1, 1, 1, 1, 1],
       [1, 1, 2, 2, 2, 1],
       [1, 2, 2, 2, 2, 1],
       [1, 2, 2, 2, 2, 1],
       [1, 1, 2, 2, 2, 1],
       [1, 1, 1, 1, 1, 1]], dtype=int8)
```

Here two markers were used to designate an object (marker = 2) and the background (marker = 1). The order in which these are processed is arbitrary: moving the marker for the background to the lower right corner of the array yields a different result:

```python
>>> markers = np.array([[0, 0, 0, 0, 0, 0, 0],
                      ... [0, 0, 0, 0, 0, 0, 0],
                      ... [0, 0, 0, 0, 0, 0, 0],
                      ... [0, 0, 0, 0, 0, 0, 0],
                      ... [0, 0, 0, 0, 0, 0, 0],
                      ... [0, 0, 0, 0, 0, 0, 0]], np.int8)
```

The result is that the object (marker = 2) is smaller because the second marker was processed earlier. This may not be the desired effect if the first marker was supposed to designate a background object. Therefore `watershed_ift` treats markers with a negative value explicitly as background markers and processes them after the normal markers. For instance, replacing the first marker by a negative marker gives a result similar to the first example:

```python
>>> markers = np.array([[0, 0, 0, 0, 0, 0, 0],
    [0, 0, 0, 0, 0, 0, 0],
    [0, 0, 0, 0, 0, 0, 0],
    [0, 0, 0, 0, 0, 0, 0],
    [0, 0, 0, 0, 0, 0, 0],
    [0, 0, 0, 0, 0, 0, 0],
    [0, 0, 0, 0, 0, 0, 0]], np.int8)
>>> watershed_ift(input, markers)
array([[-1, -1, -1, -1, -1, -1, -1],
    [-1, 2, 2, 2, -1, -1],
    [-1, 2, 2, 2, -1, -1],
    [-1, 2, 2, 2, -1, -1],
    [-1, -1, 2, 2, -1, -1],
    [-1, -1, -1, -1, -1, -1]], dtype=int8)
```

The connectivity of the objects is defined by a structuring element. If no structuring element is provided, one is generated by calling `generate_binary_structure` (see Binary morphology) using a connectivity of one (which in 2D is a 4-connected structure.) For example, using an 8-connected structure with the last example yields a different object:

```python
>>> markers = np.array([[0, 0, 0, 0, 0, 0, 0],
    [0, 0, 0, 0, 0, 0, 0],
    [0, 0, 0, 0, 0, 0, 0],
    [0, 0, 0, 0, 0, 0, 0],
    [0, 0, 0, 0, 0, 0, 0],
    [0, 0, 0, 0, 0, 0, 0],
    [0, 0, 0, 0, 0, 0, 0]], np.int8)
>>> watershed_ift(input, markers, structure=np.array([[1, 1, 1], [1, 1, 1], [1, 1, 1]]))
array([[-1, -1, -1, -1, -1, -1, -1],
    [-1, 2, 2, 2, -1, -1],
    [-1, 2, 2, 2, -1, -1],
    [-1, 2, 2, 2, -1, -1],
    [-1, -1, 2, 2, -1, -1],
    [-1, -1, -1, -1, -1, -1]], dtype=int8)
```

**Note:** The implementation of `watershed_ift` limits the data types of the input to `np.uint8` and

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Object measurements

Given an array of labeled objects, the properties of the individual objects can be measured. The \texttt{find_objects} function can be used to generate a list of slices that for each object, give the smallest sub-array that fully contains the object:

- The \texttt{find_objects} function finds all objects in a labeled array and returns a list of slices that correspond to the smallest regions in the array that contains the object.

For instance:

```python
>>> a = np.array([[0, 1, 1, 0, 0, 0], [0, 1, 1, 0, 1, 0], [0, 0, 1, 1, 0, 1], [0, 0, 0, 1, 0, 0]])
>>> l, n = label(a)
>>> from scipy.ndimage import find_objects
>>> f = find_objects(l)
>>> a[f[0]]
array([[1, 1],
        [1, 1]])
>>> a[f[1]]
array([[0, 1, 0],
        [1, 1, 1],
        [0, 1, 0]])
```

The function \texttt{find_objects} returns slices for all objects, unless the \texttt{max_label} parameter is larger than zero, in which case only the first \texttt{max_label} objects are returned. If an index is missing in the \texttt{label} array, \texttt{None} is return instead of a slice. For example:

```python
>>> from scipy.ndimage import find_objects
>>> find_objects([[1, 0, 3, 4], max_label = 3])
[(slice(0, 1, None),), None, (slice(2, 3, None),)]
```

The list of slices generated by \texttt{find_objects} is useful to find the position and dimensions of the objects in the array, but can also be used to perform measurements on the individual objects. Say we want to find the sum of the intensities of an object in image:

```python
>>> image = np.arange(4 * 6).reshape(4, 6)
>>> mask = np.array([[0, 1, 1, 0, 0, 0], [0, 1, 1, 0, 1, 0], [0, 0, 0, 1, 1, 0], [0, 0, 0, 0, 1, 0]])
>>> labels = label(mask)[0]
>>> slices = find_objects(labels)
```

Then we can calculate the sum of the elements in the second object:

```python
>>> np.where(labels[slices[1]] == 2, image[slices[1]], 0).sum()
80
```

That is however not particularly efficient, and may also be more complicated for other types of measurements. Therefore a few measurements functions are defined that accept the array of object labels and the index of the object to be measured. For instance calculating the sum of the intensities can be done by:

```python
>>> from scipy.ndimage import sum as ndi_sum
>>> ndi_sum(image, labels, 2)
80
```
For large arrays and small objects it is more efficient to call the measurement functions after slicing the array:

```python
>>> ndi_sum(image[slices[1]], labels[slices[1]], 2)
80
```

Alternatively, we can do the measurements for a number of labels with a single function call, returning a list of results. For instance, to measure the sum of the values of the background and the second object in our example we give a list of labels:

```python
>>> ndi_sum(image, labels, [0, 2])
array([178.0, 80.0])
```

The measurement functions described below all support the `index` parameter to indicate which object(s) should be measured. The default value of `index` is `None`. This indicates that all elements where the label is larger than zero should be treated as a single object and measured. Thus, in this case the `labels` array is treated as a mask defined by the elements that are larger than zero. If `index` is a number or a sequence of numbers it gives the labels of the objects that are measured. If `index` is a sequence, a list of the results is returned. Functions that return more than one result, return their result as a tuple if `index` is a single number, or as a tuple of lists, if `index` is a sequence.

- The `sum` function calculates the sum of the elements of the object with label(s) given by `index`, using the `labels` array for the object labels. If `index` is `None`, all elements with a non-zero label value are treated as a single object. If `label` is `None`, all elements of `input` are used in the calculation.

- The `mean` function calculates the mean of the elements of the object with label(s) given by `index`, using the `labels` array for the object labels. If `index` is `None`, all elements with a non-zero label value are treated as a single object. If `label` is `None`, all elements of `input` are used in the calculation.

- The `variance` function calculates the variance of the elements of the object with label(s) given by `index`, using the `labels` array for the object labels. If `index` is `None`, all elements with a non-zero label value are treated as a single object. If `label` is `None`, all elements of `input` are used in the calculation.

- The `standard_deviation` function calculates the standard deviation of the elements of the object with label(s) given by `index`, using the `labels` array for the object labels. If `index` is `None`, all elements with a non-zero label value are treated as a single object. If `label` is `None`, all elements of `input` are used in the calculation.

- The `minimum` function calculates the minimum of the elements of the object with label(s) given by `index`, using the `labels` array for the object labels. If `index` is `None`, all elements with a non-zero label value are treated as a single object. If `label` is `None`, all elements of `input` are used in the calculation.

- The `maximum` function calculates the maximum of the elements of the object with label(s) given by `index`, using the `labels` array for the object labels. If `index` is `None`, all elements with a non-zero label value are treated as a single object. If `label` is `None`, all elements of `input` are used in the calculation.

- The `minimum_position` function calculates the position of the minimum of the elements of the object with label(s) given by `index`, using the `labels` array for the object labels. If `index` is `None`, all elements with a non-zero label value are treated as a single object. If `label` is `None`, all elements of `input` are used in the calculation.

- The `maximum_position` function calculates the position of the maximum of the elements of the object with label(s) given by `index`, using the `labels` array for the object labels. If `index` is `None`, all elements with a non-zero label value are treated as a single object. If `label` is `None`, all elements of `input` are used in the calculation.

- The `extrema` function calculates the minimum, the maximum, and their positions, of the elements of the object with label(s) given by `index`, using the `labels` array for the object labels. If `index` is `None`, all elements with a non-zero label value are treated as a single object. If `label` is `None`, all elements
of \texttt{input} are used in the calculation. The result is a tuple giving the minimum, the maximum, the position of the minimum and the position of the maximum. The result is the same as a tuple formed by the results of the functions \texttt{minimum}, \texttt{maximum}, \texttt{minimum\_position}, and \texttt{maximum\_position} that are described above.

- The \texttt{center\_of\_mass} function calculates the center of mass of the of the object with label(s) given by \texttt{index}, using the \texttt{labels} array for the object labels. If \texttt{index} is  \texttt{None}, all elements with a non-zero label value are treated as a single object. If \texttt{label} is \texttt{None}, all elements of \texttt{input} are used in the calculation.

- The \texttt{histogram} function calculates a histogram of the of the object with label(s) given by \texttt{index}, using the \texttt{labels} array for the object labels. If \texttt{index} is \texttt{None}, all elements with a non-zero label value are treated as a single object. If \texttt{label} is \texttt{None}, all elements of \texttt{input} are used in the calculation. Histograms are defined by their minimum (\texttt{min}), maximum (\texttt{max}) and the number of bins (\texttt{bins}). They are returned as one-dimensional arrays of type \texttt{np.int32}.

### Extending \texttt{scipy.ndimage} in C

A few functions in \texttt{scipy.ndimage} take a callback argument. This can be either a python function or a \texttt{scipy.LowLevelCallable} containing a pointer to a C function. Using a C function will generally be more efficient since it avoids the overhead of calling a python function on many elements of an array. To use a C function you must write a C extension that contains the callback function and a Python function that returns a \texttt{scipy.LowLevelCallable} containing a pointer to the callback.

An example of a function that supports callbacks is \texttt{geometric\_transform}, which accepts a callback function that defines a mapping from all output coordinates to corresponding coordinates in the input array. Consider the following python example which uses \texttt{geometric\_transform} to implement a shift function.

```python
from scipy import ndimage

def transform(output_coordinates, shift):
    input_coordinates = output_coordinates[0] - shift, output_coordinates[1] - shift
    return input_coordinates

im = np.arange(12).reshape(4, 3).astype(np.float64)
shift = 0.5
print(ndimage.geometric_transform(im, transform, extra_arguments=(shift,)))
```

We can also implement the callback function with the following C code.

```c
/* example.c */
#include <Python.h>
#include <numpy/npy_common.h>

static int _transform(npy_intp *output_coordinates, double *input_coordinates, int output_rank, int input_rank, void *user_data)
{
    npy_intp i;
    double shift = *(double *)user_data;

    for (i = 0; i < input_rank; i++) {
        input_coordinates[i] = output_coordinates[i] - shift;
    }
    return 1;
}
```

(continues on next page)
static char *transform_signature = "int (npy_intp *, double *, int, int, void *)";

static PyObject *
py_get_transform(PyObject *obj, PyObject *args)
{
    if (!PyArg_ParseTuple(args, "")) return NULL;
    return PyCapsule_New(_transform, transform_signature, NULL);
}

static PyMethodDef ExampleMethods[] = {
    {"get_transform", (PyCFunction)py_get_transform, METH_VARARGS, ""},
    {NULL, NULL, 0, NULL}
};

/* Initialize the module */
#if PY_VERSION_HEX >= 0x03000000
static struct PyModuleDef example = {
    PyModuleDef_HEAD_INIT,
    "example",
    NULL,
    -1,
    ExampleMethods,
    NULL,
    NULL,
    NULL
};

PyMODINIT_FUNC
PyInit_example(void)
{
    return PyModule_Create(&example);
}
#else
PyMODINIT_FUNC
initexample(void)
{
    Py_InitModule("example", ExampleMethods);
}
#endif

More information on writing Python extension modules can be found here. If the C code is in the file example.c, then it can be compiled with the following setup.py,

```python
from distutils.core import setup, Extension
import numpy

shift = Extension('example',
    ['example.c'],
    include_dirs=[numpy.get_include()])
```

(continues on next page)
```python
setup(name='example',
       ext_modules=[shift])
```

and now running the script

```python
import ctypes
import numpy as np
from scipy import ndimage, LowLevelCallable

from example import get_transform

shift = 0.5

user_data = ctypes.c_double(shift)
ptr = ctypes.cast(ctypes.pointer(user_data), ctypes.c_void_p)
callback = LowLevelCallable(get_transform(), ptr)
im = np.arange(12).reshape(4, 3).astype(np.float64)
print(ndimage.geometric_transform(im, callback))
```

produces the same result as the original python script.

In the C version _transform is the callback function and the parameters output_coordinates and input_coordinates play the same role as they do in the python version while output_rank and input_rank provide the equivalents of len(output_coordinates) and len(input_coordinates). The variable shift is passed through user_data instead of extra_arguments. Finally, the C callback function returns an integer status which is one upon success and zero otherwise.

The function py_transform wraps the callback function in a PyCapsule. The main steps are:

- Initialize a PyCapsule. The first argument is a pointer to the callback function.
- The second argument is the function signature which must match exactly the one expected by ndimage.
- Above, we used scipy.LowLevelCallable to specify user_data that we generated with ctypes.
  A different approach would be to supply the data in the capsule context, that can be set by :cfunc:`PyCapsule_SetContext` and omit specifying user_data in scipy.LowLevelCallable. However, in this approach we would need to deal with allocation/freeing of the data — freeing the data after the capsule is destroyed can be done by specifying a non-NULL callback function in the third argument of :cfunc:`PyCapsule_New`.

C callback functions for ndimage all follow this scheme. The next section lists the ndimage functions that accept a C callback function and gives the prototype of the function.

See also:

The functions that support low-level callback arguments are:

generic_filter, generic_filter1d, geometric_transform

Below, we show alternative ways to write the code, using Cython, ctypes, or cffi instead of writing wrapper code in C.

**Numba**

Numba provides a way to write low-level functions easily in Python. We can write the above using Numba as:

```python
402 Chapter 4. Tutorial
```
# example.py
import numpy as np
import ctypes
from scipy import ndimage, LowLevelCallable
from numba import cfunc, types, carray
@cfunc(types.intc(types.CPointer(types.intp),
    types.CPointer(types.double),
    types.intc,
    types.intc,
    types.voidptr))
def transform(output_coordinates_ptr, input_coordinates_ptr,
    output_rank, input_rank, user_data):
    input_coordinates = carray(input_coordinates_ptr, (input_rank,))
    output_coordinates = carray(output_coordinates_ptr, (output_rank,))
    shift = carray(user_data, (1,), types.double)[0]
    for i in range(input_rank):
        input_coordinates[i] = output_coordinates[i] - shift
    return 1
shift = 0.5
# Then call the function
user_data = ctypes.c_double(shift)
ptr = ctypes.cast(ctypes.pointer(user_data), ctypes.c_void_p)
callback = LowLevelCallable(transform.ctypes, ptr)
im = np.arange(12).reshape(4, 3).astype(np.float64)
print(ndimage.geometric_transform(im, callback))

Cython
Functionally the same code as above can be written in Cython with somewhat less boilerplate as follows.

# example.pyx
from numpy cimport npy_intp as intp
cdef api int transform(intp *output_coordinates, double *input_coordinates,
    int output_rank, int input_rank, void *user_data):
    cdef intp i
    cdef double shift = (<double *>user_data)[0]
    for i in range(input_rank):
        input_coordinates[i] = output_coordinates[i] - shift
    return 1

# script.py
import ctypes
import numpy as np
from scipy import ndimage, LowLevelCallable

(continues on next page)
import example

shift = 0.5

user_data = ctypes.c_double(shift)
ptr = ctypes.cast(ctypes.pointer(user_data), ctypes.c_void_p)
callback = LowLevelCallable.from_cython(example, "transform", ptr)
im = np.arange(12).reshape(4, 3).astype(np.float64)
print(ndimage.geometric_transform(im, callback))

cffi
With cffi, you can interface with a C function residing in a shared library (DLL). First, we need to write the shared library, which we do in C — this example is for Linux/OSX:

```c
#include <stdint.h>

int _transform(intptr_t *output_coordinates, double *input_coordinates,
               int output_rank, int input_rank, void *user_data)
{
    int i;
    double shift = *(double *)user_data;

    for (i = 0; i < input_rank; i++) {
        input_coordinates[i] = output_coordinates[i] - shift;
    }
    return 1;
}
```

The Python code calling the library is:

```python
import os
import numpy as np
from scipy import ndimage, LowLevelCallable
import cffi

# Construct the FFI object, and copypaste the function declaration
ffi = cffi.FFI()
ffi.cdef(""
    int _transform(intptr_t *output_coordinates, double *input_coordinates,
                   int output_rank, int input_rank, void *user_data);
""
)

# Open library
lib = ffi.dlopen(os.path.abspath("example.so"))
```
# Do the function call
user_data = ffi.new('double *', 0.5)
callback = LowLevelCallable(lib._transform, user_data)
im = np.arange(12).reshape(4, 3).astype(np.float64)
print(ndimage.geometric_transform(im, callback))

You can find more information in the cffi documentation.

cypes
With cypes, the C code and the compilation of the so/DLL is as for cffi above. The Python code is different:

```python
# script.py
import os
import ctypes
import numpy as np
from scipy import ndimage, LowLevelCallable
lib = ctypes.CDLL(os.path.abspath('example.so'))
shift = 0.5
user_data = ctypes.c_double(shift)
ptr = ctypes.cast(ctypes.pointer(user_data), ctypes.c_void_p)

# Ctypes has no built-in intptr type, so override the signature
# instead of trying to get it via ctypes
callback = LowLevelCallable(lib._transform, ptr,
                            "int _transform(intptr_t *, double *, int, int, void *)")

# Perform the call
im = np.arange(12).reshape(4, 3).astype(np.float64)
print(ndimage.geometric_transform(im, callback))

You can find more information in the ctypes documentation.

References

4.1.15 File IO (scipy.io)

See also:
numpy-reference.routines.io (in numpy)

MATLAB files

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>loadmat(file_name[, mdict, appendmat])</td>
<td>Load MATLAB file.</td>
</tr>
<tr>
<td>savemat(file_name, mdict[, appendmat, ...])</td>
<td>Save a dictionary of names and arrays into a MATLAB-style .mat file.</td>
</tr>
<tr>
<td>whosmat(file_name[, appendmat])</td>
<td>List variables inside a MATLAB file.</td>
</tr>
</tbody>
</table>

The basic functions
We'll start by importing scipy.io and calling it sio for convenience:
>>> import scipy.io as sio

If you are using IPython, try tab completing on `sio`. Among the many options, you will find:

```python
sio.loadmat
sio.savemat
sio.whosmat
```

These are the high-level functions you will most likely use when working with MATLAB files. You’ll also find:

```python
sio.matlab
```

This is the package from which `loadmat`, `savemat` and `whosmat` are imported. Within `sio.matlab`, you will find the `mio` module. This module contains the machinery that `loadmat` and `savemat` use. From time to time you may find yourself re-using this machinery.

**How do I start?**

You may have a `.mat` file that you want to read into Scipy. Or, you want to pass some variables from Scipy / Numpy into MATLAB.

To save us using a MATLAB license, let’s start in Octave. Octave has MATLAB-compatible save and load functions. Start Octave (`octave` at the command line for me):

```
octave:1> a = 1:12
a =
    1 2 3 4 5 6 7 8 9 10 11 12
octave:2> a = reshape(a, [1 3 4])
a =
ans(:,:,1) =
    1 2 3
ans(:,:,2) =
    4 5 6
ans(:,:,3) =
    7 8 9
ans(:,:,4) =
    10 11 12
octave:3> save -6 octave_a.mat a % MATLAB 6 compatible
octave:4> ls octave_a.mat octave_a.mat
```

Now, to Python:
```python
>>> mat_contents = sio.loadmat('octave_a.mat')
>>> mat_contents
{'a': array([[ 1.,  4.,  7., 10.],
             [ 2.,  5.,  8., 11.],
             [ 3.,  6.,  9., 12.]],
            '__version__': '1.0',
            '__header__': 'MATLAB 5.0 MAT-file, written by
Octave 3.6.3, 2013-02-17 21:02:11 UTC',
            '__globals__': []}
>>> oct_a = mat_contents['a']
>>> oct_a
array([[ 1.,  4.,  7., 10.],
        [ 2.,  5.,  8., 11.],
        [ 3.,  6.,  9., 12.]])
>>> oct_a.shape
(1, 3, 4)
```

Now let’s try the other way round:

```python
>>> import numpy as np
>>> vect = np.arange(10)
>>> vect.shape
(10,)
>>> sio.savemat('np_vector.mat', {'vect':vect})
```

Then back to Octave:

```
octave:8> load np_vector.mat
octave:9> vect =
    0   1   2   3   4   5   6   7   8   9
octave:10> size(vect)
ans =
    1   10
```

If you want to inspect the contents of a MATLAB file without reading the data into memory, use the `whosmat` command:

```python
>>> sio.whosmat('octave_a.mat')
[('a', (1, 3, 4), 'double')]
```

`whosmat` returns a list of tuples, one for each array (or other object) in the file. Each tuple contains the name, shape and data type of the array.

**MATLAB structs**

MATLAB structs are a little bit like Python dicts, except the field names must be strings. Any MATLAB object can be a value of a field. As for all objects in MATLAB, structs are in fact arrays of structs, where a single struct is an array of shape (1, 1).

```octave
octave:11> my_struct = struct('field1', 1, 'field2', 2)
my_struct =
```
octave:12> save -6 octave_struct.mat my_struct
We can load this in Python:

```python
>>> mat_contents = sio.loadmat('octave_struct.mat')
>>> mat_contents
{'my_struct': array([[[1.0], [2.0]]],
                     dtype=[('field1', 'O'), ('field2', 'O')]),
             '__version__': '1.0', '__header__':
             '--MATLAB 5.0 MAT-file, written by Octave 3.6.3, 2013-02-17 21:23:14 UTC',
             '__globals__': []}
>>> oct_struct = mat_contents['my_struct']
>>> oct_struct.shape
(1, 1)
>>> val = oct_struct[0,0]
>>> val
([[1.0], [2.0]])
>>> val['field1']
array([[1.0]])
>>> val['field2']
array([[2.0]])
>>> val.dtype
dtype([('field1', 'O'), ('field2', 'O'))]
```

In versions of Scipy from 0.12.0, MATLAB structs come back as numpy structured arrays, with fields named for the struct fields. You can see the field names in the `dtype` output above. Note also:

```python
>>> val = oct_struct[0,0]
```

and:

```octave
octave:13> size(my_struct)
ans = 
     1   1
```

So, in MATLAB, the struct array must be at least 2D, and we replicate that when we read into Scipy. If you want all length 1 dimensions squeezed out, try this:

```python
>>> mat_contents = sio.loadmat('octave_struct.mat', squeeze_me=True)
>>> oct_struct = mat_contents['my_struct']
```

Sometimes, it’s more convenient to load the MATLAB structs as python objects rather than numpy structured arrays - it can make the access syntax in python a bit more similar to that in MATLAB. In order to do this, use the `struct_as_record=False` parameter setting to `loadmat`.
>>> mat_contents = sio.loadmat('octave_struct.mat', struct_as_record=False)
>>> oct_struct = mat_contents['my_struct']
>>> oct_struct[0,0].field1
array([[ 1.]])

struct_as_record=False works nicely with squeeze_me:

>>> mat_contents = sio.loadmat('octave_struct.mat', struct_as_record=False, squeeze_me=True)
>>> oct_struct = mat_contents['my_struct']
>>> oct_struct.shape # but no - it's a scalar
Traceback (most recent call last):
  File "<stdin>" , line 1, in <module>
AttributeError: 'mat_struct' object has no attribute 'shape'
>>> type(oct_struct)
<class 'scipy.io.matlab.mio5_params.mat_struct'>
>>> oct_struct.field1
1.0

Saving struct arrays can be done in various ways. One simple method is to use dicts:

>>> a_dict = {'field1': 0.5, 'field2': 'a string'}
>>> sio.savemat('saved_struct.mat', {'a_dict': a_dict})

loaded as:

octave:21> load saved_struct
octave:22> a_dict
a_dict =

scalar structure containing the fields:

    field2 = a string
    field1 = 0.50000

You can also save structs back again to MATLAB (or Octave in our case) like this:

>>> dt = [(('f1', 'f8'), ('f2', 'S10'))]
>>> arr = np.zeros((2,), dtype=dt)
>>> arr
array([[0. , b'', 0. , b'']
       [0. , b'']],
      dtype=[('f1', '<f8'), ('f2', 'S10')])
>>> arr[0]['f1'] = 0.5
>>> arr[0]['f2'] = 'python'
>>> arr[1]['f1'] = 99
>>> arr[1]['f2'] = 'not perl'
>>> sio.savemat('np_struct_arr.mat', {'arr': arr})

MATLAB cell arrays
Cell arrays in MATLAB are rather like python lists, in the sense that the elements in the arrays can contain any type of MATLAB object. In fact they are most similar to numpy object arrays, and that is how we load them into numpy.
octave:14> my_cells = {1, [2, 3]}
my_cells =
{[1,1] = 1
 [1,2] =
     2 3
}

octave:15> save -6 octave_cells.mat my_cells

Back to Python:

```python
>>> mat_contents = sio.loadmat('octave_cells.mat')
>>> oct_cells = mat_contents['my_cells']
>>> print(oct_cells.dtype)
object
>>> val = oct_cells[0,0]
>>> print(val)
array([[ 1.]])
>>> print(val.dtype)
float64
```

Saving to a MATLAB cell array just involves making a numpy object array:

```python
>>> obj_arr = np.zeros((2,), dtype=np.object)
>>> obj_arr[0] = 1
>>> obj_arr[1] = 'a string'
>>> print(obj_arr)
array([1, 'a string'], dtype=object)
```

```python
>>> sio.savemat('np_cells.mat', {'obj_arr':obj_arr})
```

octave:16> load np_cells.mat
octave:17> obj_arr
obj_arr =
{[1,1] = 1
 [2,1] = a string
}

IDL files

```python
readsav(file_name[, idict, python_dict, ...]) Read an IDL .sav file.
```

Matrix Market files

```python
mminfo(source) Return size and storage parameters from Matrix Market file-like ‘source’.
mmread(source) Reads the contents of a Matrix Market file-like ‘source’ into a matrix.
```

Continued on next page
Table 3 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>mmwrite</code></td>
<td>Writes the sparse or dense array <code>a</code> to Matrix Market</td>
</tr>
<tr>
<td></td>
<td>file-like <code>target</code>.</td>
</tr>
</tbody>
</table>

Wav sound files (**scipy.io.wavfile**)

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>read</code></td>
<td>Open a WAV file</td>
</tr>
<tr>
<td><code>write</code></td>
<td>Write a numpy array as a WAV file.</td>
</tr>
</tbody>
</table>

Arff files (**scipy.io.arff**)

Module to read ARFF files, which are the standard data format for WEKA.

ARFF is a text file format which support numerical, string and data values. The format can also represent missing data and sparse data.

**Notes**

The ARFF support in **scipy.io** provides file reading functionality only. For more extensive ARFF functionality, see **liac-arff**.

See the **WEKA website** for more details about the ARFF format and available datasets.

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>loadarff</code></td>
<td>Read an arff file.</td>
</tr>
</tbody>
</table>

Netcdf (**scipy.io.netcdf**)

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>netcdf_file</code></td>
<td>A file object for NetCDF data.</td>
</tr>
</tbody>
</table>

Allows reading of NetCDF files (version of **pupyrene** package)
CHAPTER
FIVE

DEVELOPER’S GUIDE

Explanations of how to start contributing to SciPy, and descriptions of maintenance activities and policies.

5.1 SciPy Code of Conduct

5.1.1 Introduction

This code of conduct applies to all spaces managed by the SciPy project, including all public and private mailing lists, issue trackers, wikis, blogs, Twitter, and any other communication channel used by our community. The SciPy project does not organise in-person events, however events related to our community should have a code of conduct similar in spirit to this one.

This code of conduct should be honored by everyone who participates in the SciPy community formally or informally, or claims any affiliation with the project, in any project-related activities and especially when representing the project, in any role.

This code is not exhaustive or complete. It serves to distill our common understanding of a collaborative, shared environment and goals. Please try to follow this code in spirit as much as in letter, to create a friendly and productive environment that enriches the surrounding community.

5.1.2 Specific Guidelines

We strive to:

1. Be open. We invite anyone to participate in our community. We prefer to use public methods of communication for project-related messages, unless discussing something sensitive. This applies to messages for help or project-related support, too; not only is a public support request much more likely to result in an answer to a question, it also ensures that any inadvertent mistakes in answering are more easily detected and corrected.

2. Be empathetic, welcoming, friendly, and patient. We work together to resolve conflict, and assume good intentions. We may all experience some frustration from time to time, but we do not allow frustration to turn into a personal attack. A community where people feel uncomfortable or threatened is not a productive one.

3. Be collaborative. Our work will be used by other people, and in turn we will depend on the work of others. When we make something for the benefit of the project, we are willing to explain to others how it works, so that they can build on the work to make it even better. Any decision we make will affect users and colleagues, and we take those consequences seriously when making decisions.

4. Be inquisitive. Nobody knows everything! Asking questions early avoids many problems later, so we encourage questions, although we may direct them to the appropriate forum. We will try hard to be responsive and helpful.
5. Be careful in the words that we choose. We are careful and respectful in our communication and we take responsibility for our own speech. Be kind to others. Do not insult or put down other participants. We will not accept harassment or other exclusionary behaviour, such as:

- Violent threats or language directed against another person.
- Sexist, racist, or otherwise discriminatory jokes and language.
- Posting sexually explicit or violent material.
- Posting (or threatening to post) other people’s personally identifying information (“doxing”).
- Sharing private content, such as emails sent privately or non-publicly, or unlogged forums such as IRC channel history, without the sender’s consent.
- Personal insults, especially those using racist or sexist terms.
- Unwelcome sexual attention.
- Excessive profanity. Please avoid swearwords; people differ greatly in their sensitivity to swearing.
- Repeated harassment of others. In general, if someone asks you to stop, then stop.
- Advocating for, or encouraging, any of the above behaviour.

5.1.3 Diversity Statement

The SciPy project welcomes and encourages participation by everyone. We are committed to being a community that everyone enjoys being part of. Although we may not always be able to accommodate each individual’s preferences, we try our best to treat everyone kindly.

No matter how you identify yourself or how others perceive you: we welcome you. Though no list can hope to be comprehensive, we explicitly honour diversity in: age, culture, ethnicity, genotype, gender identity or expression, language, national origin, neurotype, phenotype, political beliefs, profession, race, religion, sexual orientation, socioeconomic status, subculture and technical ability, to the extent that these do not conflict with this code of conduct.

Though we welcome people fluent in all languages, SciPy development is conducted in English.

Standards for behaviour in the SciPy community are detailed in the Code of Conduct above. Participants in our community should uphold these standards in all their interactions and help others to do so as well (see next section).

5.1.4 Reporting Guidelines

We know that it is painfully common for internet communication to start at or devolve into obvious and flagrant abuse. We also recognize that sometimes people may have a bad day, or be unaware of some of the guidelines in this Code of Conduct. Please keep this in mind when deciding on how to respond to a breach of this Code.

For clearly intentional breaches, report those to the Code of Conduct committee (see below). For possibly unintentional breaches, you may reply to the person and point out this code of conduct (either in public or in private, whatever is most appropriate). If you would prefer not to do that, please feel free to report to the Code of Conduct Committee directly, or ask the Committee for advice, in confidence.

You can report issues to the SciPy Code of Conduct committee, at scipy-conduct@googlegroups.com. Currently, the committee consists of:

- Stefan van der Walt
- Nathaniel J. Smith
- Ralf Gommers
If your report involves any members of the committee, or if they feel they have a conflict of interest in handling it, then they will recuse themselves from considering your report. Alternatively, if for any reason you feel uncomfortable making a report to the committee, then you can also contact:

- Chair of the SciPy Steering Committee: Ralf Gommers, or
- Senior NumFOCUS staff: conduct@numfocus.org

5.1.5 Incident reporting resolution & Code of Conduct enforcement

This section summarizes the most important points, more details can be found in CoC_reporting_manual.

We will investigate and respond to all complaints. The SciPy Code of Conduct Committee and the SciPy Steering Committee (if involved) will protect the identity of the reporter, and treat the content of complaints as confidential (unless the reporter agrees otherwise).

In case of severe and obvious breaches, e.g. personal threat or violent, sexist or racist language, we will immediately disconnect the originator from SciPy communication channels; please see the manual for details.

In cases not involving clear severe and obvious breaches of this code of conduct, the process for acting on any received code of conduct violation report will be:

1. acknowledge report is received
2. reasonable discussion/feedback
3. mediation (if feedback didn’t help, and only if both reporter and reportee agree to this)
4. enforcement via transparent decision (see CoC_resolutions) by the Code of Conduct Committee

The committee will respond to any report as soon as possible, and at most within 72 hours.

5.1.6 Endnotes

We are thankful to the groups behind the following documents, from which we drew content and inspiration:

- The Apache Foundation Code of Conduct
- The Contributor Covenant
- Jupyter Code of Conduct
- Open Source Guides - Code of Conduct

5.2 Contributing to SciPy

This document aims to give an overview of how to contribute to SciPy. It tries to answer commonly asked questions, and provide some insight into how the community process works in practice. Readers who are familiar with the SciPy community and are experienced Python coders may want to jump straight to the git workflow documentation.

There are a lot of ways you can contribute:

- Contributing new code
- Fixing bugs and other maintenance work
- Improving the documentation
- Reviewing open pull requests
- Triaging issues
- Working on the scipy.org website
Contributing new code

If you have been working with the scientific Python toolstack for a while, you probably have some code lying
around of which you think “this could be useful for others too”. Perhaps it’s a good idea then to contribute
it to SciPy or another open source project. The first question to ask is then, where does this code belong?
That question is hard to answer here, so we start with a more specific one: what code is suitable for putting
into SciPy? Almost all of the new code added to scipy has in common that it’s potentially useful in multiple
scientific domains and it fits in the scope of existing scipy submodules. In principle new submodules can be
added too, but this is far less common. For code that is specific to a single application, there may be an
existing project that can use the code. Some scikits (scikit-learn, scikit-image, statsmodels, etc.) are good
examples here; they have a narrower focus and because of that more domain-specific code than SciPy.

Now if you have code that you would like to see included in SciPy, how do you go about it? After checking
that your code can be distributed in SciPy under a compatible license (see FAQ for details), the first step is to
discuss on the scipy-dev mailing list. All new features, as well as changes to existing code, are discussed and
decided on there. You can, and probably should, already start this discussion before your code is finished.

Assuming the outcome of the discussion on the mailing list is positive and you have a function or piece of
code that does what you need it to do, what next? Before code is added to SciPy, it at least has to have
good documentation, unit tests and correct code style.

1. Unit tests

   In principle you should aim to create unit tests that exercise all the code that you are adding. This
gives some degree of confidence that your code runs correctly, also on Python versions and
hardware or OSes that you don’t have available yourself. An extensive description of how to write
unit tests is given in the NumPy testing guidelines.

2. Documentation

   Clear and complete documentation is essential in order for users to be able to find and understand
the code. Documentation for individual functions and classes – which includes at least a basic
description, type and meaning of all parameters and returns values, and usage examples in doctest
format – is put in docstrings. Those docstrings can be read within the interpreter, and are compiled
into a reference guide in html and pdf format. Higher-level documentation for key (areas of)
functionality is provided in tutorial format and/or in module docstrings. A guide on how to write
documentation is given in how to document.

3. Code style

   Uniformity of style in which code is written is important to others trying to understand the code.
SciPy follows the standard Python guidelines for code style, PEP8. In order to check that your
code conforms to PEP8, you can use the pep8 package style checker. Most IDEs and text editors
have settings that can help you follow PEP8, for example by translating tabs by four spaces. Using
pyflakes to check your code is also a good idea.

At the end of this document a checklist is given that may help to check if your code fulfills all requirements
for inclusion in SciPy.

Another question you may have is: where exactly do I put my code? To answer this, it is useful to understand
how the SciPy public API (application programming interface) is defined. For most modules the API is two
levels deep, which means your new function should appear as scipy.submodule.my_new_func. my_new_func
can be put in an existing or new file under /scipy/<submodule>/, its name is added to the __all__ list
in that file (which lists all public functions in the file), and those public functions are then imported in
/scipy/<submodule>/__init__.py. Any private functions/classes should have a leading underscore (_) in
their name. A more detailed description of what the public API of SciPy is, is given in SciPy API.
Once you think your code is ready for inclusion in SciPy, you can send a pull request (PR) on Github. We won’t go into the details of how to work with git here, this is described well in the git workflow section of the NumPy documentation and on the Github help pages. When you send the PR for a new feature, be sure to also mention this on the scipy-dev mailing list. This can prompt interested people to help review your PR. Assuming that you already got positive feedback before on the general idea of your code/feature, the purpose of the code review is to ensure that the code is correct, efficient and meets the requirements outlined above. In many cases the code review happens relatively quickly, but it’s possible that it stalls. If you have addressed all feedback already given, it’s perfectly fine to ask on the mailing list again for review (after a reasonable amount of time, say a couple of weeks, has passed). Once the review is completed, the PR is merged into the “master” branch of SciPy.

The above describes the requirements and process for adding code to SciPy. It doesn’t yet answer the question though how decisions are made exactly. The basic answer is: decisions are made by consensus, by everyone who chooses to participate in the discussion on the mailing list. This includes developers, other users and yourself. Aiming for consensus in the discussion is important – SciPy is a project by and for the scientific Python community. In those rare cases that agreement cannot be reached, the maintainers of the module in question can decide the issue.

5.2.2 Contributing by helping maintain existing code

The previous section talked specifically about adding new functionality to SciPy. A large part of that discussion also applies to maintenance of existing code. Maintenance means fixing bugs, improving code quality, documenting existing functionality better, adding missing unit tests, keeping build scripts up-to-date, etc. The SciPy issue list contains all reported bugs, build/documentation issues, etc. Fixing issues helps improve the overall quality of SciPy, and is also a good way of getting familiar with the project. You may also want to fix a bug because you ran into it and need the function in question to work correctly. The discussion on code style and unit testing above applies equally to bug fixes. It is usually best to start by writing a unit test that shows the problem, i.e. it should pass but doesn’t. Once you have that, you can fix the code so that the test does pass. That should be enough to send a PR for this issue. Unlike when adding new code, discussing this on the mailing list may not be necessary - if the old behavior of the code is clearly incorrect, no one will object to having it fixed. It may be necessary to add some warning or deprecation message for the changed behavior. This should be part of the review process.

Note: Pull requests that only change code style, e.g. fixing some PEP8 issues in a file, are discouraged. Such PRs are often not worth cluttering the git annotate history, and take reviewer time that may be better spent in other ways. Code style cleanups of code that is touched as part of a functional change are fine however.

5.2.3 Reviewing pull requests

Reviewing open pull requests (PRs) is very welcome, and a valuable way to help increase the speed at which the project moves forward. If you have specific knowledge/experience in a particular area (say “optimization algorithms” or “special functions”) then reviewing PRs in that area is especially valuable - sometimes PRs with technical code have to wait for a long time to get merged due to a shortage of appropriate reviewers.

We encourage everyone to get involved in the review process; it’s also a great way to get familiar with the code base. Reviewers should ask themselves some or all of the following questions:

- Was this change adequately discussed (relevant for new features and changes in existing behavior)?
- Is the feature scientifically sound? Algorithms may be known to work based on literature; otherwise, closer look at correctness is valuable.
- Is the intended behavior clear under all conditions (e.g. unexpected inputs like empty arrays or nan/inf values)?
• Does the code meet the quality, test and documentation expectation outline under Contributing new code?

If we do not know you yet, consider introducing yourself.

5.2.4 Other ways to contribute

There are many ways to contribute other than contributing code.

Triaging issues (investigating bug reports for validity and possible actions to take) is also a useful activity. SciPy has many hundreds of open issues; closing invalid ones and correctly labeling valid ones (ideally with some first thoughts in a comment) allows prioritizing maintenance work and finding related issues easily when working on an existing function or submodule.

Participating in discussions on the scipy-user and scipy-dev mailing lists is a contribution in itself. Everyone who writes to those lists with a problem or an idea would like to get responses, and writing such responses makes the project and community function better and appear more welcoming.

The scipy.org website contains a lot of information on both SciPy the project and SciPy the community, and it can always use a new pair of hands. The sources for the website live in their own separate repo: https://github.com/scipy/scipy.org

5.2.5 Recommended development setup

Since Scipy contains parts written in C, C++, and Fortran that need to be compiled before use, make sure you have the necessary compilers and Python development headers installed. Having compiled code also means that importing Scipy from the development sources needs some additional steps, which are explained below.

First fork a copy of the main Scipy repository in Github onto your own account and then create your local repository via:

```
$ git clone git@github.com:YOURUSERNAME/scipy.git scipy
$ cd scipy
$ git remote add upstream git://github.com/scipy/scipy.git
```

To build the development version of Scipy and run tests, spawn interactive shells with the Python import paths properly set up etc., do one of:

```
$ python runtests.py -v
$ python runtests.py -v -s optimize
$ python runtests.py -v -t scipy.special.tests.test_basic::test_xlogy
$ python runtests.py --ipython
$ python runtests.py --python somescript.py
$ python runtests.py --bench
```

This builds Scipy first, so the first time it may take some time. If you specify -n, the tests are run against the version of Scipy (if any) found on current PYTHONPATH. Note: if you run into a build issue, more detailed build documentation can be found in :doc:`building/index` and at https://github.com/scipy/scipy/tree/master/doc/source/building

Using runtests.py is the recommended approach to running tests. There are also a number of alternatives to it, for example in-place build or installing to a virtualenv. See the FAQ below for details.

Some of the tests in Scipy are very slow and need to be separately enabled. See the FAQ below for details.
5.2.6 SciPy structure

All SciPy modules should follow the following conventions. In the following, a SciPy module is defined as a Python package, say yyy, that is located in the scipy/ directory.

- Ideally, each SciPy module should be as self-contained as possible. That is, it should have minimal dependencies on other packages or modules. Even dependencies on other SciPy modules should be kept to a minimum. A dependency on NumPy is of course assumed.

- Directory yyy/ contains:
  - A file setup.py that defines configuration(parent_package='', top_path=None) function for numpy.distutils.
  - A directory tests/ that contains files test_<name>.py corresponding to modules yyy/<name>{.py,.so,/}.

- Private modules should be prefixed with an underscore _, for instance yyy/_somemodule.py.

- User-visible functions should have good documentation following the Numpy documentation style, see how to document

- The __init__.py of the module should contain the main reference documentation in its docstring. This is connected to the Sphinx documentation under doc/ via Sphinx’s automodule directive.

  The reference documentation should first give a categorized list of the contents of the module using autosummary:: directives, and after that explain points essential for understanding the use of the module.

  Tutorial-style documentation with extensive examples should be separate, and put under doc/source/tutorial/

See the existing Scipy submodules for guidance.

For further details on Numpy distutils, see:

https://github.com/numpy/numpy/blob/master/doc/DISTUTILS.rst.txt

5.2.7 Useful links, FAQ, checklist

Checklist before submitting a PR

- Are there unit tests with good code coverage?
- Do all public function have docstrings including examples?
- Is the code style correct (PEP8, pyflakes)
- Is the commit message formatted correctly?
- Is the new functionality tagged with .. versionadded:: X.Y.Z (with X.Y.Z the version number of the next release - can be found in setup.py)?
- Is the new functionality mentioned in the release notes of the next release?
- Is the new functionality added to the reference guide?
- In case of larger additions, is there a tutorial or more extensive module-level description?
- In case compiled code is added, is it integrated correctly via setup.py
- If you are a first-time contributor, did you add yourself to THANKS.txt? Please note that this is perfectly normal and desirable - the aim is to give every single contributor credit, and if you don’t add yourself it’s simply extra work for the reviewer (or worse, the reviewer may forget).
- Did you check that the code can be distributed under a BSD license?
Useful SciPy documents

- The **how to document** guidelines
- NumPy/SciPy testing guidelines
- SciPy API
- The SciPy Roadmap
- NumPy/SciPy git workflow
- How to submit a good bug report

FAQ

**I based my code on existing Matlab/R/... code I found online, is this OK?**

It depends. SciPy is distributed under a BSD license, so if the code that you based your code on is also BSD licensed or has a BSD-compatible license (e.g. MIT, PSF) then it’s OK. Code which is GPL or Apache licensed, has no clear license, requires citation or is free for academic use only can’t be included in SciPy. Therefore if you copied existing code with such a license or made a direct translation to Python of it, your code can’t be included. If you’re unsure, please ask on the scipy-dev mailing list.

**Why is SciPy under the BSD license and not, say, the GPL?**

Like Python, SciPy uses a “permissive” open source license, which allows proprietary re-use. While this allows companies to use and modify the software without giving anything back, it is felt that the larger user base results in more contributions overall, and companies often publish their modifications anyway, without being required to. See John Hunter’s BSD pitch.

**How do I set up a development version of SciPy in parallel to a released version that I use to do my job/research?**

One simple way to achieve this is to install the released version in site-packages, by using a binary installer or pip for example, and set up the development version in a virtualenv. First install `virtualenv` (optionally use `virtualenvwrapper`), then create your virtualenv (named scipy-dev here) with:

```bash
$ virtualenv scipy-dev
```

Now, whenever you want to switch to the virtual environment, you can use the command `source scipy-dev/bin/activate`, and `deactivate` to exit from the virtual environment and back to your previous shell. With scipy-dev activated, install first Scipy’s dependencies:

```bash
$ pip install Numpy pytest Cython
```

After that, you can install a development version of Scipy, for example via:

```bash
$ python setup.py install
```

The installation goes to the virtual environment.

**How do I set up an in-place build for development**

For development, you can set up an in-place build so that changes made to .py files have effect without rebuild. First, run:

```bash
$ python setup.py build_ext -i
```

Then you need to point your PYTHONPATH environment variable to this directory. Some IDEs (Spyder for example) have utilities to manage PYTHONPATH. On Linux and OSX, you can run the command:
and on Windows

$ set PYTHONPATH=/path/to/scipy

Now editing a Python source file in SciPy allows you to immediately test and use your changes (in .py files), by simply restarting the interpreter.

Are there any video examples for installing from source, setting up a development environment, etc...?

Currently, there are two video demonstrations for Anaconda Python on macOS:

Anaconda SciPy Dev Part I (macOS) is a four-minute overview of installing Anaconda, building SciPy from source, and testing changes made to SciPy from the Spyder IDE.

Anaconda SciPy Dev Part II (macOS) shows how to use a virtual environment to easily switch between the “pre-built version” of SciPy installed with Anaconda and your “source-built version” of SciPy created according to Part I.

Are there any video examples of the basic development workflow?

SciPy Development Workflow is a five-minute example of fixing a bug and submitting a pull request. While it’s intended as a followup to Anaconda SciPy Dev Part I (macOS) and Anaconda SciPy Dev Part II (macOS), the process is similar for other development setups.

Can I use a programming language other than Python to speed up my code?

Yes. The languages used in SciPy are Python, Cython, C, C++ and Fortran. All of these have their pros and cons. If Python really doesn’t offer enough performance, one of those languages can be used. Important concerns when using compiled languages are maintainability and portability. For maintainability, Cython is clearly preferred over C/C++/Fortran. Cython and C are more portable than C++/Fortran. A lot of the existing C and Fortran code in SciPy is older, battle-tested code that was only wrapped in (but not specifically written for) Python/SciPy. Therefore the basic advice is: use Cython. If there’s specific reasons why C/C++/Fortran should be preferred, please discuss those reasons first.

How do I debug code written in C/C++/Fortran inside Scipy?

The easiest way to do this is to first write a Python script that invokes the C code whose execution you want to debug. For instance mytest.py:

```python
from scipy.special import hyp2f1
print(hyp2f1(5.0, 1.0, -1.8, 0.95))
```

Now, you can run:

```
gdb --args python runtests.py -g --python mytest.py
```

If you didn’t compile with debug symbols enabled before, remove the build directory first. While in the debugger:

```
(gdb) break cephes_hyp2f1
(gdb) run
```

The execution will now stop at the corresponding C function and you can step through it as usual. Instead of plain gdb you can of course use your favourite alternative debugger; run it on the python binary with arguments runtests.py -g --python mytest.py.

How do I enable additional tests in Scipy?
Some of the tests in Scipy’s test suite are very slow and not enabled by default. You can run the full suite via:

```bash
$ python runtests.py -g -m full
```

This invokes the test suite `import scipy; scipy.test("full")`, enabling also slow tests.

There is an additional level of very slow tests (several minutes), which are disabled also in this case. They can be enabled by setting the environment variable `SCIPY_XSLOW=1` before running the test suite.

### 5.3 Building from sources

**Note:** If you are only trying to install SciPy, see *Installing and upgrading*.

Build instructions for different operating systems:

#### 5.3.1 Building From Source on Linux

**Generic instructions**

To build NumPy/SciPy from source, get the source package, unpack it, and:

```bash
python setup.py install --user  # installs to your home directory
```

or

```bash
python setup.py build
python setup.py install --prefix=$HOME/local
```

Before building, you will also need to install packages that NumPy and SciPy depend on:

- BLAS and LAPACK libraries (optional but strongly recommended for NumPy, required for SciPy): typically ATLAS + OpenBLAS, or MKL.
- C and Fortran compilers (typically gcc and gfortran).
- Python header files (typically a package named python-dev or python-devel)
- Unless you are building from released source packages, the Cython compiler is necessary (typically in a package named cython). For building recent SciPy, it is possible that you need Cython in a newer version than is available in your distribution.

Typically, you will want to install all of the above from packages supplied by your Linux distribution, as building them yourself is complicated. If you need to use specific BLAS/LAPACK libraries, you can do

```bash
export BLAS=/path/to/libblas.so
export LAPACK=/path/to/liblapack.so
export ATLAS=/path/to/libatlas.so
python setup.py ...
```

If you don’t want to any LAPACK, just do “export LAPACK=”.

You will find below additional installation instructions and advice for many major Linux distributions.
Specific instructions

- **Debian / Ubuntu**
- **Fedora 26**
- **Intel C compiler and MKL**
  - Intel MKL 11.0 (updated Dec 2012)

### Debian / Ubuntu
To build from source the following packages are needed:

```
sudo apt-get install gcc gfortran python-dev libopenblas-dev liblapack-dev cython
```

To customize which BLAS is used, you can setup a `site.cfg` file. See the `site.cfg.example` file in the numpy source for the options you can set.

Note that Debian and Ubuntu package optimized BLAS libraries in a exchangeable way. You can install libraries such as ATLAS or OpenBLAS and change the default one used via the alternatives mechanism:

```
$ sudo apt-get install libopenblas-base libatlas3-base
$ update-alternatives --list libblas.so.3
/usr/lib/atlas-base/atlas/libblas.so.3
/usr/lib/libblas/libblas.so.3
/usr/lib/openblas-base/libopenblas.so.0

$ sudo update-alternatives --set libblas.so.3 /usr/lib/openblas-base/libopenblas.so.0
```

See `/usr/share/doc/libatlas3-base/README.Debian` for instructions on how to build optimized ATLAS packages for your specific CPU. The packaged OpenBLAS chooses the optimal code at runtime so it does not need recompiling unless the packaged version does not yet support the used CPU.

You can also use a library you built yourself by preloading it. This does not require administrator rights.

```
LD_PRELOAD=/path/to/libatlas.so.3 ./my-application
```

### Fedora 26
To install scipy build requirements, you can do:

```
sudo dnf install gcc-gfortran python3-devel python2-devel openblas-devel lapack-devel....
```

### Intel C compiler and MKL
**Intel MKL 11.0 (updated Dec 2012)**

Add the following lines to site.cfg in your top level NumPy directory to use Intel® MKL for Intel® 64 (or earlier known as em64t) architecture, considering the default installation path of Intel® MKL which is bundled with Intel® Composer XE SP1 version on Linux:

```
[mkl]
library_dirs = /opt/intel/composer_xe_2013/mkl/lib/intel64
include_dirs = /opt/intel/composer_xe_2013/mkl/include
mkl_libs = mkl_intel_lp64,mkl_intel_thread,mkl_core
```

If you are building NumPy for 32 bit, please add as the following

```
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```
Instead of the layered linking approach for the Intel® MKL as shown above, you may also use the dynamic interface lib mkl_rt.lib. So, for both the ia32 and intel64 architecture make the change as below

```python
mkl_libs = mkl_rt
```

Modify cc_exe in numpy/numpy/distutils/intelccompiler.py to be something like:

```python
cc_exe = 'icc -O2 -g -openmp -avx'
```

Here we use, default optimizations (-O2), OpenMP threading (-openmp) and Intel® AVX optimizations for Intel® Xeon E5 or E3 Series which are based on Intel® SandyBridge Architecture (-avx). Run icc -help for more information on processor-specific options.

Compile and install NumPy with the Intel compiler (on 64-bit platforms replace “intel” with “intelem”):

```python
python setup.py config --compiler=intel build_clib --compiler=intel build_ext --
                   --compiler=intel install
```

Compile and install SciPy with the Intel compilers (on 64-bit platforms replace “intel” with “intelem”):

```python
python setup.py config --compiler=intel --fcompiler=intel build_clib --compiler=intel --
                       --fcompiler=intel build_ext --compiler=intel --fcompiler=intel install
```

You’ll have to set LD_LIBRARY_PATH to Intel® MKL libraries (exact values will depend on your architecture, compiler and library versions) and OpenMP library for NumPy to work. If you build NumPy for Intel® 64 platforms:

```shell
```

If you build NumPy for ia32 bit platforms:

```shell
```

### 5.3.2 Building From Source on Windows

- **Overview**
- **Building the Released SciPy**
  - Building OpenBLAS
  - Installing OpenBLAS
  - Building SciPy
- **Building Against an Older Numpy Version**
- **Additional Resources**
Overview

Compared to OSX and Linux, building NumPy and SciPy on Windows is more difficult, largely due to the lack of compatible, open-source libraries like LAPACK or ATLAS that are necessary to build both libraries and have them perform relatively well. It is not possible to just call a one-liner on the command prompt as you would on other platforms via `sudo apt-get install` machinery.

This document describes one option to build OpenBLAS and SciPy from source that was validated for scipy 1.0.0. However, in light of all the work currently being done, do not expect these instructions to be accurate in the long-run and be sure to check up on any of the open source projects mentioned for the most up-to-date information. For more information on all of these projects, the Mingwpy website is an excellent source of in-depth information than this document will provide.

Building the Released SciPy

This section provides the step-by-step process to build the released scipy. If you want to build completely from source, you should estimate at least three hours to build all libraries and compile SciPy. Feel free to stop and inspect any step at any time, but for this section, we’ll just mention the steps without providing an in-depth explanation for the reasons behind them. If you have further questions about what we’re doing, more in-depth documentation is provided in the sections below. Also, please make sure to read this section before proceeding, as the presence or absence of error messages in general is not a good indication of whether you’ve completed a step correctly. Each step creates particular files, and what ultimately matters is whether you have built the required files rather than whether error messages appeared in your terminal.

Building OpenBLAS

First, we need to install the software required to build OpenBLAS, which is the BLAS library that we’re going to use. Because the software to build OpenBLAS is different than that required to build SciPy and because OpenBLAS takes a long time to build, we’re going to start building OpenBLAS first and then explain what to do next while the OpenBLAS build is running. Alternatively, if you’d rather download a pre-built OpenBLAS, download the one of the pre-built zip files and skip to the Installing OpenBLAS section below.

Otherwise, install MSYS2 using these instructions including the `pacman` update instructions. Occasionally during the updates the terminal might ask you to close the terminal but then might refuse to be closed and hang. If this happens you can kill it via Task Manager and continue with the instructions. Make sure to install the correct architecture for the SciPy that you want to build (eg. 32 or 64 bit). Now, you have three options for opening a terminal which are MSYS2, MINGW (32 or 64 bit). After updating all the packages, now we are ready to install some more package bundles that we will need. Open a MSYS2 terminal and type the following depending on the architecture of your choice; run the following for a 32-bit build

```
pacman -S --needed base-devel mingw-w64-i686-toolchain mingw-w64-i686-cmake git
```

and for 64-bit

```
pacman -S --needed base-devel mingw-w64-x86_64-toolchain mingw-w64-x86_64-cmake git
```

It will prompt to whether install everything in these packages and you can simply accept all via hitting enter key at each step.

We should be aware of the fact that these tools also install Python2, very similar to a virtual environment, which is only usable within an MSYS2 terminal and we are not going to use it at any point.

If you already have a GitHub repository folder where you keep your own repos, it is better to use that location to keep things nice and tidy since we are going to clone yet another repository to obtain the source code, hence

```
cd /c/<wherever the GitHub repo folder is>/GitHub
```
You don’t necessarily need to build in that particular location, but it should be somewhere convenient. To make sure that we’re ready to build, type the following in the terminal:

```make
gfortran
gcc
```

These commands should give errors as we have not provided any arguments to them. However an error also implies that they are accessible on the path. Now clone the repository required to build OpenBLAS:

```bash
git clone https://github.com/matthew-brett/build-openblas.git
cd build-openblas
git submodule update --init --recursive
```

If any of these commands fail, you’re not ready to build. Go back and make sure that MSYS2 is installed correctly and has the required packages enabled. Now, let’s set some environment variables. In the MSYS2 terminal, type the following.

```bash
export OPENBLAS_COMMIT=5f998ef
export OPENBLAS_ROOT="C:\opt"
export BUILD_BITS=64
```

Please check these variables’ purpose for a moment. More specifically, make sure that you have read/write access to the path that OPENBLAS_ROOT points to. The output of the OpenBLAS build will be collected in this folder. Make sure that the OPENBLAS_COMMIT points to the correct OpenBLAS commit that you want to build in the cloned repo. In the future, build_openblas repository might get updated and you might want to get those updates by changing the commit. Make sure that the architecture is correctly set to either 32 or 64 bit. And after you’ve made sure of that, start the OpenBLAS build with:

```bash
./build_openblas.sh
```

Building OpenBLAS is challenging. The build may fail with an error after a few hours but may also fail silently and produce an incorrect binary. Please, if you have any issues, report them so that we can save the next person’s time.

While you’re waiting on OpenBLAS to finish building, go ahead and install build tools from Microsoft, since these take a while to install and you’ll need them later.

After the build_openblas.sh script has completed (probably with an error), there should be an openblas.a file somewhere on your system. If OPENBLAS_ROOT was set to C:\opt, then you might see a line like this in the MSYS2 terminal:

```
Copying the static library to /c/opt/64/lib
```

**Installing OpenBLAS**

If you see that line, then you might have OpenBLAS correctly built, even if other failures occurred. Look in that folder for openblas.a. If you find a file called something like libopenblas_5f998ef_gcc7_2_0.a, just rename it to openblas.a and continue. If the file isn’t there, then poke around and try to find the file elsewhere in OPENBLAS_ROOT. If you don’t have that file, you’ll probably need to find out what happened and then build OpenBLAS again. But if you have that file, we’ll assume that you’ve completed this step correctly. Proceeding on that assumption, let’s build SciPy.

**Before continuing, make sure that you don’t have other copies of either openblas.lib or libopenblas.lib on your computer elsewhere. Multiple copies could result in later build errors that will be difficult to debug. You may verify that the openblas library was correctly picked up by looking for the following in your build log:**
**FOUND:**

```python
define_macros = [(\'HAVE_CBLAS\', None)]
```

**Building SciPy**

Once you have built OpenBLAS, it's time to build SciPy. Before continuing make sure to install the following software for building on the latest Python version. For building on other Python versions, see the WindowsCompilers page.

1. Install Microsoft Visual Studio 2015 or 2017 Community Edition (use the build tools from Microsoft)

2. Finally, install Python from https://python.org/ (make sure to check the box to install pip)

After you’ve installed the required software, open an MSYS2 terminal, change to a good location to build, and clone SciPy.

```bash
cd C:\Users\MyUser\Downloads
git clone https://github.com/scipy/scipy.git
```

Now we need to copy the `openblas.a` file that we’ve built earlier to the correct location. If your Python is installed somewhere like the following:

```
C:\Users\<user name>\AppData\Local\Programs\Python\Python36\python.exe
```

Then you’ll need to put the `openblas.a` file somewhere like the following:

```
C:\Users\<user name>\AppData\Local\Programs\Python\Python36\Lib
```

Adjust the location accordingly based on where `python.exe` is located. Now for a sanity check. Type the following and press enter.

```
gfortran
```

If you see an error with the above command, `gfortran` is not correctly installed. Go back to the “Building OpenBLAS” section and make sure that you have installed the correct tools.

Now install the dependencies that we need to build and test SciPy. **It’s important that you specify the full path to the native Python interpreter so that the built-in MSYS2 Python will not be used. Attempting to build with the MSYS2 Python will not work correctly.**

18 October 2017 Until NumPy 1.14 is officially released, we have to work with the latest development version of the NumPy repository. See the NumPy documentation...

```bash
/p/c/Users/<user name>/AppData/Local/Programs/Python/Python36/python.exe \
-m pip install numpy cython pytest pytest-xdist pytest-faulthandler
```

Please note that this is a simpler procedure than what is used for the official binaries. **Your binaries will only work with the latest NumPy (v1.14.0dev and higher).** For building against older Numpy versions, see Building Against an Older Numpy Version. Make sure that you are in the same directory where `setup.py` is (you should be if you have not changed directories):

```
ls setup.py
```

Assuming that you have set up everything correctly, you should be ready to build. Run the following commands:

---

5.3. **Building from sources** 427
Congratulations, you’ve built SciPy!

**Building Against an Older Numpy Version**

If you want to build SciPy to work with an older numpy version, then you will need to replace the Numpy “distutils” folder with the folder from the latest numpy. The following powershell snippet can upgrade Numpy distutils while retaining an older Numpy ABI.

```
$NumpyDir = $((python -c 'import os; import numpy; print(os.path.dirname(numpy.__file__)) _') | Out-String).Trim()
rm -r -Force "$NumpyDir\distutils"
$tmpdir = New-TemporaryFile | %{ rm $_; mkdir $_ }
git clone -q --depth=1 -b master https://github.com/numpy/numpy.git $tmpdir
mv $tmpdir\numpy\distutils $NumpyDir
```

**Additional Resources**

As discussed in the overview, this document is not meant to provide extremely detailed explanations on how to build NumPy and SciPy on Windows. This is largely because currently, there is no single superior way to do so and because the process for building these libraries on Windows is under development. It is likely that any information will go out of date relatively soon. If you wish to receive more assistance, please reach out to the NumPy and SciPy mailing lists, which can be found here. There are many developers out there, working on this issue right now, and they would certainly be happy to help you out! Google is also a good resource, as there are many people out there who use NumPy and SciPy on Windows, so it would not be surprising if your question or problem has already been addressed.

### 5.3.3 Building From Source on Mac OSX

These instructions describe how to build NumPy and SciPy libraries from source.

If you just want to use NumPy or SciPy, install pre-built binaries as described in /install.

**Python**

Apple ships its own version of Python with OS X. However, we strongly recommend installing the official Python distribution.

Alternatively, use Python from one of the OS X package managers (Homebrew, MacPorts, Fink).

**Compilers (C/C++/FORTRAN/Cython)**

Though virtually any commercial C/C++ compiler may be used with SciPy, OS X comes with GNU C compilers pre-installed. The only thing missing is the GNU FORTRAN compiler.

We recommend gfortran; this is a free, open source, F95 compiler. We suggest you use the following binaries:

- gfortran installed via Homebrew, or,

  - [http://r.research.att.com/tools/gcc-42-5666.3-darwin11.pkg](http://r.research.att.com/tools/gcc-42-5666.3-darwin11.pkg) (for Xcode 4.2 or higher)

See this site for the most recent links.

Unless you are building from released source packages, the Cython compiler is also needed.
BLAS/LAPACK Installation

You will also need to install a library providing the BLAS and LAPACK interfaces. ATLAS, OpenBLAS, and MKL all work. OpenBLAS can be installed via Homebrew.

As of Scipy version 1.2.0, we do not support compiling against the system Accelerate library for BLAS and LAPACK. It does not support a sufficiently recent LAPACK interface.

Version-specific notes

This section notes only things specific to one version of OS X or Python. The build instructions in Obtaining and Building NumPy and SciPy apply to all versions.

Obtaining and Building NumPy and SciPy

You may install NumPy and SciPy either by checking out the source files from the Git repositories, or unpacking them from a source archive file from /scipylib/download. If you choose the latter, simply expand the archive (generally a gzipped tar file), otherwise check out the following branches from the repository:

```
$ git clone https://github.com/numpy/numpy.git
$ git clone https://github.com/scipy/scipy.git
```

Both NumPy and SciPy are built as follows:

```
$ python setup.py build
$ python setup.py install
```

The above applies to the official Python distribution, which is 32-bit only for 2.6 while 32/64-bit bundles are available for 2.7 and 3.x. For alternative 64-bit Pythons (either from Apple or home-built) on Snow Leopard, you may need to extend your build flags to specify the architecture by setting LDFLAGS and FFLAGS.

Note that with distutils (setup.py) given build flags like LDFLAGS do not extend but override the defaults, so you have to specify all necessary flags. Only try this if you know what you’re doing!

After a successful build, you may try running the built-in unit tests for SciPy:

```
$ python
>>> import numpy as np
>>> np.test('full')
>>> import scipy
>>> scipy.test()
```

Be sure not to import numpy or scipy while you’re in the numpy/scipy source tree. Change directory first.

If you have any problems installing SciPy on your Mac based on these instructions, please check the scipy-users and scipy-dev mailing list archives for possible solutions. If you are still stuck, feel free to join scipy-users for further assistance. Please have the following information ready:

- Your OS version
- The versions of gcc and gfortran and where you obtained gfortran
  - $ gcc --version
  - $ gfortran --version
- The versions of numpy and scipy that you are trying to install
- The full output of $ python setup.py build
5.4 SciPy Developer Guide

5.4.1 Decision making process

SciPy has a formal governance model, documented in *SciPy project governance*. The section below documents in an informal way what happens in practice for decision making about code and commit rights. The formal governance model is leading, the below is only provided for context.

**Code**

Any significant decisions on adding (or not adding) new features, breaking backwards compatibility or making other significant changes to the codebase should be made on the scipy-dev mailing list after a discussion (preferably with full consensus).

Any non-trivial change (where trivial means a typo, or a one-liner maintenance commit) has to go in through a pull request (PR). It has to be reviewed by another developer. In case review doesn’t happen quickly enough and it is important that the PR is merged quickly, the submitter of the PR should send a message to mailing list saying he/she intends to merge that PR without review at time X for reason Y unless someone reviews it before then.

Changes and new additions should be tested. Untested code is broken code.

**Commit rights**

Who gets commit rights is decided by the SciPy Steering Council; changes in commit rights will then be announced on the scipy-dev mailing list.

5.4.2 Deciding on new features

The general decision rule to accept a proposed new feature has so far been conditional on:

1. The method is applicable in many fields and “generally agreed” to be useful,
2. Fits the topic of the submodule, and does not require extensive support frameworks to operate,
3. The implementation looks sound and unlikely to need much tweaking in the future (e.g., limited expected maintenance burden), and
4. Someone wants to do it.

Although it’s difficult to give hard rules on what “generally useful and generally agreed to work” means, it may help to weigh the following against each other:

- Is the method used/useful in different domains in practice? How much domain-specific background knowledge is needed to use it properly?
- Consider the code already in the module. Is what you are adding an omission? Does it solve a problem that you’d expect the module be able to solve? Does it supplement an existing feature in a significant way?
- Consider the equivalence class of similar methods / features usually expected. Among them, what would in principle be the minimal set so that there's not a glaring omission in the offered features remaining? How much stuff would that be? Does including a representative one of them cover most use cases? Would it in principle sound reasonable to include everything from the minimal set in the module?
- Is what you are adding something that is well understood in the literature? If not, how sure are you that it will turn out well? Does the method perform well compared to other similar ones?
- Note that the twice-a-year release cycle and backward-compatibility policy makes correcting things later on more difficult.
The scopes of the submodules also vary, so it’s probably best to consider each as if it’s a separate project - “numerical evaluation of special functions” is relatively well-defined, but “commonly needed optimization algorithms” less so.

5.4.3 Development on GitHub

SciPy development largely takes place on GitHub; this section describes the expected way of working for issues, pull requests and managing the main scipy repository.

Labels and Milestones

Each issue and pull request normally gets at least two labels: one for the topic or component (scipy.stats, Documentation, etc.), and one for the nature of the issue or pull request (enhancement, maintenance, defect, etc.). Other labels that may be added depending on the situation:

- easy-fix: for issues suitable to be tackled by new contributors.
- needs-work: for pull requests that have review comments that haven’t been addressed for a while.
- needs-decision: for issues or pull requests that need a decision.
- needs-champion: for pull requests that were not finished by the original author, but are worth resurrecting.
- backport-candidate: bugfixes that should be considered for backporting by the release manager.

A milestone is created for each version number for which a release is planned. Issues that need to be addressed and pull requests that need to be merged for a particular release should be set to the corresponding milestone. After a pull request is merged, its milestone (and that of the issue it closes) should be set to the next upcoming release - this makes it easy to get an overview of changes and to add a complete list of those to the release notes.

Dealing with pull requests

- When merging contributions, a committer is responsible for ensuring that those meet the requirements outlined in Contributing to SciPy. Also check that new features and backwards compatibility breaks were discussed on the scipy-dev mailing list.
- New code goes in via a pull request (PR).
- Merge new code with the green button. In case of merge conflicts, ask the PR submitter to rebase (this may require providing some git instructions).
- Backports and trivial additions to finish a PR (really trivial, like a typo or PEP8 fix) can be pushed directly.
- For PRs that add new features or are in some way complex, wait at least a day or two before merging it. That way, others get a chance to comment before the code goes in.
- Squashing commits or cleaning up commit messages of a PR that you consider too messy is OK. Make sure though to retain the original author name when doing this.
- Make sure that the labels and milestone on a merged PR are set correctly.
- When you want to reject a PR: if it’s very obvious you can just close it and explain why, if not obvious then it’s a good idea to first explain why you think the PR is not suitable for inclusion in Scipy and then let a second committer comment or close.
Backporting

All pull requests (whether they contain enhancements, bug fixes or something else), should be made against master. Only bug fixes are candidates for backporting to a maintenance branch. The backport strategy for SciPy is to (a) only backport fixes that are important, and (b) to only backport when it’s reasonably sure that a new bugfix release on the relevant maintenance branch will be made. Typically, the developer who merges an important bugfix adds the backport-candidate label and pings the release manager, who decides on whether and when the backport is done. After the backport is completed, the backport-candidate label has to be removed again.

Release notes

When a PR gets merged, consider if the changes need to be mentioned in the release notes. What needs mentioning: new features, backwards incompatible changes, deprecations, and “other changes” (anything else noteworthy enough, see older release notes for the kinds of things worth mentioning).

Release note entries are maintained on the wiki, (e.g. https://github.com/scipy/scipy/wiki/Release-note-entries-for-SciPy-1.1.0). The release manager will gather content from there and integrate it into the html docs. We use this mechanism to avoid merge conflicts that would happen if every PR touched the same file under doc/release/ directly.

Changes can be monitored (Atom feed) and pulled (the wiki is a git repo: https://github.com/scipy/scipy.wiki.git).

Other

PR status page: When new commits get added to a pull request, GitHub doesn’t send out any notifications. The needs-work label may not be justified anymore though. This page gives an overview of PRs that were updated, need review, need a decision, etc.

Cross-referencing: Cross-referencing issues and pull requests on GitHub is often useful. GitHub allows doing that by using gh-xxxx or #xxxx with xxxx the issue/PR number. The gh-xxxx format is strongly preferred, because it’s clear that that is a GitHub link. Older issues contain #xxxx which is about Trac (what we used pre-GitHub) tickets.

PR naming convention: Pull requests, issues and commit messages usually start with a three-letter abbreviation like ENH: or BUG: This is useful to quickly see what the nature of the commit/PR/issue is. For the full list of abbreviations, see writing the commit message.

5.4.4 Licensing

SciPy is distributed under the modified (3-clause) BSD license. All code, documentation and other files added to SciPy by contributors is licensed under this license, unless another license is explicitly specified in the source code. Contributors keep the copyright for code they wrote and submit for inclusion to SciPy.

Other licenses that are compatible with the modified BSD license that SciPy uses are 2-clause BSD, MIT and PSF. Incompatible licenses are GPL, Apache and custom licenses that require attribution/citation or prohibit use for commercial purposes.

It regularly happens that PRs are submitted with content copied or derived from unlicensed code. Such contributions cannot be accepted for inclusion in SciPy. What is needed in such cases is to contact the original author and ask him to relicense his code under the modified BSD (or a compatible) license. If the original author agrees to this, add a comment saying so to the source files and forward the relevant email to the scipy-dev mailing list.

What also regularly happens is that code is translated or derived from code in R, Octave (both GPL-licensed) or a commercial application. Such code also cannot be included in SciPy. Simply implementing functionality with the same API as found in R/Octave/... is fine though, as long as the author doesn’t look at the original incompatibly-licensed source code.
5.4.5 Version numbering

SciPy version numbering complies to PEP 440. Released final versions, which are the only versions appearing on PyPI, are numbered MAJOR.MINOR.MICRO where:

- **MAJOR** is an integer indicating the major version. It changes very rarely; a change in MAJOR indicates large (possibly backwards-incompatible) changes.
- **MINOR** is an integer indicating the minor version. Minor versions are typically released twice a year and can contain new features, deprecations and bug-fixes.
- **MICRO** is an integer indicating a bug-fix version. Bug-fix versions are released when needed, typically one or two per minor version. They cannot contain new features or deprecations.

Released alpha, beta and rc (release candidate) versions are numbered like final versions but with postfixes a#, b# and rc# respectively, with # an integer. Development versions are postfixed with . dev0+<git-commit-hash>.

Examples of valid SciPy version strings are:

```
0.16.0
0.15.1
0.14.0a1
0.14.0b2
0.14.0rc1
0.17.0.dev0+ac53f09
```

An installed SciPy version contains these version identifiers:

```
scipy.__version__           # complete version string, including git commit hash for dev versions
scipy.version.short_version # string, only major.minor.micro
scipy.version.version       # string, same as scipy.__version__
scipy.version.full_version  # string, same as scipy.__version__
scipy.version.release       # bool, development or (alpha/beta/rc/final) released
scipy.version.git_revision  # string, git commit hash from which scipy was built
```

5.4.6 Deprecations

There are various reasons for wanting to remove existing functionality: it’s buggy, the API isn’t understandable, it’s superseded by functionality with better performance, it needs to be moved to another SciPy submodule, etc.

In general it’s not a good idea to remove something without warning users about that removal first. Therefore this is what should be done before removing something from the public API:

1. Propose to deprecate the functionality on the scipy-dev mailing list and get agreement that that’s OK.
2. Add a DeprecationWarning for it, which states that the functionality was deprecated, and in which release.
3. Mention the deprecation in the release notes for that release.
4. Wait till at least 6 months after the release date of the release that introduced the DeprecationWarning before removing the functionality.
5. Mention the removal of the functionality in the release notes.
The 6 months waiting period in practice usually means waiting two releases. When introducing the warning, also ensure that those warnings are filtered out when running the test suite so they don’t pollute the output.

It’s possible that there is reason to want to ignore this deprecation policy for a particular deprecation; this can always be discussed on the scipy-dev mailing list.

## 5.4.7 Distributing

Distributing Python packages is nontrivial - especially for a package with complex build requirements like Scipy - and subject to change. For an up-to-date overview of recommended tools and techniques, see the Python Packaging User Guide. This document discusses some of the main issues and considerations for Scipy.

### Dependencies

Dependencies are things that a user has to install in order to use (or build/test) a package. They usually cause trouble, especially if they’re not optional. Scipy tries to keep its dependencies to a minimum; currently they are:

**Unconditional run-time dependencies:**
- Numpy

**Conditional run-time dependencies:**
- nose (to run the test suite)
- asv (to run the benchmarks)
- matplotlib (for some functions that can produce plots)
- Pillow (for image loading/saving)
- scikits.umfpack (optionally used in sparse.linalg)
- mpmath (for more extended tests in special)

**Unconditional build-time dependencies:**
- Numpy
- A BLAS and LAPACK implementation (reference BLAS/LAPACK, ATLAS, OpenBLAS, MKL, Accelerate are all known to work)
- (for development versions) Cython

**Conditional build-time dependencies:**
- setuptools
- wheel (python setup.py bdist_wheel)
- Sphinx (docs)
- matplotlib (docs)
- LaTeX (pdf docs)
- Pillow (docs)

Furthermore of course one needs C, C++ and Fortran compilers to build Scipy, but those we don’t consider to be dependencies and are therefore not discussed here. For details, see https://scipy.github.io/devdocs/building/.
When a package provides useful functionality and it's proposed as a new dependency, consider also if it makes sense to vendor (i.e. ship a copy of it with scipy) the package instead. For example, six and decorator are vendored in scipy._lib.

The only dependency that is reported to pip is Numpy, see install_requires in Scipy's main setup.py. The other dependencies aren't needed for Scipy to function correctly, and the one unconditional build dependency that pip knows how to install (Cython) we prefer to treat like a compiler rather than a Python package that pip is allowed to upgrade.

**Issues with dependency handling**

There are some serious issues with how Python packaging tools handle dependencies reported by projects. Because Scipy gets regular bug reports about this, we go in a bit of detail here.

Scipy only reports its dependency on Numpy via install_requires if Numpy isn’t installed at all on a system. This will only change when there are either 32-bit and 64-bit Windows wheels for Numpy on PyPI or when pip upgrade becomes available (with sane behavior, unlike pip install -U, see this PR). For more details, see this summary.

The situation with setup_requires is even worse; pip doesn’t handle that keyword at all, while setuptools has issues (here's a current one) and invokes easy_install which comes with its own set of problems (note that Scipy doesn’t support easy_install at all anymore; issues specific to it will be closed as “wontfix”).

**Supported Python and Numpy versions**

The Python versions that Scipy supports are listed in the list of PyPI classifiers in setup.py, and mentioned in the release notes for each release. All newly released Python versions will be supported as soon as possible. The general policy on dropping support for a Python version is that (a) usage of that version has to be quite low (say <5% of users) and (b) the version isn’t included in an active long-term support release of one of the main Linux distributions anymore. Scipy typically follows Numpy, which has a similar policy. The final decision on dropping support is always taken on the scipy-dev mailing list.

The lowest supported Numpy version for a Scipy version is mentioned in the release notes and is encoded in scipy/__init__.py and the install_requires field of setup.py. Typically the latest Scipy release supports 3 or 4 minor versions of Numpy. That may become more if the frequency of Numpy releases increases (it’s about 1x/year at the time of writing). Support for a particular Numpy version is typically dropped if (a) that Numpy version is several years old, and (b) the maintenance cost of keeping support is starting to outweigh the benefits. The final decision on dropping support is always taken on the scipy-dev mailing list.

Supported versions of optional dependencies and compilers is less clearly documented, and also isn’t tested well or at all by Scipy’s Continuous Integration setup. Issues regarding this are dealt with as they come up in the issue tracker or mailing list.

**Building binary installers**

**Note:** This section is only about building Scipy binary installers to distribute. For info on building Scipy on the same machine as where it will be used, see this scipy.org page.

There are a number of things to take into consideration when building binaries and distributing them on PyPI or elsewhere.

**General**

- A binary is specific for a single Python version (because different Python versions aren’t ABI-compatible, at least up to Python 3.4).
- Build against the lowest Numpy version that you need to support, then it will work for all Numpy versions with the same major version number (Numpy does maintain backwards ABI compatibility).
Windows

- The currently most easily available toolchain for building Python.org compatible binaries for Scipy is installing MSVC (see https://wiki.python.org/moin/WindowsCompilers) and mingw64-gfortran. Support for this configuration requires numpy.distutils from Numpy >= 1.14.dev and a gcc/gfortran-compiled static openblas.a. This configuration is currently used in the Appveyor configuration for https://github.com/MacPython/scipy-wheels

- For 64-bit Windows installers built with a free toolchain, use the method documented at https://github.com/numpy/numpy/wiki/Mingw-static-toolchain. That method will likely be used for Scipy itself once it’s clear that the maintenance of that toolchain is sustainable long-term. See the MingwPy project and this thread for details.

- The other way to produce 64-bit Windows installers is with icc, ifort plus MKL (or MSVC instead of icc). For Intel toolchain instructions see this article and for (partial) MSVC instructions see this wiki page.

- Older Scipy releases contained a .exe “superpack” installer. Those contain 3 complete builds (no SSE, SSE2, SSE3), and were built with https://github.com/numpy/numpy/vendor. That build setup is known to not work well anymore and is no longer supported. It used g77 instead of gfortran, due to complex DLL distribution issues (see gh-2829). Because the toolchain is no longer supported, g77 support isn’t needed anymore and Scipy can now include Fortran 90/95 code.

OS X

- To produce OS X wheels that work with various Python versions (from python.org, Homebrew, MacPython), use the build method provided by https://github.com/MacPython/scipy-wheels.

- DMG installers for the Python from python.org on OS X can still be produced by tools/scipy-macosx-installer/. Scipy doesn’t distribute those installers anymore though, now that there are binary wheels on PyPi.

Linux

- PyPi-compatible Linux wheels can be produced via the manylinux project. The corresponding build setup for TravisCI for Scipy is set up in https://github.com/MacPython/scipy-wheels.

Other Linux build-setups result to PyPi incompatible wheels, which would need to be distributed via custom channels, e.g. in a Wheelhouse, see at the wheel and Wheelhouse docs.

5.4.8 Making a SciPy release

At the highest level, this is what the release manager does to release a new Scipy version:

1. Propose a release schedule on the scipy-dev mailing list.
2. Create the maintenance branch for the release.
3. Tag the release.
4. Build all release artifacts (sources, installers, docs).
5. Upload the release artifacts.
6. Announce the release.
7. Port relevant changes to release notes and build scripts to master.

In this guide we attempt to describe in detail how to perform each of the above steps. In addition to those steps, which have to be performed by the release manager, here are descriptions of release-related activities and conventions of interest:

- Backporting
• *Labels and Milestones*
• versioning
• *Supported Python and Numpy versions*
• deprecations

**Proposing a release schedule**

A typical release cycle looks like:

- Create the maintenance branch
- Release a beta version
- Release a “release candidate” (RC)
- If needed, release one or more new RCs
- Release the final version once there are no issues with the last release candidate

There’s usually at least one week between each of the above steps. Experience shows that a cycle takes between 4 and 8 weeks for a new minor version. Bug-fix versions don’t need a beta or RC, and can be done much quicker.

Ideally the final release is identical to the last RC, however there may be minor differences — it’s up to the release manager to judge the risk of that. Typically, if compiled code or complex pure Python code changes then a new RC is needed, while a simple bug-fix that’s backported from master doesn’t require a new RC.

To propose a schedule, send a list with estimated dates for branching and beta/rc/final releases to scipy-dev. In the same email, ask everyone to check if there are important issues/PRs that need to be included and aren’t tagged with the Milestone for the release or the “backport-candidate” label.

**Creating the maintenance branch**

Before branching, ensure that the release notes are updated as far as possible. Include the output of `tools/gh_lists.py` and `tools/authors.py` in the release notes.

Maintenance branches are named `maintenance/<major>.<minor>.x` (e.g. 0.19.x). To create one, simply push a branch with the correct name to the scipy repo. Immediately after, push a commit where you increment the version number on the master branch and add release notes for that new version. Send an email to scipy-dev to let people know that you’ve done this.

**Tagging a release**

First ensure that you have set up GPG correctly. See https://github.com/scipy/scipy/issues/4919 for a discussion of signing release tags, and https://keyring.debian.org/creating-key.html for instructions on creating a GPG key if you do not have one.

To make your key more readily identifiable as you, consider sending your key to public keyservers, with a command such as:

```
gpg --send-keys <yourkeyid>
```

Check that all relevant commits are in the branch. In particular, check issues and PRs under the Milestone for the release (https://github.com/scipy/scipy/milestones), PRs labeled “backport-candidate”, and that the release notes are up-to-date and included in the html docs.

Then edit `setup.py` to get the correct version number (set `ISRELEASED = True`) and commit it with a message like `REL: set version to <version-number>`. Don’t push this commit to the Scipy repo yet.
Finally tag the release locally with `git tag -s <v1.x.y>` (the `-s` ensures the tag is signed). Continue with building release artifacts (next section). Only push the release commit to the scipy repo once you have built the sdists and docs successfully. Then continue with building wheels. Only push the release tag to the repo once all wheels have been built successfully on TravisCI and Appveyor (if it fails, you have to move the tag otherwise - which is bad practice). Finally, after pushing the tag, also push a second commit which increment the version number and sets `ISRELEASED` to False again.

### Building release artifacts

Here is a complete list of artifacts created for a release:

- source archives (.tar.gz, .zip and .tar.xz for GitHub Releases, only .tar.gz is uploaded to PyPI)
- Binary wheels for Windows, Linx and OS X
- Documentation (html, pdf)
- A README file
- A Changelog file

Source archives, Changelog and README are built by running `paver release` in the repo root, and end up in `REPO_ROOT/release/`. Do this after you’ve created the signed tag locally. If this completes without issues, push the release commit (not the tag, see section above) to the scipy repo.

To build wheels, push a commit to the master branch of [https://github.com/MacPython/scipy-wheels](https://github.com/MacPython/scipy-wheels). This triggers builds for all needed Python versions on TravisCI. Update and check the `.travis.yml` and `appveyor.yml` config files what commit to build, and what Python and Numpy are used for the builds (it needs to be the lowest supported Numpy version for each Python version). See the README file in the scipy-wheels repo for more details.

The TravisCI and Appveyor builds run the tests from the built wheels and if they pass, upload the wheels to a container pointed to at [https://github.com/MacPython/scipy-wheels](https://github.com/MacPython/scipy-wheels)

From there you can download them for uploading to PyPI. This can be done in an automated fashion with `terrryfy` (note the `-n` switch which makes it only download the wheels and skip the upload to PyPI step - we want to be able to check the wheels and put their checksums into README first):

```
$ python wheel-uploader -n -v -c -u https://3f23b170c54c2533c070-1c8a9b3114517dc5fe17b7c3f8c63a43.ssl.cf2.rackcdn.com --w REPO_ROOT/release/installers --t win scipy 0.19.0
```

```
$ python wheel-uploader -n -v -c -u https://3f23b170c54c2533c070-1c8a9b3114517dc5fe17b7c3f8c63a43.ssl.cf2.rackcdn.com --w REPO_ROOT/release/installers --t macosx scipy 0.19.0
```

```
$ python wheel-uploader -n -v -c -u https://3f23b170c54c2533c070-1c8a9b3114517dc5fe17b7c3f8c63a43.ssl.cf2.rackcdn.com --w REPO_ROOT/release/installers --t manylinux1 scipy 0.19.0
```

The correct URL to use is shown in [https://github.com/MacPython/scipy-wheels](https://github.com/MacPython/scipy-wheels) and should agree with the above one.

After this, we want to regenerate the README file, in order to have the MD5 and SHA256 checksums of the just downloaded wheels in it. Run:

```
$ paver write_release_and_log
```

### Uploading release artifacts

For a release there are currently five places on the web to upload things to:
• PyPI (tarballs, wheels)
• Github releases (tarballs, release notes, Changelog)
• scipy.org (an announcement of the release)
• docs.scipy.org (html/pdf docs)

**PyPI:**

Upload first the wheels and then the sdist:

```
twine upload -s REPO_ROOT/release/installers/*.*.whl
twine upload -s REPO_ROOT/release/installers/scipy-1.x.y.tar.gz
```

**Github Releases:**

Use GUI on https://github.com/scipy/scipy/releases to create release and upload all release artifacts.

**scipy.org:**

Sources for the site are in https://github.com/scipy/scipy.org. Update the News section in www/index.rst and then do make upload USERNAME=yourusername.

**docs.scipy.org:**

First build the scipy docs, by running make dist in scipy/doc/. Verify that they look OK, then upload them to the doc server with make upload USERNAME=rgommers RELEASE=0.19.0. Note that SSH access to the doc server is needed; ask @pv (server admin) or @rgommers (can upload) if you don’t have that.

The sources for the website itself are maintained in https://github.com/scipy/docs.scipy.org/. Add the new Scipy version in the table of releases in index.rst. Push that commit, then do make upload USERNAME=yourusername.

**Wrapping up**

Send an email announcing the release to the following mailing lists:

• scipy-dev
• scipy-user
• numpy-discussion
• python-announce (not for beta/rc releases)

For beta and rc versions, ask people in the email to test (run the scipy tests and test against their own code) and report issues on Github or scipy-dev.

After the final release is done, port relevant changes to release notes, build scripts, author name mapping in tools/authors.py and any other changes that were only made on the maintenance branch to master.

### 5.4.9 Module-Specific Instructions

Some SciPy modules have specific development workflows that it is useful to be aware of while contributing.

**scipy.special**

Many of the functions in special are vectorized versions of scalar functions. The scalar functions are written by hand and the necessary loops for vectorization are generated automatically. This section discusses the steps necessary to add a new vectorized special function.

The first step in adding a new vectorized function is writing the corresponding scalar function. This can be done in Cython, C, C++, or Fortran. If starting from scratch then Cython should be preferred because the
code is easier to maintain for developers only familiar with Python. If the primary code is in Fortran then it is necessary to write a C wrapper around the code; for examples of such wrappers see specfun_wrappers.c. After implementing the scalar function, register the new function by adding a line to the FUNC string in generate_ufuncs.py. The docstring for that file explains the format. Also add documentation for the new function by adding an entry to add_newdocs.py; look in the file for examples.

5.5 SciPy project governance

The purpose of this document is to formalize the governance process used by the SciPy project in both ordinary and extraordinary situations, and to clarify how decisions are made and how the various elements of our community interact, including the relationship between open source collaborative development and work that may be funded by for-profit or non-profit entities.

5.5.1 The Project

The SciPy Project (The Project) is an open source software project. The goal of The Project is to develop open source software for scientific computing in Python, and in particular the scipy package. The Software developed by The Project is released under the BSD (or similar) open source license, developed openly and hosted on public GitHub repositories under the scipy GitHub organization.

The Project is developed by a team of distributed developers, called Contributors. Contributors are individuals who have contributed code, documentation, designs or other work to the Project. Anyone can be a Contributor. Contributors can be affiliated with any legal entity or none. Contributors participate in the project by submitting, reviewing and discussing GitHub Pull Requests and Issues and participating in open and public Project discussions on GitHub, mailing lists, and other channels. The foundation of Project participation is openness and transparency.

The Project Community consists of all Contributors and Users of the Project. Contributors work on behalf of and are responsible to the larger Project Community and we strive to keep the barrier between Contributors and Users as low as possible.

The Project is not a legal entity, nor does it currently have any formal relationships with legal entities.

5.5.2 Governance

This section describes the governance and leadership model of The Project.

The foundations of Project governance are:

- Openness & Transparency
- Active Contribution
- Institutional Neutrality

Traditionally, Project leadership was provided by a subset of Contributors, called Core Developers, whose active and consistent contributions have been recognized by their receiving “commit rights” to the Project GitHub repositories. In general all Project decisions are made through consensus among the Core Developers with input from the Community.

While this approach has served us well, as the Project grows we see a need for a more formal governance model. The SciPy Core Developers expressed a preference for a leadership model which includes a BDFL (Benevolent Dictator for Life). Therefore, moving forward The Project leadership will consist of a BDFL and Steering Council.
BDFL

The Project will have a BDFL (Benevolent Dictator for Life), who is currently Pauli Virtanen. As Dictator, the BDFL has the authority to make all final decisions for The Project. As Benevolent, the BDFL, in practice chooses to defer that authority to the consensus of the community discussion channels and the Steering Council (see below). It is expected, and in the past has been the case, that the BDFL will only rarely assert his/her final authority. Because rarely used, we refer to BDFL’s final authority as a “special” or “overriding” vote. When it does occur, the BDFL override typically happens in situations where there is a deadlock in the Steering Council or if the Steering Council asks the BDFL to make a decision on a specific matter. To ensure the benevolence of the BDFL, The Project encourages others to fork the project if they disagree with the overall direction the BDFL is taking. The BDFL may delegate his/her authority on a particular decision or set of decisions to any other Council member at his/her discretion.

The BDFL can appoint his/her successor, but it is expected that the Steering Council would be consulted on this decision. If the BDFL is unable to appoint a successor, the Steering Council will make this decision - preferably by consensus, but if needed by a majority vote.

Note that the BDFL can step down at any time, and acting in good faith, will also listen to serious calls to do so. Also note that the BDFL is more a role for fallback decision making rather than that of a director/CEO.

Steering Council

The Project will have a Steering Council that consists of Project Contributors who have produced contributions that are substantial in quality and quantity, and sustained over at least one year. The overall role of the Council is to ensure, through working with the BDFL and taking input from the Community, the long-term well-being of the project, both technically and as a community.

The Council will have a Chair, who is tasked with keeping the organisational aspects of the functioning of the Council and the Project on track. The Council will also appoint a Release Manager for the Project, who has final responsibility for one or more releases.

During the everyday project activities, council members participate in all discussions, code review and other project activities as peers with all other Contributors and the Community. In these everyday activities, Council Members do not have any special power or privilege through their membership on the Council. However, it is expected that because of the quality and quantity of their contributions and their expert knowledge of the Project Software and Services that Council Members will provide useful guidance, both technical and in terms of project direction, to potentially less experienced contributors.

The Steering Council and its Members play a special role in certain situations. In particular, the Council may:

- Make decisions about the overall scope, vision and direction of the project.
- Make decisions about strategic collaborations with other organizations or individuals.
- Make decisions about specific technical issues, features, bugs and pull requests. They are the primary mechanism of guiding the code review process and merging pull requests.
- Make decisions about the Services that are run by The Project and manage those Services for the benefit of the Project and Community.
- Make decisions when regular community discussion does not produce consensus on an issue in a reasonable time frame.
- Update policy documents such as this one.

Council membership

To become eligible for being a Steering Council Member an individual must be a Project Contributor who has produced contributions that are substantial in quality and quantity, and sustained over at least one year. Potential Council Members are nominated by existing Council members and voted upon by the existing Council after asking if the potential Member is interested and willing to serve in that capacity. The
Council will be initially formed from the set of existing Core Developers who, as of January 2017, have been significantly active over the last two years.

When considering potential Members, the Council will look at candidates with a comprehensive view of their contributions. This will include but is not limited to code, code review, infrastructure work, mailing list and chat participation, community help/building, education and outreach, design work, etc. We are deliberately not setting arbitrary quantitative metrics (like “100 commits in this repo”) to avoid encouraging behavior that plays to the metrics rather than the project’s overall well-being. We want to encourage a diverse array of backgrounds, viewpoints and talents in our team, which is why we explicitly do not define code as the sole metric on which council membership will be evaluated.

If a Council member becomes inactive in the project for a period of one year, they will be considered for removal from the Council. Before removal, inactive Member will be approached to see if they plan on returning to active participation. If not they will be removed immediately upon a Council vote. If they plan on returning to active participation soon, they will be given a grace period of one year. If they don’t return to active participation within that time period they will be removed by vote of the Council without further grace period. All former Council members can be considered for membership again at any time in the future, like any other Project Contributor. Retired Council members will be listed on the project website, acknowledging the period during which they were active in the Council.

The Council reserves the right to eject current Members, other than the BDFL, if they are deemed to be actively harmful to the project’s well-being, and attempts at communication and conflict resolution have failed.

A list of current Steering Council Members is maintained at the page governance-people.

**Council Chair**
The Chair will be appointed by the Steering Council. The Chair can stay on as long as he/she wants, but may step down at any time and will listen to serious calls to do so (similar to the BDFL role). The Chair will be responsible for:

- Starting a review of the technical direction of the project (as captured by the SciPy Roadmap) bi-yearly, around mid-April and mid-October.
- At the same times of the year, summarizing any relevant organisational updates and issues in the preceding period, and asking for feedback/suggestions on the mailing list.
- Ensuring the composition of the Steering Council stays current.
- Ensuring matters discussed in private by the Steering Council get summarized on the mailing list to keep the Community informed.
- Ensuring other important organisational documents (e.g. Code of Conduct, Fiscal Sponsorship Agreement) stay current after they are added.

**Release Manager**
The Release Manager has final responsibility for making a release. This includes:

- Proposing of and deciding on the timing of a release.
- Determining the content of a release in case there is no consensus on a particular change or feature.
- Creating the release and announcing it on the relevant public channels.

For more details on what those responsibilities look like in practice, see making-a-release.

**Conflict of interest**
It is expected that the BDFL and Council Members will be employed at a wide range of companies, universities and non-profit organizations. Because of this, it is possible that Members will have conflict of interests. Such conflict of interests include, but are not limited to:

- Financial interests, such as investments, employment or contracting work, outside of The Project that may influence their work on The Project.
• Access to proprietary information of their employer that could potentially leak into their work with the Project.

All members of the Council, BDFL included, shall disclose to the rest of the Council any conflict of interest they may have. Members with a conflict of interest in a particular issue may participate in Council discussions on that issue, but must recuse themselves from voting on the issue. If the BDFL has recused his/herself for a particular decision, the Council will appoint a substitute BDFL for that decision.

Private communications of the Council
Unless specifically required, all Council discussions and activities will be public and done in collaboration and discussion with the Project Contributors and Community. The Council will have a private mailing list that will be used sparingly and only when a specific matter requires privacy. When private communications and decisions are needed, the Council will do its best to summarize those to the Community after removing personal/private/sensitive information that should not be posted to the public internet.

Council decision making
If it becomes necessary for the Steering Council to produce a formal decision, then they will use a form of the Apache Foundation voting process. This is a formalized version of consensus, in which +1 votes indicate agreement, -1 votes are vetoes (and must be accompanied with a rationale, as above), and one can also vote fractionally (e.g. -0.5, +0.5) if one wishes to express an opinion without registering a full veto. These numeric votes are also often used informally as a way of getting a general sense of people’s feelings on some issue, and should not normally be taken as formal votes. A formal vote only occurs if explicitly declared, and if this does occur then the vote should be held open for long enough to give all interested Council Members a chance to respond – at least one week.

In practice, we anticipate that for most Steering Council decisions (e.g., voting in new members) a more informal process will suffice.

5.5.3 Institutional Partners and Funding
The Steering Council is the primary leadership for the project. No outside institution, individual or legal entity has the ability to own, control, usurp or influence the project other than by participating in the Project as Contributors and Council Members. However, because institutions can be an important funding mechanism for the project, it is important to formally acknowledge institutional participation in the project. These are Institutional Partners.

An Institutional Contributor is any individual Project Contributor who contributes to the project as part of their official duties at an Institutional Partner. Likewise, an Institutional Council Member is any Project Steering Council Member who contributes to the project as part of their official duties at an Institutional Partner.

With these definitions, an Institutional Partner is any recognized legal entity in any country that employs at least 1 Institutional Contributor or Institutional Council Member. Institutional Partners can be for-profit or non-profit entities.

Institutions become eligible to become an Institutional Partner by employing individuals who actively contribute to The Project as part of their official duties. To state this another way, the only way for a Partner to influence the project is by actively contributing to the open development of the project, in equal terms to any other member of the community of Contributors and Council Members. Merely using Project Software in institutional context does not allow an entity to become an Institutional Partner. Financial gifts do not enable an entity to become an Institutional Partner. Once an institution becomes eligible for Institutional Partnership, the Steering Council must nominate and approve the Partnership.

If at some point an existing Institutional Partner stops having any contributing employees, then a one year grace period commences. If at the end of this one year period they continue not to have any contributing employees, then their Institutional Partnership will lapse, and resuming it will require going through the normal process for new Partnerships.

An Institutional Partner is free to pursue funding for their work on The Project through any legal means.
This could involve a non-profit organization raising money from private foundations and donors or a for-profit company building proprietary products and services that leverage Project Software and Services. Funding acquired by Institutional Partners to work on The Project is called Institutional Funding. However, no funding obtained by an Institutional Partner can override the Steering Council. If a Partner has funding to do SciPy work and the Council decides to not pursue that work as a project, the Partner is free to pursue it on their own. However in this situation, that part of the Partner’s work will not be under the SciPy umbrella and cannot use the Project trademarks in a way that suggests a formal relationship.

Institutional Partner benefits are:

- Acknowledgement on the SciPy website and in talks.
- Ability to acknowledge their own funding sources on the SciPy website and in talks.
- Ability to influence the project through the participation of their Council Member.
- Council Members invited to SciPy Developer Meetings.

A list of current Institutional Partners is maintained at the page governance-people.

5.5.4 Document history

https://github.com/scipy/scipy/commits/master/doc/source/dev/governance/governance.rst

5.5.5 Acknowledgements

Substantial portions of this document were adapted from the Jupyter/IPython project’s governance document and NumPy’s governance document.

5.5.6 License

To the extent possible under law, the authors have waived all copyright and related or neighboring rights to the SciPy project governance document, as per the CC-0 public domain dedication / license.

To get an overview of where help or new features are desired or planned, see the roadmap:

5.6 SciPy Roadmap

Most of this roadmap is intended to provide a high-level view on what is most needed per SciPy submodule in terms of new functionality, bug fixes, etc. Besides important “business as usual” changes, it contains ideas for major new features - those are marked as such, and are expected to take significant dedicated effort. Things not mentioned in this roadmap are not necessarily unimportant or out of scope, however we (the SciPy developers) want to provide to our users and contributors a clear picture of where SciPy is going and where help is needed most.

5.6.1 General

This roadmap will be evolving together with SciPy. Updates can be submitted as pull requests. For large or disruptive changes you may want to discuss those first on the scipy-dev mailing list.

API changes

In general, we want to evolve the API to remove known warts as much as possible, however as much as possible without breaking backwards compatibility.

Also, it should be made (even) more clear what is public and what is private in SciPy. Everything private should be named starting with an underscore as much as possible.
Test coverage

Test coverage of code added in the last few years is quite good, and we aim for a high coverage for all new code that is added. However, there is still a significant amount of old code for which coverage is poor. Bringing that up to the current standard is probably not realistic, but we should plug the biggest holes.

Besides coverage there is also the issue of correctness - older code may have a few tests that provide decent statement coverage, but that doesn’t necessarily say much about whether the code does what it says on the box. Therefore code review of some parts of the code (stats, signal and ndimage in particular) is necessary.

Documentation

The documentation is in good shape. Expanding of current docstrings and putting them in the standard NumPy format should continue, so the number of reST errors and glitches in the html docs decreases. Most modules also have a tutorial in the reference guide that is a good introduction, however there are a few missing or incomplete tutorials - this should be fixed.

Other

Regarding Cython code:

- It’s not clear how much functionality can be Cythonized without making the .so files too large. This needs measuring.
- Cython’s old syntax for using NumPy arrays should be removed and replaced with Cython/memoryviews.

Regarding build environments:

- SciPy builds from source on Windows now with a MSVC + MinGW-w64 gfortran toolchain. This still needs to prove itself, but is looking good so far.
- Support for Accelerate will be dropped, likely in SciPy 1.1.0. If there is enough interest, we may want to write wrappers so the BLAS part of Accelerate can still be used.

Continuous integration is in good shape, it covers Windows, macOS and Linux, as well as a range of versions of our dependencies and building release quality wheels.

5.6.2 Modules

cluster

This module is in good shape.

constants

This module is basically done, low-maintenance and without open issues.

fftpack

Needed:

- solve issues with single precision: large errors, disabled for difficult sizes
- fix caching bug
- Bluestein algorithm (or chirp Z-transform)
- deprecate fftpack.convolve as public function (was not meant to be public)
There's a large overlap with `numpy.fft`. This duplication has to change (both are too widely used to deprecate one); in the documentation we should make clear that `scipy.fftpack` is preferred over `numpy.fft`. If there are differences in signature or functionality, the best version should be picked case by case (example: numpy's `rfft` is preferred, see gh-2487).

**integrate**

Needed for ODE solvers:

- Documentation is pretty bad, needs fixing
- A new ODE solver interface (`solve_ivp`) was added in SciPy 1.0.0. In the future we can consider (soft-)deprecating the older API.

The numerical integration functions are in good shape. Support for integrating complex-valued functions and integrating multiple intervals (see gh-3325) could be added.

**interpolate**

Ideas for new features:

- Spline fitting routines with better user control.
- Integration and differentiation and arithmetic routines for splines
- Transparent tensor-product splines.
- NURBS support.
- Mesh refinement and coarsening of B-splines and corresponding tensor products.

**io**

`wavfile`;

- PCM float will be supported, for anything else use `audiolab` or other specialized libraries.
- Raise errors instead of warnings if data not understood.

Other sub-modules (matlab, netcdf, idl, harwell-boeing, arff, matrix market) are in good shape.

**linalg**

`scipy.linalg` is in good shape. We have started requiring more recent LAPACK versions (minimum version increases from 3.1.0 to 3.4.0 in SciPy 1.2.0); we want to add support for newer features in LAPACK.

Needed:

- Reduce duplication of functions with `numpy.linalg`, make APIs consistent.
- `get_lapack_funcs` should always use `flapack`
- Wrap more LAPACK functions
- One too many func for LU decomposition, remove one

Ideas for new features:

- Add type-generic wrappers in the Cython BLAS and LAPACK
- Make many of the linear algebra routines into gufuncs
misc

scipy.misc will be removed as a public module. Most functions in it have been moved to another submodule or deprecated. The few that are left:

- doccer: move to scipy._lib (making it private)
- info, who: these are NumPy functions
- derivative, central_diff_weight: remove, possibly replacing them with more extensive functionality for numerical differentiation.

ndimage

Underlying ndimage is a powerful interpolation engine. Unfortunately, it was never decided whether to use a pixel model ((1, 1) elements with centers (0.5, 0.5)) or a data point model (values at points on a grid). Over time, it seems that the data point model is better defined and easier to implement. We therefore propose to move to this data representation for 1.0, and to vet all interpolation code to ensure that boundary values, transformations, etc. are correctly computed. Addressing this issue will close several issues, including #1323, #1903, #2045 and #2640.

The morphology interface needs to be standardized:

- binary dilation/erosion/opening/closing take a “structure” argument, whereas their grey equivalent take size (has to be a tuple, not a scalar), footprint, or structure.
- a scalar should be acceptable for size, equivalent to providing that same value for each axis.
- for binary dilation/erosion/opening/closing, the structuring element is optional, whereas it’s mandatory for grey. Grey morphology operations should get the same default.
- other filters should also take that default value where possible.

odr

Rename the module to regression or fitting, include optimize.curve_fit. This module will then provide a home for other fitting functionality - what exactly needs to be worked out in more detail, a discussion can be found at https://github.com/scipy/scipy/pull/448.

optimize

Overall this module is in reasonably good shape, however it is missing a few more good global optimizers as well as large-scale optimizers. These should be added. Other things that are needed:

- deprecate the fmin_* functions in the documentation, minimize is preferred.
- clearly define what’s out of scope for this module.

signal

Convolution and correlation: (Relevant functions are convolve, correlate, fftconvolve, convolve2d, correlate2d, and sepfir2d.) Eliminate the overlap with ndimage (and elsewhere). From numpy, scipy.signal and scipy.ndimage (and anywhere else we find them), pick the “best of class” for 1-D, 2-D and n-d convolution and correlation, put the implementation somewhere, and use that consistently throughout SciPy.

B-splines: (Relevant functions are bspline, cubic, quadratic, gauss_spline, cspline1d, qspline1d, cspline2d, qspline2d, cspline1d_eval, and spline_filter.) Move the good stuff to interpolate (with appropriate API changes to match how things are done in interpolate), and eliminate any duplication.

Filter design: merge firwin and firwin2 so firwin2 can be removed.
Continuous-Time Linear Systems: remove \texttt{lsim2}, \texttt{impulse2}, \texttt{step2}. The \texttt{lsim}, \texttt{impulse} and \texttt{step} functions now “just work” for any input system. Further improve the performance of \texttt{ltisys} (fewer internal transformations between different representations). Fill gaps in \texttt{lti} system conversion functions.

Second Order Sections: Make SOS filtering equally capable as existing methods. This includes \texttt{ltisys} objects, an \texttt{filtic} equivalent, and numerically stable conversions to and from other filter representations. SOS filters could be considered as the default filtering method for \texttt{ltisys} objects, for their numerical stability.

Wavelets: what’s there now doesn’t make much sense. Continuous wavelets only at the moment - decide whether to completely rewrite or remove them. Discrete wavelet transforms are out of scope (PyWavelets does a good job for those).

\textbf{sparse}

The sparse matrix formats are getting feature-complete but are slow ... reimplement parts in Cython?

- Small matrices are slower than PySparse, needs fixing

There are a lot of formats. These should be kept, but improvements/optimizations should go into CSR/CSC, which are the preferred formats. LIL may be the exception, it’s inherently inefficient. It could be dropped if DOK is extended to support all the operations LIL currently provides. Alternatives are being worked on, see \url{https://github.com/ev-br/sparr} and \url{https://github.com/perimosocordiae/sparray}.

Ideas for new features:

- Sparse arrays now act like np.matrix. We want sparse \texttt{arrays}.

\textbf{sparse.csgraph}

This module is in good shape.

\textbf{sparse.linalg}

Arpack is in good shape.

\textbf{isolve}:

- callback keyword is inconsistent
- tol keyword is broken, should be relative tol
- Fortran code not re-entrant (but we don’t solve, maybe re-use from PyKrilov)

\textbf{dsolve}:

- add sparse Cholesky or incomplete Cholesky
- look at CHOLMOD

Ideas for new features:

- Wrappers for PROPACK for faster sparse SVD computation.

\textbf{spatial}

QHull wrappers are in good shape.

Needed:

- \texttt{KDTree} will be removed, and \texttt{cKDTree} will be renamed to \texttt{KDTree} in a backwards-compatible way.
- \texttt{distance\_wrap.c} needs to be cleaned up (maybe rewrite in Cython).
special

Though there are still a lot of functions that need improvements in precision, probably the only show-stoppers are hypergeometric functions, parabolic cylinder functions, and spheroidal wave functions. Three possible ways to handle this:

1. Get good double-precision implementations. This is doable for parabolic cylinder functions (in progress). I think it’s possible for hypergeometric functions, though maybe not in time. For spheroidal wave functions this is not possible with current theory.

2. Port Boost’s arbitrary precision library and use it under the hood to get double precision accuracy. This might be necessary as a stopgap measure for hypergeometric functions; the idea of using arbitrary precision has been suggested before by @nmayorov and in gh-5349. Likely necessary for spheroidal wave functions, this could be reused: https://github.com/radelman/scattering.

3. Add clear warnings to the documentation about the limits of the existing implementations.

stats

stats.distributions is in good shape.

gaussian_kde is in good shape but limited. It should not be expanded probably, this fits better in Statsmodels (which already has a lot more KDE functionality).

5.6.3 New modules under discussion

diff

Currently Scipy doesn’t provide much support for numerical differentiation. A new scipy.diff module for that is discussed in https://github.com/scipy/scipy/issues/2035. There’s also a fairly detailed GSoC proposal to build on, see here. There has been a second (unsuccessful) GSoC project in 2017. Recent discussion and the host of alternatives available make it unlikely that a new scipy.diff submodule will be added in the near future.

There is also approx_derivative in optimize, which is still private but could form a solid basis for this module.

transforms

This module was discussed previously, mainly to provide a home for discrete wavelet transform functionality. Other transforms could fit as well, for example there’s a PR for a Hankel transform. Note: this is on the back burner, because the plans to integrate PyWavelets DWT code has been put on hold.
The exact API of all functions and classes, as given by the docstrings. The API documents expected types and allowed features for all functions, and all parameters available for the algorithms.

### 6.1 Clustering package (scipy.cluster)

**scipy.cluster.vq**

Clustering algorithms are useful in information theory, target detection, communications, compression, and other areas. The *vq* module only supports vector quantization and the k-means algorithms.

**scipy.cluster.hierarchy**

The *hierarchy* module provides functions for hierarchical and agglomerative clustering. Its features include generating hierarchical clusters from distance matrices, calculating statistics on clusters, cutting linkages to generate flat clusters, and visualizing clusters with dendrograms.

### 6.2 K-means clustering and vector quantization (scipy.cluster.vq)

Provides routines for k-means clustering, generating code books from k-means models, and quantizing vectors by comparing them with centroids in a code book.

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>whiten(obs[, check_finite])</code></td>
<td>Normalize a group of observations on a per feature basis.</td>
</tr>
<tr>
<td><code>vq(obs, code_book[, check_finite])</code></td>
<td>Assign codes from a code book to observations.</td>
</tr>
<tr>
<td><code>kmeans(obs, k_or_guess[, iter, thresh, ...])</code></td>
<td>Performs k-means on a set of observation vectors forming k clusters.</td>
</tr>
<tr>
<td><code>kmeans2(data, k[, iter, thresh, minit, ...])</code></td>
<td>Classify a set of observations into k clusters using the k-means algorithm.</td>
</tr>
</tbody>
</table>

#### 6.2.1 scipy.cluster.vq.whiten

**scipy.cluster.vq.whiten(obs, check_finite=True)**

Normalize a group of observations on a per feature basis.

Before running k-means, it is beneficial to rescale each feature dimension of the observation set with whitening. Each feature is divided by its standard deviation across all observations to give it unit variance.

**Parameters**

- **obs** [ndarray] Each row of the array is an observation. The columns are the features seen during each observation.
>>> #     f0    f1    f2
>>> obs = [[ 1.,  1.,  1.], #o0
         ... [ 2.,  2.,  2.], #o1
         ... [ 3.,  3.,  3.], #o2
         ... [ 4.,  4.,  4.]]  #o3

check_finite
[bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default: True

Returns
result [ndarray] Contains the values in obs scaled by the standard deviation of each column.

Examples

```python
>>> from scipy.cluster.vq import whiten
>>> features = np.array([[1.9, 2.3, 1.7],
                        ... [1.5, 2.5, 2.2],
                        ... [0.8, 0.6, 1.7]])
>>> whiten(features)
array([[ 4.17944278,  2.69811351,  7.21248917],
       [ 3.29956009,  2.93273208,  9.33380951],
       [ 1.75976538,  0.7038557 ,  7.21248917]])
```

6.2.2 scipy.cluster.vq.vq

scipy.cluster.vq.vq(obs, code_book, check_finite=True)
Assigns codes from a code book to observations.

Assigns a code from a code book to each observation. Each observation vector in the ‘M’ by ‘N’ obs array is compared with the centroids in the code book and assigned the code of the closest centroid.

The features in obs should have unit variance, which can be achieved by passing them through the whiten function. The code book can be created with the k-means algorithm or a different encoding algorithm.

Parameters
obs [ndarray] Each row of the ‘M’ x ‘N’ array is an observation. The columns are the “features” seen during each observation. The features must be whitened first using the whiten function or something equivalent.

code_book [ndarray] The code book is usually generated using the k-means algorithm. Each row of the array holds a different code, and the columns are the features of the code.

```python
>>> #     f0    f1    f2    f3
>>> code_book = [
               ... [ 1.,  2.,  3.,  4.], #c0
               ... [ 1.,  2.,  3.,  4.], #c1
               ... [ 1.,  2.,  3.,  4.]] #c2
```

check_finite [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default: True
Returns

code [ndarray] A length M array holding the code book index for each observation.
dist [ndarray] The distortion (distance) between the observation and its nearest code.

Examples

```python
>>> from numpy import array  
>>> from scipy.cluster.vq import vq
>>> code_book = array([[1.,1.,1.],
                     ...                     [2.,2.,2.]])
>>> features = array([[ 1.9,2.3,1.7],
                     ...                     [ 1.5,2.5,2.2],
                     ...                     [ 0.8,0.6,1.7]])

>>> vq(features,code_book)
(array([1, 1, 0],'i'), array([ 0.43588989, 0.73484692, 0.83066239]))
```

6.2.3 scipy.cluster.vq.kmeans

scipy.cluster.vq.kmeans(obs, k_or_guess, iter=20, thresh=1e-05, check_finite=True)

Performs k-means on a set of observation vectors forming k clusters.

The k-means algorithm adjusts the classification of the observations into clusters and updates the
center coordinates until the position of the centroids is stable over successive iterations. In this im-
plementation of the algorithm, the stability of the centroids is determined by comparing the absolute
value of the change in the average Euclidean distance between the observations and their corresponding
centroids against a threshold. This yields a code book mapping centroids to codes and vice versa.

Parameters

obs [ndarray] Each row of the M by N array is an observation vector. The columns
are the features seen during each observation. The features must be whitened first
with the whiten function.

k_or_guess [int or ndarray] The number of centroids to generate. A code is assigned to each
centroid, which is also the row index of the centroid in the code_book matrix
generated.
The initial k centroids are chosen by randomly selecting observations from the
observation matrix. Alternatively, passing a k by N array specifies the initial k
centroids.

iter [int, optional] The number of times to run k-means, returning the codebook with
the lowest distortion. This argument is ignored if initial centroids are specified
with an array for the k_or_guess parameter. This parameter does not represent
the number of iterations of the k-means algorithm.

thresh [float, optional] Terminates the k-means algorithm if the change in distortion since
the last k-means iteration is less than or equal to thresh.

check_finite [bool, optional] Whether to check that the input matrices contain only finite num-
bers. Disabling may give a performance gain, but may result in problems (crashes,
non-termination) if the inputs do contain infinities or NaNs. Default: True

Returns

codebook [ndarray] A k by N array of k centroids. The i’th centroid codebook[i] is represented
with the code i. The centroids and codes generated represent the lowest distortion
seen, not necessarily the globally minimal distortion.
distortion
[float] The mean (non-squared) Euclidean distance between the observations passed
and the centroids generated. Note the difference to the standard definition of
distortion in the context of the K-means algorithm, which is the sum of the squared
distances.

See also:

kmeans2

a different implementation of k-means clustering with more methods for generating initial centroids
but without using a distortion change threshold as a stopping criterion.

whiten

must be called prior to passing an observation matrix to kmeans.

Examples

```python
>>> from numpy import array
>>> from scipy.cluster.vq import vq, kmeans, whiten
>>> import matplotlib.pyplot as plt
>>> features = array([[1.9, 2.3],
                      ...                    [1.5, 2.5],
                      ...                    [0.8, 0.6],
                      ...                    [0.4, 1.8],
                      ...                    [0.1, 0.1],
                      ...                    [0.2, 1.8],
                      ...                    [2.0, 0.5],
                      ...                    [0.3, 1.5],
                      ...                    [1.0, 1.0]])
>>> whitened = whiten(features)
>>> book = np.array((whitened[0],whitened[2]))
>>> kmeans(whitened,book)
(array([[ 2.3110306 , 2.86287398], # random
         [ 0.93218041, 1.24398691]], 0.85684700941625547)
```

```python
>>> from numpy import random
>>> random.seed((1000,2000))
>>> codes = 3
>>> kmeans(whitened,codes)
(array([[ 2.3110306 , 2.86287398], # random
         [ 1.32544402, 0.6607529],
         [ 0.40782893, 2.02786907]]), 0.5196582527686241)
```

```python
>>> # Create 50 datapoints in two clusters a and b
>>> pts = 50
>>> a = np.random.multivariate_normal([0, 0], [[4, 1], [1, 4]], size=pts)
>>> b = np.random.multivariate_normal([30, 10],
>>>   ... [[10, 2], [2, 1]],
>>>   ... size=pts)
>>> features = np.concatenate((a, b))
>>> # Whiten data
>>> whitened = whiten(features)
>>> # Find 2 clusters in the data
```

(continues on next page)
>>> codebook, distortion = kmeans(whitened, 2)
>>> # Plot whitened data and cluster centers in red
>>> plt.scatter(whitened[:, 0], whitened[:, 1])
>>> plt.scatter(codebook[:, 0], codebook[:, 1], c='r')
>>> plt.show()

6.2.4 scipy.cluster.vq.kmeans2

scipy.cluster.vq.kmeans2(data, k, iter=10, thresh=1e-05, minit='random', missing='warn', check_finite=True)

Classify a set of observations into k clusters using the k-means algorithm.

The algorithm attempts to minimize the Euclidian distance between observations and centroids. Several initialization methods are included.

Parameters

- **data** [ndarray] A ‘M’ by ‘N’ array of ‘M’ observations in ‘N’ dimensions or a length ‘M’ array of ‘M’ one-dimensional observations.
- **k** [int or ndarray] The number of clusters to form as well as the number of centroids to generate. If minit initialization string is ‘matrix’, or if a ndarray is given instead, it is interpreted as initial cluster to use instead.
- **iter** [int, optional] Number of iterations of the k-means algorithm to run. Note that this differs in meaning from the iters parameter to the kmeans function.
- **thresh** [float, optional] (not used yet)
  - ‘random’: generate k centroids from a Gaussian with mean and variance estimated from the data.
  - ‘points’: choose k observations (rows) at random from data for the initial centroids.
  - ‘++’: choose k observations accordingly to the kmeans++ method (careful seeding)
  - ‘matrix’: interpret the k parameter as a k by M (or length k array for one-dimensional data) array of initial centroids.
missing  [str, optional] Method to deal with empty clusters. Available methods are ‘warn’ and ‘raise’:
   ‘warn’: give a warning and continue.
   ‘raise’: raise an ClusterError and terminate the algorithm.

check_finite  [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default: True

Returns

- centroid  [ndarray] A ‘k’ by ‘N’ array of centroids found at the last iteration of k-means.
- label  [ndarray] label[i] is the code or index of the centroid the i’th observation is closest to.

References

[1]

6.2.5 Background information

The k-means algorithm takes as input the number of clusters to generate, k, and a set of observation vectors to cluster. It returns a set of centroids, one for each of the k clusters. An observation vector is classified with the cluster number or centroid index of the centroid closest to it.

A vector v belongs to cluster i if it is closer to centroid i than any other centroids. If v belongs to i, we say centroid i is the dominating centroid of v. The k-means algorithm tries to minimize distortion, which is defined as the sum of the squared distances between each observation vector and its dominating centroid. The minimization is achieved by iteratively reclassifying the observations into clusters and recalculating the centroids until a configuration is reached in which the centroids are stable. One can also define a maximum number of iterations.

Since vector quantization is a natural application for k-means, information theory terminology is often used. The centroid index or cluster index is also referred to as a “code” and the table mapping codes to centroids and vice versa is often referred as a “code book”. The result of k-means, a set of centroids, can be used to quantize vectors. Quantization aims to find an encoding of vectors that reduces the expected distortion.

All routines expect obs to be a M by N array where the rows are the observation vectors. The codebook is a k by N array where the i’th row is the centroid of code word i. The observation vectors and centroids have the same feature dimension.

As an example, suppose we wish to compress a 24-bit color image (each pixel is represented by one byte for red, one for blue, and one for green) before sending it over the web. By using a smaller 8-bit encoding, we can reduce the amount of data by two thirds. Ideally, the colors for each of the 256 possible 8-bit encoding values should be chosen to minimize distortion of the color. Running k-means with k=256 generates a code book of 256 codes, which fills up all possible 8-bit sequences. Instead of sending a 3-byte value for each pixel, the 8-bit centroid index (or code word) of the dominating centroid is transmitted. The code book is also sent over the wire so each 8-bit code can be translated back to a 24-bit pixel value representation. If the image of interest was of an ocean, we would expect many 24-bit blues to be represented by 8-bit codes. If it was an image of a human face, more flesh tone colors would be represented in the code book.

6.3 Hierarchical clustering (scipy.cluster.hierarchy)

These functions cut hierarchical clusterings into flat clusterings or find the roots of the forest formed by a cut by providing the flat cluster ids of each observation.
SciPy Reference Guide, Release 1.2.0

6.3.1 scipy.cluster.hierarchy.fcluster

scipy.cluster.hierarchy.fcluster(Z, t[, criterion='inconsistent', depth=2, R=None, monocrit=None])

Form flat clusters from the hierarchical clustering defined by the given linkage matrix.

Parameters

- **Z** [ndarray] The hierarchical clustering encoded with the matrix returned by the `linkage` function.
- **t** [scalar] For criteria ‘inconsistent’, ‘distance’ or ‘monocrit’, this is the threshold to apply when forming flat clusters.
- **criterion** [str, optional] The criterion to use in forming flat clusters. This can be any of the following values:
  - `inconsistent`[] If a cluster node and all its descendants have an inconsistent value less than or equal to \( t \) then all its leaf descendants belong to the same flat cluster. When no non-singleton cluster meets this criterion, every node is assigned to its own cluster. (Default)
  - `distance`[] Forms flat clusters so that the original observations in each flat cluster have no greater a cophenetic distance than \( t \).
  - `maxclust`[] Finds a minimum threshold \( r \) so that the cophenetic distance between any two original observations in the same flat cluster is no more than \( r \) and no more than \( t \) flat clusters are formed.
  - `monocrit`[] Forms a flat cluster from a cluster node \( c \) with index \( i \) when \( \text{monocrit}[j] \leq t \). For example, to threshold on the maximum mean distance as computed in the inconsistency matrix \( R \) with a threshold of 0.8 do:

\[
MR = \text{maxRstat}(Z, R, 3)
\]

\[
\text{cluster}(Z, t=0.8, \text{criterion}='\text{monocrit}', \text{monocrit}=MR)
\]

- `maxclust_monocrit`[] Forms a flat cluster from a non-singleton cluster node \( c \) when \( \text{monocrit}[i] \leq r \) for all cluster indices \( i \) below and including \( c \). \( r \) is minimized such that no more than \( t \) flat clusters are formed. monocrit must be monotonic. For example, to minimize the threshold \( t \) on maximum inconsistency values so that no more than 3 flat clusters are formed, do:

\[
MI = \text{maxinconsts}(Z, R)
\]

\[
\text{cluster}(Z, t=3, \text{criterion}='\text{maxclust_monocrit}', \text{monocrit}=MI)
\]

- **depth** [int, optional] The maximum depth to perform the inconsistency calculation. It has no meaning for the other criteria. Default is 2.
- **R** [ndarray, optional] The inconsistency matrix to use for the ‘inconsistent’ criterion. This matrix is computed if not provided.
monocrit
[ndarray, optional] An array of length n-1. monocrit[i] is the statistics upon which non-singleton i is thresholded. The monocrit vector must be monotonic, i.e. given a node c with index i, for all node indices j corresponding to nodes below c, monocrit[i] >= monocrit[j].

Returns

fcluster [ndarray] An array of length n. T[i] is the flat cluster number to which original observation i belongs.

See also:

linkage
for information about hierarchical clustering methods work.

Examples

```python
>>> from scipy.cluster.hierarchy import ward, fcluster
>>> from scipy.spatial.distance import pdist

All cluster linkage methods - e.g. scipy.cluster.hierarchy.ward generate a linkage matrix Z as their output:

```n```n```n
```
>>> X = [[0, 0], [0, 1], [1, 0],
      ... [0, 4], [0, 3], [1, 4],
      ... [4, 0], [3, 0], [4, 1],
      ... [4, 4], [3, 4], [4, 3]]
```n```n```n
```n```n
```
>>> Z = ward(pdist(X))
```n```n```n
```
array([[ 0. , 1. , 1. , 2. ],
       [ 3. , 4. , 1. , 2. ],
       [ 6. , 7. , 1. , 2. ],
       [ 9. , 10. , 1. , 2. ],
       [ 2. , 12. , 1.29099445, 3. ],
       [ 5. , 13. , 1.29099445, 3. ],
       [ 8. , 14. , 1.29099445, 3. ],
       [11. , 15. , 1.29099445, 3. ],
       [16. , 17. , 5.77350269, 6. ],
       [18. , 19. , 5.77350269, 6. ],
       [20. , 21. , 8.16496581, 12. ]])
```

This matrix represents a dendrogram, where the first and second elements are the two clusters merged at each step, the third element is the distance between these clusters, and the fourth element is the size of the new cluster - the number of original data points included.

scipy.cluster.hierarchy.fcluster can be used to flatten the dendrogram, obtaining as a result an assignation of the original data points to single clusters.

This assignation mostly depends on a distance threshold t - the maximum inter-cluster distance allowed:

```python
>>> fcluster(Z, t=0.9, criterion='distance')
array([ 1,  2,  3,  4,  5,  6,  7,  8,  9, 10, 11, 12], dtype=int32)
```
In the first case, the threshold $t$ is too small to allow any two samples in the data to form a cluster, so 12 different clusters are returned.

In the second case, the threshold is large enough to allow the first 4 points to be merged with their nearest neighbors. So here only 8 clusters are returned.

The third case, with a much higher threshold, allows for up to 8 data points to be connected - so 4 clusters are returned here.

Lastly, the threshold of the fourth case is large enough to allow for all data points to be merged together - so a single cluster is returned.

### 6.3.2 scipy.cluster.hierarchy.fclusterdata

`scipy.cluster.hierarchy.fclusterdata(X, t, criterion='inconsistent', metric='euclidean', depth=2, method='single', R=None)`

Clusters the original observations in the n-by-m data matrix $X$ (n observations in m dimensions), using the euclidean distance metric to calculate distances between original observations, performs hierarchical clustering using the single linkage algorithm, and forms flat clusters using the inconsistency method with $t$ as the cut-off threshold.

A one-dimensional array $T$ of length $n$ is returned. $T[i]$ is the index of the flat cluster to which the original observation $i$ belongs.

**Parameters**

- **X**
  - [(N, M) ndarray] N by M data matrix with N observations in M dimensions.
  - [scalar]

- **t**
  - For criteria ‘inconsistent’, ‘distance’ or ‘monocrit’, this is the threshold to apply when forming flat clusters.
  - For ‘maxclust’ or ‘maxclust_monocrit’ criteria, this would be max number of clusters requested.

- **criterion**
  - [str, optional] Specifies the criterion for forming flat clusters. Valid values are ‘inconsistent’ (default), ‘distance’, or ‘maxclust’ cluster formation algorithms. See `fcluster` for descriptions.

- **metric**
  - [str, optional] The distance metric for calculating pairwise distances. See `distance.pdist` for descriptions and linkage to verify compatibility with the linkage method.

- **depth**
  - [int, optional] The maximum depth for the inconsistency calculation. See `inconsistent` for more information.

- **method**
  - [str, optional] The linkage method to use (single, complete, average, weighted, median centroid, ward). See `linkage` for more information. Default is “single”.

- **R**
  - [ndarray, optional] The inconsistency matrix. It will be computed if necessary if it is not passed.

**Returns**
fclusterdata
[ndarray] A vector of length n. T[i] is the flat cluster number to which original observation i belongs.

See also:
scipy.spatial.distance.pdist
pairwise distance metrics

Notes
This function is similar to the MATLAB function clusterdata.

Examples

```python
>>> from scipy.cluster.hierarchy import fclusterdata
```

This is a convenience method that abstracts all the steps to perform in a typical Scipy’s hierarchical clustering workflow.

- Transform the input data into a condensed matrix with scipy.spatial.distance.pdist.
- Apply a clustering method.
- Obtain flat clusters at a user defined distance threshold t using scipy.cluster.hierarchy.fcluster.

```python
>>> X = [[0, 0], [0, 1], [1, 0],
      ..., [0, 4], [0, 3], [1, 4],
      ... [4, 0], [3, 0], [4, 1],
      ... [4, 4], [3, 4], [4, 3]]
```

```python
>>> fclusterdata(X, t=1)
array([3, 3, 3, 4, 4, 4, 2, 2, 2, 1, 1, 1], dtype=int32)
```

The output here (for the dataset X, distance threshold t, and the default settings) is four clusters with three data points each.

6.3.3 scipy.cluster.hierarchy.leaders

scipy.cluster.hierarchy.leaders(Z, T)

Returns the root nodes in a hierarchical clustering.

For each flat cluster j of the k flat clusters represented in the n-sized flat cluster assignment vector T, this function finds the lowest cluster node i in the linkage tree Z such that:

- leaf descendants belong only to flat cluster j (i.e. T[p]==j for all p in S(i) where S(i) is the set of leaf ids of descendant leaf nodes with cluster node i)
- there does not exist a leaf that is not a descendant with i that also belongs to cluster j (i.e. T[q]!=j for all q not in S(i)). If this condition is violated, T is not a valid cluster assignment vector, and an exception will be thrown.

Parameters

Z [ndarray] The hierarchical clustering encoded as a matrix. See linkage for more information.

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T [ndarray] The flat cluster assignment vector.

Returns

L [ndarray] The leader linkage node id's stored as a k-element 1-D array where k is the number of flat clusters found in T.

L[j]=i is the linkage cluster node id that is the leader of flat cluster with id M[j]. If i < n, i corresponds to an original observation, otherwise it corresponds to a non-singleton cluster.

M [ndarray] The leader linkage node id's stored as a k-element 1-D array where k is the number of flat clusters found in T. This allows the set of flat cluster ids to be any arbitrary set of k integers.

For example: if L[3]=2 and M[3]=8, the flat cluster with id 8's leader is linkage node 2.

See also:

fcluster

for the creation of flat cluster assignments.

Examples

```python
>>> from scipy.cluster.hierarchy import ward, fcluster, leaders
>>> from scipy.spatial.distance import pdist

Given a linkage matrix Z - obtained after apply a clustering method to a dataset X - and a flat cluster assignment array T:

```
>>> L, M = leaders(Z, T)
>>> L
array([16, 17, 18, 19], dtype=int32)

(remember that indexes 0-11 point to the 12 data points in X whereas indexes 12-22 point to the 11 rows of Z)

`scipy.cluster.hierarchy.leaders` also returns the indexes of the flat clusters in T:

>>> M
array([1, 2, 3, 4], dtype=int32)

These are routines for agglomerative clustering.

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>linkage(y[, method, metric, optimal_ordering])</code></td>
<td>Perform hierarchical/agglomerative clustering.</td>
</tr>
<tr>
<td><code>single(y)</code></td>
<td>Perform single/min/nearest linkage on the condensed distance matrix y.</td>
</tr>
<tr>
<td><code>complete(y)</code></td>
<td>Perform complete/max/farthest point linkage on a condensed distance matrix.</td>
</tr>
<tr>
<td><code>average(y)</code></td>
<td>Perform average/UPGMA linkage on a condensed distance matrix.</td>
</tr>
<tr>
<td><code>weighted(y)</code></td>
<td>Perform weighted/WPGMA linkage on the condensed distance matrix.</td>
</tr>
<tr>
<td><code>centroid(y)</code></td>
<td>Perform centroid/UPGMC linkage.</td>
</tr>
<tr>
<td><code>median(y)</code></td>
<td>Perform median/WPGMC linkage.</td>
</tr>
<tr>
<td><code>ward(y)</code></td>
<td>Perform Ward’s linkage on a condensed distance matrix.</td>
</tr>
</tbody>
</table>

6.3.4 `scipy.cluster.hierarchy.linkage`

`scipy.cluster.hierarchy.linkage(y, method='single', metric='euclidean', optimal_ordering=False)`

Perform hierarchical/agglomerative clustering.

The input y may be either a 1d condensed distance matrix or a 2d array of observation vectors.

If y is a 1d condensed distance matrix, then y must be a \(\binom{n}{2}\) sized vector where n is the number of original observations paired in the distance matrix. The behavior of this function is very similar to the MATLAB linkage function.

A \((n-1) \times 4\) matrix Z is returned. At the i-th iteration, clusters with indices \(Z[i, 0]\) and \(Z[i, 1]\) are combined to form cluster \(n+i\). A cluster with an index less than \(n\) corresponds to one of the \(n\) original observations. The distance between clusters \(Z[i, 0]\) and \(Z[i, 1]\) is given by \(Z[i, 2]\). The fourth value \(Z[i, 3]\) represents the number of original observations in the newly formed cluster.

The following linkage methods are used to compute the distance \(d(s,t)\) between two clusters \(s\) and \(t\). The algorithm begins with a forest of clusters that have yet to be used in the hierarchy being formed. When two clusters \(s\) and \(t\) from this forest are combined into a single cluster \(u\), \(s\) and \(t\) are removed from the forest, and \(u\) is added to the forest. When only one cluster remains in the forest, the algorithm stops, and this cluster becomes the root.

A distance matrix is maintained at each iteration. The \(d[i,j]\) entry corresponds to the distance between cluster \(i\) and \(j\) in the original forest.

At each iteration, the algorithm must update the distance matrix to reflect the distance of the newly formed cluster \(u\) with the remaining clusters in the forest.
Suppose there are \(|u|\) original observations \(u[0], \ldots, u[|u| - 1]\) in cluster \(u\) and \(|v|\) original objects \(v[0], \ldots, v[|v| - 1]\) in cluster \(v\). Recall \(s\) and \(t\) are combined to form cluster \(u\). Let \(v\) be any remaining cluster in the forest that is not \(u\).

The following are methods for calculating the distance between the newly formed cluster \(u\) and each \(v\).

- **method='single'** assigns
  \[
  d(u, v) = \min(dist(u[i], v[j]))
  \]
  for all points \(i\) in cluster \(u\) and \(j\) in cluster \(v\). This is also known as the Nearest Point Algorithm.

- **method='complete'** assigns
  \[
  d(u, v) = \max(dist(u[i], v[j]))
  \]
  for all points \(i\) in cluster \(u\) and \(j\) in cluster \(v\). This is also known by the Farthest Point Algorithm or Voor Hees Algorithm.

- **method='average'** assigns
  \[
  d(u, v) = \frac{\sum_{ij} d(u[i], v[j])}{(|u| + |v|)}
  \]
  for all points \(i\) and \(j\) where \(|u|\) and \(|v|\) are the cardinalities of clusters \(u\) and \(v\), respectively. This is also called the UPGMA algorithm.

- **method='weighted'** assigns
  \[
  d(u, v) = (dist(s, v) + dist(t, v)) / 2
  \]
  where cluster \(u\) was formed with cluster \(s\) and \(t\) and \(v\) is a remaining cluster in the forest. (also called WPGMA)

- **method='centroid'** assigns
  \[
  dist(s, t) = ||c_s - c_t||_2
  \]
  where \(c_s\) and \(c_t\) are the centroids of clusters \(s\) and \(t\), respectively. When two clusters \(s\) and \(t\) are combined into a new cluster \(u\), the new centroid is computed over all the original objects in clusters \(s\) and \(t\). The distance then becomes the Euclidean distance between the centroid of \(u\) and the centroid of a remaining cluster \(v\) in the forest. This is also known as the UPGMC algorithm.

- **method='median'** assigns \(d(s, t)\) like the centroid method. When two clusters \(s\) and \(t\) are combined into a new cluster \(u\), the average of centroids \(s\) and \(t\) give the new centroid \(u\). This is also known as the WPGMC algorithm.

- **method='ward'** uses the Ward variance minimization algorithm. The new entry \(d(u, v)\) is computed as follows,
  \[
  d(u, v) = \sqrt{\frac{|v| + |s|}{T} d(v, s)^2 + \frac{|v| + |t|}{T} d(v, t)^2 - \frac{|v|}{T} d(s, t)^2}
  \]
  where \(u\) is the newly joined cluster consisting of clusters \(s\) and \(t\), \(v\) is an unused cluster in the forest, \(T = |v| + |s| + |t|\), and \(|*|\) is the cardinality of its argument. This is also known as the incremental algorithm.

**Warning:** When the minimum distance pair in the forest is chosen, there may be two or more pairs with the same minimum distance. This implementation may choose a different minimum than the MATLAB version.
Parameters

- **y** [ndarray] A condensed distance matrix. A condensed distance matrix is a flat array containing the upper triangular of the distance matrix. This is the form that `pdist` returns. Alternatively, a collection of \(m\) observation vectors in \(n\) dimensions may be passed as an \(m \times n\) array. All elements of the condensed distance matrix must be finite, i.e. no NaNs or infs.

- **method** [str, optional] The linkage algorithm to use. See the Linkage Methods section below for full descriptions.

- **metric** [str or function, optional] The distance metric to use in the case that \(y\) is a collection of observation vectors; ignored otherwise. See the `pdist` function for a list of valid distance metrics. A custom distance function can also be used.

- **optimal_ordering** [bool, optional] If True, the linkage matrix will be reordered so that the distance between successive leaves is minimal. This results in a more intuitive tree structure when the data are visualized. defaults to False, because this algorithm can be slow, particularly on large datasets [2]. See also the `optimal_leaf_ordering` function. New in version 1.0.0.

Returns

- **Z** [ndarray] The hierarchical clustering encoded as a linkage matrix.

See also:

- `scipy.spatial.distance.pdist`
- pairwise distance metrics

Notes

1. For method ‘single’ an optimized algorithm based on minimum spanning tree is implemented. It has time complexity \(O(n^2)\). For methods ‘complete’, ‘average’, ‘weighted’ and ‘ward’ an algorithm called nearest-neighbors chain is implemented. It also has time complexity \(O(n^2)\). For other methods a naive algorithm is implemented with \(O(n^3)\) time complexity. All algorithms use \(O(n^2)\) memory. Refer to [1] for details about the algorithms.

2. Methods ‘centroid’, ‘median’ and ‘ward’ are correctly defined only if Euclidean pairwise metric is used. If \(y\) is passed as precomputed pairwise distances, then it is a user responsibility to assure that these distances are in fact Euclidean, otherwise the produced result will be incorrect.

References

[1], [2]

Examples

```python
>>> from scipy.cluster.hierarchy import dendrogram, linkage
>>> from matplotlib import pyplot as plt
>>> X = [[i] for i in [2, 8, 0, 4, 1, 9, 9, 0]]

>>> Z = linkage(X, 'ward')
>>> fig = plt.figure(figsize=(25, 10))
>>> dn = dendrogram(Z)
```

```python
>>> Z = linkage(X, 'single')
>>> fig = plt.figure(figsize=(25, 10))
>>> dn = dendrogram(Z)
>>> plt.show()
```
6.3. Hierarchical clustering (scipy.cluster.hierarchy)
6.3.5 scipy.cluster.hierarchy.single

scipy.cluster.hierarchy.single(y)

Perform single/min/nearest linkage on the condensed distance matrix y.

Parameters:

- y : [ndarray] The upper triangular of the distance matrix. The result of \texttt{pdist} is returned in this form.

Returns:


See also:

- \texttt{linkage}
  for advanced creation of hierarchical clusterings.

- \texttt{scipy.spatial.distance.pdist}
  pairwise distance metrics

Examples:

\begin{verbatim}
>>> from scipy.cluster.hierarchy import single, fcluster
>>> from scipy.spatial.distance import pdist

First we need a toy dataset to play with:

```
  x x x x
 x   x
 x   x
 x x x x
```

```
>>> X = [[0, 0], [0, 1], [1, 0],
       [0, 4], [0, 3], [1, 4],
       [4, 0], [3, 0], [4, 1],
       [4, 4], [3, 4], [4, 3]]
```

Then we get a condensed distance matrix from this dataset:

```
>>> y = pdist(X)
```

Finally, we can perform the clustering:

```
>>> Z = single(y)
```

```
array([[ 0.,  1.,  1.,  2.],
       [ 2., 12.,  1.,  3.],
       [ 3.,  4.,  1.,  2.],
       [ 5., 14.,  1.,  3.],
       [ 6.,  7.,  1.,  2.],
       [ 8., 16.,  1.,  3.],
       [ 9., 10.,  1.,  2.],
       [11., 18.,  1.,  3.],
       [13., 15.,  2.,  6.]], dtype=float32)
```

(continues on next page)
The linkage matrix $Z$ represents a dendrogram - see `scipy.cluster.hierarchy.linkage` for a detailed explanation of its contents.

We can use `scipy.cluster.hierarchy.fcluster` to see to which cluster each initial point would belong given a distance threshold:

```python
>>> fcluster(Z, 0.9, criterion='distance')
array([ 7, 8, 9, 10, 11, 12, 4, 5, 6, 1, 2, 3], dtype=int32)
>>> fcluster(Z, 1, criterion='distance')
array([3, 3, 3, 4, 4, 4, 2, 2, 2, 1, 1, 1], dtype=int32)
>>> fcluster(Z, 2, criterion='distance')
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1], dtype=int32)
```

Also `scipy.cluster.hierarchy.dendrogram` can be used to generate a plot of the dendrogram.

### 6.3.6 `scipy.cluster.hierarchy.complete`

`scipy.cluster.hierarchy.complete(y)`  
Perform complete/max/farthest point linkage on a condensed distance matrix.

**Parameters**

- `y` [ndarray] The upper triangular of the distance matrix. The result of `pdist` is returned in this form.

**Returns**

- `Z` [ndarray] A linkage matrix containing the hierarchical clustering. See the `linkage` function documentation for more information on its structure.

**See also:**

- `linkage` for advanced creation of hierarchical clusterings.
- `scipy.spatial.distance.pdist` pairwise distance metrics

**Examples**

```python
>>> from scipy.cluster.hierarchy import complete, fcluster
>>> from scipy.spatial.distance import pdist
```

First we need a toy dataset to play with:

```
x x x x
x x
x x
x x x x
```
Then we get a condensed distance matrix from this dataset:

```python
>>> y = pdist(X)
```

Finally, we can perform the clustering:

```python
>>> Z = complete(y)
```

```python
array([[ 0. , 1. , 1. , 2. ],
       [ 3. , 4. , 1. , 2. ],
       [ 6. , 7. , 1. , 2. ],
       [ 9. , 10. , 1. , 2. ],
       [ 2. , 12. , 1.41421356, 3. ],
       [ 5. , 13. , 1.41421356, 3. ],
       [ 8. , 14. , 1.41421356, 3. ],
       [11. , 15. , 1.41421356, 3. ],
       [16. , 17. , 4.12310563, 6. ],
       [18. , 19. , 4.12310563, 6. ],
       [20. , 21. , 5.65685425, 12. ]])
```

The linkage matrix $Z$ represents a dendrogram - see `scipy.cluster.hierarchy.linkage` for a detailed explanation of its contents.

We can use `scipy.cluster.hierarchy.fcluster` to see to which cluster each initial point would belong given a distance threshold:

```python
>>> fcluster(Z, 0.9, criterion='distance')
array([1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12], dtype=int32)
```

```python
>>> fcluster(Z, 1.5, criterion='distance')
array([1, 1, 1, 2, 2, 3, 3, 4, 4, 4, 4, 4], dtype=int32)
```

```python
>>> fcluster(Z, 4.5, criterion='distance')
array([1, 1, 1, 1, 1, 2, 2, 2, 2, 2, 2, 2], dtype=int32)
```

```python
>>> fcluster(Z, 6, criterion='distance')
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1], dtype=int32)
```

Also `scipy.cluster.hierarchy.dendrogram` can be used to generate a plot of the dendrogram.

### 6.3.7 `scipy.cluster.hierarchy.average`

`scipy.cluster.hierarchy.average(y)`

Perform average/UPGMA linkage on a condensed distance matrix.

**Parameters**

- **y** [ndarray] The upper triangular of the distance matrix. The result of `pdist` is returned in this form.

**Returns**

- **Z** [ndarray] A linkage matrix containing the hierarchical clustering. See `linkage` for more information on its structure.
See also:

linkage

for advanced creation of hierarchical clusterings.

scipy.spatial.distance.pdist

pairwise distance metrics

Examples

```python
>>> from scipy.cluster.hierarchy import average, fcluster
>>> from scipy.spatial.distance import pdist
```

First we need a toy dataset to play with:

```
x   x   x   x
x   x
x   x
x   x   x   x
```

```python
>>> X = [[0, 0], [0, 1], [1, 0],
      ... [0, 4], [0, 3], [1, 4],
      ... [4, 0], [3, 0], [4, 1],
      ... [4, 4], [3, 4], [4, 3]]
```

Then we get a condensed distance matrix from this dataset:

```python
>>> y = pdist(X)
```

Finally, we can perform the clustering:

```python
>>> Z = average(y)
>>> Z
array([[ 0.  , 1.  , 1.  , 2.  ],
       [ 3.  , 4.  , 1.  , 2.  ],
       [ 6.  , 7.  , 1.  , 2.  ],
       [ 9.  , 10. , 1.  , 2.  ],
       [ 2.  , 12. , 1.20710678, 3.  ],
       [ 5.  , 13. , 1.20710678, 3.  ],
       [ 8.  , 14. , 1.20710678, 3.  ],
       [11.  , 15. , 1.20710678, 3.  ],
       [16.  , 17. , 3.39675184, 6.  ],
       [18.  , 19. , 3.39675184, 6.  ],
       [20.  , 21. , 4.09206523, 12. ]])
```

The linkage matrix Z represents a dendrogram - see `scipy.cluster.hierarchy.linkage` for a detailed explanation of its contents.

We can use `scipy.cluster.hierarchy.fcluster` to see to which cluster each initial point would belong given a distance threshold:

```python
>>> fcluster(Z, 0.9, criterion='distance')
array([1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12], dtype=int32)
```
Also `scipy.cluster.hierarchy.dendrogram` can be used to generate a plot of the dendrogram.

### 6.3.8 `scipy.cluster.hierarchy.weighted`

`scipy.cluster.hierarchy.weighted(y)`

Perform weighted/WPGMA linkage on the condensed distance matrix.

See `linkage` for more information on the return structure and algorithm.

**Parameters**

- `y` [ndarray] The upper triangular of the distance matrix. The result of `pdist` is returned in this form.

**Returns**

- `Z` [ndarray] A linkage matrix containing the hierarchical clustering. See `linkage` for more information on its structure.

See also:

- `linkage` for advanced creation of hierarchical clusterings.
- `scipy.spatial.distance.pdist` pairwise distance metrics

**Examples**

```python
>>> from scipy.cluster.hierarchy import weighted, fcluster
>>> from scipy.spatial.distance import pdist
```

First we need a toy dataset to play with:

```
 x x x x
 x   x
 x   x
 x x x x
```

```python
>>> X = [[0, 0], [0, 1], [1, 0],
      ... [0, 4], [0, 3], [1, 4],
      ... [4, 0], [3, 0], [4, 1],
      ... [4, 4], [3, 4], [4, 3]]
```

Then we get a condensed distance matrix from this dataset:

```python
>>> y = pdist(X)
```
Finally, we can perform the clustering:

```python
>>> Z = weighted(y)
>>> Z
array([[ 0. ,  1. ,  1. ,  2. ],
       [ 6. ,  7. ,  1. ,  2. ],
       [ 3. ,  4. ,  1. ,  2. ],
       [ 9. , 11. ,  1. ,  2. ],
       [ 2. , 12. , 1.20710678, 3. ],
       [ 8. , 13. , 1.20710678, 3. ],
       [ 5. , 14. , 1.20710678, 3. ],
       [10. , 15. , 1.20710678, 3. ],
       [18. , 19. , 3.05595762, 6. ],
       [16. , 17. , 3.32379407, 6. ],
       [20. , 21. , 4.06357713, 12. ]])
```

The linkage matrix Z represents a dendrogram - see `scipy.cluster.hierarchy.linkage` for a detailed explanation of its contents.

We can use `scipy.cluster.hierarchy.fcluster` to see to which cluster each initial point would belong given a distance threshold:

```python
>>> fcluster(Z, 0.9, criterion='distance')
array([ 7,  8,  9,  1,  2,  3, 10, 11, 12,  4,  6,  5], dtype=int32)
>>> fcluster(Z, 1.5, criterion='distance')
array([ 3,  3,  1,  1,  1,  4,  4,  2,  2,  2], dtype=int32)
>>> fcluster(Z, 4, criterion='distance')
array([ 2,  2,  1,  1,  1,  2,  2,  1,  1,  1], dtype=int32)
>>> fcluster(Z, 6, criterion='distance')
array([ 1,  1,  1,  1,  1,  1,  1,  1,  1,  1], dtype=int32)
```

Also `scipy.cluster.hierarchy.dendrogram` can be used to generate a plot of the dendrogram.

### 6.3.9 scipy.cluster.hierarchy.centroid

`scipy.cluster.hierarchy.centroid(y)`

Perform centroid/UPGMC linkage.

See `linkage` for more information on the input matrix, return structure, and algorithm.

The following are common calling conventions:

1. `Z = centroid(y)`
   
   Performs centroid/UPGMC linkage on the condensed distance matrix y.

2. `Z = centroid(X)`
   
   Performs centroid/UPGMC linkage on the observation matrix X using Euclidean distance as the distance metric.

**Parameters**

- `y` [ndarray] A condensed distance matrix. A condensed distance matrix is a flat array containing the upper triangular of the distance matrix. This is the form that `pdist` returns. Alternatively, a collection of m observation vectors in n dimensions may be passed as a m by n array.

**Returns**
Z: [ndarray] A linkage matrix containing the hierarchical clustering. See the linkage function documentation for more information on its structure.

See also:

linkage
for advanced creation of hierarchical clusterings.

scipy.spatial.distance.pdist
pairwise distance metrics

Examples

```python
>>> from scipy.cluster.hierarchy import centroid, fcluster
>>> from scipy.spatial.distance import pdist

First we need a toy dataset to play with:

```
x x x x
x  x
x  x
x x x x
```

```python
>>> X = [[0, 0], [0, 1], [1, 0], ...
...   [0, 4], [0, 3], [1, 4], ...
...   [4, 0], [3, 0], [4, 1], ...
...   [4, 4], [3, 4], [4, 3]]

Then we get a condensed distance matrix from this dataset:

```python
>>> y = pdist(X)

Finally, we can perform the clustering:

```python
>>> Z = centroid(y)
>>> Z
array([[ 0. , 1. , 1. , 2. ],
       [ 3. , 4. , 1. , 2. ],
       [ 9. , 10., 1. , 2. ],
       [ 6. , 7. , 1. , 2. ],
       [ 2. , 12., 1.11803399, 3. ],
       [ 5. , 13., 1.11803399, 3. ],
       [ 8. , 15., 1.11803399, 3. ],
       [11. , 14., 1.11803399, 3. ],
       [18. , 19., 3.33333333, 6. ],
       [16. , 17., 3.33333333, 6. ],
       [20. , 21., 3.33333333, 12. ]])
```

The linkage matrix Z represents a dendrogram - see scipy.cluster.hierarchy.linkage for a detailed explanation of its contents.

We can use scipy.cluster.hierarchy.fcluster to see to which cluster each initial point would belong given a distance threshold:
>>> fcluster(Z, 0.9, criterion='distance')
array([ 7,  8,  9, 10, 11, 12,  1,  2,  3,  4,  5,  6], dtype=int32)
>>> fcluster(Z, 1.1, criterion='distance')
array([5, 5, 6, 7, 8, 1, 1, 2, 3, 3, 4], dtype=int32)
>>> fcluster(Z, 2, criterion='distance')
array([3, 3, 4, 4, 1, 1, 1, 2, 2, 2], dtype=int32)
>>> fcluster(Z, 4, criterion='distance')
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1], dtype=int32)

Also `scipy.cluster.hierarchy.dendrogram` can be used to generate a plot of the dendrogram.

### 6.3.10 `scipy.cluster.hierarchy.median`

`scipy.cluster.hierarchy.median(y)`

Perform median/WPGMC linkage.

See `linkage` for more information on the return structure and algorithm.

The following are common calling conventions:

1. `Z = median(y)`
   - Performs median/WPGMC linkage on the condensed distance matrix `y`. See `linkage` for more information on the return structure and algorithm.

2. `Z = median(X)`
   - Performs median/WPGMC linkage on the observation matrix `X` using Euclidean distance as the distance metric. See `linkage` for more information on the return structure and algorithm.

**Parameters**

- `y` [ndarray] A condensed distance matrix. A condensed distance matrix is a flat array containing the upper triangular of the distance matrix. This is the form that `pdist` returns. Alternatively, a collection of `m` observation vectors in `n` dimensions may be passed as a `m` by `n` array.

**Returns**

- `Z` [ndarray] The hierarchical clustering encoded as a linkage matrix.

**See also:**

- `linkage` for advanced creation of hierarchical clusterings.
- `scipy.spatial.distance.pdist` pairwise distance metrics

**Examples**

```python
from scipy.cluster.hierarchy import median, fcluster
from scipy.spatial.distance import pdist
```

First we need a toy dataset to play with:

```
x x x x
x x
```

(continues on next page)
Then we get a condensed distance matrix from this dataset:

```python
>>> y = pdist(X)
```

Finally, we can perform the clustering:

```python
>>> Z = median(y)
>>> Z
array([[ 0. , 1. , 1. , 2. ],
[ 3. , 4. , 1. , 2. ],
[ 9. , 10. , 1. , 2. ],
[ 6. , 7. , 1. , 2. ],
[ 2. , 12. , 1.11803399, 3. ],
[ 5. , 13. , 1.11803399, 3. ],
[ 8. , 15. , 1.11803399, 3. ],
[11. , 14. , 1.11803399, 3. ],
[18. , 19. , 3. , 6. ],
[16. , 17. , 3.5 , 6. ],
[20. , 21. , 3.25 , 12. ]])
```

The linkage matrix `Z` represents a dendrogram - see `scipy.cluster.hierarchy.linkage` for a detailed explanation of its contents.

We can use `scipy.cluster.hierarchy.fcluster` to see to which cluster each initial point would belong given a distance threshold:

```python
>>> fcluster(Z, 0.9, criterion='distance')
array([7, 8, 9, 10, 11, 12, 1, 2, 3, 4, 5, 6], dtype=int32)
>>> fcluster(Z, 1.1, criterion='distance')
array([5, 5, 6, 7, 7, 8, 1, 1, 2, 3, 3, 4], dtype=int32)
>>> fcluster(Z, 2, criterion='distance')
array([3, 3, 3, 4, 4, 4, 1, 1, 2, 2, 2], dtype=int32)
>>> fcluster(Z, 4, criterion='distance')
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1], dtype=int32)
```

Also `scipy.cluster.hierarchy.dendrogram` can be used to generate a plot of the dendrogram.

### 6.3.11 scipy.cluster.hierarchy.ward

`scipy.cluster.hierarchy.ward(y)`
Perform Ward’s linkage on a condensed distance matrix.

See `linkage` for more information on the return structure and algorithm.

The following are common calling conventions:

1. `Z = ward(y)` Performs Ward’s linkage on the condensed distance matrix `y`. 
2. `Z = ward(X)` Performs Ward’s linkage on the observation matrix `X` using Euclidean distance as the distance metric.

**Parameters**

`y` [ndarray] A condensed distance matrix. A condensed distance matrix is a flat array containing the upper triangular of the distance matrix. This is the form that `pdist` returns. Alternatively, a collection of `m` observation vectors in `n` dimensions may be passed as an `m` by `n` array.

**Returns**

`Z` [ndarray] The hierarchical clustering encoded as a linkage matrix. See `linkage` for more information on the return structure and algorithm.

See also:

`linkage`

for advanced creation of hierarchical clusterings.

`scipy.spatial.distance.pdist`

pairwise distance metrics

**Examples**

```python
>>> from scipy.cluster.hierarchy import ward, fcluster
>>> from scipy.spatial.distance import pdist
```

First we need a toy dataset to play with:

```
x x x x
x   x
x   x
x x x x
```

```python
>>> X = [[0, 0], [0, 1], [1, 0],
       [0, 4], [0, 3], [1, 4],
       [4, 0], [3, 0], [4, 1],
       [4, 4], [3, 4], [4, 3]]
```

Then we get a condensed distance matrix from this dataset:

```python
>>> y = pdist(X)
```

Finally, we can perform the clustering:

```python
>>> Z = ward(y)
>>> Z
array([[ 0. , 1. , 1. , 2. ],
       [ 3. , 4. , 1. , 2. ],
       [ 6. , 7. , 1. , 2. ],
       [ 9. , 10. , 1. , 2. ],
       [ 2. , 12. , 1.29099445, 3. ],
       [ 5. , 13. , 1.29099445, 3. ]],
      dtype=object)
```

(continues on next page)
The linkage matrix $Z$ represents a dendrogram - see `scipy.cluster.hierarchy.linkage` for a detailed explanation of its contents.

We can use `scipy.cluster.hierarchy.fcluster` to see to which cluster each initial point would belong given a distance threshold:

```python
>>> fcluster(Z, 0.9, criterion='distance')
array([ 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12], dtype=int32)
>>> fcluster(Z, 1.1, criterion='distance')
array([1, 1, 2, 3, 4, 5, 6, 7, 8], dtype=int32)
>>> fcluster(Z, 3, criterion='distance')
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1], dtype=int32)
>>> fcluster(Z, 9, criterion='distance')
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1], dtype=int32)
```

Also `scipy.cluster.hierarchy.dendrogram` can be used to generate a plot of the dendrogram.

These routines compute statistics on hierarchies.

<table>
<thead>
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<th>Function</th>
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<tr>
<td><code>cophenet(Z[, Y])</code></td>
<td>Calculate the cophenetic distances between each observation in the hierarchical clustering defined by the linkage Z.</td>
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<tr>
<td><code>from_mlab_linkage(Z)</code></td>
<td>Convert a linkage matrix generated by MATLAB(TM) to a new linkage matrix compatible with this module.</td>
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<td><code>inconsistent(Z[, d])</code></td>
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<td><code>maxinconsts(Z, R)</code></td>
<td>Return the maximum inconsistency coefficient for each non-singleton cluster and its children.</td>
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<td><code>maxRstat(Z, R, i)</code></td>
<td>Return the maximum statistic for each non-singleton cluster and its children.</td>
</tr>
<tr>
<td><code>to_mlab_linkage(Z)</code></td>
<td>Convert a linkage matrix to a MATLAB(TM) compatible one.</td>
</tr>
</tbody>
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### 6.3.12 scipy.cluster.hierarchy.cophenet

`scipy.cluster.hierarchy.cophenet(Z, Y=None)`

Calculate the cophenetic distances between each observation in the hierarchical clustering defined by the linkage Z.

Suppose $p$ and $q$ are original observations in disjoint clusters $s$ and $t$, respectively and $s$ and $t$ are joined by a direct parent cluster $u$. The cophenetic distance between observations $i$ and $j$ is simply the distance between clusters $s$ and $t$.

**Parameters**

...
The hierarchical clustering encoded as an array (see \texttt{linkage} function).

\[ \text{Y} \] (ndarray (optional)) Calculates the cophenetic correlation coefficient \( c \) of a hierarchical clustering defined by the linkage matrix \( Z \) of a set of \( n \) observations in \( m \) dimensions. \( Y \) is the condensed distance matrix from which \( Z \) was generated.

**Returns**

- \( c \) [ndarray] The cophenetic correlation distance (if \( Y \) is passed).
- \( d \) [ndarray] The cophenetic distance matrix in condensed form. The \( ij \) th entry is the cophenetic distance between original observations \( i \) and \( j \).

**See also:**

\texttt{linkage}

for a description of what a linkage matrix is.

\texttt{scipy.spatial.distance.squareform}

transforming condensed matrices into square ones.

**Examples**

```python
>>> from scipy.cluster.hierarchy import single, cophenet
>>> from scipy.spatial.distance import pdist, squareform
```

Given a dataset \( X \) and a linkage matrix \( Z \), the cophenetic distance between two points of \( X \) is the distance between the largest two distinct clusters that each of the points:

```python
>>> X = [[0, 0], [0, 1], [1, 0],
...      [0, 4], [0, 3], [1, 4],
...      [4, 0], [3, 0], [4, 1],
...      [4, 4], [3, 4], [4, 3]]
```

\( X \) corresponds to this dataset

```
x x x x
x  x
x x x
x x x
```

```python
>>> Z = single(pdist(X))
>>> Z
array([[0., 1., 1., 2.],
       [2., 12., 1., 3.],
       [3., 4., 1., 2.],
       [5., 14., 1., 3.],
       [6., 7., 1., 2.],
       [8., 16., 1., 3.],
       [9., 10., 1., 2.],
       [11., 18., 1., 3.],
       [13., 15., 2., 6.],
       [17., 20., 2., 9.],
       [19., 21., 2., 12.]])
```

```python
>>> cophenet(Z)
array([[1., 1., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2.,
```

(continues on next page)
The output of the `scipy.cluster.hierarchy.cophenet` method is represented in condensed form. We can use `scipy.spatial.distance.squareform` to see the output as a regular matrix (where each element \( ij \) denotes the cophenetic distance between each \( i, j \) pair of points in \( X \)):

```python
>>> squareform(cophenet(Z))
array([[0., 1., 1., 2., 2., 2., 2., 2., 2., 2., 2., 2.],
      [1., 0., 1., 2., 2., 2., 2., 2., 2., 2., 2., 2.],
      [1., 1., 0., 2., 2., 2., 2., 2., 2., 2., 2., 2.],
      [2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2.],
      [2., 2., 2., 1., 2., 2., 2., 2., 2., 2., 2., 2.],
      [2., 2., 2., 1., 0., 2., 2., 2., 2., 2., 2., 2.],
      [2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2.],
      [2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2.],
      [2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2.],
      [2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2.],
])
```

In this example, the cophenetic distance between points on \( X \) that are very close (i.e. in the same corner) is 1. For other pairs of points is 2, because the points will be located in clusters at different corners - thus the distance between these clusters will be larger.

### 6.3.13 scipy.cluster.hierarchy.from_mlab_linkage

`scipy.cluster.hierarchy.from_mlab_linkage(Z)`

Convert a linkage matrix generated by MATLAB(TM) to a new linkage matrix compatible with this module.

The conversion does two things:

- the indices are converted from \( 1..N \) to \( 0..(N-1) \) form, and
- a fourth column \( Z[:,3] \) is added where \( Z[i,3] \) represents the number of original observations (leaves) in the non-singleton cluster \( i \).

This function is useful when loading in linkages from legacy data files generated by MATLAB.

**Parameters**

- **Z**  

**Returns**

- **ZS**  
  [ndarray] A linkage matrix compatible with `scipy.cluster.hierarchy`.

See also:

- `linkage`  
  for a description of what a linkage matrix is.

- `to_mlab_linkage`  
  transform from Scipy to MATLAB format.
Examples

```python
>>> import numpy as np
>>> from scipy.cluster.hierarchy import ward, from_mlab_linkage
```

Given a linkage matrix in MATLAB format `mZ`, we can use `scipy.cluster.hierarchy.from_mlab_linkage` to import it into Scipy format:

```python
>>> mZ = np.array([[1, 2, 1], [4, 5, 1], [7, 8, 1],
    [10, 11, 1], [3, 13, 1.29099445],
    [6, 14, 1.29099445],
    [9, 15, 1.29099445],
    [12, 16, 1.29099445],
    [17, 18, 5.77350269],
    [19, 20, 5.77350269],
    [21, 22, 8.16496581]])
```

```python
>>> Z = from_mlab_linkage(mZ)
>>> Z
array([[ 0.,  1.,  1.,  2. ],
    [ 3.,  4.,  1.,  2. ],
    [ 6.,  7.,  1.,  2. ],
    [ 9., 10.,  1.,  2. ],
    [ 2., 12., 1.29099445, 3. ],
    [ 5., 13., 1.29099445, 3. ],
    [ 8., 14., 1.29099445, 3. ],
    [11., 15., 1.29099445, 3. ],
    [16., 17.,  5.77350269, 6. ],
    [18., 19.,  5.77350269, 6. ],
    [20., 21.,  8.16496581, 12. ]])
```

As expected, the linkage matrix `Z` returned includes an additional column counting the number of original samples in each cluster. Also, all cluster indexes are reduced by 1 (MATLAB format uses 1-indexing, whereas Scipy uses 0-indexing).

### 6.3.14 `scipy.cluster.hierarchy.inconsistent`

`scipy.cluster.hierarchy.inconsistent(Z, d=2)`

Calculate inconsistency statistics on a linkage matrix.

**Parameters**

- `Z` [ndarray] The \((n-1)\) by 4 matrix encoding the linkage (hierarchical clustering). See `linkage` documentation for more information on its form.

- `d` [int, optional] The number of links up to \(d\) levels below each non-singleton cluster.

**Returns**

- `R` [ndarray] A \((n-1)\) by 4 matrix where the \(i\)'th row contains the link statistics for the non-singleton cluster \(i\). The link statistics are computed over the link heights for links \(d\) levels below the cluster \(i\). \(R[i,0]\) and \(R[i,1]\) are the mean and standard deviation of the link heights, respectively; \(R[i,2]\) is the number of links included in the calculation; and \(R[i,3]\) is the inconsistency coefficient,

\[
\frac{Z[i,2] - R[i,0]}{R[i,1]}\]
Notes
This function behaves similarly to the MATLAB(TM) inconsistent function.

Examples
```python
>>> from scipy.cluster.hierarchy import inconsistent, linkage
>>> from matplotlib import pyplot as plt
>>> X = [i for i in [2, 8, 0, 4, 1, 9, 9, 0]]
>>> Z = linkage(X, 'ward')
>>> print(Z)
[[ 5. 6. 0. 2. ]
 [ 2. 7. 0. 2. ]
 [ 0. 4. 1. 2. ]
 [ 1. 8. 1.15470054 3. ]
 [ 9. 10. 2.12132034 4. ]
 [ 3. 12. 4.11096096 5. ]
>>> inconsistent(Z)
array([[ 0. , 0. , 1. , 0. ],
 [0. , 0. , 1. , 0. ],
 [ 1. , 0. , 1. , 0. ],
 [0.57735027, 0.81649658, 2. , 0.70710678],
 [1.04044011, 1.06123822, 3. , 1.01850858],
 [3.11614065, 1.4068837 , 2. , 0.70710678],
 [6.44583366, 6.76770586, 3. , 1.12682288]])
```

6.3.15 scipy.cluster.hierarchy.maxinconsts

scipy.cluster.hierarchy.maxinconsts(Z, R)

Return the maximum inconsistency coefficient for each non-singleton cluster and its children.

Parameters

Z [ndarray] The hierarchical clustering encoded as a matrix. See linkage for more information.

R [ndarray] The inconsistency matrix.

Returns

MI [ndarray] A monotonic (n-1)-sized numpy array of doubles.

See also:

linkage

for a description of what a linkage matrix is.

inconsistent

for the creation of an inconsistency matrix.

Examples
```python
>>> from scipy.cluster.hierarchy import median, inconsistent, maxinconsts
>>> from scipy.spatial.distance import pdist

Given a data set X, we can apply a clustering method to obtain a linkage matrix Z. scipy.cluster.
hierarchy.inconsistent can be also used to obtain the inconsistency matrix R associated to this
clustering process:
```
Here `scipy.cluster.hierarchy.maxinconsts` can be used to compute the maximum value of the inconsistency statistic (the last column of $R$) for each non-singleton cluster and its children:

```python
>>> maxinconsts(Z, R)
array([10. , 0. , 0. , 0. , 0.70710678, 0.70710678, 0.70710678, 0.70710678, 1.15470054, 1.15470054, 1.15470054])
```

### 6.3.16 `scipy.cluster.hierarchy.maxdists`

`scipy.cluster.hierarchy.maxdists(Z)`

Return the maximum distance between any non-singleton cluster.

**Parameters**

- $Z$ [ndarray] The hierarchical clustering encoded as a matrix. See `linkage` for more information.

**Returns**

- `maxdists` [ndarray] A (n-1) sized numpy array of doubles; MD[i] represents the maximum distance between any cluster (including singletons) below and including the node
with index i. More specifically, \( MD[i] = \text{Z}[Q(i)-n, 2].\max() \) where \( Q(i) \) is the set of all node indices below and including node i.

See also:

**linkage**

for a description of what a linkage matrix is.

**is_monotonic**

for testing for monotonicity of a linkage matrix.

**Examples**

```python
>>> from scipy.cluster.hierarchy import median, maxdists
>>> from scipy.spatial.distance import pdist

Given a linkage matrix \( \text{Z} \), `scipy.cluster.hierarchy.maxdists` computes for each new cluster generated (i.e. for each row of the linkage matrix) what is the maximum distance between any two child clusters.

Due to the nature of hierarchical clustering, in many cases this is going to be just the distance between the two child clusters that were merged to form the current one - that is, \( \text{Z}[;,:2] \).

However, for non-monotonic cluster assignments such as `scipy.cluster.hierarchy.median` clustering this is not always the case: There may be cluster formations were the distance between the two clusters merged is smaller than the distance between their children.

We can see this in an example:

```python
>>> X = [[0, 0], [0, 1], [1, 0],
      ... [0, 4], [0, 3], [1, 4],
      ... [4, 0], [3, 0], [4, 1],
      ... [4, 4], [3, 4], [4, 3]]
>>> Z = median(pdist(X))
>>> Z
array([[ 0., 1., 1., 2. ],
       [ 3., 4., 1., 2. ],
       [ 9., 10., 1., 2. ],
       [ 6., 7., 1., 2. ],
       [ 2., 12., 1.11803399, 3. ],
       [ 5., 13., 1.11803399, 3. ],
       [ 8., 15., 1.11803399, 3. ],
       [11., 14., 1.11803399, 3. ],
       [18., 19., 3., 6. ],
       [16., 17., 3.5 , 6. ],
       [20., 21., 3.25 , 12. ]])
>>> maxdists(Z)
array([1. , 1. , 1. , 1.11803399, 1.11803399, 1.11803399, 3. , 3.5 , 3.5 ])
```

Note that while the distance between the two clusters merged when creating the last cluster is 3.25, there are two children (clusters 16 and 17) whose distance is larger (3.5). Thus, `scipy.cluster.hierarchy.maxdists` returns 3.5 in this case.
6.3.17  scipy.cluster.hierarchy.maxRstat

scipy.cluster.hierarchy.maxRstat(Z, R, i)

Return the maximum statistic for each non-singleton cluster and its children.

Parameters

Z  [array_like] The hierarchical clustering encoded as a matrix. See linkage for more information.
R  [array_like] The inconsistency matrix.
i  [int] The column of R to use as the statistic.

Returns

MR  [ndarray] Calculates the maximum statistic for the i'th column of the inconsistency matrix R for each non-singleton cluster node. MR[j] is the maximum over R[Q(j)-n, i] where Q(j) the set of all node ids corresponding to nodes below and including j.

See also:

linkage

for a description of what a linkage matrix is.
inconsistent

for the creation of an inconsistency matrix.

Examples

```python
>>> from scipy.cluster.hierarchy import median, inconsistent, maxRstat
>>> from scipy.spatial.distance import pdist

Given a data set X, we can apply a clustering method to obtain a linkage matrix Z. scipy.cluster hierarchy.inconsistent can be also used to obtain the inconsistency matrix R associated to this clustering process:

```python
>>> X = [[0, 0], [0, 1], [1, 0],
      ... [0, 4], [0, 3], [1, 4],
      ... [4, 0], [3, 0], [4, 1],
      ... [4, 4], [3, 4], [4, 3]]

>>> Z = median(pdist(X))
>>> R = inconsistent(Z)
>>> R
array([[1.  , 0.  , 0.4 , 0.  ],
       [1.  , 0.  , 0.4 , 0.  ],
       [1.  , 0.  , 0.4 , 0.  ],
       [1.  , 0.  , 1.  , 0.  ],
       [1.  , 0.  , 0.4 , 0.  ],
       [1.05901699, 0.08346263, 2.  , 0.70710678],
       [1.05901699, 0.08346263, 2.  , 0.70710678],
       [1.05901699, 0.08346263, 2.  , 0.70710678],
       [1.74535599, 1.08655358, 3.  , 1.15470054],
       [1.91202266, 1.37522872, 3.  , 1.15470054],
       [3.25  , 0.25  , 3.  , 0.  ]])
```
`scipy.cluster.hierarchy.maxRstat` can be used to compute the maximum value of each column of \( R \), for each non-singleton cluster and its children:

```python
>>> maxRstat(Z, R, 0)
array([[1., 1., 1., 1.05901699, 1.05901699, 1.05901699, 1.74535599, 1.91202266, 3.25]])
>>> maxRstat(Z, R, 1)
array([[0., 0. , 0. , 0. , 0.08346263, 0.08346263, 0.08346263, 1.08655358, 1.37522872]])
>>> maxRstat(Z, R, 3)
array([[0. , 0. , 0. , 0. , 0.70710678, 0.70710678, 0.70710678, 1.15470054, 1.15470054]])
```

### 6.3.18 scipy.cluster.hierarchy.to_mlab_linkage

`scipy.cluster.hierarchy.to_mlab_linkage(Z)`

Convert a linkage matrix to a MATLAB(TM) compatible one.

Converts a linkage matrix \( Z \) generated by the linkage function of this module to a MATLAB(TM) compatible one. The return linkage matrix has the last column removed and the cluster indices are converted to 1..\( N \) indexing.

**Parameters**

- \( Z \) [ndarray] A linkage matrix generated by `scipy.cluster.hierarchy`.

**Returns**

- `to_mlab_linkage` [ndarray] A linkage matrix compatible with MATLAB(TM)’s hierarchical clustering functions.

The return linkage matrix has the last column removed and the cluster indices are converted to 1..\( N \) indexing.

**See also:**

- `linkage` for a description of what a linkage matrix is.
- `from_mlab_linkage` transform from Matlab to Scipy format.

**Examples**

```python
>>> from scipy.cluster.hierarchy import ward, to_mlab_linkage
>>> from scipy.spatial.distance import pdist

>>> X = [[0, 0], [0, 1], [1, 0], [0, 4], [0, 3], [1, 4], [4, 0], [3, 0], [4, 1], [4, 4], [3, 4], [4, 3]]
```
After a linkage matrix Z has been created, we can use `scipy.cluster.hierarchy.to_mlab_linkage` to convert it into MATLAB format:

```python
>>> mZ = to_mlab_linkage(Z)
>>> mZ
array([[ 1. ,  2. ,  1. ],
       [ 4. ,  5. ,  1. ],
       [ 7. ,  8. ,  1. ],
       [10. , 11. ,  1. ],
       [ 3. , 13. , 1.29099445],
       [ 6. , 14. , 1.29099445],
       [ 9. , 15. , 1.29099445],
       [12. , 16. , 1.29099445],
       [17. , 18. , 5.77350269],
       [19. , 20. , 5.77350269],
       [21. , 22. , 8.16496581]])
```

The new linkage matrix `mZ` uses 1-indexing for all the clusters (instead of 0-indexing). Also, the last column of the original linkage matrix has been dropped.

Routines for visualizing flat clusters.

```python
dendrogram(Z[, p, truncate_mode, ...])
```

Plot the hierarchical clustering as a dendrogram.

### 6.3.19 scipy.cluster.hierarchy.dendrogram

```python
scipy.cluster.hierarchy.dendrogram(Z, p=30, truncate_mode=None, color_threshold=None,
get_leaves=True, orientation='top', labels=None, count_sort=False, distance_sort=False,
show_leaf_counts=True, no_plot=False, no_labels=False,
leaf_font_size=None, leaf_rotation=None, leaf_label_func=None,
show_contracted=False, link_color_func=None, ax=None,
above_threshold_color='b')
```

Plot the hierarchical clustering as a dendrogram.

The dendrogram illustrates how each cluster is composed by drawing a U-shaped link between a non-singleton cluster and its children. The top of the U-link indicates a cluster merge. The two legs of the U-link indicate which clusters were merged. The length of the two legs of the U-link represents the distance between the child clusters. It is also the cophenetic distance between original observations in
the two children clusters.

**Parameters**

- **Z** [ndarray] The linkage matrix encoding the hierarchical clustering to render as a dendrogram. See the `linkage` function for more information on the format of Z.
- **p** [int, optional] The p parameter for `truncate_mode`.
- **truncate_mode** [str, optional] The dendrogram can be hard to read when the original observation matrix from which the linkage is derived is large. Truncation is used to condense the dendrogram. There are several modes:
  - *None* No truncation is performed (default). Note: 'none' is an alias for None that's kept for backward compatibility.
  - 'lastp' The last p non-singleton clusters formed in the linkage are the only non-leaf nodes in the linkage; they correspond to rows Z[n-p-2:end] in Z. All other non-singleton clusters are contracted into leaf nodes.
  - 'level' No more than p levels of the dendrogram tree are displayed. A “level” includes all nodes with p merges from the last merge. Note: 'mtica' is an alias for 'level' that's kept for backward compatibility.
- **color_threshold** [double, optional] For brevity, let t be the color_threshold. Colors all the descendent links below a cluster node k the same color if k is the first node below the cut threshold t. All links connecting nodes with distances greater than or equal to the threshold are colored blue. If t is less than or equal to zero, all nodes are colored blue. If color_threshold is None or ‘default’, corresponding with MATLAB(TM) behavior, the threshold is set to 0.7*max(Z[:,2]).
- **get_leaves** [bool, optional] Includes a list R['leaves']=H in the result dictionary. For each i, H[i] == j, cluster node j appears in position i in the left-to-right traversal of the leaves, where j < 2n - 1 and i < n.
- **orientation** [str, optional] The direction to plot the dendrogram, which can be any of the following strings:
  - 'top' Plots the root at the top, and plot descendent links going downwards. (default).
  - 'bottom' Plots the root at the bottom, and plot descendent links going upwards.
  - 'left' Plots the root at the left, and plot descendent links going right.
  - 'right' Plots the root at the right, and plot descendent links going left.
- **labels** [ndarray, optional] By default labels is None so the index of the original observation is used to label the leaf nodes. Otherwise, this is an n-sized list (or tuple). The labels[i] value is the text to put under the i th leaf node only if it corresponds to an original observation and not a non-singleton cluster.
- **count_sort** [str or bool, optional] For each node n, the order (visually, from left-to-right) n’s two descendent links are plotted is determined by this parameter, which can be any of the following values:
  - False Nothing is done.
  - 'ascending' or True The child with the minimum number of original objects in its cluster is plotted first.
  - 'descending' The child with the maximum number of original objects in its cluster is plotted first.

Note distance_sort and count_sort cannot both be True.
distance_sort

[str or bool, optional] For each node n, the order (visually, from left-to-right) n’s two descendent links are plotted is determined by this parameter, which can be any of the following values:

False: Nothing is done.
'ascending' or True: The child with the minimum distance between its direct descendents is plotted first.
'descending': The child with the maximum distance between its direct descendents is plotted first.

Note distance_sort and count_sort cannot both be True.

show_leaf_counts

[bool, optional] When True, leaf nodes representing \( k > 1 \) original observation are labeled with the number of observations they contain in parentheses.

no_plot

[bool, optional] When True, the final rendering is not performed. This is useful if only the data structures computed for the rendering are needed or if matplotlib is not available.

no_labels

[bool, optional] When True, no labels appear next to the leaf nodes in the rendering of the dendrogram.

leaf_rotation

[double, optional] Specifies the angle (in degrees) to rotate the leaf labels. When unspecified, the rotation is based on the number of nodes in the dendrogram (default is 0).

leaf_font_size

[int, optional] Specifies the font size (in points) of the leaf labels. When unspecified, the size based on the number of nodes in the dendrogram.

leaf_label_func

[lambda or function, optional] When leaf_label_func is a callable function, for each leaf with cluster index \( k < 2^n - 1 \). The function is expected to return a string with the label for the leaf. Indices \( k < n \) correspond to original observations while indices \( k \geq n \) correspond to non-singleton clusters.

For example, to label singletons with their node id and non-singletons with their id, count, and inconsistency coefficient, simply do:

```python
# First define the leaf label function.
def llf(id):
    if id < n:
        return str(id)
    else:
        return '[%d %d %1.2f]' % (id, count, R[n-id,3])
# The text for the leaf nodes is going to be big so force
# a rotation of 90 degrees.
dendrogram(Z, leaf_label_func=llf, leaf_rotation=90)
```

show_contracted

[bool, optional] When True the heights of non-singleton nodes contracted into a leaf node are plotted as crosses along the link connecting that leaf node. This really is only useful when truncation is used (see truncate_mode parameter).

link_color_func

[callable, optional] If given, link_color_function is called with each non-singleton id corresponding to each U-shaped link it will paint. The function is expected to
return the color to paint the link, encoded as a matplotlib color string code. For example:

```python
dendrogram(Z, link_color_func=lambda k: colors[k])
```

colors the direct links below each untruncated non-singleton node \( k \) using `colors[k]`.

*ax*  
[matplotlib Axes instance, optional] If None and no_plot is not True, the dendrogram will be plotted on the current axes. Otherwise if no_plot is not True the dendrogram will be plotted on the given `Axes` instance. This can be useful if the dendrogram is part of a more complex figure.

above_threshold_color  
[str, optional] This matplotlib color string sets the color of the links above the color_threshold. The default is ‘b’.

**Returns**

* R  
[dict] A dictionary of data structures computed to render the dendrogram. Its has the following keys:

  * 'color_list'  
A list of color names. The \( k \)'th element represents the color of the \( k \)'th link.

  * 'icoord' and 'dcoord'  
Each of them is a list of lists. Let `icoord = [I1, I2, ..., Ip]` where `Ik = [xk1, xk2, xk3, xk4]` and `dcoord = [D1, D2, ..., Dp]` where `Dk = [yk1, yk2, yk3, yk4]`, then the \( k \)'th link painted is \((xk1, yk1) - (xk2, yk2) - (xk3, yk3) - (xk4, yk4)\).

  * 'ivl'  
A list of labels corresponding to the leaf nodes.

  * 'leaves'  
For each \( i \), \( H[i] == j \), cluster node \( j \) appears in position \( i \) in the left-to-right traversal of the leaves, where \( j < 2n - 1 \) and \( i < n \). If \( j \) is less than \( n \), the \( i \)-th leaf node corresponds to an original observation. Otherwise, it corresponds to a non-singleton cluster.

See also:

* linkage, set_link_color_palette

Notes

It is expected that the distances in \( Z[:, 2] \) be monotonic, otherwise crossings appear in the dendrogram.

Examples

```python
>>> from scipy.cluster import hierarchy
>>> import matplotlib.pyplot as plt
```

A very basic example:

```python
>>> ytdist = np.array([662., 877., 255., 412., 996., 295., 468., 268.,
                     400., 754., 564., 138., 219., 869., 669.])
>>> Z = hierarchy.linkage(ytdist, 'single')
>>> plt.figure()
>>> dn = hierarchy.dendrogram(Z)
```

Now plot in given axes, improve the color scheme and use both vertical and horizontal orientations:

```python
>>> hierarchy.set_link_color_palette(['m', 'c', 'y', 'k'])
>>> fig, axes = plt.subplots(1, 2, figsize=(8, 3))
>>> dn1 = hierarchy.dendrogram(Z, ax=axes[0], above_threshold_color='y',
```

(continues on next page)
These are data structures and routines for representing hierarchies as tree objects.

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
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<tbody>
<tr>
<td><code>ClusterNode(id, left, right, dist, count)</code></td>
<td>A tree node class for representing a cluster.</td>
</tr>
<tr>
<td><code>leaves_list(Z)</code></td>
<td>Return a list of leaf node ids.</td>
</tr>
<tr>
<td><code>to_tree(Z, rd)</code></td>
<td>Convert a linkage matrix into an easy-to-use tree object.</td>
</tr>
<tr>
<td><code>cut_tree(Z, n_clusters, height)</code></td>
<td>Given a linkage matrix $Z$, return the cut tree.</td>
</tr>
<tr>
<td><code>optimal_leaf_ordering(Z, y, metric)</code></td>
<td>Given a linkage matrix $Z$ and distance, reorder the cut tree.</td>
</tr>
</tbody>
</table>

### 6.3. Hierarchical clustering (`scipy.cluster.hierarchy`)
6.3.20 scipy.cluster.hierarchy.ClusterNode

class scipy.cluster.hierarchy.ClusterNode(id, left=None, right=None, dist=0, count=1)

A tree node class for representing a cluster.

Leaf nodes correspond to original observations, while non-leaf nodes correspond to non-singleton clusters.

The to_tree function converts a matrix returned by the linkage function into an easy-to-use tree representation.

All parameter names are also attributes.

Parameters

- **id** [int] The node id.
- **left** [ClusterNode instance, optional] The left child tree node.
- **right** [ClusterNode instance, optional] The right child tree node.
- **dist** [float, optional] Distance for this cluster in the linkage matrix.
- **count** [int, optional] The number of samples in this cluster.

See also:

to_tree

for converting a linkage matrix Z into a tree object.

Methods

- **get_count()** The number of leaf nodes (original observations) belonging to the cluster node nd.
- **get_id()** The identifier of the target node.
- **get_left()** Return a reference to the left child tree object.
- **get_right()** Return a reference to the right child tree object.
- **is_leaf()** Return True if the target node is a leaf.
- **pre_order([func])** Perform pre-order traversal without recursive function calls.

scipy.cluster.hierarchy.ClusterNode.get_count

ClusterNode.get_count()

The number of leaf nodes (original observations) belonging to the cluster node nd. If the target node is a leaf, 1 is returned.

Returns

- **get_count** [int] The number of leaf nodes below the target node.

scipy.cluster.hierarchy.ClusterNode.get_id

ClusterNode.get_id()

The identifier of the target node.

For 0 <= i < n, i corresponds to original observation i. For n <= i < 2n-1, i corresponds to non-singleton cluster formed at iteration i-n.

Returns

- **id** [int] The identifier of the target node.
scipy.cluster.hierarchy.ClusterNode.get_left

ClusterNode.get_left()
Return a reference to the left child tree object.

Returns
left : [ClusterNode]
The left child of the target node. If the node is a leaf, None is returned.

scipy.cluster.hierarchy.ClusterNode.get_right

ClusterNode.get_right()
Return a reference to the right child tree object.

Returns
right : [ClusterNode]
The right child of the target node. If the node is a leaf, None is returned.

scipy.cluster.hierarchy.ClusterNode.is_leaf

ClusterNode.is_leaf()
Return True if the target node is a leaf.

Returns
leafness : [bool] True if the target node is a leaf node.

scipy.cluster.hierarchy.ClusterNode.pre_order

ClusterNode.pre_order(func=<function ClusterNode.<lambda>>)
Perform pre-order traversal without recursive function calls.

When a leaf node is first encountered, func is called with the leaf node as its argument, and its
result is appended to the list.

For example, the statement:

```python
ids = root.pre_order(lambda x: x.id)
```

returns a list of the node ids corresponding to the leaf nodes of the tree as they appear from left
to right.

Parameters

func : [function] Applied to each leaf ClusterNode object in the pre-order traversal.
Given the i-th leaf node in the pre-order traversal n[i], the result of
func(n[i]) is stored in L[i]. If not provided, the index of the original observation
to which the node corresponds is used.

Returns

L : [list] The pre-order traversal.

6.3.21 scipy.cluster.hierarchy.leaves_list

scipy.cluster.hierarchy.leaves_list(Z)
Return a list of leaf node ids.

The return corresponds to the observation vector index as it appears in the tree from left to right. Z
is a linkage matrix.
Parameters

\( Z \) [ndarray] The hierarchical clustering encoded as a matrix. \( Z \) is a linkage matrix. See \textit{linkage} for more information.

Returns

leaves_list [ndarray] The list of leaf node ids.

See also:

dendrogram

for information about dendrogram structure.

Examples

```python
>>> from scipy.cluster.hierarchy import ward, dendrogram, leaves_list
>>> from scipy.spatial.distance import pdist
>>> from matplotlib import pyplot as plt

>>> X = [[0, 0], [0, 1], [1, 0],
      ... [0, 4], [0, 3], [1, 4],
      ... [4, 0], [3, 0], [4, 1],
      ... [4, 4], [3, 4], [4, 3]]

>>> Z = ward(pdist(X))

The linkage matrix \( Z \) represents a dendrogram, that is, a tree that encodes the structure of the clustering performed. \textit{scipy.cluster.hierarchy.leaves_list} shows the mapping between indexes in the \( X \) dataset and leaves in the dendrogram:

```
6.3.22 scipy.cluster.hierarchy.to_tree

scipy.cluster.hierarchy.to_tree(Z, rd=False)

Convert a linkage matrix into an easy-to-use tree object.

The reference to the root ClusterNode object is returned (by default).

Each ClusterNode object has a left, right, dist, id, and count attribute. The left and right attributes point to ClusterNode objects that were combined to generate the cluster. If both are None then the ClusterNode object is a leaf node, its count must be 1, and its distance is meaningless but set to 0.

Note: This function is provided for the convenience of the library user. ClusterNodes are not used as input to any of the functions in this library.

Parameters

- Z [ndarray] The linkage matrix in proper form (see the linkage function documentation).
- rd [bool, optional] When False (default), a reference to the root ClusterNode object is returned. Otherwise, a tuple (r, d) is returned. r is a reference to the root node while d is a list of ClusterNode objects - one per original entry in the linkage matrix plus entries for all clustering steps. If a cluster id is less than the number of samples n in the data that the linkage matrix describes, then it corresponds to a singleton cluster (leaf node). See linkage for more information on the assignment of cluster ids to clusters.

Returns

- tree [ClusterNode or tuple (ClusterNode, list of ClusterNode)] If rd is False, a ClusterNode. If rd is True, a list of length 2*n - 1, with n the number of samples. See the description of rd above for more details.

See also:

linkage, is_valid_linkage, ClusterNode

Examples

```python
>>> from scipy.cluster import hierarchy
>>> x = np.random.rand(10).reshape(5, 2)
>>> Z = hierarchy.linkage(x)
>>> hierarchy.to_tree(Z)
<scipy.cluster.hierarchy.ClusterNode object at ...>
>>> rootnode, nodelist = hierarchy.to_tree(Z, rd=True)
>>> rootnode
<scipy.cluster.hierarchy.ClusterNode object at ...>
>>> len(nodelist)
9
```

6.3.23 scipy.cluster.hierarchy.cut_tree

scipy.cluster.hierarchy.cut_tree(Z, n_clusters=None, height=None)

Given a linkage matrix Z, return the cut tree.

Parameters

- n_clusters [array_like, optional] Number of clusters in the tree at the cut point.
**height**  [array_like, optional] The height at which to cut the tree. Only possible for ultrametric trees.

**Returns**  
cutree  [array] An array indicating group membership at each agglomeration step. I.e., for a full cut tree, in the first column each data point is in its own cluster. At the next step, two nodes are merged. Finally all singleton and non-singleton clusters are in one group. If \( n_{\text{clusters}} \) or \( \text{height} \) is given, the columns correspond to the columns of \( n_{\text{clusters}} \) or \( \text{height} \).

**Examples**

```python
>>> from scipy import cluster
>>> np.random.seed(23)
>>> X = np.random.randn(50, 4)
>>> Z = cluster.hierarchy.ward(X)
>>> cutree = cluster.hierarchy.cut_tree(Z, n_clusters=[5, 10])
>>> cutree[:,:10]
array([[0, 0],
       [1, 1],
       [2, 2],
       [3, 3],
       [3, 4],
       [2, 2],
       [0, 0],
       [1, 5],
       [3, 6],
       [4, 7]])
```

6.3.24  **scipy.cluster.hierarchy.optimal_leaf_ordering**

scipy.cluster.hierarchy.optimal_leaf_ordering(\( Z, y, \text{metric='euclidean'} \))  

Given a linkage matrix \( Z \) and distance, reorder the cut tree.

**Parameters**

- **Z**  [ndarray] The hierarchical clustering encoded as a linkage matrix. See \( \text{linkage} \) for more information on the return structure and algorithm.
- **y**  [ndarray] The condensed distance matrix from which \( Z \) was generated. Alternatively, a collection of \( m \) observation vectors in \( n \) dimensions may be passed as a \( m \times n \) array.
- **metric**  [str or function, optional] The distance metric to use in the case that \( y \) is a collection of observation vectors; ignored otherwise. See the \( \text{pdist} \) function for a list of valid distance metrics. A custom distance function can also be used.

**Returns**

- **Z_ordered**  [ndarray] A copy of the linkage matrix \( Z \), reordered to minimize the distance between adjacent leaves.

**Examples**

```python
>>> from scipy.cluster import hierarchy
>>> np.random.seed(23)
>>> X = np.random.randn(10,10)
>>> Z = hierarchy.ward(X)
```
>>> hierarchy.leaves_list(Z)
array([0, 5, 3, 9, 6, 8, 1, 4, 2, 7], dtype=int32)
>>> hierarchy.leaves_list(hierarchy.optimal_leaf_ordering(Z, X))
array([3, 9, 0, 5, 8, 2, 7, 4, 1, 6], dtype=int32)

These are predicates for checking the validity of linkage and inconsistency matrices as well as for checking isomorphism of two flat cluster assignments.

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>is_valid_im(R[, warning, throw, name])</code></td>
<td>Return True if the inconsistency matrix passed is valid.</td>
</tr>
<tr>
<td><code>is_valid_linkage(Z[, warning, throw, name])</code></td>
<td>Check the validity of a linkage matrix.</td>
</tr>
<tr>
<td><code>is_isomorphic(T1, T2)</code></td>
<td>Determine if two different cluster assignments are equivalent.</td>
</tr>
<tr>
<td><code>is_monotonic(Z)</code></td>
<td>Return True if the linkage passed is monotonic.</td>
</tr>
<tr>
<td><code>correspond(Z, Y)</code></td>
<td>Check for correspondence between linkage and condensed distance matrices.</td>
</tr>
<tr>
<td><code>num_obs_linkage(Z)</code></td>
<td>Return the number of original observations of the linkage matrix passed.</td>
</tr>
</tbody>
</table>

### 6.3.25 scipy.cluster.hierarchy.is_valid_im

**scipy.cluster.hierarchy.is_valid_im(R, warning=False, throw=False, name=None)**

Return True if the inconsistency matrix passed is valid.

It must be a $n$ by 4 array of doubles. The standard deviations $R[:,1]$ must be nonnegative. The link counts $R[:,2]$ must be positive and no greater than $n - 1$.

**Parameters**

- **R** [ndarray] The inconsistency matrix to check for validity.
- **warning** [bool, optional] When True, issues a Python warning if the linkage matrix passed is invalid.
- **throw** [bool, optional] When True, throws a Python exception if the linkage matrix passed is invalid.
- **name** [str, optional] This string refers to the variable name of the invalid linkage matrix.

**Returns**

- **b** [bool] True if the inconsistency matrix is valid.

**See also:**

- `linkage`
  
  for a description of what a linkage matrix is.

- `inconsistent`
  
  for the creation of an inconsistency matrix.

**Examples**

```python
>>> from scipy.cluster.hierarchy import ward, inconsistent, is_valid_im
>>> from scipy.spatial.distance import pdist
```
Given a data set \( X \), we can apply a clustering method to obtain a linkage matrix \( Z \). \texttt{scipy.cluster.hierarchy.inconsistent} can be also used to obtain the inconsistency matrix \( R \) associated to this clustering process:

```python
>>> X = [[0, 0], [0, 1], [1, 0],
      ... [0, 4], [0, 3], [1, 4],
      ... [4, 0], [3, 0], [4, 1],
      ... [4, 4], [3, 4], [4, 3]]
```

```python
>>> Z = ward(pdist(X))
>>> R = inconsistent(Z)
```

```python
>>> Z
array([[ 0. , 1. , 1. , 2. ],
       [ 3. , 4. , 1. , 2. ],
       [ 6. , 7. , 1. , 2. ],
       [ 9. , 10. , 1. , 2. ],
       [ 2. , 12. , 1.29099445, 3. ],
       [ 5. , 13. , 1.29099445, 3. ],
       [ 8. , 14. , 1.29099445, 3. ],
       [11. , 15. , 1.29099445, 3. ],
       [16. , 17. , 5.77350269, 6. ],
       [18. , 19. , 5.77350269, 6. ],
       [20. , 21. , 8.16496581, 12. ]])
```

```python
>>> R
array([[1. , 0. , 1. , 0. ],
       [1. , 0. , 1. , 0. ],
       [1. , 0. , 1. , 0. ],
       [1. , 0. , 1. , 0. ],
       [1.14549722, 0.20576415, 2. , 0.70710678],
       [1.14549722, 0.20576415, 2. , 0.70710678],
       [1.14549722, 0.20576415, 2. , 0.70710678],
       [1.14549722, 0.20576415, 2. , 0.70710678],
       [2.78516386, 2.58797734, 3. , 1.15470054],
       [2.78516386, 2.58797734, 3. , 1.15470054],
       [6.57065706, 1.38071187, 3. , 1.15470054]])
```

Now we can use \texttt{scipy.cluster.hierarchy.is_valid_im} to verify that \( R \) is correct:

```python
>>> is_valid_im(R)
True
```

However, if \( R \) is wrongly constructed (e.g one of the standard deviations is set to a negative value) then the check will fail:

```python
>>> R[-1,1] = R[-1,1] * -1
>>> is_valid_im(R)
False
```

### 6.3.26 \texttt{scipy.cluster.hierarchy.is_valid_linkage}

\texttt{scipy.cluster.hierarchy.is_valid_linkage}(Z, warning=False, throw=False, name=None)

Check the validity of a linkage matrix.

A linkage matrix is valid if it is a two dimensional array (type double) with \( n \) rows and 4 columns. The first two columns must contain indices between 0 and \( 2n - 1 \). For a given row \( i \), the following two
expressions have to hold:

\[ 0 \leq Z[i, 0] \leq i + n - 10 \leq Z[i, 1] \leq i + n - 1 \]

I.e. a cluster cannot join another cluster unless the cluster being joined has been generated.

**Parameters**

- **Z** [array_like] Linkage matrix.
- **warning** [bool, optional] When True, issues a Python warning if the linkage matrix passed is invalid.
- **throw** [bool, optional] When True, throws a Python exception if the linkage matrix passed is invalid.
- **name** [str, optional] This string refers to the variable name of the invalid linkage matrix.

**Returns**

- **b** [bool] True if the inconsistency matrix is valid.

See also:

- **linkage** for a description of what a linkage matrix is.

**Examples**

```python
>>> from scipy.cluster.hierarchy import ward, is_valid_linkage
>>> from scipy.spatial.distance import pdist

All linkage matrices generated by the clustering methods in this module will be valid (i.e. they will have the appropriate dimensions and the two required expressions will hold for all the rows).

We can check this using `scipy.cluster.hierarchy.is_valid_linkage`:

```python
>>> X = [[0, 0], [0, 1], [1, 0],
      ... [0, 4], [0, 3], [1, 4],
      ... [4, 0], [3, 0], [4, 1],
      ... [4, 4], [3, 4], [4, 3]]
```

```python
>>> Z = ward(pdist(X))
>>> Z
array([[ 0.   ,  1.   ,  1.   ,  2.   ],
       [ 3.   ,  4.   ,  1.   ,  2.   ],
       [ 6.   ,  7.   ,  1.   ,  2.   ],
       [ 9.   , 10.   ,  1.   ,  2.   ],
       [ 2.   , 12.   ,  1.29099445,  3.   ],
       [ 5.   , 13.   ,  1.29099445,  3.   ],
       [ 8.   , 14.   ,  1.29099445,  3.   ],
       [11.   , 15.   ,  1.29099445,  3.   ],
       [16.   , 17.   , 5.77350269,  6.   ],
       [18.   , 19.   , 5.77350269,  6.   ],
       [20.   , 21.   , 8.16496581, 12.   ]])
```

```python
>>> is_valid_linkage(Z)
True
```

However, if we create a linkage matrix in a wrong way - or if we modify a valid one in a way that any of the required expressions don’t hold anymore, then the check will fail:
>>> Z[3][1] = 20  # the cluster number 20 is not defined at this point
>>> is_valid_linkage(Z)
False

6.3.27 `scipy.cluster.hierarchy.is_isomorphic`

`scipy.cluster.hierarchy.is_isomorphic(T1, T2)`

Determine if two different cluster assignments are equivalent.

**Parameters**

- `T1`  
  [array_like] An assignment of singleton cluster ids to flat cluster ids.

- `T2`  
  [array_like] An assignment of singleton cluster ids to flat cluster ids.

**Returns**

- `b`  
  [bool] Whether the flat cluster assignments `T1` and `T2` are equivalent.

**See also:**

- `linkage`
  for a description of what a linkage matrix is.

- `fcluster`
  for the creation of flat cluster assignments.

**Examples**

```python
>>> from scipy.cluster.hierarchy import fcluster, is_isomorphic
>>> from scipy.cluster.hierarchy import single, complete
>>> from scipy.spatial.distance import pdist
```

Two flat cluster assignments can be isomorphic if they represent the same cluster assignment, with different labels.

For example, we can use the `scipy.cluster.hierarchy.single:` method and flatten the output to four clusters:

```python
>>> X = [[0, 0], [0, 1], [1, 0],
      ... [0, 4], [0, 3], [1, 4],
      ... [4, 0], [3, 0], [4, 1],
      ... [4, 4], [3, 4], [4, 3]]
```

```python
>>> Z = single(pdist(X))
>>> T = fcluster(Z, 1, criterion='distance')
>>> T
array([3, 3, 3, 4, 4, 4, 2, 2, 2, 1, 1, 1], dtype=int32)
```

We can then do the same using the `scipy.cluster.hierarchy.complete:` method:

```python
>>> Z = complete(pdist(X))
>>> T_ = fcluster(Z, 1.5, criterion='distance')
>>> T_
array([1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4], dtype=int32)
```
As we can see, in both cases we obtain four clusters and all the data points are distributed in the same way - the only thing that changes are the flat cluster labels (3 => 1, 4 => 2, 2 => 3 and 4 => 1), so both cluster assignments are isomorphic:

```python
>>> is_isomorphic(T, T_)
True
```

### 6.3.28 scipy.cluster.hierarchy.is_monotonic

**scipy.cluster.hierarchy.is_monotonic(Z)**

Return True if the linkage passed is monotonic.

The linkage is monotonic if for every cluster \( s \) and \( t \) joined, the distance between them is no less than the distance between any previously joined clusters.

**Parameters**

- \( Z \) [ndarray] The linkage matrix to check for monotonicity.

**Returns**

- \( b \) [bool] A boolean indicating whether the linkage is monotonic.

**See also:**

- `linkage`

  for a description of what a linkage matrix is.

**Examples**

```python
>>> from scipy.cluster.hierarchy import median, ward, is_monotonic
>>> from scipy.spatial.distance import pdist

By definition, some hierarchical clustering algorithms - such as `scipy.cluster.hierarchy.ward` - produce monotonic assignments of samples to clusters; however, this is not always true for other hierarchical methods - e.g. `scipy.cluster.hierarchy.median`.

Given a linkage matrix \( Z \) (as the result of a hierarchical clustering method) we can test programmatically whether if is has the monotonicity property or not, using `scipy.cluster.hierarchy.is_monotonic`:

```python
>>> X = [[0, 0], [0, 1], [1, 0],
... [0, 4], [0, 3], [1, 4],
... [4, 0], [3, 0], [4, 1],
... [4, 4], [3, 4], [4, 3]]

>>> Z = ward(pdist(X))
>>> Z
array([[ 0. , 1. , 1. , 2. ],
       [ 3. , 4. , 1. , 2. ],
       [ 6. , 7. , 1. , 2. ],
       [ 9. , 10. , 1. , 2. ],
       [ 2. , 12. , 1.29099445, 3. ],
       [ 5. , 13. , 1.29099445, 3. ],
       [ 8. , 14. , 1.29099445, 3. ],
       [11. , 15. , 1.29099445, 3. ],
       [16. , 17. , 5.77350269, 6. ]], dtype=object)
```

(continues on next page)
>>> is_monotonic(Z)
True

>>> Z = median(pdist(X))

>>> Z
array([[ 0. ,  1. ,  1. ,  2. ],
       [ 3. ,  4. ,  1. ,  2. ],
       [ 9. , 10. ,  1. ,  2. ],
       [ 6. ,  7. ,  1. ,  2. ],
       [ 2. , 12. , 1.11803399,  3. ],
       [ 5. , 13. , 1.11803399,  3. ],
       [ 8. , 15. , 1.11803399,  3. ],
       [11. , 14. , 1.11803399,  3. ],
       [18. , 19. ,  3. ,   6. ],
       [16. , 17. ,  3.5 ,   6. ],
       [20. , 21. ,  3.25 ,  12. ]])

>>> is_monotonic(Z)
False

Note that this method is equivalent to just verifying that the distances in the third column of the linkage matrix appear in a monotonically increasing order.

### 6.3.29 scipy.cluster.hierarchy.correspond

**scipy.cluster.hierarchy.correspond(Z, Y)**

Check for correspondence between linkage and condensed distance matrices.

They must have the same number of original observations for the check to succeed.

This function is useful as a sanity check in algorithms that make extensive use of linkage and distance matrices that must correspond to the same set of original observations.

**Parameters**

- **Z**  
  [array_like] The linkage matrix to check for correspondence.

- **Y**  
  [array_like] The condensed distance matrix to check for correspondence.

**Returns**

- **b**  
  [bool] A boolean indicating whether the linkage matrix and distance matrix could possibly correspond to one another.

**See also:**

- **linkage**

  for a description of what a linkage matrix is.

**Examples**

```python
>>> from scipy.cluster.hierarchy import ward, correspond
>>> from scipy.spatial.distance import pdist
```

This method can be used to check if a given linkage matrix Z has been obtained from the application of a cluster method over a dataset X:
```python
>>> X = [[0, 0], [0, 1], [1, 0],
... [0, 4], [0, 3], [1, 4],
... [4, 0], [3, 0], [4, 1],
... [4, 4], [3, 4], [4, 3]]
>>> X_condensed = pdist(X)
>>> Z = ward(X_condensed)
```

Here we can compare $Z$ and $X$ (in condensed form):

```python
>>> correspond(Z, X_condensed)
True
```

### 6.3.30 scipy.cluster.hierarchy.num_obs_linkage

`scipy.cluster.hierarchy.num_obs_linkage(Z)`

Return the number of original observations of the linkage matrix passed.

**Parameters**

$Z$  
[array] The linkage matrix on which to perform the operation.

**Returns**

$n$  
[int] The number of original observations in the linkage.

**Examples**

```python
>>> from scipy.cluster.hierarchy import ward, num_obs_linkage
>>> from scipy.spatial.distance import pdist

>>> X = [[0, 0], [0, 1], [1, 0],
... [0, 4], [0, 3], [1, 4],
... [4, 0], [3, 0], [4, 1],
... [4, 4], [3, 4], [4, 3]]

>>> Z = ward(pdist(X))
```

$Z$ is a linkage matrix obtained after using the Ward clustering method with $X$, a dataset with 12 data points.

```python
>>> num_obs_linkage(Z)
12
```

Utility routines for plotting:

- `set_link_color_palette(palette)`: Set list of matplotlib color codes for use by dendrogram.

### 6.3.31 scipy.cluster.hierarchy.set_link_color_palette

`scipy.cluster.hierarchy.set_link_color_palette(palette)`

Set list of matplotlib color codes for use by dendrogram.

Note that this palette is global (i.e. setting it once changes the colors for all subsequent calls to `dendrogram`) and that it affects only the colors below `color_threshold`.  

6.3. Hierarchical clustering (`scipy.cluster.hierarchy`)
Note that `dendrogram` also accepts a custom coloring function through its `link_color_func` keyword, which is more flexible and non-global.

**Parameters**

- `palette` ([list of str or None]) A list of matplotlib color codes. The order of the color codes is the order in which the colors are cycled through when color thresholding in the dendrogram. If `None`, resets the palette to its default (which is `['g', 'r', 'c', 'm', 'y', 'k']`).

**Returns**

- `None`

**See also:**

- `dendrogram`

**Notes**

Ability to reset the palette with `None` added in Scipy 0.17.0.

**Examples**

```python
>>> from scipy.cluster import hierarchy
>>> ytdist = np.array([662., 877., 255., 412., 996., 295., 468., 268., ...
                      400., 754., 564., 138., 219., 869., 669.])
>>> Z = hierarchy.linkage(ytdist, 'single')
>>> dn = hierarchy.dendrogram(Z, no_plot=True)
>>> dn['color_list']
['g', 'b', 'b', 'b', 'b']
>>> hierarchy.set_link_color_palette(['c', 'm', 'y', 'k'])
>>> dn = hierarchy.dendrogram(Z, no_plot=True)
>>> dn['color_list']
['c', 'b', 'b', 'b', 'b']
>>> dn = hierarchy.dendrogram(Z, no_plot=True, color_threshold=267,
                           ... above_threshold_color='k')
>>> dn['color_list']
['c', 'm', 'm', 'k', 'k']
```

Now reset the color palette to its default:

```python
>>> hierarchy.set_link_color_palette(None)
```

### 6.3.32 References

- MATLAB and MathWorks are registered trademarks of The MathWorks, Inc.
- Mathematica is a registered trademark of The Wolfram Research, Inc.

### 6.4 Constants (`scipy.constants`)

Physical and mathematical constants and units.
6.4.1 Mathematical constants

<table>
<thead>
<tr>
<th>pi</th>
<th>Pi</th>
</tr>
</thead>
<tbody>
<tr>
<td>golden</td>
<td>Golden ratio</td>
</tr>
<tr>
<td>golden_ratio</td>
<td>Golden ratio</td>
</tr>
</tbody>
</table>

6.4.2 Physical constants

<table>
<thead>
<tr>
<th>c</th>
<th>speed of light in vacuum</th>
</tr>
</thead>
<tbody>
<tr>
<td>speed_of_light</td>
<td>speed of light in vacuum</td>
</tr>
<tr>
<td>mu_0</td>
<td>the magnetic constant (\mu_0)</td>
</tr>
<tr>
<td>epsilon_0</td>
<td>the electric constant (vacuum permittivity), (\epsilon_0)</td>
</tr>
<tr>
<td>h</td>
<td>the Planck constant (h)</td>
</tr>
<tr>
<td>Planck</td>
<td>the Planck constant (h)</td>
</tr>
<tr>
<td>hbar</td>
<td>(h = h/(2\pi))</td>
</tr>
<tr>
<td>G</td>
<td>Newtonian constant of gravitation</td>
</tr>
<tr>
<td>gravitational_constant</td>
<td>Newtonian constant of gravitation</td>
</tr>
<tr>
<td>g</td>
<td>standard acceleration of gravity</td>
</tr>
<tr>
<td>e</td>
<td>elementary charge</td>
</tr>
<tr>
<td>elementary_charge</td>
<td>elementary charge</td>
</tr>
<tr>
<td>R</td>
<td>molar gas constant</td>
</tr>
<tr>
<td>gas_constant</td>
<td>molar gas constant</td>
</tr>
<tr>
<td>alpha</td>
<td>fine-structure constant</td>
</tr>
<tr>
<td>fine_structure</td>
<td>fine-structure constant</td>
</tr>
<tr>
<td>N_A</td>
<td>Avogadro constant</td>
</tr>
<tr>
<td>Avogadro</td>
<td>Avogadro constant</td>
</tr>
<tr>
<td>k</td>
<td>Boltzmann constant</td>
</tr>
<tr>
<td>Boltzmann</td>
<td>Boltzmann constant</td>
</tr>
<tr>
<td>sigma</td>
<td>Stefan-Boltzmann constant (\sigma)</td>
</tr>
<tr>
<td>Stefan_Boltzmann</td>
<td>Stefan-Boltzmann constant (\sigma)</td>
</tr>
<tr>
<td>Wien</td>
<td>Wien displacement law constant</td>
</tr>
<tr>
<td>Rydberg</td>
<td>Rydberg constant</td>
</tr>
<tr>
<td>m_e</td>
<td>electron mass</td>
</tr>
<tr>
<td>electron_mass</td>
<td>electron mass</td>
</tr>
<tr>
<td>m_p</td>
<td>proton mass</td>
</tr>
<tr>
<td>proton_mass</td>
<td>proton mass</td>
</tr>
<tr>
<td>m_n</td>
<td>neutron mass</td>
</tr>
<tr>
<td>neutron_mass</td>
<td>neutron mass</td>
</tr>
</tbody>
</table>

Constants database

In addition to the above variables, \texttt{scipy.constants} also contains the 2014 CODATA recommended values [Rc437f0a4090e-CODATA2014] database containing more physical constants.

<table>
<thead>
<tr>
<th>value(key)</th>
<th>Value in \texttt{physical_constants} indexed by key</th>
</tr>
</thead>
<tbody>
<tr>
<td>unit(key)</td>
<td>Unit in \texttt{physical_constants} indexed by key</td>
</tr>
<tr>
<td>precision(key)</td>
<td>Relative precision in \texttt{physical_constants} indexed by key</td>
</tr>
<tr>
<td>find([sub, disp])</td>
<td>Return list of \texttt{physical_constant} keys containing a given string.</td>
</tr>
</tbody>
</table>

Continued on next page
**Table 10 – continued from previous page**

<table>
<thead>
<tr>
<th><strong>ConstantWarning</strong></th>
<th>Accessing a constant no longer in current CODATA data set</th>
</tr>
</thead>
</table>

scipy.constants.value

```python
scipy.constants.value(key)
```

Value in physical_constants indexed by key

**Parameters**

- `key` [Python string or unicode] Key in dictionary `physical_constants`

**Returns**

- `value` [float] Value in `physical_constants` corresponding to `key`

**See also:**

codata

Contains the description of `physical_constants`, which, as a dictionary literal object, does not itself possess a docstring.

**Examples**

```python
>>> from scipy import constants
>>> constants.value(u'elementary charge')
1.6021766208e-19
```

scipy.constants.unit

```python
scipy.constants.unit(key)
```

Unit in physical_constants indexed by key

**Parameters**

- `key` [Python string or unicode] Key in dictionary `physical_constants`

**Returns**

- `unit` [Python string] Unit in `physical_constants` corresponding to `key`

**See also:**

codata

Contains the description of `physical_constants`, which, as a dictionary literal object, does not itself possess a docstring.

**Examples**

```python
>>> from scipy import constants
>>> constants.unit(u'proton mass')
'kg'
```

scipy.constants.precision

```python
scipy.constants.precision(key)
```

Relative precision in physical_constants indexed by key

**Parameters**

- `key` [Python string or unicode] Key in dictionary `physical_constants`

**Returns**
prec  [float] Relative precision in physical_constants corresponding to key

See also:

codata

Contains the description of physical_constants, which, as a dictionary literal object, does not itself possess a docstring.

Examples

```python
>>> from scipy import constants
>>> constants.precision('proton mass')
1.2555138746605121e-08
```

scipy.constants.find

scipy.constants.find(sub=None, disp=False)

Return list of physical_constant keys containing a given string.

Parameters

- `sub` [str, unicode] Sub-string to search keys for. By default, return all keys.
- `disp` [bool] If True, print the keys that are found, and return None. Otherwise, return the list of keys without printing anything.

Returns

- `keys` [list or None] If `disp` is False, the list of keys is returned. Otherwise, None is returned.

See also:

codata

Contains the description of physical_constants, which, as a dictionary literal object, does not itself possess a docstring.

Examples

```python
>>> from scipy.constants import find, physical_constants

Which keys in the physical_constants dictionary contain ‘boltzmann’?

```python
>>> find('boltzmann')
['Boltzmann constant',
 'Boltzmann constant in Hz/K',
 'Boltzmann constant in eV/K',
 'Boltzmann constant in inverse meters per kelvin',
 'Stefan-Boltzmann constant']
```

Get the constant called ‘Boltzmann constant in Hz/K’:

```python
>>> physical_constants['Boltzmann constant in Hz/K']
(20836612000.0, 'Hz K^-1', 12000.0)
```

Find constants with ‘radius’ in the key:

```python
>>> find('radius')
['Bohr radius',
 (continues on next page)
'classical electron radius',
'deuteron rms charge radius',
'proton rms charge radius']

```python
>>> physical_constants['classical electron radius']
(2.8179403227e-15, 'm', 1.9e-24)
```

**scipy.constants.ConstantWarning**

Exception `scipy.constants.ConstantWarning`

Accessing a constant no longer in current CODATA data set

**scipy.constants.physical_constants**

Dictionary of physical constants, of the format `physical_constants[name] = (value, unit, uncertainty)`.

Available constants:

<table>
<thead>
<tr>
<th>Constant</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>alpha particle mass</td>
<td>6.64465723e-27 kg</td>
</tr>
<tr>
<td>alpha particle mass energy equivalent</td>
<td>5.971920097e-10 J</td>
</tr>
<tr>
<td>alpha particle mass energy equivalent in MeV</td>
<td>372.379378 MeV</td>
</tr>
<tr>
<td>alpha particle mass in u</td>
<td>4.001506179127 u</td>
</tr>
<tr>
<td>alpha particle molar mass</td>
<td>0.004001506179127 kg mol⁻¹</td>
</tr>
<tr>
<td>alpha particle-electron mass ratio</td>
<td>7294.29954136</td>
</tr>
<tr>
<td>alpha particle-proton mass ratio</td>
<td>3.9725968907</td>
</tr>
<tr>
<td>Angstrom star</td>
<td>1.00001495e-10 m</td>
</tr>
<tr>
<td>atomic mass constant</td>
<td>1.66053904e-27 kg</td>
</tr>
<tr>
<td>atomic mass constant energy equivalent</td>
<td>1.492418062e-10 J</td>
</tr>
<tr>
<td>atomic mass constant energy equivalent in MeV</td>
<td>931.4940954 MeV</td>
</tr>
<tr>
<td>atomic mass unit-electron volt relationship</td>
<td>931494095.4 eV</td>
</tr>
<tr>
<td>atomic mass unit-hartree relationship</td>
<td>34231776.902 Eₜ</td>
</tr>
<tr>
<td>atomic mass unit-hertz relationship</td>
<td>2.253427206e+23 Hz</td>
</tr>
<tr>
<td>atomic mass unit-inverse meter relationship</td>
<td>751300661660000.0 m⁻¹</td>
</tr>
<tr>
<td>atomic mass unit-joule relationship</td>
<td>1.492418062e-10 J</td>
</tr>
<tr>
<td>atomic mass unit-kilogram relationship</td>
<td>10809543800000.0 K</td>
</tr>
<tr>
<td>atomic mass unit-kilogram relationship</td>
<td>1.66053904e+27 kg</td>
</tr>
<tr>
<td>atomic unit of 1st hyperpolarizability</td>
<td>3.206361329e-53 C⁻³ m⁻³ J⁻²</td>
</tr>
<tr>
<td>atomic unit of 2nd hyperpolarizability</td>
<td>6.235380085e-65 C⁻⁴ m⁻⁴ J⁻³</td>
</tr>
<tr>
<td>atomic unit of action</td>
<td>1.0545718e-34 J s</td>
</tr>
<tr>
<td>atomic unit of charge</td>
<td>1.6021766208e-19 C</td>
</tr>
<tr>
<td>atomic unit of charge density</td>
<td>1081202377000.0 C m⁻³</td>
</tr>
<tr>
<td>atomic unit of current</td>
<td>0.006623618183 A</td>
</tr>
<tr>
<td>atomic unit of electric dipole mom.</td>
<td>8.478353552e-30 C m</td>
</tr>
<tr>
<td>atomic unit of electric field</td>
<td>514220670700.0 V m⁻¹</td>
</tr>
<tr>
<td>atomic unit of electric field gradient</td>
<td>9.717362356e+21 V m⁻²</td>
</tr>
<tr>
<td>atomic unit of electric polarizability</td>
<td>1.648777237e+41 C⁻² m⁻² J⁻¹</td>
</tr>
<tr>
<td>atomic unit of electric potential</td>
<td>27.21138602 V</td>
</tr>
<tr>
<td>atomic unit of electric quadrupole mom.</td>
<td>4.486551484e-40 C m⁻²</td>
</tr>
<tr>
<td>atomic unit of energy</td>
<td>4.35974465e-18 J</td>
</tr>
<tr>
<td>atomic unit of force</td>
<td>8.23872336e-08 N</td>
</tr>
<tr>
<td>atomic unit of length</td>
<td>5.2917721067e+11 m</td>
</tr>
<tr>
<td>atomic unit of mag. dipole mom.</td>
<td>1.854801999e-23 J T⁻¹</td>
</tr>
<tr>
<td>atomic unit of mag. flux density</td>
<td>235061.755 T</td>
</tr>
</tbody>
</table>

Continue on next page
| **atomic unit of magnetizability** | 7.8910368886e-29 J T^-2 |
| **atomic unit of mass** | 9.10938356e-31 kg |
| **atomic unit of mom. um** | 1.992851882e-24 kg m s^-1 |
| **atomic unit of permittivity** | 1.11265065636183e-10 F m^-1 |
| **atomic unit of time** | 2.41884326509e-17 s |
| **atomic unit of velocity** | 2187691.26277 m s^-1 |
| **Avogadro constant** | 6.022140857e+23 mol^-1 |
| **Bohr magneton** | 9.274009994e-24 J T^-1 |
| **Bohr magneton in eV/T** | 5.7883818012e-05 eV T^-1 |
| **Bohr magneton in Hz/T** | 13996245042.0 Hz T^-1 |
| **Bohr magneton in inverse meters per tesla** | 46.6844814 m^-1 T^-1 |
| **Bohr magneton in K/T** | 0.6717405 K T^-1 |
| **Bohr radius** | 5.2917721067e-11 m |
| **Boltzmann constant** | 1.38064852e-23 J K^-1 |
| **Boltzmann constant in eV/K** | 8.6173303e-05 eV K^-1 |
| **Boltzmann constant in Hz/K** | 20836612000.0 Hz K^-1 |
| **Boltzmann constant in inverse meters per kelvin** | 69.503457 m^-1 K^-1 |
| **characteristic impedance of vacuum** | 376.73031346177066 ohm |
| **classical electron radius** | 2.8179403227e-15 m |
| **Compton wavelength** | 2.4263102367e-12 m |
| **Compton wavelength over 2 pi** | 3.8615926764e-13 m |
| **conductance quantum** | 7.74809173e-05 S |
| **conventional value of Josephson constant** | 483597900000000.0 Hz V^-1 |
| **conventional value of von Klitzing constant** | 25812.807 ohm |
| **Cu x unit** | 1.00207697e-13 m |
| **deuteron g factor** | 0.8574382311 |
| **deuteron mag. mom.** | 4.33073504e-27 J T^-1 |
| **deuteron mag. mom. to Bohr magneton ratio** | 0.000469754554 |
| **deuteron mag. mom. to nuclear magneton ratio** | 0.8574382311 |
| **deuteron mass** | 3.343583719e-27 kg |
| **deuteron mass energy equivalent** | 3.05063183e-10 J |
| **deuteron mass energy equivalent in MeV** | 1875.612928 MeV |
| **deuteron mass in u** | 2.01353212745 u |
| **deuteron molar mass** | 0.00201353212745 kg mol^-1 |
| **deuteron rms charge radius** | 2.1413e-15 m |
| **deuteron-electron mag. mom. ratio** | -0.0004664345535 |
| **deuteron-electron mass ratio** | 3670.48296785 |
| **deuteron-neutron mag. mom. ratio** | -0.44820652 |
| **deuteron-proton mag. mom. ratio** | 0.3070122077 |
| **deuteron-proton mass ratio** | 1.99900750087 |
| **electric constant** | 8.854187817620389e-12 F m^-1 |
| **electron charge to mass quotient** | -175882002400.0 C kg^-1 |
| **electron g factor** | -2.00231930436182 |
| **electron gyromag. ratio** | 17608596400.0 s^-1 T^-1 |
| **electron gyromag. ratio over 2 pi** | 28024.95164 MHz T^-1 |
| **electron mag. mom.** | -9.28476462e-24 J T^-1 |
| **electron mag. mom. anomaly** | 0.00115965218091 |
| **electron mag. mom. to Bohr magneton ratio** | -1.00115965218091 |
| **electron mag. mom. to nuclear magneton ratio** | -1838.28197234 |
| **electron mass** | 9.10938356e-31 kg |

Continued on next page
Table 11 – continued from previous page

<table>
<thead>
<tr>
<th>Description</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>electron mass energy equivalent</td>
<td>8.18710565e-14 J</td>
</tr>
<tr>
<td>electron mass energy equivalent in MeV</td>
<td>0.5109989461 MeV</td>
</tr>
<tr>
<td>electron mass in u</td>
<td>0.0005485799907 u</td>
</tr>
<tr>
<td>electron molar mass</td>
<td>5.485799907e-07 kg mol^-1</td>
</tr>
<tr>
<td>electron to alpha particle mass ratio</td>
<td>0.000137093554798</td>
</tr>
<tr>
<td>electron to shielded helion mag. mom. ratio</td>
<td>864.058257</td>
</tr>
<tr>
<td>electron to shielded proton mag. mom. ratio</td>
<td>-658.2275971</td>
</tr>
<tr>
<td>electron volt</td>
<td>1.6021766208e-19 J</td>
</tr>
<tr>
<td>electron volt-atomic mass unit relationship</td>
<td>1.0735441105e-09 u</td>
</tr>
<tr>
<td>electron volt-hartree relationship</td>
<td>0.03674932248 E_h</td>
</tr>
<tr>
<td>electron volt-inverse meter relationship</td>
<td>806554.4050 m^-1</td>
</tr>
<tr>
<td>electron volt-joule relationship</td>
<td>1.6021766208e-19 J</td>
</tr>
<tr>
<td>electron volt-kelvin relationship</td>
<td>11604.5221 K</td>
</tr>
<tr>
<td>electron volt-kilogram relationship</td>
<td>1.782661907e-36 kg</td>
</tr>
<tr>
<td>electron-deuteron mag. mom. ratio</td>
<td>-2143.92349</td>
</tr>
<tr>
<td>electron-deuteron mass ratio</td>
<td>0.00002724431704784</td>
</tr>
<tr>
<td>electron-helion mass ratio</td>
<td>0.0001819543074854</td>
</tr>
<tr>
<td>electron-muon mag. mom. ratio</td>
<td>206.766988</td>
</tr>
<tr>
<td>electron-muon mass ratio</td>
<td>0.0048363317</td>
</tr>
<tr>
<td>electron-neutron mag. mom. ratio</td>
<td>960.9205</td>
</tr>
<tr>
<td>electron-neutron mass ratio</td>
<td>0.00054386734428</td>
</tr>
<tr>
<td>electron-proton mag. mom. ratio</td>
<td>-658.2106866</td>
</tr>
<tr>
<td>electron-proton mass ratio</td>
<td>0.000544617021352</td>
</tr>
<tr>
<td>electron-tau mass ratio</td>
<td>0.000287592</td>
</tr>
<tr>
<td>electron-triton mass ratio</td>
<td>0.00018192000062203</td>
</tr>
<tr>
<td>elementary charge</td>
<td>1.6021766208e-19 C</td>
</tr>
<tr>
<td>elementary charge over h</td>
<td>241798926200000.0 A J^-1</td>
</tr>
<tr>
<td>Faraday constant</td>
<td>96485.33289 C mol^-1</td>
</tr>
<tr>
<td>Faraday constant for conventional electric current</td>
<td>96485.3251 C mol^-1</td>
</tr>
<tr>
<td>Fermi coupling constant</td>
<td>1.1663787e-05 GeV^-2</td>
</tr>
<tr>
<td>fine-structure constant</td>
<td>0.0072973525664</td>
</tr>
<tr>
<td>first radiation constant</td>
<td>3.74177179e-16 W m^-2</td>
</tr>
<tr>
<td>first radiation constant for spectral radiance</td>
<td>1.191042953e-16 W m^-2 sr^-1</td>
</tr>
<tr>
<td>Hartree energy</td>
<td>4.35974465e-18 J</td>
</tr>
<tr>
<td>Hartree energy in eV</td>
<td>27.21138602 eV</td>
</tr>
<tr>
<td>hartree-atomic mass unit relationship</td>
<td>2.9212623197e-08 u</td>
</tr>
<tr>
<td>hartree-electron volt relationship</td>
<td>27.21138602 eV</td>
</tr>
<tr>
<td>hartree-hertz relationship</td>
<td>657968392071000.0 Hz</td>
</tr>
<tr>
<td>hartree-inverse meter relationship</td>
<td>21947463.13702 m^-1</td>
</tr>
<tr>
<td>hartree-joule relationship</td>
<td>4.35974465e-18 J</td>
</tr>
<tr>
<td>hartree-kelvin relationship</td>
<td>315775.13 K</td>
</tr>
<tr>
<td>hartree-kilogram relationship</td>
<td>4.850870129e-35 kg</td>
</tr>
<tr>
<td>helion g factor</td>
<td>-4.255250616</td>
</tr>
<tr>
<td>helion mag. mom.</td>
<td>-1.074617522e-26 J T^-1</td>
</tr>
<tr>
<td>helion mag. mom. to Bohr magneton ratio</td>
<td>-0.001158740958</td>
</tr>
<tr>
<td>helion mag. mom. to nuclear magneton ratio</td>
<td>-2.127625308</td>
</tr>
<tr>
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<tr>
<td>Triton mass energy equivalent in MeV</td>
<td>$2808.92112$ MeV</td>
</tr>
<tr>
<td>Triton mass in u</td>
<td>$3.0155007162$ u</td>
</tr>
<tr>
<td>Triton molar mass</td>
<td>$0.00301550071632$ kg mol$^{-1}$</td>
</tr>
<tr>
<td>Triton-electron mass ratio</td>
<td>$5496.92153588$</td>
</tr>
<tr>
<td>Triton-proton mass ratio</td>
<td>$2.99371703348$</td>
</tr>
<tr>
<td>Unified atomic mass unit</td>
<td>$1.66053904e-27$ kg</td>
</tr>
<tr>
<td>Von Klitzing constant</td>
<td>$25812.8077729$ ohm</td>
</tr>
<tr>
<td>Weak mixing angle</td>
<td>$0.2223$</td>
</tr>
<tr>
<td>Wien frequency displacement law constant</td>
<td>$58789238000.0$ Hz K$^{-1}$</td>
</tr>
<tr>
<td>Wien wavelength displacement law constant</td>
<td>$0.0028977772$ m K</td>
</tr>
<tr>
<td>(220) lattice spacing of silicon</td>
<td>$1.920155714e-10$ m</td>
</tr>
</tbody>
</table>
6.4.3 Units

SI prefixes

<table>
<thead>
<tr>
<th>Prefix</th>
<th>Symbol</th>
<th>Exponent</th>
</tr>
</thead>
<tbody>
<tr>
<td>yotta</td>
<td>y</td>
<td>$10^{24}$</td>
</tr>
<tr>
<td>zetta</td>
<td>z</td>
<td>$10^{21}$</td>
</tr>
<tr>
<td>exa</td>
<td>E</td>
<td>$10^{18}$</td>
</tr>
<tr>
<td>peta</td>
<td>P</td>
<td>$10^{15}$</td>
</tr>
<tr>
<td>tera</td>
<td>T</td>
<td>$10^{12}$</td>
</tr>
<tr>
<td>giga</td>
<td>G</td>
<td>$10^9$</td>
</tr>
<tr>
<td>mega</td>
<td>M</td>
<td>$10^6$</td>
</tr>
<tr>
<td>kilo</td>
<td>k</td>
<td>$10^3$</td>
</tr>
<tr>
<td>hecto</td>
<td>h</td>
<td>$10^2$</td>
</tr>
<tr>
<td>deka</td>
<td>da</td>
<td>$10^1$</td>
</tr>
<tr>
<td>deci</td>
<td>d</td>
<td>$10^{-1}$</td>
</tr>
<tr>
<td>centi</td>
<td>c</td>
<td>$10^{-2}$</td>
</tr>
<tr>
<td>milli</td>
<td>m</td>
<td>$10^{-3}$</td>
</tr>
<tr>
<td>micro</td>
<td>u</td>
<td>$10^{-6}$</td>
</tr>
<tr>
<td>nano</td>
<td>n</td>
<td>$10^{-9}$</td>
</tr>
<tr>
<td>pico</td>
<td>p</td>
<td>$10^{-12}$</td>
</tr>
<tr>
<td>femto</td>
<td>f</td>
<td>$10^{-15}$</td>
</tr>
<tr>
<td>atto</td>
<td>a</td>
<td>$10^{-18}$</td>
</tr>
<tr>
<td>zepto</td>
<td>z</td>
<td>$10^{-21}$</td>
</tr>
</tbody>
</table>

Binary prefixes

<table>
<thead>
<tr>
<th>Prefix</th>
<th>Symbol</th>
<th>Exponent</th>
</tr>
</thead>
<tbody>
<tr>
<td>kibi</td>
<td>ki</td>
<td>$2^{10}$</td>
</tr>
<tr>
<td>mebi</td>
<td>mi</td>
<td>$2^{20}$</td>
</tr>
<tr>
<td>gibi</td>
<td>gi</td>
<td>$2^{30}$</td>
</tr>
<tr>
<td>tebi</td>
<td>te</td>
<td>$2^{40}$</td>
</tr>
<tr>
<td>pebi</td>
<td>pe</td>
<td>$2^{50}$</td>
</tr>
<tr>
<td>exbi</td>
<td>ex</td>
<td>$2^{60}$</td>
</tr>
<tr>
<td>zebi</td>
<td>ze</td>
<td>$2^{70}$</td>
</tr>
<tr>
<td>yobi</td>
<td>yo</td>
<td>$2^{80}$</td>
</tr>
</tbody>
</table>
### Mass

<table>
<thead>
<tr>
<th>Unit</th>
<th>Conversion</th>
</tr>
</thead>
<tbody>
<tr>
<td>gram</td>
<td>$10^{-3}$ kg</td>
</tr>
<tr>
<td>metric_ton</td>
<td>$10^3$ kg</td>
</tr>
<tr>
<td>grain</td>
<td>one grain in kg</td>
</tr>
<tr>
<td>lb</td>
<td>one pound (avoirdupois) in kg</td>
</tr>
<tr>
<td>pound</td>
<td>one pound (avoirdupois) in kg</td>
</tr>
<tr>
<td>blob</td>
<td>one inch version of a slug in kg</td>
</tr>
<tr>
<td>slinch</td>
<td>one inch version of a slug in kg</td>
</tr>
<tr>
<td>slug</td>
<td>one slug in kg (added in 1.0.0)</td>
</tr>
<tr>
<td>oz</td>
<td>one ounce in kg</td>
</tr>
<tr>
<td>ounce</td>
<td>one ounce in kg</td>
</tr>
<tr>
<td>stone</td>
<td>one stone in kg</td>
</tr>
<tr>
<td>grain</td>
<td>one grain in kg</td>
</tr>
<tr>
<td>long_ton</td>
<td>one long ton in kg</td>
</tr>
<tr>
<td>short_ton</td>
<td>one short ton in kg</td>
</tr>
<tr>
<td>troy_ounce</td>
<td>one Troy ounce in kg</td>
</tr>
<tr>
<td>troy_pound</td>
<td>one Troy pound in kg</td>
</tr>
<tr>
<td>carat</td>
<td>one carat in kg</td>
</tr>
<tr>
<td>m_u</td>
<td>atomic mass constant (in kg)</td>
</tr>
<tr>
<td>u</td>
<td>atomic mass constant (in kg)</td>
</tr>
<tr>
<td>atomic_mass</td>
<td>atomic mass constant (in kg)</td>
</tr>
</tbody>
</table>

### Angle

<table>
<thead>
<tr>
<th>Unit</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>degree</td>
<td>degree in radians</td>
</tr>
<tr>
<td>arcmin</td>
<td>arc minute in radians</td>
</tr>
<tr>
<td>arcminute</td>
<td>arc minute in radians</td>
</tr>
<tr>
<td>arcsec</td>
<td>arc second in radians</td>
</tr>
<tr>
<td>arcsecond</td>
<td>arc second in radians</td>
</tr>
</tbody>
</table>

### Time

<table>
<thead>
<tr>
<th>Unit</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>minute</td>
<td>one minute in seconds</td>
</tr>
<tr>
<td>hour</td>
<td>one hour in seconds</td>
</tr>
<tr>
<td>day</td>
<td>one day in seconds</td>
</tr>
<tr>
<td>week</td>
<td>one week in seconds</td>
</tr>
<tr>
<td>year</td>
<td>one year (365 days) in seconds</td>
</tr>
<tr>
<td>Julian_year</td>
<td>one Julian year (365.25 days) in seconds</td>
</tr>
</tbody>
</table>
### Length

<table>
<thead>
<tr>
<th>Unit</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>inch</td>
<td>one inch in meters</td>
</tr>
<tr>
<td>foot</td>
<td>one foot in meters</td>
</tr>
<tr>
<td>yard</td>
<td>one yard in meters</td>
</tr>
<tr>
<td>mile</td>
<td>one mile in meters</td>
</tr>
<tr>
<td>mil</td>
<td>one mil in meters</td>
</tr>
<tr>
<td>pt</td>
<td>one point in meters</td>
</tr>
<tr>
<td>point</td>
<td>one point in meters</td>
</tr>
<tr>
<td>survey_foot</td>
<td>one survey foot in meters</td>
</tr>
<tr>
<td>survey_mile</td>
<td>one survey mile in meters</td>
</tr>
<tr>
<td>nautical_mile</td>
<td>one nautical mile in meters</td>
</tr>
<tr>
<td>fermi</td>
<td>one Fermi in meters</td>
</tr>
<tr>
<td>angstrom</td>
<td>one Angstrom in meters</td>
</tr>
<tr>
<td>micron</td>
<td>one micron in meters</td>
</tr>
<tr>
<td>au</td>
<td>one astronomical unit in meters</td>
</tr>
<tr>
<td>astronomical_unit</td>
<td>one astronomical unit in meters</td>
</tr>
<tr>
<td>light_year</td>
<td>one light year in meters</td>
</tr>
<tr>
<td>parsec</td>
<td>one parsec in meters</td>
</tr>
</tbody>
</table>

### Pressure

<table>
<thead>
<tr>
<th>Unit</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>atm</td>
<td>standard atmosphere in pascals</td>
</tr>
<tr>
<td>atmosphere</td>
<td>standard atmosphere in pascals</td>
</tr>
<tr>
<td>bar</td>
<td>one bar in pascals</td>
</tr>
<tr>
<td>torr</td>
<td>one torr (mmHg) in pascals</td>
</tr>
<tr>
<td>mmHg</td>
<td>one torr (mmHg) in pascals</td>
</tr>
<tr>
<td>psi</td>
<td>one psi in pascals</td>
</tr>
</tbody>
</table>

### Area

<table>
<thead>
<tr>
<th>Unit</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>hectare</td>
<td>one hectare in square meters</td>
</tr>
<tr>
<td>acre</td>
<td>one acre in square meters</td>
</tr>
</tbody>
</table>

### Volume

<table>
<thead>
<tr>
<th>Unit</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>liter</td>
<td>one liter in cubic meters</td>
</tr>
<tr>
<td>litre</td>
<td>one liter in cubic meters</td>
</tr>
<tr>
<td>gallon</td>
<td>one gallon (US) in cubic meters</td>
</tr>
<tr>
<td>gallon_US</td>
<td>one gallon (US) in cubic meters</td>
</tr>
<tr>
<td>gallon_imp</td>
<td>one gallon (UK) in cubic meters</td>
</tr>
<tr>
<td>fluid_ounce</td>
<td>one fluid ounce (US) in cubic meters</td>
</tr>
<tr>
<td>fluid_ounce_US</td>
<td>one fluid ounce (US) in cubic meters</td>
</tr>
<tr>
<td>fluid_ounce_imp</td>
<td>one fluid ounce (UK) in cubic meters</td>
</tr>
<tr>
<td>bbl</td>
<td>one barrel in cubic meters</td>
</tr>
<tr>
<td>barrel</td>
<td>one barrel in cubic meters</td>
</tr>
</tbody>
</table>
**Speed**

<table>
<thead>
<tr>
<th>Unit</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>kmh</td>
<td>kilometers per hour in meters per second</td>
</tr>
<tr>
<td>mph</td>
<td>miles per hour in meters per second</td>
</tr>
<tr>
<td>mach</td>
<td>one Mach (approx., at 15 °C, 1 atm) in meters per second</td>
</tr>
<tr>
<td>speed_of_sound</td>
<td>one Mach (approx., at 15 °C, 1 atm) in meters per second</td>
</tr>
<tr>
<td>knot</td>
<td>one knot in meters per second</td>
</tr>
</tbody>
</table>

**Temperature**

<table>
<thead>
<tr>
<th>Unit</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>zero_Celsius</td>
<td>zero of Celsius scale in Kelvin</td>
</tr>
<tr>
<td>degree_Fahrenheit</td>
<td>one Fahrenheit (only differences) in Kelvins</td>
</tr>
</tbody>
</table>

```
convert_temperature(val, old_scale, new_scale) Convert from a temperature scale to another one among Celsius, Kelvin, Fahrenheit and Rankine scales.
```

```python
scipy.constants.convert_temperature
```

Convert from a temperature scale to another one among Celsius, Kelvin, Fahrenheit and Rankine scales.

**Parameters**

- **val** [array_like] Value(s) of the temperature(s) to be converted expressed in the original scale.
- **old_scale**: str Specifies as a string the original scale from which the temperature value(s) will be converted. Supported scales are Celsius (‘Celsius’, ‘celsius’, ‘C’ or ‘c’), Kelvin (‘Kelvin’, ‘kelvin’, ‘K’, ‘k’), Fahrenheit (‘Fahrenheit’, ‘fahrenheit’, ‘F’ or ‘f’) and Rankine (‘Rankine’, ‘rankine’, ‘R’, ‘r’).
- **new_scale**: str Specifies as a string the new scale to which the temperature value(s) will be converted. Supported scales are Celsius (‘Celsius’, ‘celsius’, ‘C’ or ‘c’), Kelvin (‘Kelvin’, ‘kelvin’, ‘K’, ‘k’), Fahrenheit (‘Fahrenheit’, ‘fahrenheit’, ‘F’ or ‘f’) and Rankine (‘Rankine’, ‘rankine’, ‘R’, ‘r’).

**Returns**

- **res** [float or array of floats] Value(s) of the converted temperature(s) expressed in the new scale.

**Notes**

New in version 0.18.0.

**Examples**

```python
>>> from scipy.constants import convert_temperature
>>> convert_temperature(np.array([-40, 40.0]), 'Celsius', 'Kelvin')
array([ 233.15, 313.15])
```
### Energy

<table>
<thead>
<tr>
<th>Unit</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>eV</td>
<td>one electron volt in Joules</td>
</tr>
<tr>
<td>electron_volt</td>
<td>one electron volt in Joules</td>
</tr>
<tr>
<td>calorie</td>
<td>one calorie (thermochemical) in Joules</td>
</tr>
<tr>
<td>calorie_th</td>
<td>one calorie (thermochemical) in Joules</td>
</tr>
<tr>
<td>calorie_IT</td>
<td>one calorie (International Steam Table calorie, 1956) in Joules</td>
</tr>
<tr>
<td>erg</td>
<td>one erg in Joules</td>
</tr>
<tr>
<td>Btu</td>
<td>one British thermal unit (International Steam Table) in Joules</td>
</tr>
<tr>
<td>Btu_IT</td>
<td>one British thermal unit (International Steam Table) in Joules</td>
</tr>
<tr>
<td>Btu_th</td>
<td>one British thermal unit (thermochemical) in Joules</td>
</tr>
<tr>
<td>ton_TNT</td>
<td>one ton of TNT in Joules</td>
</tr>
</tbody>
</table>

### Power

<table>
<thead>
<tr>
<th>Unit</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>hp</td>
<td>one horsepower in watts</td>
</tr>
<tr>
<td>horsepower</td>
<td>one horsepower in watts</td>
</tr>
</tbody>
</table>

### Force

<table>
<thead>
<tr>
<th>Unit</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dyn</td>
<td>one dyne in newtons</td>
</tr>
<tr>
<td>dyne</td>
<td>one dyne in newtons</td>
</tr>
<tr>
<td>lbf</td>
<td>one pound force in newtons</td>
</tr>
<tr>
<td>pound_force</td>
<td>one pound force in newtons</td>
</tr>
<tr>
<td>kgf</td>
<td>one kilogram force in newtons</td>
</tr>
<tr>
<td>kilogram_force</td>
<td>one kilogram force in newtons</td>
</tr>
</tbody>
</table>

### Optics

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>lambda2nu</td>
<td>Convert wavelength to optical frequency</td>
</tr>
<tr>
<td>nu2lambda</td>
<td>Convert optical frequency to wavelength.</td>
</tr>
</tbody>
</table>

#### scipy.constants.lambda2nu

Convert wavelength to optical frequency

**Parameters**

- `lambda_` [array_like] Wavelength(s) to be converted.

**Returns**

- `nu` [float or array of floats] Equivalent optical frequency.

**Notes**

Computes $\nu = \frac{c}{\lambda}$ where $c = 299792458.0$, i.e., the (vacuum) speed of light in meters/second.

**Examples**

```python
>>> from scipy.constants import lambda2nu, speed_of_light
>>> lambda2nu(np.array((1, speed_of_light)))
array([ 2.99792458e+08, 1.00000000e+00])
```
scipy.constants.nu2lambda

scipy.constants.nu2lambda(nu)

Convert optical frequency to wavelength.

**Parameters**

nu [array_like] Optical frequency to be converted.

**Returns**

lambda [float or array of floats] Equivalent wavelength(s).

**Notes**

Computes $\lambda = \frac{c}{\nu}$ where $c = 299792458.0$, i.e., the (vacuum) speed of light in meters/second.

**Examples**

```python
>>> from scipy.constants import nu2lambda, speed_of_light
>>> nu2lambda(np.array((1, speed_of_light)))
array([ 2.99792458e+08, 1.00000000e+00])
```

6.4.4 References

6.5 Discrete Fourier transforms (scipy.fftpack)

6.5.1 Fast Fourier Transforms (FFTs)

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>fft</code></td>
<td>Return discrete Fourier transform of real or complex sequence.</td>
</tr>
<tr>
<td><code>ifft</code></td>
<td>Return discrete inverse Fourier transform of real or complex sequence.</td>
</tr>
<tr>
<td><code>fft2</code></td>
<td>2-D discrete Fourier transform.</td>
</tr>
<tr>
<td><code>ifft2</code></td>
<td>2-D discrete inverse Fourier transform of real or complex sequence.</td>
</tr>
<tr>
<td><code>fftn</code></td>
<td>Return multidimensional discrete Fourier transform.</td>
</tr>
<tr>
<td><code>ifftn</code></td>
<td>Return inverse multi-dimensional discrete Fourier transform.</td>
</tr>
<tr>
<td><code>rfft</code></td>
<td>Discrete Fourier transform of a real sequence.</td>
</tr>
<tr>
<td><code>irfft</code></td>
<td>Return inverse discrete Fourier transform of real sequence x.</td>
</tr>
<tr>
<td><code>dct</code></td>
<td>Return the Discrete Cosine Transform of arbitrary type sequence x.</td>
</tr>
<tr>
<td><code>idct</code></td>
<td>Return the Inverse Discrete Cosine Transform of an arbitrary type sequence.</td>
</tr>
<tr>
<td><code>dctn</code></td>
<td>Return multidimensional Discrete Cosine Transform along the specified axes.</td>
</tr>
<tr>
<td><code>idctn</code></td>
<td>Return multidimensional Discrete Cosine Transform along the specified axes.</td>
</tr>
<tr>
<td><code>dst</code></td>
<td>Return the Discrete Sine Transform of arbitrary type sequence x.</td>
</tr>
<tr>
<td><code>idst</code></td>
<td>Return the Inverse Discrete Sine Transform of an arbitrary type sequence.</td>
</tr>
<tr>
<td><code>dstn</code></td>
<td>Return multidimensional Discrete Sine Transform along the specified axes.</td>
</tr>
</tbody>
</table>

Continued on next page
Table 14 – continued from previous page

idstn(x[, type, shape, axes, norm, overwrite_x]) Return multidimensional Discrete Sine Transform along the specified axes.

scipy.fftpack.fft

scipy.fftpack.fft(x, n=None, axis=-1, overwrite_x=False)

Return discrete Fourier transform of real or complex sequence.

The returned complex array contains $y(0)$, $y(1)$, ..., $y(n-1)$ where

$$y(j) = \left( x \ast \exp(-2\pi i sqrt(-1) \ast j \ast np.arange(n)/n) \right).\text{sum}().$$

Parameters

- **x** [array_like] Array to Fourier transform.
- **n** [int, optional] Length of the Fourier transform. If $n < x.shape[axis]$, $x$ is truncated. If $n > x.shape[axis]$, $x$ is zero-padded. The default results in $n = x.shape[axis]$.
- **axis** [int, optional] Axis along which the fft's are computed; the default is over the last axis (i.e., $axis=-1$).
- **overwrite_x** [bool, optional] If True, the contents of $x$ can be destroyed; the default is False.

Returns

- **z** [complex ndarray] with the elements:

  \[
  \begin{align*}
  [y(0), y(1), \ldots, y(n/2), y(-n/2), \ldots, y(-1)] & \text{ if } n \text{ is even} \\
  [y(0), y(1), \ldots, y((n-1)/2), y(-(n-1)/2), \ldots, y(-1)] & \text{ if } n \text{ is odd}
  \end{align*}
  \]

where:

\[
y(j) = \sum_{k=0}^{n-1} x[k] \ast \exp(-sqrt(-1) \ast j \ast k \ast 2 \pi/n), \quad j = 0..n-1
\]

See also:

- **ifft**
  - Inverse FFT
- **rfft**
  - FFT of a real sequence

Notes

The packing of the result is “standard”: If $A = \text{fft}(a, n)$, then $A[0]$ contains the zero-frequency term, $A[1:n/2]$ contains the positive-frequency terms, and $A[n/2:]$ contains the negative-frequency terms, in order of decreasingly negative frequency. So for an 8-point transform, the frequencies of the result are $[0, 1, 2, 3, -4, -3, -2, -1]$. To rearrange the fft output so that the zero-frequency component is centered, like $[-4, -3, -2, -1, 0, 1, 2, 3]$, use $fftshift$.

Both single and double precision routines are implemented. Half precision inputs will be converted to single precision. Non floating-point inputs will be converted to double precision. Long-double precision inputs are not supported.

This function is most efficient when $n$ is a power of two, and least efficient when $n$ is prime.

Note that if $x$ is real-valued then $A[j] = A[n-j].conjugate()$. If $x$ is real-valued and $n$ is even then $A[n/2]$ is real.
If the data type of $x$ is real, a “real FFT” algorithm is automatically used, which roughly halves the computation time. To increase efficiency a little further, use $rfft$, which does the same calculation, but only outputs half of the symmetrical spectrum. If the data is both real and symmetrical, the $dct$ can again double the efficiency, by generating half of the spectrum from half of the signal.

**Examples**

```python
>>> from scipy.fftpack import fft, ifft
>>> x = np.arange(5)
>>> np.allclose(fft(ifft(x)), x, atol=1e-15)  # within numerical accuracy.
True
```

**scipy.fftpack.ifft**

Return discrete inverse Fourier transform of real or complex sequence.

The returned complex array contains $y(0)$, $y(1)$, ..., $y(n-1)$ where

$$y(j) = (x \ast \exp(2\pi\sqrt{-1}\ast j/n)).\text{mean}().$$

**Parameters**

- **x**  
  [array_like] Transformed data to invert.

- **n**  
  [int, optional] Length of the inverse Fourier transform. If $n < x.shape[axis]$, $x$ is truncated. If $n > x.shape[axis]$, $x$ is zero-padded. The default results in $n = x.shape[axis]$.

- **axis**  
  [int, optional] Axis along which the ifft’s are computed; the default is over the last axis (i.e., $axis=-1$).

- **overwrite_x**  
  [bool, optional] If True, the contents of $x$ can be destroyed; the default is False.

**Returns**

- **ifft**  

**See also:**

- **fft**

  Forward FFT

**Notes**

Both single and double precision routines are implemented. Half precision inputs will be converted to single precision. Non floating-point inputs will be converted to double precision. Long-double precision inputs are not supported.

This function is most efficient when $n$ is a power of two, and least efficient when $n$ is prime.

If the data type of $x$ is real, a “real IFFT” algorithm is automatically used, which roughly halves the computation time.

**Examples**

```python
>>> from scipy.fftpack import fft, ifft
>>> import numpy as np
>>> x = np.arange(5)
>>> np.allclose(ifft(fft(x)), x, atol=1e-15)  # within numerical accuracy.
True
```
**scipy.fftpack.fft2**

`scipy.fftpack.fft2(x, shape=None, axes=(-2, -1), overwrite_x=False)`  
2-D discrete Fourier transform.  
Return the two-dimensional discrete Fourier transform of the 2-D argument `x`.  
See also:

`fftn`  
for detailed information.

**scipy.fftpack.ifft2**

`scipy.fftpack.ifft2(x, shape=None, axes=(-2, -1), overwrite_x=False)`  
2-D discrete inverse Fourier transform of real or complex sequence.  
Return inverse two-dimensional discrete Fourier transform of arbitrary type sequence `x`.  
See `ifft` for more information.  
See also:

`fft2`, `ifft`

**scipy.fftpack.fftn**

`scipy.fftpack.fftn(x, shape=None, axes=None, overwrite_x=False)`  
Return multidimensional discrete Fourier transform.  
The returned array contains:

\[
y[j_1, \ldots, j_d] = \sum_{k_1=0}^{n_1-1} \ldots \sum_{k_d=0}^{n_d-1} x[k_1, \ldots, k_d] \prod_{i=1}^{d} \exp(-\sqrt{-1} \cdot 2 \cdot \pi / n_i \cdot j_i \cdot k_i)
\]

where `d = len(x.shape)` and `n = x.shape`.  

**Parameters**

- `x`  
  [array_like] The (n-dimensional) array to transform.  
- `shape`  
  [int or array_like of ints or None, optional] The shape of the result. If both `shape` and `axes` (see below) are None, `shape` is `x.shape`; if `shape` is None but `axes` is not None, then `shape` is `scipy.take(x.shape, axes, axis=0)`. If `shape[i] > x.shape[i]`, the i-th dimension is padded with zeros. If `shape[i] < x.shape[i]`, the i-th dimension is truncated to length `shape[i]`. If any element of `shape` is -1, the size of the corresponding dimension of `x` is used.  
- `axes`  
  [int or array_like of ints or None, optional] The axes of `x` (y if `shape` is not None) along which the transform is applied. The default is over all axes.  
- `overwrite_x`  
  [bool, optional] If True, the contents of `x` can be destroyed. Default is False.  

**Returns**

- `y`  
  [complex-valued n-dimensional numpy array] The (n-dimensional) DFT of the input array.  

See also:

`fftn`
Notes
If \( x \) is real-valued, then \( y[\ldots, j_i, \ldots] = y[\ldots, n_i-j_i, \ldots].\text{conjugate()} \).

Both single and double precision routines are implemented. Half precision inputs will be converted to single precision. Non floating-point inputs will be converted to double precision. Long-double precision inputs are not supported.

Examples

```python
>>> from scipy.fftpack import fftn, ifftn
>>> y = (-np.arange(16), 8 - np.arange(16), np.arange(16))
>>> np.allclose(y, fftn(ifftn(y)))
True
```

scipy.fftpack.ifftn

scipy.fftpack.ifftn(x, shape=None, axes=None, overwrite_x=False)

Return inverse multi-dimensional discrete Fourier transform.

The sequence can be of an arbitrary type.

The returned array contains:

\[
y[j_1, \ldots, j_d] = \frac{1}{p} \sum_{k_1=0..n_1-1} \cdots \sum_{k_d=0..n_d-1} x[k_1, \ldots, k_d] \prod_{i=1..d} \exp\left(\frac{-1}{2} \cdot pi/n_i \cdot j_i \cdot k_i\right)
\]

where \( d = \text{len(x.shape)} \), \( n = \text{x.shape} \), and \( p = \prod_{i=1..d} n_i \).

For description of parameters see `fftn`.

See also:

`fftn`

for detailed information.

Examples

```python
>>> from scipy.fftpack import fftn, ifftn
>>> import numpy as np
>>> y = (-np.arange(16), 8 - np.arange(16), np.arange(16))
>>> np.allclose(y, ifftn(fftn(y)))
True
```

scipy.fftpack.rfft

scipy.fftpack.rfft(x, n=None, axis=-1, overwrite_x=False)

Discrete Fourier transform of a real sequence.

Parameters

- **x**: [array_like, real-valued] The data to transform.
- **n**: [int, optional] Defines the length of the Fourier transform. If \( n \) is not specified (the default) then \( n = x.shape[axis] \). If \( n < x.shape[axis] \), \( x \) is truncated, if \( n > x.shape[axis] \), \( x \) is zero-padded.
- **axis**: [int, optional] The axis along which the transform is applied. The default is the last axis.
- **overwrite_x**: [bool, optional] If set to true, the contents of \( x \) can be overwritten. Default is False.
**Returns**

\[ z \] [real ndarray] The returned real array contains:

\[
[y(0), \text{Re}(y(1)), \text{Im}(y(1)), \ldots, \text{Re}(y(n/2))] \quad \text{if } n \text{ is even}
\]

\[
[y(0), \text{Re}(y(1)), \text{Im}(y(1)), \ldots, \text{Re}(y(n/2)), \text{Im}(y(n/2))] \quad \text{if } n \text{ is odd}
\]

where:

\[
y(j) = \sum_{k=0}^{n-1} x[k] \cdot \exp(-\sqrt{-1} \cdot j \cdot k^2 \cdot \pi / n)
\]

\[
j = 0 \ldots n-1
\]

See also:

*fft*, *irfft*, *numpy.fft.rfft*

**Notes**

Within numerical accuracy, \( y == \text{rfft}(\text{irfft}(y)) \).

Both single and double precision routines are implemented. Half precision inputs will be converted to single precision. Non floating-point inputs will be converted to double precision. Long-double precision inputs are not supported.

To get an output with a complex datatype, consider using the related function *numpy.fft.rfft*.

**Examples**

```python
>>> from scipy.fftpack import fft, rfft
>>> a = [9, -9, 1, 3]
>>> fft(a)
array([ 4. +0.j, 8.+12.j, 16. +0.j, 8.-12.j])
>>> rfft(a)
array([ 4., 8., 12., 16.])
```

**scipy.fftpack.irfft**

*scipy.fftpack.irfft\(x, n=None, axis=-1, overwrite_x=False)\)*

Return inverse discrete Fourier transform of real sequence \(x\).

The contents of \(x\) are interpreted as the output of the *rfft* function.

**Parameters**

- **x** [array_like] Transformed data to invert.
- **n** [int, optional] Length of the inverse Fourier transform. If \(n < x\text{.shape}[axis]\), \(x\) is truncated. If \(n > x\text{.shape}[axis]\), \(x\) is zero-padded. The default results in \(n = x\text{.shape}[axis]\).
- **axis** [int, optional] Axis along which the ifft’s are computed; the default is over the last axis (i.e., axis=-1).
- **overwrite_x** [bool, optional] If True, the contents of \(x\) can be destroyed; the default is False.

**Returns**

- **irfft** [ndarray of floats] The inverse discrete Fourier transform.

See also:

*rfft, ifft, numpy.fft.irfft*
Notes
The returned real array contains:

\[ [y(0), y(1), \ldots, y(n-1)] \]

where for n is even:

\[
y(j) = \frac{1}{n} \left( \sum_{k=1}^{n/2-1} \left( x[2k-1] + \sqrt{-1} \cdot x[2k] \right) \right) * \exp(\sqrt{-1} \cdot j \cdot k \cdot 2 \cdot \pi / n) + c.c. + x[0] + (-1) ** (j) \cdot x[n-1]
\]

and for n is odd:

\[
y(j) = \frac{1}{n} \left( \sum_{k=1}^{(n-1)/2} \left( x[2k-1] + \sqrt{-1} \cdot x[2k] \right) \right) * \exp(\sqrt{-1} \cdot j \cdot k \cdot 2 \cdot \pi / n) + c.c. + x[0]
\]

c.c. denotes complex conjugate of preceding expression.

For details on input parameters, see \texttt{rfft}.

To process (conjugate-symmetric) frequency-domain data with a complex datatype, consider using the related function \texttt{numpy.fft.irfft}.

Examples

```python
>>> from scipy.fftpack import rfft, irfft
>>> a = [1.0, 2.0, 3.0, 4.0, 5.0]
>>> irfft(a)
array([ 2.6 , -3.16405192, 1.24398433, -1.14955713, 1.46962473])
>>> irfft(rfft(a))
array([1., 2., 3., 4., 5.])
```

\texttt{scipy.fftpack.dct}

\texttt{scipy.fftpack.dct}(\texttt{x}, \texttt{type=2}, \texttt{n=None}, \texttt{axis=-1}, \texttt{norm=None}, \texttt{overwrite_x=False})

Return the Discrete Cosine Transform of arbitrary type sequence \texttt{x}.

Parameters

- \texttt{x} [array_like] The input array.
- \texttt{type} [{1, 2, 3, 4}, optional] Type of the DCT (see Notes). Default type is 2.
- \texttt{n} [int, optional] Length of the transform. If \texttt{n < x.shape[axis]}, \texttt{x} is truncated. If \texttt{n > x.shape[axis]}, \texttt{x} is zero-padded. The default results in \texttt{n = x.shape[axis]}.
- \texttt{axis} [int, optional] Axis along which the dct is computed; the default is over the last axis (i.e., \texttt{axis}=-1).
- \texttt{norm} [{None, ‘ortho’}, optional] Normalization mode (see Notes). Default is None.
- \texttt{overwrite_x} [bool, optional] If True, the contents of \texttt{x} can be destroyed; the default is False.

Returns

- \texttt{y} [ndarray of real] The transformed input array.

See also:

- \texttt{idct}

Inverse DCT
Notes
For a single dimension array \( x \), \( \text{dct}(x, \text{norm}='\text{ortho}') \) is equal to MATLAB \( \text{dct}(x) \).

There are theoretically 8 types of the DCT, only the first 4 types are implemented in scipy. ‘The’ DCT generally refers to DCT type 2, and ‘the’ Inverse DCT generally refers to DCT type 3.

Type I
There are several definitions of the DCT-I; we use the following (for \( \text{norm} = \text{None} \)):

\[
y[k] = x[0] + (-1)^k x[N-1] + 2 \sum_{n=1}^{N-2} x[n] \cos(\pi k n / (N-1))
\]

If \( \text{norm} = '\text{ortho}' \), \( x[0] \) and \( x[N-1] \) are multiplied by a scaling factor of \( \sqrt{2} \), and \( y[k] \) is multiplied by a scaling factor \( f \):

\[
f = 0.5 \times \sqrt{1 / (N-1)} \text{ if } k = 0 \text{ or } N-1, \\
f = 0.5 \times \sqrt{2 / (N-1)} \text{ otherwise.}
\]

New in version 1.2.0: Orthonormalization in DCT-I.

Note: The DCT-I is only supported for input size > 1.

Type II
There are several definitions of the DCT-II; we use the following (for \( \text{norm} = \text{None} \)):

\[
y[k] = 2 \sum_{n=0}^{N-1} x[n] \cos(\pi k (2n+1) / (2N)), \quad 0 \leq k < N.
\]

If \( \text{norm} = '\text{ortho}' \), \( y[k] \) is multiplied by a scaling factor \( f \):

\[
f = \sqrt{1 / (4N)} \text{ if } k = 0, \\
f = \sqrt{1 / (2N)} \text{ otherwise.}
\]

Which makes the corresponding matrix of coefficients orthonormal \( (O^O' = I_d) \).

Type III
There are several definitions, we use the following (for \( \text{norm} = \text{None} \)):

\[
y[k] = x[0] + 2 \sum_{n=1}^{N-1} x[n] \cos(\pi (k+0.5) n / N), \quad 0 \leq k < N.
\]

or, for \( \text{norm} = '\text{ortho}' \) and \( 0 \leq k < N \):

\[
y[k] = x[0] / \sqrt{N} + \sqrt{2/N} \sum_{n=1}^{N-1} x[n] \cos(\pi (k+0.5) n / N)
\]

The (unnormalized) DCT-III is the inverse of the (unnormalized) DCT-II, up to a factor \( 2N \). The orthonormalized DCT-III is exactly the inverse of the orthonormalized DCT-II.

Type IV
There are several definitions of the DCT-IV; we use the following (for norm=None):

\[
N-1
y[k] = 2 * \sum_{n=0}^{N-1} x[n] \cos(\pi(2k+1)(2n+1)/(4N)), \quad 0 \leq k < N.
\]

If norm='ortho', \(y[k]\) is multiplied by a scaling factor \(f\):

\[
f = 0.5 \sqrt{2/N}
\]

New in version 1.2.0: Support for DCT-IV.

References
[1], [2]

Examples
The Type 1 DCT is equivalent to the FFT (though faster) for real, even-symmetrical inputs. The output is also real and even-symmetrical. Half of the FFT input is used to generate half of the FFT output:

```python
>>> from scipy.fftpack import fft, dct
>>> fft(np.array([4., 3., 5., 10., 5., 3.])).real
array([ 30., -8., 6., -2., 6., -8.])
>>> dct(np.array([4., 3., 5., 10.]), 1)
array([ 30., -8., 6., -2.])
```

**scipy.fftpack.idct**

\[
\text{scipy.fftpack.idct}(x, \text{type}=2, n=None, axis=-1, \text{norm}=\text{None}, \text{overwrite}_x=False)
\]

Return the Inverse Discrete Cosine Transform of an arbitrary type sequence.

**Parameters**

- **x** [array_like] The input array.
- **type** [{1, 2, 3, 4}, optional] Type of the DCT (see Notes). Default type is 2.
- **n** [int, optional] Length of the transform. If \(n < x.\text{shape}[\text{axis}]\), \(x\) is truncated. If \(n > x.\text{shape}[\text{axis}]\), \(x\) is zero-padded. The default results in \(n = x.\text{shape}[\text{axis}]\).
- **axis** [int, optional] Axis along which the idct is computed; the default is over the last axis (i.e., \(\text{axis}=-1\)).
- **norm** [{None, ‘ortho’}, optional] Normalization mode (see Notes). Default is None.
- **overwrite_x** [bool, optional] If True, the contents of \(x\) can be destroyed; the default is False.

**Returns**

- **idct** [ndarray of real] The transformed input array.

See also:

dct

Forward DCT

**Notes**

For a single dimension array \(x\), \text{idct}(x, \text{norm}='\text{ortho}') is equal to MATLAB \text{idct}(x).

‘The’ IDCT is the IDCT of type 2, which is the same as DCT of type 3.

IDCT of type 1 is the DCT of type 1, IDCT of type 2 is the DCT of type 3, and IDCT of type 3 is the DCT of type 2. IDCT of type 4 is the DCT of type 4. For the definition of these types, see \text{dct}.  

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Examples
The Type 1 DCT is equivalent to the DFT for real, even-symmetrical inputs. The output is also real and even-symmetrical. Half of the IFFT input is used to generate half of the IFFT output:

```python
>>> from scipy.fftpack import ifft, idct
>>> ifft(np.array([ 30., -8.,  6., -2.,  6., -8.])).real
array([ 4.,  3.,  5., 10.,  5.,  3.])
>>> idct(np.array([ 30., -8.,  6., -2.]), 1) / 6
array([ 4.,  3.,  5., 10.])
```

`scipy.fftpack.dctn`

`scipy.fftpack.dctn(x, type=2, shape=None, axes=None, norm=None, overwrite_x=False)`
Return multidimensional Discrete Cosine Transform along the specified axes.

Parameters
- `x` [array_like] The input array.
- `type` [{1, 2, 3, 4}, optional] Type of the DCT (see Notes). Default type is 2.
- `shape` [int or array_like of ints or None, optional] The shape of the result. If both `shape` and `axes` (see below) are None, `shape` is `x.shape`; if `shape` is None but `axes` is not None, then `shape` is `scipy.take(x.shape, axes, axis=0)`. If `shape[i] > x.shape[i]`, the i-th dimension is padded with zeros. If `shape[i] < x.shape[i]`, the i-th dimension is truncated to length `shape[i]`. If any element of `shape` is -1, the size of the corresponding dimension of `x` is used.
- `axes` [int or array_like of ints or None, optional] Axes along which the DCT is computed. The default is over all axes.
- `norm` [{None, ‘ortho’}, optional] Normalization mode (see Notes). Default is None.
- `overwrite_x` [bool, optional] If True, the contents of `x` can be destroyed; the default is False.

Returns
- `y` [ndarray of real] The transformed input array.

See also:
- `idctn`
  Inverse multidimensional DCT

Notes
For full details of the DCT types and normalization modes, as well as references, see `dct`.

Examples
```python
>>> from scipy.fftpack import dctn, idctn
>>> y = np.random.randn(16, 16)
>>> np.allclose(y, idctn(dctn(y, norm='ortho'), norm='ortho'))
True
```

`scipy.fftpack.idctn`

`scipy.fftpack.idctn(x, type=2, shape=None, axes=None, norm=None, overwrite_x=False)`
Return multidimensional Discrete Cosine Transform along the specified axes.

Parameters
- `x` [array_like] The input array.
type  [{1, 2, 3, 4}, optional] Type of the DCT (see Notes). Default type is 2.
shape [int or array_like of ints or None, optional] The shape of the result. If both shape and axes (see below) are None, shape is x.shape; if shape is None but axes is not None, then shape is scipy.take(x.shape, axes, axis=0). If shape[i] > x.shape[i], the i-th dimension is padded with zeros. If shape[i] < x.shape[i], the i-th dimension is truncated to length shape[i]. If any element of shape is -1, the size of the corresponding dimension of x is used.
axes [int or array_like of ints or None, optional] Axes along which the IDCT is computed. The default is over all axes.
norm [{None, ‘ortho’}, optional] Normalization mode (see Notes). Default is None.
overwrite_x [bool, optional] If True, the contents of x can be destroyed; the default is False.

Returns
y [ndarray of real] The transformed input array.

See also:
dctn multidimensional DCT

Notes
For full details of the IDCT types and normalization modes, as well as references, see idct.

Examples
>>> from scipy.fftpack import dctn, idctn
>>> y = np.random.randn(16, 16)
>>> np.allclose(y, idctn(dctn(y, norm='ortho'), norm='ortho'))
True

scipy.fftpack.dst

scipy.fftpack.dst(x, type=2, n=None, axis=-1, norm=None, overwrite_x=False)
Return the Discrete Sine Transform of arbitrary type sequence x.

Parameters
x [array_like] The input array.
type [{1, 2, 3, 4}, optional] Type of the DST (see Notes). Default type is 2.
n [int, optional] Length of the transform. If n < x.shape[axis], x is truncated. If n > x.shape[axis], x is zero-padded. The default results in n = x.shape[axis].
axis [int, optional] Axis along which the dst is computed; the default is over the last axis (i.e., axis=-1).
norm [{None, ‘ortho’}, optional] Normalization mode (see Notes). Default is None.
overwrite_x [bool, optional] If True, the contents of x can be destroyed; the default is False.

Returns
dst [ndarray of reals] The transformed input array.

See also:
idst

Inverse DST
Notes
For a single dimension array $x$.

There are theoretically 8 types of the DST for different combinations of even/odd boundary conditions and boundary offsets \[^1\], only the first 3 types are implemented in Scipy.

**Type I**

There are several definitions of the DST-I; we use the following for `norm=None`. DST-I assumes the input is odd around $n=-1$ and $n=N$.

$$y[k] = 2 \sum_{n=0}^{N-1} x[n] \sin\left(\pi \frac{(k+1)(n+1)}{N+1}\right)$$

Note that the DST-I is only supported for input size $> 1$ The (unnormalized) DST-I is its own inverse, up to a factor $2(N+1)$. The orthonormalized DST-I is exactly its own inverse.

**Type II**

There are several definitions of the DST-II; we use the following for `norm=None`. DST-II assumes the input is odd around $n=-1/2$ and $n=N-1/2$; the output is odd around $k=-1$ and even around $k=N-1$.

$$y[k] = 2 \sum_{n=0}^{N-1} x[n] \sin\left(\pi \frac{(k+1)(n+0.5)}{N}\right), \quad 0 < k < N.$$  

if `norm='ortho'`, $y[k]$ is multiplied by a scaling factor $f$

$$f = \sqrt{1/(4*N)} \text{ if } k == 0$$

$$f = \sqrt{1/(2*N)} \text{ otherwise.}$$

**Type III**

There are several definitions of the DST-III, we use the following (for `norm=None`). DST-III assumes the input is odd around $n=-1$ and even around $n=N-1$.

$$y[k] = x[N-1] * (-1)^k + 2 \sum_{n=0}^{N-2} x[n] \sin\left(\pi \frac{(k+0.5)(n+1)}{N}\right), \quad 0 < k < N.$$  

The (unnormalized) DST-III is the inverse of the (unnormalized) DST-II, up to a factor $2N$. The orthonormalized DST-III is exactly the inverse of the orthonormalized DST-II.

New in version 0.11.0.

**Type IV**

There are several definitions of the DST-IV, we use the following (for `norm=None`). DST-IV assumes the input is odd around $n=-0.5$ and even around $n=N-0.5$.

$$y[k] = 2 \sum_{n=0}^{N-1} x[n] \sin\left(\pi \frac{(k+0.5)(n+0.5)}{N}\right), \quad 0 < k < N.$$  

The (unnormalized) DST-IV is its own inverse, up to a factor $2N$. The orthonormalized DST-IV is exactly its own inverse.

New in version 1.2.0: Support for DST-IV.
scipy.fftpack.idst

scipy.fftpack.idst(x, type=2, n=None, axis=-1, norm=None, overwrite_x=False)

Return the Inverse Discrete Sine Transform of an arbitrary type sequence.

Parameters

- x: [array_like] The input array.
- type: [{1, 2, 3, 4}, optional] Type of the DST (see Notes). Default type is 2.
- n: [int, optional] Length of the transform. If n < x.shape[axis], x is truncated. If n > x.shape[axis], x is zero-padded. The default results in n = x.shape[axis].
- axis: [int, optional] Axis along which the idst is computed; the default is over the last axis (i.e., axis=-1).
- norm: [{None, ‘ortho’}, optional] Normalization mode (see Notes). Default is None.
- overwrite_x: [bool, optional] If True, the contents of x can be destroyed; the default is False.

Returns

idst: [ndarray of real] The transformed input array.

See also:

dst

Forward DST

Notes

‘The’ IDST is the IDST of type 2, which is the same as DST of type 3.

IDST of type 1 is the DST of type 1, IDST of type 2 is the DST of type 3, and IDST of type 3 is the DST of type 2. For the definition of these types, see dst.

New in version 0.11.0.

scipy.fftpack.dstn

scipy.fftpack.dstn(x, type=2, shape=None, axes=None, norm=None, overwrite_x=False)

Return multidimensional Discrete Sine Transform along the specified axes.

Parameters

- x: [array_like] The input array.
- type: [{1, 2, 3, 4}, optional] Type of the DCT (see Notes). Default type is 2.
- shape: [int or array_like of ints or None, optional] The shape of the result. If both shape and axes (see below) are None, shape is x.shape; if shape is None but axes is not None, then shape is scipy.take(x.shape, axes, axis=0). If shape[i] > x.shape[i], the i-th dimension is padded with zeros. If shape[i] < x.shape[i], the i-th dimension is truncated to length shape[i]. If any element of shape is -1, the size of the corresponding dimension of x is used.
- axes: [int or array_like of ints or None, optional] Axes along which the DCT is computed. The default is over all axes.
- norm: [{None, ‘ortho’}, optional] Normalization mode (see Notes). Default is None.
- overwrite_x: [bool, optional] If True, the contents of x can be destroyed; the default is False.

Returns

See also:

dst

Forward DST

Notes

‘The’ DST is the DST of type 2, which is the same as DCT of type 3.

DST of type 1 is the DCT of type 1, DST of type 2 is the DCT of type 3, and DST of type 3 is the DCT of type 2. For the definition of these types, see dst.

New in version 0.11.0.
y [ndarray of real] The transformed input array.

See also:

idstn

Inverse multidimensional DST

Notes

For full details of the DST types and normalization modes, as well as references, see dst.

Examples

```python
>>> from scipy.fftpack import dstn, idstn
>>> y = np.random.randn(16, 16)
>>> np.allclose(y, idstn(dstn(y, norm='ortho'), norm='ortho'))
True
```

scipy.fftpack.idstn

scipy.fftpack.idstn(x, type=2, shape=None, axes=None, norm=None, overwrite_x=False)

Return multidimensional Discrete Sine Transform along the specified axes.

Parameters

- **x** [array_like] The input array.
- **type** [{1, 2, 3, 4}, optional] Type of the DCT (see Notes). Default type is 2.
- **shape** [int or array_like of ints or None, optional] The shape of the result. If both `shape` and `axes` (see below) are None, `shape` is `x.shape`; if `shape` is None but `axes` is not None, then `shape` is `scipy.take(x.shape, axes, axis=0)`. If `shape[i] > x.shape[i]`, the i-th dimension is padded with zeros. If `shape[i] < x.shape[i]`, the i-th dimension is truncated to length `shape[i]`. If any element of `shape` is -1, the size of the corresponding dimension of `x` is used.
- **axes** [int or array_like of ints or None, optional] Axes along which the IDCT is computed. The default is over all axes.
- **norm** [{None, ‘ortho’}, optional] Normalization mode (see Notes). Default is None.
- **overwrite_x** [bool, optional] If True, the contents of `x` can be destroyed; the default is False.

Returns

- **y** [ndarray of real] The transformed input array.

See also:

dctn

multidimensional DST

Notes

For full details of the IDST types and normalization modes, as well as references, see idst.

Examples

```python
>>> from scipy.fftpack import dstn, idstn
>>> y = np.random.randn(16, 16)
>>> np.allclose(y, idstn(dstn(y, norm='ortho'), norm='ortho'))
True
```
### 6.5.2 Differential and pseudo-differential operators

- **diff(x[, order, period, _cache])**
  - Return k-th derivative (or integral) of a periodic sequence x.

- **tilbert(x[, h, period, _cache])**
  - Return h-Tilbert transform of a periodic sequence x.

- **itilbert(x[, h, period, _cache])**
  - Return inverse h-Tilbert transform of a periodic sequence x.

- **hilbert(x[, _cache])**
  - Return Hilbert transform of a periodic sequence x.

- **ihilbert(x)**
  - Return inverse Hilbert transform of a periodic sequence x.

- **cs_diff(x, a, b[, period, _cache])**
  - Return (a,b)-cosh/sinh pseudo-derivative of a periodic sequence.

- **sc_diff(x, a, b[, period, _cache])**
  - Return (a,b)-sinh/cosh pseudo-derivative of a periodic sequence x.

- **ss_diff(x, a, b[, period, _cache])**
  - Return (a,b)-sinh/sinh pseudo-derivative of a periodic sequence x.

- **cc_diff(x, a, b[, period, _cache])**
  - Return (a,b)-cosh/cosh pseudo-derivative of a periodic sequence.

- **shift(x, a[, period, _cache])**
  - Shift periodic sequence x by a: y(u) = x(u+a).

**scipy.fftpack.diff**

```python
scipy.fftpack.diff(x, order=1, period=None, _cache=())
```

Return k-th derivative (or integral) of a periodic sequence x.

If x_j and y_j are Fourier coefficients of periodic functions x and y, respectively, then:

\[
y_j = \text{pow}(\sqrt{-1} \cdot j \cdot 2 \cdot \pi / \text{period}, \text{order}) \cdot x_j
\]

\[
y_0 = 0 \text{ if order is not } 0.
\]

**Parameters**

- **x** [array_like] Input array.
- **order** [int, optional] The order of differentiation. Default order is 1. If order is negative, then integration is carried out under the assumption that \(x_0 = 0\).
- **period** [float, optional] The assumed period of the sequence. Default is \(2 \cdot \pi\).

**Notes**

If \(\sum(x, \text{axis}=0) = 0\) then \(\text{diff}(	ext{diff}(x, k), -k) = x\) (within numerical accuracy).

For odd order and even \(\text{len}(x)\), the Nyquist mode is taken zero.

**scipy.fftpack.tilbert**

```python
scipy.fftpack.tilbert(x, h, period=None, _cache=())
```

Return h-Tilbert transform of a periodic sequence x.

If x_j and y_j are Fourier coefficients of periodic functions x and y, respectively, then:

\[
y_j = \sqrt{-1} \cdot \text{coth}(j \cdot h \cdot 2 \cdot \pi / \text{period}) \cdot x_j
\]

\[
y_0 = 0
\]

**Parameters**

- **x** [array_like] The input array to transform.
**h** [float] Defines the parameter of the Tilbert transform.

**period** [float, optional] The assumed period of the sequence. Default period is 2*pi.

**Returns**

**tilbert** [ndarray] The result of the transform.

**Notes**

If \( \text{sum}(x, \text{axis}=0) = 0 \) and \( n = \text{len}(x) \) is odd then \( \text{tilbert}(\text{itilbert}(x)) = x \).

If \( 2 \cdot \pi \cdot h / \text{period} \) is approximately 10 or larger, then numerically \( \text{tilbert} = \text{hilbert} \) (theoretically oo-Tilbert == Hilbert).

For even \( \text{len}(x) \), the Nyquist mode of \( x \) is taken zero.

### scipy.fftpack.itilbert

**scipy.fftpack.itilbert**

**scipy.fftpack.itilbert**\( (x, h, \text{period}=\text{None}, \_\text{cache}={} \)\)

Return inverse h-Tilbert transform of a periodic sequence \( x \).

If \( x_j \) and \( y_j \) are Fourier coefficients of periodic functions \( x \) and \( y \), respectively, then:

\[
\begin{align*}
y_j &= -\sqrt{-1} \cdot \tanh(j \cdot h \cdot 2 \cdot \pi / \text{period}) \cdot x_j \\
y_0 &= 0
\end{align*}
\]

For more details, see **tilbert**.

### scipy.fftpack.hilbert

**scipy.fftpack.hilbert**

**scipy.fftpack.hilbert**\( (x, \_\text{cache}=\{ \)\)

Return Hilbert transform of a periodic sequence \( x \).

If \( x_j \) and \( y_j \) are Fourier coefficients of periodic functions \( x \) and \( y \), respectively, then:

\[
\begin{align*}
y_j &= \sqrt{-1} \cdot \text{sign}(j) \cdot x_j \\
y_0 &= 0
\end{align*}
\]

**Parameters**

\( x \) [array_like] The input array, should be periodic.

\( \_\text{cache} \) [dict, optional] Dictionary that contains the kernel used to do a convolution with.

**Returns**

\( y \) [ndarray] The transformed input.

**See also:**

**scipy.signal.hilbert**

Compute the analytic signal, using the Hilbert transform.

**Notes**

If \( \text{sum}(x, \text{axis}=0) = 0 \) then \( \text{hilbert}(\text{ihilbert}(x)) = x \).

For even \( \text{len}(x) \), the Nyquist mode of \( x \) is taken zero.

The sign of the returned transform does not have a factor -1 that is more often than not found in the definition of the Hilbert transform. Note also that **scipy.signal.hilbert** does have an extra -1 factor compared to this function.
scipy.fftpack.ihilbert

scipy.fftpack.ihilbert(x)
Return inverse Hilbert transform of a periodic sequence x.

If \( x_j \) and \( y_j \) are Fourier coefficients of periodic functions \( x \) and \( y \), respectively, then:

\[
\begin{align*}
y_j &= -\sqrt{-1} \cdot \text{sign}(j) \cdot x_j \\
y_0 &= 0
\end{align*}
\]

scipy.fftpack.cs_diff

scipy.fftpack.cs_diff(x, a, b, period=None, _cache={})
Return \((a,b)\)-cosh/sinh pseudo-derivative of a periodic sequence.

If \( x_j \) and \( y_j \) are Fourier coefficients of periodic functions \( x \) and \( y \), respectively, then:

\[
\begin{align*}
y_j &= -\sqrt{-1} \cdot \cosh(j \cdot a \cdot 2 \cdot \pi / \text{period}) / \sinh(j \cdot b \cdot 2 \cdot \pi / \text{period}) \cdot x_j \\
y_0 &= 0
\end{align*}
\]

Parameters

- \( x \) [array_like]: The array to take the pseudo-derivative from.
- \( a, b \) [float]: Defines the parameters of the cosh/sinh pseudo-differential operator.
- \( \text{period} \) [float, optional]: The period of the sequence. Default period is 2\(*\pi\).

Returns

- \( \text{cs_diff} \) [ndarray]: Pseudo-derivative of periodic sequence \( x \).

Notes

For even len(\( x \)), the Nyquist mode of \( x \) is taken as zero.

scipy.fftpack.sc_diff

scipy.fftpack.sc_diff(x, a, b, period=None, _cache={})
Return \((a,b)\)-sinh/cosh pseudo-derivative of a periodic sequence \( x \).

If \( x_j \) and \( y_j \) are Fourier coefficients of periodic functions \( x \) and \( y \), respectively, then:

\[
\begin{align*}
y_j &= \sqrt{-1} \cdot \sinh(j \cdot a \cdot 2 \cdot \pi / \text{period}) / \cosh(j \cdot b \cdot 2 \cdot \pi / \text{period}) \cdot x_j \\
y_0 &= 0
\end{align*}
\]

Parameters

- \( x \) [array_like]: Input array.
- \( a, b \) [float]: Defines the parameters of the sinh/cosh pseudo-differential operator.
- \( \text{period} \) [float, optional]: The period of the sequence \( x \). Default is 2\(*\pi\).

Notes

\( \text{sc_diff}(\text{cs_diff}(x,a,b),b,a) == x \) For even len(\( x \)), the Nyquist mode of \( x \) is taken as zero.

scipy.fftpack.ss_diff

scipy.fftpack.ss_diff(x, a, b, period=None, _cache={})
Return \((a,b)\)-sinh/sinh pseudo-derivative of a periodic sequence \( x \).

If \( x_j \) and \( y_j \) are Fourier coefficients of periodic functions \( x \) and \( y \), respectively, then:

\[
\begin{align*}
y_j &= \sqrt{-1} \cdot \sinh(j \cdot a \cdot 2 \cdot \pi / \text{period}) / \cosh(j \cdot b \cdot 2 \cdot \pi / \text{period}) \cdot x_j \\
y_0 &= 0
\end{align*}
\]

Parameters

- \( x \) [array_like]: Input array.
- \( a, b \) [float]: Defines the parameters of the sinh/cosh pseudo-differential operator.
- \( \text{period} \) [float, optional]: The period of the sequence \( x \). Default is 2\(*\pi\).

Notes

\( \text{sc_diff}(\text{cs_diff}(x,a,b),b,a) == x \) For even len(\( x \)), the Nyquist mode of \( x \) is taken as zero.
\[ y_j = \frac{\sinh(ja \cdot 2\pi/\text{period})}{\sinh(jb \cdot 2\pi/\text{period})} \cdot x_j \]
\[ y_0 = \frac{a}{b} \cdot x_0 \]

**Parameters**
- **x** [array_like] The array to take the pseudo-derivative from.
- **a, b** Defines the parameters of the sinh/sinh pseudo-differential operator.
- **period** [float, optional] The period of the sequence x. Default is 2*\(\pi\).

**Notes**
`ss_diff(ss_diff(x, a, b), b, a) == x`

`scipy.fftpack.cc_diff`

`scipy.fftpack.cc_diff(x, a, b, period=None, _cache={})`

Return (a,b)-cosh/cosh pseudo-derivative of a periodic sequence.

If \(x_j\) and \(y_j\) are Fourier coefficients of periodic functions \(x\) and \(y\), respectively, then:

\[ y_j = \frac{\cosh(ja \cdot 2\pi/\text{period})}{\cosh(jb \cdot 2\pi/\text{period})} \cdot x_j \]

**Parameters**
- **x** [array_like] The array to take the pseudo-derivative from.
- **a, b** [float] Defines the parameters of the sinh/sinh pseudo-differential operator.
- **period** [float, optional] The period of the sequence x. Default is 2*\(\pi\).

**Returns**
- **cc_diff** [ndarray] Pseudo-derivative of periodic sequence \(x\).

**Notes**
`cc_diff(cc_diff(x, a, b), b, a) == x`

`scipy.fftpack.shift`

`scipy.fftpack.shift(x, a, period=None, _cache={})`

Shift periodic sequence \(x\) by \(a\): \(y(u) = x(u+a)\).

If \(x_j\) and \(y_j\) are Fourier coefficients of periodic functions \(x\) and \(y\), respectively, then:

\[ y_j = \exp(j \cdot a \cdot 2\pi/\text{period} \cdot \sqrt{-1}) \cdot x_f \]

**Parameters**
- **x** [array_like] The array to take the pseudo-derivative from.
- **a** [float] Defines the parameters of the sinh/sinh pseudo-differential operator.
- **period** [float, optional] The period of the sequences \(x\) and \(y\). Default period is 2*\(\pi\).

### 6.5.3 Helper functions

- **fftshift(x, axes)** Shift the zero-frequency component to the center of the spectrum.

- **ifftshift(x, axes)** The inverse of `fftshift`.

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<th>Description</th>
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<td><code>fftfreq(n[, d])</code></td>
<td>Return the Discrete Fourier Transform sample frequencies.</td>
</tr>
<tr>
<td><code>rfftfreq(n[, d])</code></td>
<td>DFT sample frequencies (for usage with rfft, irfft).</td>
</tr>
<tr>
<td><code>next_fast_len(target)</code></td>
<td>Find the next fast size of input data to <code>fft</code>, for zero-padding, etc.</td>
</tr>
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</table>

**scipy.fftpack.fftshift**

`scipy.fftpack.fftshift(x, axes=None)`  
Shift the zero-frequency component to the center of the spectrum.  

This function swaps half-spaces for all axes listed (defaults to all). Note that `y[0]` is the Nyquist component only if `len(x)` is even.  

**Parameters**

- `x` : array_like  
  Input array.
- `axes` : int or shape tuple, optional  
  Axes over which to shift. Default is None, which shifts all axes.

**Returns**

- `y` : ndarray  
  The shifted array.

**See also:**

`ifftshift`  
The inverse of `fftshift`.

**Examples**

```python
>>> freqs = np.fft.fftfreq(10, 0.1)
>>> freqs
array([ 0., 1., 2., 3., 4., -5., -4., -3., -2., -1.])
```

```python
>>> np.fft.fftshift(freqs)
array([-5., -4., -3., -2., -1.,  0.,  1.,  2.,  3.,  4.])
```

Shift the zero-frequency component only along the second axis:

```python
>>> freqs = np.fft.fftfreq(9, d=1./9).reshape(3, 3)
>>> freqs
array([[ 0.,  1.,  2.],
       [ 3.,  4., -4.],
       [-3., -2., -1.]])
```

```python
>>> np.fft.fftshift(freqs, axes=(1,))
array([[ 2.,  0.,  1.],
       [-4.,  3.,  4.],
       [-1., -3., -2.]])
```

**scipy.fftpack.ifftshift**

`scipy.fftpack.ifftshift(x, axes=None)`  
The inverse of `fftshift`. Although identical for even-length `x`, the functions differ by one sample for odd-length `x`.

**Parameters**
SciPy Reference Guide, Release 1.2.0

x [array_like] Input array.
axes [int or shape tuple, optional] Axes over which to calculate. Defaults to None, which shifts all axes.

Returns
y [ndarray] The shifted array.

See also:
fftshift
Shift zero-frequency component to the center of the spectrum.

Examples

```python
>>> freqs = np.fft.fftfreq(9, d=1./9).reshape(3, 3)
>>> freqs
array(
    [[ 0.,  1.,  2.],
     [ 3.,  4., -4.],
     [-3., -2., -1.]]
)
>>> np.fft.ifftshift(np.fft.fftshift(freqs))
array(
    [[ 0.,  1.,  2.],
     [ 3.,  4., -4.],
     [-3., -2., -1.]]
)
```

scipy.fftpack.fftshift

scipy.fftpack.fftshift(n, d=1.0)
Return the Discrete Fourier Transform sample frequencies.

The returned float array `f` contains the frequency bin centers in cycles per unit of the sample spacing (with zero at the start). For instance, if the sample spacing is in seconds, then the frequency unit is cycles/second.

Given a window length `n` and a sample spacing `d`:

```python
f = [0, 1, ..., n/2-1, -n/2, ..., -1] / (d*n) if n is even
f = [0, 1, ..., (n-1)/2, -(n-1)/2, ..., -1] / (d*n) if n is odd
```

Parameters

n [int] Window length.
d [scalar, optional] Sample spacing (inverse of the sampling rate). Defaults to 1.

Returns

f [ndarray] Array of length `n` containing the sample frequencies.

Examples

```python
>>> signal = np.array([-2, 8, 6, 4, 1, 0, 3, 5], dtype=float)
>>> fourier = np.fft.fft(signal)
>>> n = signal.size
>>> timestep = 0.1
>>> freq = np.fft.fftfreq(n, d=timestep)
>>> freq
array([ 0. ,  1.25,  2.5 ,  3.75, -5. , -3.75, -2.5 , -1.25])
```
scipy.fftpack.rfftfreq

scipy.fftpack.rfftfreq(n, d=1.0)

DFT sample frequencies (for usage with rfft, irfft).

The returned float array contains the frequency bins in cycles/unit (with zero at the start) given a
window length \( n \) and a sample spacing \( d \):

\[
f = \left[ 0, 1, 1, 2, 2, \ldots, \frac{n}{2} - 1, \frac{n}{2} - 1, \frac{n}{2} \right] / (d \times n) \quad \text{if } n \text{ is even}
f = \left[ 0, 1, 1, 2, 2, \ldots, \frac{n}{2} - 1, \frac{n}{2} - 1, \frac{n}{2}, \frac{n}{2} \right] / (d \times n) \quad \text{if } n \text{ is odd}
\]

Parameters

- **n** [int] Window length.
- **d** [scalar, optional] Sample spacing. Default is 1.

Returns

- **out** [ndarray] The array of length \( n \), containing the sample frequencies.

Examples

```python
>>> from scipy import fftpack
>>> sig = np.array([-2, 8, 6, 4, 1, 0, 3, 5], dtype=float)
>>> sig_fft = fftpack.rfft(sig)
>>> n = sig_fft.size
>>> timestep = 0.1
>>> freq = fftpack.rfftfreq(n, d=timestep)
>>> freq
array([ 0. , 1.25, 1.25, 2.5 , 2.5 , 3.75, 3.75, 5. ])
```

scipy.fftpack.next_fast_len

scipy.fftpack.next_fast_len(target)

Find the next fast size of input data to \texttt{fft}, for zero-padding, etc.

SciPy’s FFTPACK has efficient functions for radix \{2, 3, 4, 5\}, so this returns the next composite
of the prime factors 2, 3, and 5 which is greater than or equal to \texttt{target}. (These are also known as
5-smooth numbers, regular numbers, or Hamming numbers.)

Parameters

- **target** [int] Length to start searching from. Must be a positive integer.

Returns

- **out** [int] The first 5-smooth number greater than or equal to \texttt{target}.

Notes

New in version 0.18.0.

Examples

On a particular machine, an FFT of prime length takes 133 ms:

```python
>>> from scipy import fftpack
>>> min_len = 10007  # prime length is worst case for speed
>>> a = np.random.randn(min_len)
>>> b = fftpack.fft(a)
```

Zero-padding to the next 5-smooth length reduces computation time to 211 us, a speedup of 630 times:
>>> from scipy import fftpack
>>> b = fftpack.fft(a, 10125)
Rounding up to the next power of 2 is not optimal, taking 367 us to compute, 1.7 times as long as the 5-smooth size:

>>> b = fftpack.fft(a, 16384)
Note that fftshift, ifftshift and fftfreq are numpy functions exposed by fftpack; importing them from numpy should be preferred.

6.5.4 Convolutions (scipy.fftpack.convolve)

```python
scipy.fftpack.convolve.convolve
scipy.fftpack.convolve.convolve(x, omega[, swap_real_imag, overwrite_x]) = <fortran object>
Wrapper for convolve.

Parameters
x [input rank-1 array('d') with bounds (n)]
omega [input rank-1 array('d') with bounds (n)]

Returns
y [rank-1 array('d') with bounds (n) and x storage]

Other Parameters
overwrite_x [input int, optional] Default: 0
swap_real_imag [input int, optional] Default: 0
```

```python
scipy.fftpack.convolve.convolve_z
scipy.fftpack.convolve.convolve_z(x, omega_real, omega_imag[, overwrite_x]) = <fortran object>
Wrapper for convolve_z.

Parameters
x [input rank-1 array('d') with bounds (n)]
omega_real [input rank-1 array('d') with bounds (n)]
omega_imag [input rank-1 array('d') with bounds (n)]

Returns
y [rank-1 array('d') with bounds (n) and x storage]
```

6.5. Discrete Fourier transforms (scipy.fftpack)
Other Parameters

overwrite_x
  [input int, optional] Default: 0

scipy.fftpack.convolve.init_convolution_kernel

scipy.fftpack.convolve.init_convolution_kernel(n, kernel_func[, d, zero_nyquist, kernel_func_extra_args]) = <fortran object>

Wrapper for init_convolution_kernel.

Parameters

n     [input int]
kernel_func
  [call-back function]

Returns

omega  [rank-1 array('d') with bounds (n)]

Other Parameters

d  [input int, optional] Default: 0
kernel_func_extra_args
  [input tuple, optional] Default: ()
zero_nyquist
  [input int, optional] Default: d%2

Notes
Call-back functions:

def kernel_func(k): return kernel_func
Required arguments:
  k  : input int
Return objects:
  kernel_func : float

scipy.fftpack.convolve.destroy_convolve_cache

scipy.fftpack.convolve.destroy_convolve_cache = <fortran object>
Wrapper for destroy_convolve_cache.

6.6 Integration and ODEs (scipy.integrate)

6.6.1 Integrating functions, given function object

quad(func, a, b[, args, full_output, ...])  Compute a definite integral.
dblquad(func, a, b, gfun, hfun[, args, ...])  Compute a double integral.
tplquad(func, a, b, gfun, hfun, qfun, rfun)  Compute a triple (definite) integral.
nquad(func, ranges[, args, opts, full_output])  Integration over multiple variables.
fixed_quad(func, a, b[, args, n])  Compute a definite integral using fixed-order Gaussian quadrature.
quadtrature(func, a, b[, args, tol, rtol, ...])  Compute a definite integral using fixed-tolerance Gaussian quadrature.

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<td>romberg</td>
<td>Romberg integration of a callable function or method.</td>
</tr>
<tr>
<td>quad_explain</td>
<td>Print extra information about integrate.quad() parameters and returns.</td>
</tr>
<tr>
<td>newton_cotes</td>
<td>Return weights and error coefficient for Newton-Cotes integration.</td>
</tr>
<tr>
<td>IntegrationWarning</td>
<td>Warning on issues during integration.</td>
</tr>
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</table>

**scipy.integrate.quad**

scipy.integrate.quad(func, a, b, args=(), full_output=0, epsabs=1.49e-08, epsrel=1.49e-08, limit=50, points=None, weight=None, wvar=None, wopts=None, maxp1=50, limlst=50)

Compute a definite integral.

Integrate func from a to b (possibly infinite interval) using a technique from the Fortran library QUADPACK.

**Parameters**

- **func** [{function, scipy.LowLevelCallable}] A Python function or method to integrate. If func takes many arguments, it is integrated along the axis corresponding to the first argument.
- **a** [float] Lower limit of integration (use -numpy.inf for -infinity).
- **b** [float] Upper limit of integration (use numpy.inf for +infinity).
- **args** [tuple, optional] Extra arguments to pass to func.
- **full_output** [int, optional] Non-zero to return a dictionary of integration information. If non-zero, warning messages are also suppressed and the message is appended to the output tuple.
- **epsabs** [float or int, optional] Absolute error tolerance.
- **epsrel** [float or int, optional] Relative error tolerance.

**Returns**

- **y** [float] The integral of func from a to b.
- **abserr** [float] An estimate of the absolute error in the result.
- **infodict** [dict] A dictionary containing additional information. Run scipy.integrate.quad_explain() for more information.
- **message** A convergence message.
- **explain** Appended only with ‘cos’ or ‘sin’ weighting and infinite integration limits, it contains an explanation of the codes in infodict[‘ierlst’]

**Other Parameters**

- **epsabs** [float or int, optional] Absolute error tolerance.
- **epsrel** [float or int, optional] Relative error tolerance.
limit [float or int, optional] An upper bound on the number of subintervals used in the adaptive algorithm.

points [(sequence of floats, ints), optional] A sequence of break points in the bounded integration interval where local difficulties of the integrand may occur (e.g., singularities, discontinuities). The sequence does not have to be sorted.

weight [float or int, optional] String indicating weighting function. Full explanation for this and the remaining arguments can be found below.

wvar [optional] Variables for use with weighting functions.

wopts [optional] Optional input for reusing Chebyshev moments.

maxp1 [float or int, optional] An upper bound on the number of Chebyshev moments.

limlst [int, optional] Upper bound on the number of cycles (>=3) for use with a sinusoidal weighting and an infinite end-point.

See also:

dblquad double integral
tplquad triple integral
nquad n-dimensional integrals (uses quad recursively)

fixed_quad fixed-order Gaussian quadrature

quadrature adaptive Gaussian quadrature

odeint ODE integrator
ode ODE integrator

simps integrator for sampled data

romb integrator for sampled data

scipy.special for coefficients and roots of orthogonal polynomials

Notes
Extra information for quad() inputs and outputs

If full_output is non-zero, then the third output argument (infodict) is a dictionary with entries as tabulated below. For infinite limits, the range is transformed to (0,1) and the optional outputs are given with respect to this transformed range. Let M be the input argument limit and let K be infodict['last']. The entries are:

‘neval’
The number of function evaluations.
'last'

The number, K, of subintervals produced in the subdivision process.

'alist'

A rank-1 array of length M, the first K elements of which are the left end points of the subintervals in the partition of the integration range.

'blist'

A rank-1 array of length M, the first K elements of which are the right end points of the subintervals.

'rlist'

A rank-1 array of length M, the first K elements of which are the integral approximations on the subintervals.

'elist'

A rank-1 array of length M, the first K elements of which are the moduli of the absolute error estimates on the subintervals.

'iord'

A rank-1 integer array of length M, the first L elements of which are pointers to the error estimates over the subintervals with L = K if K <= M/2 + 2 or L = M + 1 - K otherwise. Let I be the sequence infodict['iord'] and let E be the sequence infodict['elist']. Then E[I[1]], ..., E[I[L]] forms a decreasing sequence.

If the input argument points is provided (i.e. it is not None), the following additional outputs are placed in the output dictionary. Assume the points sequence is of length P.

'pts'

A rank-1 array of length P + 2 containing the integration limits and the break points of the intervals in ascending order. This is an array giving the subintervals over which integration will occur.

'level'

A rank-1 integer array of length M (=limit), containing the subdivision levels of the subintervals, i.e., if (aa, bb) is a subinterval of (pts[1], pts[2]) where pts[0] and pts[2] are adjacent elements of infodict['pts'], then (aa, bb) has level l if |bb - aa| = |pts[2] - pts[1]| * 2**(-l).

'ndin'

A rank-1 integer array of length P + 2. After the first integration over the intervals (pts[1], pts[2]), the error estimates over some of the intervals may have been increased artificially in order to put their subdivision forward. This array has ones in slots corresponding to the subintervals for which this happens.

Weighting the integrand

The input variables, weight and wvar, are used to weight the integrand by a select list of functions. Different integration methods are used to compute the integral with these weighting functions. The possible values of weight and the corresponding weighting functions are.
wvar holds the parameter w, (alpha, beta), or c depending on the weight selected. In these expressions, a and b are the integration limits.

For the ‘cos’ and ‘sin’ weighting, additional inputs and outputs are available.

For finite integration limits, the integration is performed using a Clenshaw-Curtis method which uses Chebyshev moments. For repeated calculations, these moments are saved in the output dictionary:

‘momcom’

The maximum level of Chebyshev moments that have been computed, i.e., if M_c is infodict['momcom'] then the moments have been computed for intervals of length |b-a| * 2**(-1), l=0,1,...,M_c.

‘nnlog’

A rank-1 integer array of length M (=limit), containing the subdivision levels of the subintervals, i.e., an element of this array is equal to l if the corresponding subinterval is |b-a| * 2**(-l).

‘chebmo’

A rank-2 array of shape (25, maxp1) containing the computed Chebyshev moments. These can be passed on to an integration over the same interval by passing this array as the second element of the sequence wopts and passing infodict['momcom'] as the first element.

If one of the integration limits is infinite, then a Fourier integral is computed (assuming w neq 0). If full_output is 1 and a numerical error is encountered, besides the error message attached to the output tuple, a dictionary is also appended to the output tuple which translates the error codes in the array info['ierlst'] to English messages. The output information dictionary contains the following entries instead of ‘last’, ‘alist’, ‘blist’, ‘rlist’, and ‘elist’:

‘lst’

The number of subintervals needed for the integration (call it K_f).

‘rslist’

A rank-1 array of length M_f=limlst, whose first K_f elements contain the integral contribution over the interval (a+(k-1)c, a+kc) where c = (2*floor(|w|) + 1) * pi / |w| and k=1,2,...,K_f.

‘erlst’

A rank-1 array of length M_f containing the error estimate corresponding to the interval in the same position in infodict['rslist'].

‘ierlst’

A rank-1 integer array of length M_f containing an error flag corresponding to the interval in the same position in infodict['rslist']. See the explanation dictionary (last entry in the output tuple) for the meaning of the codes.

<table>
<thead>
<tr>
<th>weight</th>
<th>Weight function used</th>
<th>wvar</th>
</tr>
</thead>
<tbody>
<tr>
<td>'cos'</td>
<td>cos(w*x)</td>
<td>wvar = w</td>
</tr>
<tr>
<td>'sin'</td>
<td>sin(w*x)</td>
<td>wvar = w</td>
</tr>
<tr>
<td>'alg'</td>
<td>g(x) = ((x-a)**alpha)*((b-x)**beta)</td>
<td>wvar = (alpha, beta)</td>
</tr>
<tr>
<td>'alg-loga'</td>
<td>g(x)*log(x-a)</td>
<td>wvar = (alpha, beta)</td>
</tr>
<tr>
<td>'alg-logb'</td>
<td>g(x)*log(b-x)</td>
<td>wvar = (alpha, beta)</td>
</tr>
<tr>
<td>'alg-log'</td>
<td>g(x)*log(x-a)*log(b-x)</td>
<td>wvar = (alpha, beta)</td>
</tr>
<tr>
<td>'cauchy'</td>
<td>1/(x-c)</td>
<td>wvar = c</td>
</tr>
</tbody>
</table>

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Examples

Calculate \( \int_0^4 x^2 \, dx \) and compare with an analytic result

```python
>>> from scipy import integrate
>>> x2 = lambda x: x**2
>>> integrate.quad(x2, 0, 4)
(21.333333333333332, 2.3684757858670003e-13)
```

Print \( 4^3 / 3. \) # analytic result

21.3333333333

Calculate \( \int e^{-x} \, dx \)

```python
>>> invexp = lambda x: np.exp(-x)
>>> integrate.quad(invexp, 0, np.inf)
(1.0, 5.842605999138044e-11)
```

Calculate \( \int_1^0 x^2 + y^2 \, dx \) with ctypes, holding \( y \) parameter as 1:

```python
testlib.c =>
    double func(int n, double args[n]){
        return args[0]*args[0] + args[1]*args[1];}
compile to library testlib.*
```

```python
from scipy import integrate
import ctypes
lib = ctypes.CDLL('/home/.../testlib.*') # use absolute path
lib.func.restype = ctypes.c_double
lib.func.argtypes = (ctypes.c_int, ctypes.c_double)
integrate.quad(lib.func,0,1,())
#1.3333333333333333, 1.4802973661668752e-14
print((1.0**3/3.0 + 1.0) - (0.0**3/3.0 + 0.0)) #Analytic result
  #1.3333333333333333
```

Be aware that pulse shapes and other sharp features as compared to the size of the integration interval may not be integrated correctly using this method. A simplified example of this limitation is integrating a y-axis reflected step function with many zero values within the integrals bounds.

```python
>>> y = lambda x: 1 if x<=0 else 0
>>> integrate.quad(y, -1, 1)
(1.0, 1.1102230246251565e-14)
>>> integrate.quad(y, -1, 100)
(1.00000000002199108, 1.0189464580163188e-08)
>>> integrate.quad(y, -1, 10000)
(0.0, 0.0)
```
scipy.integrate.dblquad

Compute a double integral.

Return the double (definite) integral of \( \text{func}(y, x) \) from \( x = a \) to \( b \) and \( y = gfun(x) \) to \( hfun(x) \).

**Parameters**

- **func** [callable] A Python function or method of at least two variables: \( y \) must be the first argument and \( x \) the second argument.
- **a, b** [float] The limits of integration in \( x \): \( a < b \)
- **gfun** [callable or float] The lower boundary curve in \( y \) which is a function taking a single floating point argument \( (x) \) and returning a floating point result or a float indicating a constant boundary curve.
- **hfun** [callable or float] The upper boundary curve in \( y \) (same requirements as \( gfun \)).
- **args** [sequence, optional] Extra arguments to pass to \( \text{func} \).
- **epsabs** [float, optional] Absolute tolerance passed directly to the inner 1-D quadrature integration. Default is \( 1.49 \times 10^{-8} \).
- **epsrel** [float, optional] Relative tolerance of the inner 1-D integrals. Default is \( 1.49 \times 10^{-8} \).

**Returns**

- **y** [float] The resultant integral.
- **abserr** [float] An estimate of the error.

See also:

- quad
  - single integral
- tplquad
  - triple integral
- nquad
  - \( N \)-dimensional integrals
- fixed_quad
  - fixed-order Gaussian quadrature
- quadtrature
  - adaptive Gaussian quadrature
- odeint
  - ODE integrator
- ode
  - ODE integrator
- simps
  - integrator for sampled data
- romb
  - integrator for sampled data
- scipy.special
  - for coefficients and roots of orthogonal polynomials
Examples
Compute the double integral of $x \cdot y^2$ over the box $x$ ranging from 0 to 2 and $y$ ranging from 0 to 1.

```python
>>> from scipy import integrate
>>> f = lambda y, x: x * y**2
>>> integrate.dblquad(f, 0, 2, lambda x: 0, lambda x: 1)
(0.6666666666666667, 7.401486830834377e-15)
```

`scipy.integrate.tplquad`

`scipy.integrate.tplquad(func, a, b, gfun, hfun, qfun, rfun, args=(), epsabs=1.49e-08, epsrel=1.49e-08)`

Compute a triple (definite) integral.

Return the triple integral of $\text{func}(z, y, x)$ from $x = a..b$, $y = \text{gfun}(x)..\text{hfun}(x)$, and $z = \text{qfun}(x,y)..\text{rfun}(x,y)$.

**Parameters**

- **func** [function] A Python function or method of at least three variables in the order $(z, y, x)$.
- **a, b** [float] The limits of integration in $x$: $a < b$
- **gfun** [function or float] The lower boundary curve in $y$ which is a function taking a single floating point argument ($x$) and returning a floating point result or a float indicating a constant boundary curve.
- **hfun** [function or float] The upper boundary curve in $y$ (same requirements as gfun).
- **qfun** [function or float] The lower boundary surface in $z$. It must be a function that takes two floats in the order $(x, y)$ and returns a float or a float indicating a constant boundary surface.
- **rfun** [function or float] The upper boundary surface in $z$. (Same requirements as qfun.)
- **args** [tuple, optional] Extra arguments to pass to func.
- **epsabs** [float, optional] Absolute tolerance passed directly to the innermost 1-D quadrature integration. Default is 1.49e-8.
- **epsrel** [float, optional] Relative tolerance of the innermost 1-D integrals. Default is 1.49e-8.

**Returns**

- **y** [float] The resultant integral.
- **abserr** [float] An estimate of the error.

See also:

- `quad`
  Adaptive quadrature using QUADPACK
- `quadrature`
  Adaptive Gaussian quadrature
- `fixed_quad`
  Fixed-order Gaussian quadrature
- `dblquad`
  Double integrals
**nquad**
N-dimensional integrals

**romb**
Integrators for sampled data

**simps**
Integrators for sampled data

**ode**
ODE integrators

**odeint**
ODE integrators

**scipy.special**
For coefficients and roots of orthogonal polynomials

**Examples**
Compute the triple integral of \(x \times y \times z\), over \(x\) ranging from 1 to 2, \(y\) ranging from 2 to 3, \(z\) ranging from 0 to 1.

```python
>>> from scipy import integrate
>>> f = lambda z, y, x: x * y * z
>>> integrate.tplquad(f, 1, 2, lambda x: 2, lambda x: 3,
... lambda x, y: 0, lambda x, y: 1)
(1.8750000000000002, 3.324644794257407e-14)
```

**scipy.integrate.nquad**

scipy.integrate.nquad(func, ranges, args=None, opts=None, full_output=False)
Integration over multiple variables.

Wraps quad to enable integration over multiple variables. Various options allow improved integration of discontinuous functions, as well as the use of weighted integration, and generally finer control of the integration process.

**Parameters**

**func**
[(callable, scipy.LowLevelCallable)] The function to be integrated. Has arguments of \(x_0, \ldots, x_n, t_0, t_m\), where integration is carried out over \(x_0, \ldots, x_n\), which must be floats. Function signature should be \(\text{func}(x_0, x_1, \ldots, x_n, t_0, t_1, \ldots, t_m)\). Integration is carried out in order. That is, integration over \(x_0\) is the innermost integral, and \(x_n\) is the outermost.
If the user desires improved integration performance, then \(f\) may be a scipy.LowLevelCallable with one of the signatures:

- `double func(int n, double *xx)`
- `double func(int n, double *xx, void *user_data)`

where \(n\) is the number of extra parameters and \(args\) is an array of doubles of the additional parameters, the \(xx\) array contains the coordinates. The user_data is the data contained in the scipy.LowLevelCallable.

**ranges**
[iterable object] Each element of ranges may be either a sequence of 2 numbers, or else a callable that returns such a sequence. ranges[0] corresponds to integration over \(x_0\), and so on. If an element of ranges is a callable, then it will be called with
all of the integration arguments available, as well as any parametric arguments. e.g. if
func = f(x0, x1, x2, t0, t1), then ranges[0] may be defined as either
(a, b) or else as (a, b) = range0(x1, x2, t0, t1).

args [iterable object, optional] Additional arguments t0, ..., tn, required by func,
ranges, and opts.

opts [iterable object or dict, optional] Options to be passed to quad. May be empty, a
dict, or a sequence of dicts or functions that return a dict. If empty, the default
options from scipy.integrate.quad are used. If a dict, the same options are used for
all levels of integration. If a sequence, then each element of the sequence corresponds
to a particular integration. e.g. opts[0] corresponds to integration over x0, and
so on. If a callable, the signature must be the same as for ranges. The available
options together with their default values are:
• epsabs = 1.49e-08
• epsrel = 1.49e-08
• limit = 50
• points = None
• weight = None
• wvar = None
• wopts = None
For more information on these options, see quad and quad_explain.

full_output [bool, optional] Partial implementation of full_output from scipy.integrate.quad.
The number of integrand function evaluations neval can be obtained by setting
full_output=True when calling nquad.

Returns

result [float] The result of the integration.

abserr [float] The maximum of the estimates of the absolute error in the various integration
results.

out_dict [dict, optional] A dict containing additional information on the integration.

See also:

quad

1-dimensional numerical integration

dblquad, tplquad

fixed_quad

fixed-order Gaussian quadrature

quadrature

adaptive Gaussian quadrature

Examples

>>> from scipy import integrate
>>> func = lambda x0,x1,x2,x3 : x0**2 + x1*x2 - x3**3 + np.sin(x0) + (1 if (x0-.2*x3-.5-.25*x1>0) else 0)
>>> points = [[lambda x1,x2,x3 : 0.2*x3 + 0.5 + 0.25*x1], [], [], []]
>>> def opts0(*args, **kwargs):
...     return {'points':[0.2*args[2] + 0.5 + 0.25*args[0]]}
>>> integrate.nquad(func, [[0,1], [-1,1], [.13,.8], [-.15,1]],
... opt=[opts0(),{},{},{}], full_output=True)
(1.5267454070738633, 2.9437360001402324e-14, {'neval': 388962})
>>> scale = .1
>>> def func2(x0, x1, x2, x3, t0, t1):
...     return x0*x1*x3**2 + np.sin(x2) + 1 + (1 if x0+t1*x1-t0>0 else 0)
>>> def lim0(x1, x2, x3, t0, t1):
...     return [scale * (x1**2 + x2 + np.cos(x3)*t0*t1 + 1) - 1,
...             scale * (x1**2 + x2 + np.cos(x3)*t0*t1 + 1) + 1]
>>> def lim1(x2, x3, t0, t1):
...     return [scale * (x0*x2 + t1*x3) - 1,
...             scale * (x0*x2 + t1*x3) + 1]
>>> def lim2(x3, t0, t1):
...     return [scale * (x3 + t0**2*t1**3) - 1,
...             scale * (x3 + t0**2*t1**3) + 1]
>>> def lim3(t0, t1):
...     return [scale * (t0+t1) - 1, scale * (t0+t1) + 1]
>>> def opts0(x1, x2, x3, t0, t1):
...     return {'points' : [t0 - t1*x1]}
>>> def opts1(x2, x3, t0, t1):
...     return {}
>>> def opts2(x3, t0, t1):
...     return {}
>>> def opts3(t0, t1):
...     return {}
>>> integrate.nquad(func2, [lim0, lim1, lim2, lim3], args=(0,0),
...                   opts=[opts0, opts1, opts2, opts3])
(25.066666666666666, 2.7829590483937256e-13)

scipy.integrate.fixed_quad

scipy.integrate.fixed_quad(func, a, b, args=(), n=5)

Compute a definite integral using fixed-order Gaussian quadrature.

Integrate func from a to b using Gaussian quadrature of order n.

Parameters

func [callable] A Python function or method to integrate (must accept vector inputs).
If integrating a vector-valued function, the returned array must have shape (...,
len(x)).

a [float] Lower limit of integration.
b [float] Upper limit of integration.
args [tuple, optional] Extra arguments to pass to function, if any.
n [int, optional] Order of quadrature integration. Default is 5.

Returns

val [float] Gaussian quadrature approximation to the integral
none [None] Statically returned value of None

See also:

quad
    adaptive quadrature using QUADPACK
dblquad
    double integrals
tplquad
 triple integrals

romberg
 adaptive Romberg quadrature

quadrature
 adaptive Gaussian quadrature

romb
 integrators for sampled data

simps
 integrators for sampled data

cumtrapz
 cumulative integration for sampled data

ode
 ODE integrator

odeint
 ODE integrator

Examples

```python
>>> from scipy import integrate
>>> f = lambda x: x**8
>>> integrate.fixed_quad(f, 0.0, 1.0, n=4)
(0.1110884353741496, None)
>>> integrate.fixed_quad(f, 0.0, 1.0, n=5)
(0.11111111111111102, None)
>>> print(1/9.0)  # analytical result
0.1111111111111111
```

```python
>>> integrate.fixed_quad(np.cos, 0.0, np.pi/2, n=4)
(0.9999999771971152, None)
>>> integrate.fixed_quad(np.cos, 0.0, np.pi/2, n=5)
(1.000000000303107, None)
>>> np.sin(np.pi/2)-np.sin(0)  # analytical result
1.0
```

scipy.integrate.quadrature

```python
scipy.integrate.quadrature(func, a, b, args=(), tol=1.49e-08, rtol=1.49e-08, maxiter=50, vec_func=True, miniter=1)
```

Compute a definite integral using fixed-tolerance Gaussian quadrature.

Integrate `func` from `a` to `b` using Gaussian quadrature with absolute tolerance `tol`.

**Parameters**

- **func** [function] A Python function or method to integrate.
- **a** [float] Lower limit of integration.
- **b** [float] Upper limit of integration.
args  [tuple, optional] Extra arguments to pass to function.
tol, rtol [float, optional] Iteration stops when error between last two iterates is less than tol OR the relative change is less than rtol.
maxiter [int, optional] Maximum order of Gaussian quadrature.
vec_func [bool, optional] True or False if func handles arrays as arguments (is a “vector” function). Default is True.

Returns
val [float] Gaussian quadrature approximation (within tolerance) to integral.
err [float] Difference between last two estimates of the integral.

See also:
romberg
adaptive Romberg quadrature
fixed_quad
fixed-order Gaussian quadrature
quad
adaptive quadrature using QUADPACK
dblquad
double integrals
tplquad
triple integrals
romb
integrator for sampled data
simps
integrator for sampled data
cumtrapz
cumulative integration for sampled data
ode
ODE integrator
odeint
ODE integrator

Examples
>>> from scipy import integrate
>>> f = lambda x: x**8
>>> integrate.quadrature(f, 0.0, 1.0)
(0.11111111111111106, 4.163336342344337e-17)
>>> print(1/9.0)  # analytical result
0.1111111111111111
```python
>>> integrate.quadrature(np.cos, 0.0, np.pi/2)
(0.9999999999999536, 3.9611425250996035e-11)
```

```python
>>> np.sin(np.pi/2)-np.sin(0)  # analytical result
1.0
```

**scipy.integrate.romberg**

```python
scipy.integrate.romberg(function, a, b, args=(), tol=1.48e-08, rtol=1.48e-08, show=False, divmax=10, vec_func=False)
```

Romberg integration of a callable function or method.

Returns the integral of `function` (a function of one variable) over the interval `(a, b)`.

If `show` is 1, the triangular array of the intermediate results will be printed. If `vec_func` is True (default is False), then `function` is assumed to support vector arguments.

**Parameters**

- `function` [callable] Function to be integrated.
- `a` [float] Lower limit of integration.
- `b` [float] Upper limit of integration.

**Returns**

- `results` [float] Result of the integration.

**Other Parameters**

- `args` [tuple, optional] Extra arguments to pass to function. Each element of `args` will be passed as a single argument to `func`. Default is to pass no extra arguments.
- `tol`, `rtol` [float, optional] The desired absolute and relative tolerances. Defaults are 1.48e-8.
- `show` [bool, optional] Whether to print the results. Default is False.
- `vec_func` [bool, optional] Whether `func` handles arrays as arguments (i.e whether it is a “vector” function). Default is False.

**See also:**

- `fixed_quad`
  Fixed-order Gaussian quadrature.
- `quad`
  Adaptive quadrature using QUADPACK.
- `dblquad`
  Double integrals.
- `tplquad`
  Triple integrals.
- `romb`
  Integrators for sampled data.
- `simps`
  Integrators for sampled data.
cumtrapz
Cumulative integration for sampled data.

ode
ODE integrator.

odeint
ODE integrator.

References
[1]

Examples
Integrate a gaussian from 0 to 1 and compare to the error function.

```python
>>> from scipy import integrate
>>> from scipy.special import erf
>>> gaussian = lambda x: 1/np.sqrt(np.pi) * np.exp(-x**2)
>>> result = integrate.romberg(gaussian, 0, 1, show=True)
Romberg integration of <function vfunc at ...> from [0, 1]

<table>
<thead>
<tr>
<th>Steps</th>
<th>StepSize</th>
<th>Results</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1.000000</td>
<td>0.385872</td>
</tr>
<tr>
<td>2</td>
<td>0.500000</td>
<td>0.412631</td>
</tr>
<tr>
<td>4</td>
<td>0.250000</td>
<td>0.421368</td>
</tr>
<tr>
<td>8</td>
<td>0.125000</td>
<td>0.421352</td>
</tr>
<tr>
<td>16</td>
<td>0.062500</td>
<td>0.421350</td>
</tr>
<tr>
<td>32</td>
<td>0.031250</td>
<td>0.421350</td>
</tr>
</tbody>
</table>

The final result is 0.421350396475 after 33 function evaluations.

```python
>>> print("%g %g" % (2*result, erf(1)))
0.842701 0.842701
```

scipy.integrate.quad_explain
scipy.integrate.quad_explain(output=<_io.TextIOWrapper encoding='ANSI_X3.4-1968'>)

Print extra information about integrate.quad() parameters and returns.

Parameters

**output** [instance with “write” method, optional] Information about quad is passed to output.write(). Default is sys.stdout.

Returns

None

scipy.integrate.newton_cotes
scipy.integrate.newton_cotes(rn, equal=0)

Return weights and error coefficient for Newton-Cotes integration.

Suppose we have (N+1) samples of f at the positions x_0, x_1, ..., x_N. Then an N-point Newton-Cotes formula for the integral between x_0 and x_N is:

\[
\int_{x_0}^{x_N} f(x)dx = \Delta x \sum_{i=0}^{N} a_i f(x_i) + B_N(\Delta x)^{N+2} f^{N+1}(\xi)
\]
where $\xi \in [x_0, x_N]$ and $\Delta x = \frac{x_N - x_0}{N}$ is the average samples spacing.

If the samples are equally-spaced and N is even, then the error term is $B_N(\Delta x)^{N+3}f^{N+2}(\xi)$.

**Parameters**

- `rn` [int] The integer order for equally-spaced data or the relative positions of the samples with the first sample at 0 and the last at N, where $N+1$ is the length of `rn`. N is the order of the Newton-Cotes integration.
- `equal` [int, optional] Set to 1 to enforce equally spaced data.

**Returns**

- `an` [ndarray] 1-D array of weights to apply to the function at the provided sample positions.
- `B` [float] Error coefficient.

**Notes**

Normally, the Newton-Cotes rules are used on smaller integration regions and a composite rule is used to return the total integral.

**Examples**

Compute the integral of $\sin(x)$ in $[0, \pi]$:

```python
code
>>> from scipy.integrate import newton_cotes
>>> def f(x):
...     return np.sin(x)
>>> a = 0
>>> b = np.pi
>>> exact = 2
>>> for N in [2, 4, 6, 8, 10]:
...     x = np.linspace(a, b, N + 1)
...     an, B = newton_cotes(N, 1)
...     dx = (b - a) / N
...     quad = dx * np.sum(an * f(x))
...     error = abs(quad - exact)
...     print("{:2d} {:10.9f} {:5e}".format(N, quad, error))
...
2 2.094395102 9.43951e-02
4 1.998570732 1.42927e-03
6 2.000017814 1.78136e-05
8 1.999999835 1.64725e-07
10 2.000000001 1.14677e-09
```

scipy.integrate.IntegrationWarning

**exception scipy.integrate.IntegrationWarning**

Warning on issues during integration.

### 6.6.2 Integrating functions, given fixed samples

- `trapezoidal`

  - `trapz(y[, x, dx, axis])` Integrate along the given axis using the composite trapezoidal rule.

- `cumtrapz` Cumulatively integrate $y(x)$ using the composite trapezoidal rule.
Table 19 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>simps</code></td>
<td>Integrate y(x) using samples along the given axis and the composite Simpson’s rule.</td>
</tr>
<tr>
<td><code>romb</code></td>
<td>Romberg integration using samples of a function.</td>
</tr>
</tbody>
</table>

**scipy.integrate.trapz**

`scipy.integrate.trapz(y, x=None, dx=1.0, axis=-1)`

Integrate along the given axis using the composite trapezoidal rule.

Integrate $y(x)$ along given axis.

**Parameters**

- `y` : [array_like] Input array to integrate.
- `x` : [array_like, optional] The sample points corresponding to the $y$ values. If $x$ is None, the sample points are assumed to be evenly spaced $dx$ apart. The default is None.
- `dx` : [scalar, optional] The spacing between sample points when $x$ is None. The default is 1.
- `axis` : [int, optional] The axis along which to integrate.

**Returns**

- `trapz` : [float] Definite integral as approximated by trapezoidal rule.

**See also:**

`sum`, `cumsum`

**Notes**

Image [2] illustrates trapezoidal rule – $y$-axis locations of points will be taken from $y$ array, by default $x$-axis distances between points will be 1.0, alternatively they can be provided with $x$ array or with $dx$ scalar. Return value will be equal to combined area under the red lines.

**References**

[1], [2]

**Examples**

```python
>>> np.trapz([1,2,3])
4.0
>>> np.trapz([1,2,3], x=[4,6,8])
8.0
>>> np.trapz([1,2,3], dx=2)
8.0
>>> a = np.arange(6).reshape(2, 3)
>>> a
array([[0, 1, 2],
       [3, 4, 5]])
>>> np.trapz(a, axis=0)
array([ 1.5, 2.5, 3.5])
>>> np.trapz(a, axis=1)
array([ 2., 8.])
```

**scipy.integrate.cumtrapz**

`scipy.integrate.cumtrapz(y, x=None, dx=1.0, axis=-1, initial=None)`

Cumulatively integrate $y(x)$ using the composite trapezoidal rule.

**Parameters**

- `y` : [array_like] Input array to integrate.
- `x` : [array_like, optional] The sample points corresponding to the $y$ values. If $x$ is None, the sample points are assumed to be evenly spaced $dx$ apart. The default is None.
- `dx` : [scalar, optional] The spacing between sample points when $x$ is None. The default is 1.
- `axis` : [int, optional] The axis along which to integrate.
- `initial` : [scalar, optional] The starting value. Defaults to 0.

**Notes**

Image [2] illustrates trapezoidal rule – $y$-axis locations of points will be taken from $y$ array, by default $x$-axis distances between points will be 1.0, alternatively they can be provided with $x$ array or with $dx$ scalar. Return value will be equal to combined area under the red lines.

**References**

[1], [2]

**Examples**

```python
>>> np.cumtrapz([1,2,3])
array([ 1.,  2.,  3.])
>>> np.cumtrapz([1,2,3], x=[4,6,8])
array([ 1.,  2.,  3.,  4.,  6.,  8.])
>>> np.cumtrapz([1,2,3], dx=2)
array([ 1.,  3.,  5.,  7.])
>>> a = np.arange(6).reshape(2, 3)
>>> a
array([[0, 1, 2],
       [3, 4, 5]])
>>> np.cumtrapz(a, axis=0)
array([[ 1.5,  3.5,  5.5],
       [ 4.5,  6.5,  8.5]])
>>> np.cumtrapz(a, axis=1)
array([[ 1.,  4.,  7.],
       [ 3.,  6.,  9.]])
```
**Parameters**

- `y` [array_like] Values to integrate.
- `x` [array_like, optional] The coordinate to integrate along. If None (default), use spacing $dx$ between consecutive elements in $y$.
- `dx` [float, optional] Spacing between elements of $y$. Only used if $x$ is None.
- `axis` [int, optional] Specifies the axis to accumulate. Default is -1 (last axis).
- `initial` [scalar, optional] If given, insert this value at the beginning of the returned result. Typically this value should be 0. Default is None, which means no value at $x[0]$ is returned and $res$ has one element less than $y$ along the axis of integration.

**Returns**

- `res` [ndarray] The result of cumulative integration of $y$ along $axis$. If `initial` is None, the shape is such that the axis of integration has one less value than $y$. If `initial` is given, the shape is equal to that of $y$.

**See also:**

- `numpy.cumsum`, `numpy.cumprod`
- `quad`
  adaptive quadrature using QUADPACK
- `romberg`
  adaptive Romberg quadrature
- `quadrature`
  adaptive Gaussian quadrature
- `fixed_quad`
  fixed-order Gaussian quadrature
- `dblquad`
  double integrals
- `tplquad`
  triple integrals
- `romb`
  integrators for sampled data
- `ode`
  ODE integrators
- `odeint`
  ODE integrators

**Examples**

```python
>>> from scipy import integrate
>>> import matplotlib.pyplot as plt

>>> x = np.linspace(-2, 2, num=20)
>>> y = x
>>> y_int = integrate.cumtrapz(y, x, initial=0)
>>> plt.plot(x, y_int, 'ro', x, y[0] + 0.5 * x**2, 'b-')
>>> plt.show()
```
scipy.integrate.simps

**scipy.integrate.simps***(y, x=None, dx=1, axis=-1, even='avg')***

Integrate y(x) using samples along the given axis and the composite Simpson’s rule. If x is None, spacing of dx is assumed.

If there are an even number of samples, N, then there are an odd number of intervals (N-1), but Simpson’s rule requires an even number of intervals. The parameter ‘even’ controls how this is handled.

**Parameters**

- **y** [array_like] Array to be integrated.
- **x** [array_like, optional] If given, the points at which y is sampled.
- **dx** [int, optional] Spacing of integration points along axis of y. Only used when x is None. Default is 1.
- **axis** [int, optional] Axis along which to integrate. Default is the last axis.
- **even** [str {'avg', 'first', 'last'}, optional]
  - ‘avg’ [Average two results:1) use the first N-2 intervals with] a trapezoidal rule on the last interval and 2) use the last N-2 intervals with a trapezoidal rule on the first interval.
  - ‘first’ [Use Simpson’s rule for the first N-2 intervals with] a trapezoidal rule on the last interval.
  - ‘last’ [Use Simpson’s rule for the last N-2 intervals with a] trapezoidal rule on the first interval.

**See also:**

- **quad**
  - adaptive quadrature using QUADPACK
- **romberg**
  - adaptive Romberg quadrature
- **quadrature**
  - adaptive Gaussian quadrature
**fixed_quad**

fixed-order Gaussian quadrature

**dblquad**

double integrals

**tplquad**

triple integrals

**romb**

integrators for sampled data

**cumtrapz**

cumulative integration for sampled data

**ode**

ODE integrators

**odeint**

ODE integrators

**Notes**

For an odd number of samples that are equally spaced the result is exact if the function is a polynomial of order 3 or less. If the samples are not equally spaced, then the result is exact only if the function is a polynomial of order 2 or less.

**Examples**

```python
>>> from scipy import integrate
>>> x = np.arange(0, 10)
>>> y = np.arange(0, 10)

>>> integrate.simps(y, x)
40.5

>>> y = np.power(x, 3)

>>> integrate.simps(y, x)
1642.5

>>> integrate.quad(lambda x: x**3, 0, 9)[0]
1640.25

>>> integrate.simps(y, x, even='first')

1644.5
```

**scipy.integrate.romb**

**scipy.integrate.romb**(*y*, *dx=1.0*, *axis=-1*, *show=False*)

Romberg integration using samples of a function.

**Parameters**

- **y** [array_like] A vector of \(2^k + 1\) equally-spaced samples of a function.
- **dx** [float, optional] The sample spacing. Default is 1.
- **axis** [int, optional] The axis along which to integrate. Default is -1 (last axis).
show  [bool, optional] When y is a single 1-D array, then if this argument is True print
the table showing Richardson extrapolation from the samples. Default is False.

Returns
romb  [ndarray] The integrated result for axis.

See also:
quad  adaptive quadrature using QUADPACK
romberg  adaptive Romberg quadrature
quadrature  adaptive Gaussian quadrature
fixed_quad  fixed-order Gaussian quadrature
dblquad  double integrals
tplquad  triple integrals
simps  integrators for sampled data
cumtrapz  cumulative integration for sampled data
ode  ODE integrators
odeint  ODE integrators

Examples
>>> from scipy import integrate
>>> x = np.arange(10, 14.25, 0.25)
>>> y = np.arange(3, 12)

>>> integrate.romb(y)
56.0

>>> y = np.sin(np.power(x, 2.5))
>>> integrate.romb(y)
-0.742561336672229
>>> integrate.romb(y, show=True)
Richardson Extrapolation Table for Romberg Integration

<table>
<thead>
<tr>
<th>Value 1</th>
<th>Value 2</th>
<th>Value 3</th>
<th>Value 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>-0.81576</td>
<td>4.63862</td>
<td>6.45674</td>
<td>-1.10581</td>
</tr>
<tr>
<td>-3.02062</td>
<td>-3.65245</td>
<td>-2.57379</td>
<td>-3.06311</td>
</tr>
<tr>
<td>-3.05664</td>
<td>-3.06595</td>
<td>-1.34093</td>
<td>-0.92997</td>
</tr>
<tr>
<td>-0.75160</td>
<td>-0.74256</td>
<td>-0.74256</td>
<td>-0.74366</td>
</tr>
</tbody>
</table>

See also:

scipy.special for orthogonal polynomials (special) for Gaussian quadrature roots and weights for other weighting factors and regions.

6.6.3 Solving initial value problems for ODE systems

The solvers are implemented as individual classes which can be used directly (low-level usage) or through a convenience function.

scipy.integrate.solve_ivp

scipy.integrate.solve_ivp(fun, t_span, y0[, method, t_eval, ...]) Solve an initial value problem for a system of ODEs.

RK23(fun, t0, y0, t_bound[, max_step, rtol, ...]) Explicit Runge-Kutta method of order 3(2).
RK45(fun, t0, y0, t_bound[, max_step, rtol, ...]) Explicit Runge-Kutta method of order 5(4).
Radau(fun, t0, y0, t_bound[, max_step, ...]) Implicit Runge-Kutta method of Radau IIA family of order 5.
BDF(fun, t0, y0, t_bound[, max_step, rtol, ...]) Implicit method based on backward-differentiation formulas.
LSODA(fun, t0, y0, t_bound[, first_step, ...]) Adams/BDF method with automatic stiffness detection and switching.

OdeSolver(fun, t0, y0, t_bound, vectorized) Base class for ODE solvers.
DenseOutput(t_old, t) Base class for local interpolant over step made by an ODE solver.
OdeSolution(ts, interpolants) Continuous ODE solution.

This function numerically integrates a system of ordinary differential equations given an initial value:

dy / dt = f(t, y)
y(t0) = y0

Here t is a one-dimensional independent variable (time), y(t) is an n-dimensional vector-valued function (state), and an n-dimensional vector-valued function f(t, y) determines the differential equations. The goal is to find y(t) approximately satisfying the differential equations, given an initial value y(t0)=y0.

Some of the solvers support integration in the complex domain, but note that for stiff ODE solvers, the right-hand side must be complex-differentiable (satisfy Cauchy-Riemann equations [11]). To solve a problem in the complex domain, pass y0 with a complex data type. Another option is always to rewrite your problem for real and imaginary parts separately.
Parameters

fun  [callable] Right-hand side of the system. The calling signature is fun(t, y). Here t is a scalar, and there are two options for the ndarray y: It can either have shape (n,); then fun must return array_like with shape (n,). Alternatively it can have shape (n, k); then fun must return an array_like with shape (n, k), i.e. each column corresponds to a single column in y. The choice between the two options is determined by vectorized argument (see below). The vectorized implementation allows a faster approximation of the Jacobian by finite differences (required for stiff solvers).

t_span  [2-tuple of floats] Interval of integration (t0, tf). The solver starts with t=t0 and integrates until it reaches t=tf.

y0  [array_like, shape (n,)] Initial state. For problems in the complex domain, pass y0 with a complex data type (even if the initial guess is purely real).

method  [string or OdeSolver, optional] Integration method to use:
  • ‘RK45’ (default): Explicit Runge-Kutta method of order 5(4) [1]. The error is controlled assuming accuracy of the fourth-order method, but steps are taken using the fifth-order accurate formula (local extrapolation is done). A quartic interpolation polynomial is used for the dense output [2]. Can be applied in the complex domain.
  • ‘RK23’: Explicit Runge-Kutta method of order 3(2) [3]. The error is controlled assuming accuracy of the second-order method, but steps are taken using the third-order accurate formula (local extrapolation is done). A cubic Hermite polynomial is used for the dense output. Can be applied in the complex domain.
  • ‘Radau’: Implicit Runge-Kutta method of the Radau IIA family of order 5 [4]. The error is controlled with a third-order accurate embedded formula. A cubic polynomial which satisfies the collocation conditions is used for the dense output.
  • ‘BDF’: Implicit multi-step variable-order (1 to 5) method based on a backward differentiation formula for the derivative approximation [5]. The implementation follows the one described in [6]. A quasi-constant step scheme is used and accuracy is enhanced using the NDF modification. Can be applied in the complex domain.
  • ‘LSODA’: Adams/BDF method with automatic stiffness detection and switching [7], [8]. This is a wrapper of the Fortran solver from ODEPACK. You should use the ‘RK45’ or ‘RK23’ method for non-stiff problems and ‘Radau’ or ‘BDF’ for stiff problems [9]. If not sure, first try to run ‘RK45’. If needs unusually many iterations, diverges, or fails, your problem is likely to be stiff and you should use ‘Radau’ or ‘BDF’. ‘LSODA’ can also be a good universal choice, but it might be somewhat less convenient to work with as it wraps old Fortran code.
  You can also pass an arbitrary class derived from OdeSolver which implements the solver.

dense_output  [bool, optional] Whether to compute a continuous solution. Default is False.

t_eval  [array_like or None, optional] Times at which to store the computed solution, must be sorted and lie within t_span. If None (default), use points selected by the solver.

events  [callable, list of callables or None, optional] Types of events to track. Each is defined by a continuous function of time and state that becomes zero value in case of an event. Each function must have the signature event(t, y) and return a float. The solver will find an accurate value of t at which event(t, y(t)) = 0 using a root-finding algorithm. Additionally each event function might have the following attributes:
  • terminal: bool, whether to terminate integration if this event occurs. Implicitly False if not assigned.
- direction: float, direction of a zero crossing. If direction is positive, event must go from negative to positive, and vice versa if direction is negative. If 0, then either direction will count. Implicitly 0 if not assigned.

You can assign attributes like `event.terminal = True` to any function in Python. If None (default), events won’t be tracked.

vectorized
[bool, optional] Whether fun is implemented in a vectorized fashion. Default is False.

options
Options passed to a chosen solver. All options available for already implemented solvers are listed below.

first_step
[float or None, optional] Initial step size. Default is None which means that the algorithm should choose.

max_step
[float, optional] Maximum allowed step size. Default is np.inf, i.e. the step size is not bounded and determined solely by the solver.

rtol, atol
[float and array_like, optional] Relative and absolute tolerances. The solver keeps the local error estimates less than atol + rtol * abs(y). Here rtol controls a relative accuracy (number of correct digits). But if a component of y is approximately below atol, the error only needs to fall within the same atol threshold, and the number of correct digits is not guaranteed. If components of y have different scales, it might be beneficial to set different atol values for different components by passing array_like with shape (n,) for atol. Default values are 1e-3 for rtol and 1e-6 for atol.

jac
[{None, array_like, sparse_matrix, callable}, optional] Jacobian matrix of the right-hand side of the system with respect to y, required by the ‘Radau’, ‘BDF’ and ‘LSODA’ method. The Jacobian matrix has shape (n, n) and its element (i, j) is equal to \( \frac{d f_i}{d y_j} \). There are three ways to define the Jacobian:
- If array_like or sparse_matrix, the Jacobian is assumed to be constant. Not supported by ‘LSODA’.
- If callable, the Jacobian is assumed to depend on both t and y; it will be called as jac(t, y) as necessary. For the ‘Radau’ and ‘BDF’ methods, the return value might be a sparse matrix.
- If None (default), the Jacobian will be approximated by finite differences.

It is generally recommended to provide the Jacobian rather than relying on a finite-difference approximation.

jac_sparsity
[{None, array_like, sparse_matrix}, optional] Defines a sparsity structure of the Jacobian matrix for a finite-difference approximation. Its shape must be (n, n). This argument is ignored if jac is not None. If the Jacobian has only few non-zero elements in each row, providing the sparsity structure will greatly speed up the computations [10]. A zero entry means that a corresponding element in the Jacobian is always zero. If None (default), the Jacobian is assumed to be dense. Not supported by ‘LSODA’, see lband and uband instead.

lband, uband
[int or None] Parameters defining the bandwidth of the Jacobian for the ‘LSODA’ method, i.e., jac[i, j] != 0 only for i - lband <= j <= i + uband. Setting these requires your jac routine to return the Jacobian in the packed format: the returned array must have n columns and uband + lband + 1 rows in which Jacobian diagonals are written. Specifically jac_packed[uband + i - j, j] = jac[i, j]. The same format is used in scipy.linalg.solve_banded (check for an illustration). These parameters can be also used with jac=None to reduce the number of Jacobian elements estimated by finite differences.

min_step

6.6. Integration and ODEs (scipy.integrate)
[float, optional] The minimum allowed step size for ‘LSODA’ method. By default 
\texttt{min\_step} is zero.

\textbf{Returns}

Bunch object with the following fields defined:

\begin{itemize}
\item \textit{t} [ndarray, shape \{n\_points,\}] Time points.
\item \textit{y} [ndarray, shape \{n, n\_points\}] Values of the solution at \textit{t}.
\item \textit{sol} [\texttt{OdeSolution} or None] Found solution as \texttt{OdeSolution} instance; None if 
dense\_output was set to False.
\item \textit{t\_events} [list of ndarray or None] Contains for each event type a list of arrays at which an 
event of that type event was detected. None if \textit{events} was None.
\item \textit{nfev} [int] Number of evaluations of the right-hand side.
\item \textit{njev} [int] Number of evaluations of the Jacobian.
\item \textit{nlu} [int] Number of LU decompositions.
\item \textit{status} [int] Reason for algorithm termination:
    \begin{itemize}
    \item -1: Integration step failed.
    \item 0: The solver successfully reached the end of \textit{tspan}.
    \item 1: A termination event occurred.
    \end{itemize}
\item \textit{message} [string] Human-readable description of the termination reason.
\item \textit{success} [bool] True if the solver reached the interval end or a termination event occurred 
(\textit{status} \geq 0).
\end{itemize}

\textbf{References}

[1], [2], [3], [4], [5], [6], [7], [8], [9], [10], [11]

\textbf{Examples}

Basic exponential decay showing automatically chosen time points.

\begin{verbatim}
>>> from scipy.integrate import solve_ivp
>>> def exponential_decay(t, y):
...    return -0.5 * y
>>> sol = solve_ivp(exponential_decay, [0, 10], [2, 4, 8])
>>> print(sol.t)
[ 0. 0.11487653 1.26364188 3.06061781 4.85759374 6.65456967 8.4515456 10. ]
>>> print(sol.y)
[[2. 1.21305369 0.73534021 0.27066736 0.01350938]
 [4. 2.42610739 1.47068043 0.54133472 0.02701876]
 [8. 4.85221478 2.94136085 1.08266944 0.05403753]]
\end{verbatim}

Specifying points where the solution is desired.

\begin{verbatim}
>>> sol = solve_ivp(exponential_decay, [0, 10], [2, 4, 8], ...t_eval=[0, 1, 2, 4, 10])
>>> print(sol.t)
[ 0 1 2 4 10]
>>> print(sol.y)
[[2. 1.21305369 0.73534021 0.27066736 0.01350938]
 [4. 2.42610739 1.47068043 0.54133472 0.02701876]
 [8. 4.85221478 2.94136085 1.08266944 0.05403753]]
\end{verbatim}

Cannon fired upward with terminal event upon impact. The \texttt{terminal} and \texttt{direction} fields of an 
event are applied by monkey patching a function. Here \texttt{y[0]} is position and \texttt{y[1]} is velocity. The
projectile starts at position 0 with velocity +10. Note that the integration never reaches t=100 because the event is terminal.

```python
>>> def upward_cannon(t, y):
...     return [y[1], -0.5]
>>> def hit_ground(t, y):
...     return y[1]
>>> hit_ground.terminal = True
>>> hit_ground.direction = -1
>>> sol = solve_ivp(upward_cannon, [0, 100], [0, 10], events=hit_ground)
>>> print(sol.t_events)
[array([20.])]
>>> print(sol.t)
[0.00000000e+00 9.99900010e-05 1.09989001e-03 1.10988901e-02
 1.1108891e-01 1.1109890e+01 1.11099890e+01 2.00000000e+01]
```

scipy.integrate.RK23

```
class scipy.integrate.RK23(fun, t0, y0, t_bound, max_step=inf, rtol=0.001, atol=1e-06, vectorized=False, first_step=None, **extraneous)
```

Explicit Runge-Kutta method of order 3(2).

This uses the Bogacki-Shampine pair of formulas [1]. The error is controlled assuming accuracy of the second-order method, but steps are taken using the third-order accurate formula (local extrapolation is done). A cubic Hermite polynomial is used for the dense output.

Can be applied in the complex domain.

**Parameters**

`fun` [callable] Right-hand side of the system. The calling signature is `fun(t, y)`. Here `t` is a scalar and there are two options for ndarray `y`. It can either have shape (n,), then `fun` must return array_like with shape (n,). Or alternatively it can have shape (n, k), then `fun` must return array_like with shape (n, k), i.e. each column corresponds to a single column in `y`. The choice between the two options is determined by `vectorized` argument (see below).

`t0` [float] Initial time.

`y0` [array_like, shape (n,)] Initial state.

`t_bound` [float] Boundary time - the integration won’t continue beyond it. It also determines the direction of the integration.

`first_step` [float or None, optional] Initial step size. Default is `None` which means that the algorithm should choose.

`max_step` [float, optional] Maximum allowed step size. Default is `np.inf`, i.e. the step size is not bounded and determined solely by the solver.

`rtol, atol` [float and array_like, optional] Relative and absolute tolerances. The solver keeps the local error estimates less than `atol + rtol * abs(y)`. Here `rtol` controls a relative accuracy (number of correct digits). But if a component of `y` is approximately below `atol`, the error only needs to fall within the same `atol` threshold, and the number of correct digits is not guaranteed. If components of `y` have different scales, it might be beneficial to set different `atol` values for different components by passing array_like with shape (n,) for `atol`. Default values are 1e-3 for `rtol` and 1e-6 for `atol`.

`vectorized` [bool, optional] Whether `fun` is implemented in a vectorized fashion. Default is `False`. 

6.6. Integration and ODEs (scipy.integrate)
References

Attributes

- n [int] Number of equations.
- t_bound [float] Boundary time.
- direction [float] Integration direction: +1 or -1.
- t [float] Current time.
- y [ndarray] Current state.
- t_old [float] Previous time. None if no steps were made yet.
- step_size [float] Size of the last successful step. None if no steps were made yet.
- nfev [int] Number evaluations of the system’s right-hand side.
- njev [int] Number of evaluations of the Jacobian. Is always 0 for this solver as it does not use the Jacobian.
- nlu [int] Number of LU decompositions. Is always 0 for this solver.

Methods

- dense_output() Compute a local interpolant over the last successful step.
- step() Perform one integration step.

scipy.integrate.RK23.dense_output
RK23.dense_output() Compute a local interpolant over the last successful step.

Returns

- sol [DenseOutput] Local interpolant over the last successful step.

scipy.integrate.RK23.step
RK23.step() Perform one integration step.

Returns

- message [string or None] Report from the solver. Typically a reason for a failure if self.status is ‘failed’ after the step was taken or None otherwise.

scipy.integrate.RK45

class scipy.integrate.RK45(fun, t0, y0, t_bound, max_step=inf, rtol=0.001, atol=1e-06, vectorized=False, first_step=None, **extraneous)

Explicit Runge-Kutta method of order 5(4).

This uses the Dormand-Prince pair of formulas [1]. The error is controlled assuming accuracy of the fourth-order method accuracy, but steps are taken using the fifth-order accurate formula (local extrapolation is done). A quartic interpolation polynomial is used for the dense output [2].

Can be applied in the complex domain.

Parameters

- fun [callable] Right-hand side of the system. The calling signature is fun(t, y). Here t is a scalar, and there are two options for the ndarray y: It can either have shape (n,); then fun must return array_like with shape (n,). Alternatively it can have shape (n, k); then fun must return an array_like with shape (n, k), i.e. each
column corresponds to a single column in y. The choice between the two options is determined by `vectorized` argument (see below).

t0
[float] Initial time.
y0
[array_like, shape (n,)] Initial state.
t_bound
[float] Boundary time - the integration won’t continue beyond it. It also determines the direction of the integration.

`first_step`
[float or None, optional] Initial step size. Default is `None` which means that the algorithm should choose.

`max_step`
[float, optional] Maximum allowed step size. Default is `np.inf`, i.e. the step size is not bounded and determined solely by the solver.

rtol, atol
[float and array_like, optional] Relative and absolute tolerances. The solver keeps the local error estimates less than `atol + rtol * abs(y)`. Here `rtol` controls a relative accuracy (number of correct digits). But if a component of `y` is approximately below `atol`, the error only needs to fall within the same `atol` threshold, and the number of correct digits is not guaranteed. If components of `y` have different scales, it might be beneficial to set different `atol` values for different components by passing array_like with shape (n,) for `atol`. Default values are 1e-3 for `rtol` and 1e-6 for `atol`.

`vectorized`
[bool, optional] Whether `fun` is implemented in a vectorized fashion. Default is False.

References
[1], [2]

Attributes

n
[int] Number of equations.

status

t_bound
[float] Boundary time.

direction
[float] Integration direction: +1 or -1.

t
[float] Current time.

y
[ndarray] Current state.

t_old
[float] Previous time. None if no steps were made yet.

step_size
[float] Size of the last successful step. None if no steps were made yet.

nfev
[int] Number evaluations of the system’s right-hand side.

njev
[int] Number of evaluations of the Jacobian. Is always 0 for this solver as it does not use the Jacobian.

nlu
[int] Number of LU decompositions. Is always 0 for this solver.

Methods

dense_output()
Compute a local interpolant over the last successful step.

step()
Perform one integration step.

scipy.integrate.RK45.dense_output
RK45.dense_output()
Compute a local interpolant over the last successful step.

Returns

sol
[DenseOutput] Local interpolant over the last successful step.
scipy.integrate.RK45.step
RK45.step()
    Perform one integration step.

Returns
message  [string or None] Report from the solver. Typically a reason for a failure if self.status is ‘failed’ after the step was taken or None otherwise.

scipy.integrate.Radau

class scipy.integrate.Radau(fun, t0, y0, t_bound, max_step=inf, rtol=0.001, atol=1e-06, jac=None, jac_sparsity=None, vectorized=False, first_step=None, **extraneous)
    Implicit Runge-Kutta method of Radau IIA family of order 5.

The implementation follows [1]. The error is controlled with a third-order accurate embedded formula. A cubic polynomial which satisfies the collocation conditions is used for the dense output.

Parameters

fun  [callable] Right-hand side of the system. The calling signature is fun(t, y). Here t is a scalar, and there are two options for the ndarray y: It can either have shape (n,); then fun must return array_like with shape (n,). Alternatively it can have shape (n, k); then fun must return an array_like with shape (n, k), i.e. each column corresponds to a single column in y. The choice between the two options is determined by vectorized argument (see below). The vectorized implementation allows a faster approximation of the Jacobian by finite differences (required for this solver).

  t0  [float] Initial time.

  y0  [array_like, shape (n,)] Initial state.

  t_bound [float] Boundary time - the integration won’t continue beyond it. It also determines the direction of the integration.

first_step  [float or None, optional] Initial step size. Default is None which means that the algorithm should choose.

max_step  [float, optional] Maximum allowed step size. Default is np.inf, i.e. the step size is not bounded and determined solely by the solver.

rtol, atol  [float and array_like, optional] Relative and absolute tolerances. The solver keeps the local error estimates less than atol + rtol * abs(y). Here rtol controls a relative accuracy (number of correct digits). But if a component of y is approximately below atol, the error only needs to fall within the same atol threshold, and the number of correct digits is not guaranteed. If components of y have different scales, it might be beneficial to set different atol values for different components by passing array_like with shape (n,) for atol. Default values are 1e-3 for rtol and 1e-6 for atol.

jac  [(None, array_like, sparse_matrix, callable)], optional] Jacobian matrix of the right-hand side of the system with respect to y, required by this method. The Jacobian matrix has shape (n, n) and its element (i, j) is equal to $\frac{d f_i}{d y_j}$. There are three ways to define the Jacobian:

- If array_like or sparse_matrix, the Jacobian is assumed to be constant.
- If callable, the Jacobian is assumed to depend on both t and y; it will be called as jac(t, y) as necessary. For the ‘Radau’ and ‘BDF’ methods, the return value might be a sparse matrix.
- If None (default), the Jacobian will be approximated by finite differences.
It is generally recommended to provide the Jacobian rather than relying on a finite-difference approximation.

**jac_sparsity**

\[
\text{[(None, array_like, sparse matrix), optional]} \text{ Defines a sparsity structure of the Jacobian matrix for a finite-difference approximation. Its shape must be (n, n). This argument is ignored if jac is not None. If the Jacobian has only few non-zero elements in each row, providing the sparsity structure will greatly speed up the computations [2]. A zero entry means that a corresponding element in the Jacobian is always zero. If None (default), the Jacobian is assumed to be dense.}
\]

**vectorized**

\[
\text{[bool, optional]} \text{ Whether fun is implemented in a vectorized fashion. Default is False.}
\]

**References**

[1], [2]

**Attributes**

- **n**  
  \[
  \text{[int]} \text{ Number of equations.}
  \]
- **status**  
  \[
  \text{[string]} \text{ Current status of the solver: 'running', 'finished' or 'failed'.}
  \]
- **t_bound**  
  \[
  \text{[float]} \text{ Boundary time.}
  \]
- **direction**  
  \[
  \text{[float]} \text{ Integration direction: +1 or -1.}
  \]
- **t**  
  \[
  \text{[float]} \text{ Current time.}
  \]
- **y**  
  \[
  \text{[ndarray]} \text{ Current state.}
  \]
- **t_old**  
  \[
  \text{[float]} \text{ Previous time. None if no steps were made yet.}
  \]
- **step_size**  
  \[
  \text{[float]} \text{ Size of the last successful step. None if no steps were made yet.}
  \]
- **nfev**  
  \[
  \text{[int]} \text{ Number of evaluations of the right-hand side.}
  \]
- **njev**  
  \[
  \text{[int]} \text{ Number of evaluations of the Jacobian.}
  \]
- **nlu**  
  \[
  \text{[int]} \text{ Number of LU decompositions.}
  \]

**Methods**

- **dense_output()**  
  \[
  \text{Compute a local interpolant over the last successful step.}
  \]
- **step()**  
  \[
  \text{Perform one integration step.}
  \]

```python
scipy.integrate.Radau.dense_output
Radau.dense_output()  
Compute a local interpolant over the last successful step.

Returns

- **sol**  
  \[
  \text{[DenseOutput]} \text{ Local interpolant over the last successful step.}
  \]
```

```python
scipy.integrate.Radau.step
Radau.step()  
Perform one integration step.

Returns

- **message**  
  \[
  \text{[string or None]} \text{ Report from the solver. Typically a reason for a failure if self.status is 'failed' after the step was taken or None otherwise.}
  \]
```

```python
scipy.integrate.BDF
```
This is a variable order method with the order varying automatically from 1 to 5. The general framework of the BDF algorithm is described in [1]. This class implements a quasi-constant step size as explained in [2]. The error estimation strategy for the constant-step BDF is derived in [3]. An accuracy enhancement using modified formulas (NDF) [2] is also implemented.

Can be applied in the complex domain.

**Parameters**

fun [callable] Right-hand side of the system. The calling signature is `fun(t, y)`. Here `t` is a scalar, and there are two options for the ndarray `y`: It can either have shape (n,); then `fun` must return array_like with shape (n,). Alternatively it can have shape (n, k); then `fun` must return an array_like with shape (n, k), i.e. each column corresponds to a single column in `y`. The choice between the two options is determined by `vectorized` argument (see below). The vectorized implementation allows a faster approximation of the Jacobian by finite differences (required for this solver).

t0 [float] Initial time.

y0 [array_like, shape (n,)] Initial state.

t_bound [float] Boundary time - the integration won’t continue beyond it. It also determines the direction of the integration.

first_step [float or None, optional] Initial step size. Default is `None` which means that the algorithm should choose.

max_step [float, optional] Maximum allowed step size. Default is `np.inf`, i.e. the step size is not bounded and determined solely by the solver.

rtol, atol [float and array_like, optional] Relative and absolute tolerances. The solver keeps the local error estimates less than `atol + rtol * abs(y)`. Here `rtol` controls a relative accuracy (number of correct digits). But if a component of `y` is approximately below `atol`, the error only needs to fall within the same `atol` threshold, and the number of correct digits is not guaranteed. If components of `y` have different scales, it might be beneficial to set different `atol` values for different components by passing array_like with shape `(n,)` for `atol`. Default values are `1e-3` for `rtol` and `1e-6` for `atol`.

jac [(None, array_like, sparse_matrix, callable), optional] Jacobian matrix of the right-hand side of the system with respect to `y`, required by this method. The Jacobian matrix has shape `(n, n)` and its element `(i, j)` is equal to `d f_i / d y_j`. There are three ways to define the Jacobian:
- If `array_like` or `sparse_matrix`, the Jacobian is assumed to be constant.
- If callable, the Jacobian is assumed to depend on both `t` and `y`; it will be called as `jac(t, y)` as necessary. For the ‘Radau’ and ‘BDF’ methods, the return value might be a sparse matrix.
- If `None` (default), the Jacobian will be approximated by finite differences. It is generally recommended to provide the Jacobian rather than relying on a finite-difference approximation.

jac_sparsity [(None, array_like, sparse matrix), optional] Defines a sparsity structure of the Jacobian matrix for a finite-difference approximation. Its shape must be `(n, n)`. This argument is ignored if `jac` is not `None`. If the Jacobian has only few non-zero elements in each row, providing the sparsity structure will greatly speed up the computations [4]. A zero entry means that a corresponding element in the Jacobian is always zero. If `None` (default), the Jacobian is assumed to be dense.

tool
[bool, optional] Whether `fun` is implemented in a vectorized fashion. Default is False.

References
[1], [2], [3], [4]

Attributes
- `n` [int] Number of equations.
- `t_bound` [float] Boundary time.
- `direction` [float] Integration direction: +1 or -1.
- `t` [float] Current time.
- `y` [ndarray] Current state.
- `t_old` [float] Previous time. None if no steps were made yet.
- `step_size` [float] Size of the last successful step. None if no steps were made yet.
- `nfev` [int] Number of evaluations of the right-hand side.
- `njev` [int] Number of evaluations of the Jacobian.
- `nlu` [int] Number of LU decompositions.

Methods

```
dense_output()  # Compute a local interpolant over the last successful step.
step()          # Perform one integration step.
```

**scipy.integrate.BDF.dense_output**

BDF.dense_output()

Compute a local interpolant over the last successful step.

**Returns**

- `sol` [DenseOutput] Local interpolant over the last successful step.

**scipy.integrate.BDF.step**

BDF.step()

Perform one integration step.

**Returns**

- `message` [string or None] Report from the solver. Typically a reason for a failure if `self.status` is ‘failed’ after the step was taken or None otherwise.

**scipy.integrate.LSODA**

```
class scipy.integrate.LSODA(fun, t0, y0, t_bound, first_step=None, min_step=0.0, max_step=inf, rtol=0.001, atol=1e-06, jac=None, lband=None, uband=None, vectorized=False, **extraneous)
```

Adams/BDF method with automatic stiffness detection and switching.

This is a wrapper to the Fortran solver from ODEPACK [1]. It switches automatically between the nonstiff Adams method and the stiff BDF method. The method was originally detailed in [2].

**Parameters**

- `fun` [callable] Right-hand side of the system. The calling signature is `fun(t, y)`. Here `t` is a scalar, and there are two options for the `ndarray` `y`: It can either have shape `(n,)`; then `fun` must return array_like with shape `(n,)`. Alternatively it can have shape `(n, k)`: then `fun` must return an array_like with shape `(n, k)`, i.e. each column corresponds to a single column in `y`. The choice between the two options

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is determined by `vectorized` argument (see below). The vectorized implementation allows a faster approximation of the Jacobian by finite differences (required for this solver).

t0
[float] Initial time.
y0
[array_like, shape (n,)] Initial state.
t_bound
[Float] Boundary time - the integration won’t continue beyond it. It also determines the direction of the integration.

first_step
[float or None, optional] Initial step size. Default is `None` which means that the algorithm should choose.

min_step
[float, optional] Minimum allowed step size. Default is 0.0, i.e. the step size is not bounded and determined solely by the solver.

max_step
[float, optional] Maximum allowed step size. Default is np.inf, i.e. the step size is not bounded and determined solely by the solver.
rtol, atol
[float and array_like, optional] Relative and absolute tolerances. The solver keeps the local error estimates less than `atol + rtol * abs(y)`. Here `rtol` controls a relative accuracy (number of correct digits). But if a component of `y` is approximately below `atol`, the error only needs to fall within the same `atol` threshold, and the number of correct digits is not guaranteed. If components of `y` have different scales, it might be beneficial to set different `atol` values for different components by passing `array_like` with shape (n,) for `atol`. Default values are 1e-3 for `rtol` and 1e-6 for `atol`.

jac
[None or callable, optional] Jacobian matrix of the right-hand side of the system with respect to `y`. The Jacobian matrix has shape (n, n) and its element (i, j) is equal to \( \frac{d f_i}{d y_j} \). The function will be called as `jac(t, y)`. If None (default), the Jacobian will be approximated by finite differences. It is generally recommended to provide the Jacobian rather than relying on a finite-difference approximation.

lband, uband
[int or None] Parameters defining the bandwidth of the Jacobian, i.e., `jac[i, j]` != 0 only for `i - lband <= j <= i + uband`. Setting these requires your `jac` routine to return the Jacobian in the packed format: the returned array must have `n` columns and `uband + lband + 1` rows in which Jacobian diagonals are written. Specifically `jac_packed[uband + i - j , j] = jac[i, j]`. The same format is used in `scipy.linalg.solve_banded` (check for an illustration). These parameters can be also used with `jac=None` to reduce the number of Jacobian elements estimated by finite differences.

vectorized
[bool, optional] Whether `fun` is implemented in a vectorized fashion. A vectorized implementation offers no advantages for this solver. Default is False.

References
[1], [2]

Attributes

n
[int] Number of equations.
status
t_bound
[float] Boundary time.
direction
[float] Integration direction: +1 or -1.
t
[float] Current time.
y
[ndarray] Current state.
t_old
[float] Previous time. None if no steps were made yet.
nfev
[int] Number of evaluations of the right-hand side.
njev  [int] Number of evaluations of the Jacobian.

Methods

dense_output()  Compute a local interpolant over the last successful step.

step()  Perform one integration step.

scipy.integrate.LSODA.dense_output
LSODA.dense_output()
Compute a local interpolant over the last successful step.

Returns

sol  [DenseOutput] Local interpolant over the last successful step.

scipy.integrate.LSODA.step
LSODA.step()
Perform one integration step.

Returns

message  [string or None] Report from the solver. Typically a reason for a failure if self.status is ‘failed’ after the step was taken or None otherwise.

scipy.integrate.OdeSolver
class scipy.integrate.OdeSolver(fun, t0, y0, t_bound, vectorized, support_complex=False)
Base class for ODE solvers.

In order to implement a new solver you need to follow the guidelines:

1. A constructor must accept parameters presented in the base class (listed below) along with any other parameters specific to a solver.

2. A constructor must accept arbitrary extraneous arguments **extraneous, but warn that these arguments are irrelevant using common.warn_extraneous function. Do not pass these arguments to the base class.

3. A solver must implement a private method _step_impl(self) which propagates a solver one step further. It must return tuple (success, message), where success is a boolean indicating whether a step was successful, and message is a string containing description of a failure if a step failed or None otherwise.

4. A solver must implement a private method _dense_output_impl(self) which returns a DenseOutput object covering the last successful step.

5. A solver must have attributes listed below in Attributes section. Note that t_old and step_size are updated automatically.

6. Use fun(self, t, y) method for the system rhs evaluation, this way the number of function evaluations (nfev) will be tracked automatically.

7. For convenience a base class provides fun_single(self, t, y) and fun_vectorized(self, t, y) for evaluating the rhs in non-vectorized and vectorized fashions respectively (regardless of how fun from the constructor is implemented). These calls don’t increment nfev.

8. If a solver uses a Jacobian matrix and LU decompositions, it should track the number of Jacobian evaluations (njev) and the number of LU decompositions (nlu).
9. By convention the function evaluations used to compute a finite difference approximation of the Jacobian should not be counted in \( nfev \), thus use `fun_single(self, t, y)` or `fun_vectorized(self, t, y)` when computing a finite difference approximation of the Jacobian.

**Parameters**

- **fun** ([callable]) Right-hand side of the system. The calling signature is `fun(t, y)`. Here `t` is a scalar and there are two options for `ndarray y`. It can either have shape `(n,)`, then `fun` must return `array_like` with shape `(n,)`. Or alternatively it can have shape `(n, n_points)`, then `fun` must return `array_like` with shape `(n, n_points)` (each column corresponds to a single column in `y`). The choice between the two options is determined by `vectorized` argument (see below).

- **t0** ([float]) Initial time.

- **y0** ([array_like, shape (n,)]) Initial state.

- **t_bound** ([float]) Boundary time — the integration won’t continue beyond it. It also determines the direction of the integration.

- **vectorized** ([bool]) Whether `fun` is implemented in a vectorized fashion.

- **support_complex** ([bool, optional]) Whether integration in a complex domain should be supported. Generally determined by a derived solver class capabilities. Default is False.

**Attributes**

- **n** ([int]) Number of equations.

- **status** ([string]) Current status of the solver: ‘running’, ‘finished’ or ‘failed’.

- **t_bound** ([float]) Boundary time.

- **direction** ([float]) Integration direction: +1 or -1.

- **t** ([float]) Current time.

- **y** ([ndarray]) Current state.

- **t_old** ([float]) Previous time. None if no steps were made yet.

- **step_size** ([float]) Size of the last successful step. None if no steps were made yet.

- **nfev** ([int]) Number of the system’s rhs evaluations.

- **njev** ([int]) Number of the Jacobian evaluations.

- **nlu** ([int]) Number of LU decompositions.

**Methods**

- **dense_output()** Compute a local interpolant over the last successful step.

- **step()** Perform one integration step.

**scipy.integrate.OdeSolver.dense_output**

`OdeSolver.dense_output()`

Compute a local interpolant over the last successful step.

**Returns**

- **sol** ([DenseOutput]) Local interpolant over the last successful step.

**scipy.integrate.OdeSolver.step**

`OdeSolver.step()`

Perform one integration step.

**Returns**

- **message** [string or None] Report from the solver. Typically a reason for a failure if
self.status is ‘failed’ after the step was taken or None otherwise.

scipy.integrate.DenseOutput

class scipy.integrate.DenseOutput(t_old, t)
Base class for local interpolant over step made by an ODE solver.

It interpolates between \(t_{\text{min}}\) and \(t_{\text{max}}\) (see Attributes below). Evaluation outside this interval is not forbidden, but the accuracy is not guaranteed.

Attributes

- \(t_{\text{min}}, t_{\text{max}}\)
  - [float] Time range of the interpolation.

Methods

___call__(t) Evaluate the interpolant.

scipy.integrate.DenseOutput.__call__
DenseOutput.__call__(t)
Evaluate the interpolant.

Parameters

- \(t\) [float or array_like with shape (n_points,)] Points to evaluate the solution at.

Returns

- \(y\) [ndarray, shape (n,) or (n, n_points)] Computed values. Shape depends on whether \(t\) was a scalar or a 1-d array.

scipy.integrate.OdeSolution

class scipy.integrate.OdeSolution(ts, interpolants)
Continuous ODE solution.

It is organized as a collection of DenseOutput objects which represent local interpolants. It provides an algorithm to select a right interpolant for each given point.

The interpolants cover the range between \(t_{\text{min}}\) and \(t_{\text{max}}\) (see Attributes below). Evaluation outside this interval is not forbidden, but the accuracy is not guaranteed.

When evaluating at a breakpoint (one of the values in \(ts\)) a segment with the lower index is selected.

Parameters

- \(ts\) [array_like, shape (n_segments + 1,)] Time instants between which local interpolants are defined. Must be strictly increasing or decreasing (zero segment with two points is also allowed).

- interpolants [list of DenseOutput with n_segments elements] Local interpolants. An i-th interpolant is assumed to be defined between \(ts[i]\) and \(ts[i + 1]\).

Attributes

- \(t_{\text{min}}, t_{\text{max}}\)
  - [float] Time range of the interpolation.

Methods

___call__(t) Evaluate the solution.
**scipy.integrate.OdeSolution._call_**

OdeSolution._call_(t)

Evaluate the solution.

**Parameters**

- **t**
  [float or array_like with shape (n_points,)] Points to evaluate at.

**Returns**

- **y**
  [ndarray, shape (n_states,) or (n_states, n_points)]Computed values. Shape depends on whether \( t \) is a scalar or a 1-d array.

**Old API**

These are the routines developed earlier for scipy. They wrap older solvers implemented in Fortran (mostly ODEPACK). While the interface to them is not particularly convenient and certain features are missing compared to the new API, the solvers themselves are of good quality and work fast as compiled Fortran code. In some cases it might be worth using this old API.

### odeint

**odeint(func, y0, t[, args, Dfun, col_deriv, …])** Integrate a system of ordinary differential equations.

**ode(f[, jac])** A generic interface class to numeric integrators.

**complex_ode(f[, jac])** A wrapper of ode for complex systems.

### scipy.integrate.odeint

**scipy.integrate.odeint**

Integrate a system of ordinary differential equations.

**Note:** For new code, use **scipy.integrate.solve_ivp** to solve a differential equation.

Solve a system of ordinary differential equations using lsoda from the FORTRAN library odepack.

Solves the initial value problem for stiff or non-stiff systems of first order ode-s:

\[
\frac{dy}{dt} = \text{func}(y, t, \ldots) \quad [\text{or} \ \text{func}(t, y, \ldots)]
\]

where \( y \) can be a vector.

**Note:** By default, the required order of the first two arguments of \( \text{func} \) are in the opposite order of the arguments in the system definition function used by the **scipy.integrate.ode** class and the function **scipy.integrate.solve_ivp**. To use a function with the signature \( \text{func}(t, y, \ldots) \), the argument \( tfirst \) must be set to True.

**Parameters**

- **func**
  [callable(y, t, …) or callable(t, y, …)] Computes the derivative of \( y \) at \( t \). If the signature is **callable(t, y, …)**, then the argument \( tfirst \) must be set True.

- **y0**
  [array] Initial condition on \( y \) (can be a vector).

- **t**
  [array] A sequence of time points for which to solve for \( y \). The initial value point should be the first element of this sequence. This sequence must be monotonically increasing or monotonically decreasing; repeated values are allowed.
**args**  [tuple, optional] Extra arguments to pass to function.

**Dfun**  [callable(y, t, ...) or callable(t, y, ...)] Gradient (Jacobian) of func. If the signature is `callable(t, y, ...)`, then the argument `tfirst` must be set `True`.

**col_deriv**  [bool, optional] True if `Dfun` defines derivatives down columns (faster), otherwise `Dfun` should define derivatives across rows.

**full_output**  [bool, optional] True if to return a dictionary of optional outputs as the second output

**printmessg**  [bool, optional] Whether to print the convergence message

**tfirst:**  [bool, optional] If True, the first two arguments of `func` (and `Dfun`, if given) must `t, y` instead of the default `y, t`. New in version 1.1.0.

**Returns**

**y**  [array, shape (len(t), len(y0))] Array containing the value of y for each desired time `in t`, with the initial value `y0` in the first row.

**infodict**  [dict, only returned if `full_output == True`] Dictionary containing additional output information

<table>
<thead>
<tr>
<th>key</th>
<th>meaning</th>
</tr>
</thead>
<tbody>
<tr>
<td>'hu'</td>
<td>vector of step sizes successfully used for each time step.</td>
</tr>
<tr>
<td>'tcur'</td>
<td>vector with the value of <code>t</code> reached for each time step. (will always be at least as large as the input times).</td>
</tr>
<tr>
<td>'tolsf'</td>
<td>vector of tolerance scale factors, greater than 1.0, computed when a request for too much accuracy was detected.</td>
</tr>
<tr>
<td>'tsw'</td>
<td>value of <code>t</code> at the time of the last method switch (given for each time step)</td>
</tr>
<tr>
<td>'nst'</td>
<td>cumulative number of time steps</td>
</tr>
<tr>
<td>'nfe'</td>
<td>cumulative number of function evaluations for each time step</td>
</tr>
<tr>
<td>'nje'</td>
<td>cumulative number of jacobian evaluations for each time step</td>
</tr>
<tr>
<td>'nqu'</td>
<td>a vector of method orders for each successful step.</td>
</tr>
<tr>
<td>'imxer'</td>
<td>index of the component of largest magnitude in the weighted local error vector (<code>e / ewt</code>) on an error return, -1 otherwise.</td>
</tr>
<tr>
<td>'lenrw'</td>
<td>the length of the double work array required.</td>
</tr>
<tr>
<td>'leniw'</td>
<td>the length of integer work array required.</td>
</tr>
<tr>
<td>'mused'</td>
<td>a vector of method indicators for each successful time step: 1: adams (nonstiff), 2: bdf (stiff)</td>
</tr>
</tbody>
</table>

**Other Parameters**

**ml, mu**  [int, optional] If either of these are not None or non-negative, then the Jacobian is assumed to be banded. These give the number of lower and upper non-zero diagonals in this banded matrix. For the banded case, `Dfun` should return a matrix whose rows contain the non-zero bands (starting with the lowest diagonal). Thus, the return matrix `jac` from `Dfun` should have shape `(ml + mu + 1, len(y0))` when `ml >=0` or `mu >=0`. The data in `jac` must be stored such that `jac[i - j + mu, j]` holds the derivative of the `i'th equation with respect to the `j'th state variable. If `col_deriv` is True, the transpose of this `jac` must be returned.

**rtol, atol**  [float, optional] The input parameters `rtol` and `atol` determine the error control performed by the solver. The solver will control the vector, `e`, of estimated local errors in `y`, according to an inequality of the form `max-norm of (e / ewt) <= 1`, where `ewt` is a vector of positive error weights computed as `ewt = rtol * abs(y)`
+ atol. rtol and atol can be either vectors the same length as y or scalars. Defaults
to 1.49012e-8.

tcrit [ndarray, optional] Vector of critical points (e.g. singularities) where integration
care should be taken.

t0 [float, (0: solver-determined), optional] The step size to be attempted on the first
step.

h0 [float, (0: solver-determined), optional] The maximum absolute step size allowed.

hmin [float, (0: solver-determined), optional] The minimum absolute step size allowed.

ixpr [bool, optional] Whether to generate extra printing at method switches.

mxstep [int, (0: solver-determined), optional] Maximum number of (internally defined)
steps allowed for each integration point in t.

mxhnil [int, (0: solver-determined), optional] Maximum number of messages printed.

mxordn [int, (0: solver-determined), optional] Maximum order to be allowed for the non-
stiff (Adams) method.

mxords [int, (0: solver-determined), optional] Maximum order to be allowed for the stiff
(BDF) method.

See also:

solve_ivp

Solve an initial value problem for a system of ODEs.

ode

a more object-oriented integrator based on VODE.

quad

for finding the area under a curve.

Examples

The second order differential equation for the angle \( \theta \) of a pendulum acted on by gravity with
friction can be written:

\[
\frac{d^2 \theta(t)}{dt^2} + b \frac{d\theta(t)}{dt} + c \sin(\theta(t)) = 0
\]

where \( b \) and \( c \) are positive constants, and a prime (‘) denotes a derivative. To solve this equation with
odeint, we must first convert it to a system of first order equations. By defining the angular velocity
\( \omega(t) = \frac{d\theta(t)}{dt} \), we obtain the system:

\[
\begin{align*}
\frac{d\theta(t)}{dt} &= \omega(t) \\
\frac{d\omega(t)}{dt} &= -b \omega(t) - c \sin(\theta(t))
\end{align*}
\]

Let \( y \) be the vector \([\theta, \omega]\). We implement this system in python as:

```python
>>> def pend(y, t, b, c):
...     theta, omega = y
...     dydt = [omega, -b*omega - c*np.sin(theta)]
...     return dydt
...```

We assume the constants are \( b = 0.25 \) and \( c = 5.0 \):

```python
>>> b = 0.25
>>> c = 5.0
```
For initial conditions, we assume the pendulum is nearly vertical with \( \theta(0) = \pi - 0.1 \), and is initially at rest, so \( \omega(0) = 0 \). Then the vector of initial conditions is

```python
>>> y0 = [np.pi - 0.1, 0.0]
```

We will generate a solution at 101 evenly spaced samples in the interval \( 0 \leq t \leq 10 \). So our array of times is:

```python
>>> t = np.linspace(0, 10, 101)
```

Call `odeint` to generate the solution. To pass the parameters \( b \) and \( c \) to `pend`, we give them to `odeint` using the `args` argument.

```python
>>> from scipy.integrate import odeint
>>> sol = odeint(pend, y0, t, args=(b, c))
```

The solution is an array with shape \((101, 2)\). The first column is \( \theta(t) \), and the second is \( \omega(t) \). The following code plots both components.

```python
>>> import matplotlib.pyplot as plt
>>> plt.plot(t, sol[:, 0], 'b', label='\theta(t)')
>>> plt.plot(t, sol[:, 1], 'g', label='\omega(t)')
>>> plt.legend(loc='best')
>>> plt.xlabel('t')
>>> plt.grid()
>>> plt.show()
```

**scipy.integrate.ode**

**class scipy.integrate.ode\((f, jac=None)\)**

A generic interface class to numeric integrators.

Solve an equation system \( y'(t) = f(t, y) \) with \( (optional) \) \( jac = \frac{df}{dy} \).

**Note:** The first two arguments of \( f(t, y, ...) \) are in the opposite order of the arguments in the system definition function used by `scipy.integrate.odeint`.

**Parameters**

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f [callable f(t, y, *f_args)] Right-hand side of the differential equation. t is a scalar, y.shape == (n,). f_args is set by calling set_f_params(*args). f should return a scalar, array or list (not a tuple).


See also:

odeint

an integrator with a simpler interface based on lsoda from ODEPACK

quad

for finding the area under a curve

Notes

Available integrators are listed below. They can be selected using the set_integrator method.

“vode”

Real-valued Variable-coefficient Ordinary Differential Equation solver, with fixed-leading-coefficient implementation. It provides implicit Adams method (for non-stiff problems) and a method based on backward differentiation formulas (BDF) (for stiff problems).

Source: http://www.netlib.org/ode/vode.f

Warning: This integrator is not re-entrant. You cannot have two ode instances using the “vode” integrator at the same time.

This integrator accepts the following parameters in set_integrator method of the ode class:

• atol : float or sequence absolute tolerance for solution
• rtol : float or sequence relative tolerance for solution
• lband : None or int
• uband : None or int Jacobian band width, jac[i,j] != 0 for i-lband <= j <= i+uband. Setting these requires your jac routine to return the jacobian in packed format, jac_packed[i-j+uband, j] = jac[i,j]. The dimension of the matrix must be (lband+uband+1, len(y)).
• method: ‘adams’ or ‘bdf’ Which solver to use, Adams (non-stiff) or BDF (stiff)
• with_jacobian : bool This option is only considered when the user has not supplied a Jacobian function and has not indicated (by setting either band) that the Jacobian is banded. In this case, with_jacobian specifies whether the iteration method of the ODE solver’s correction step is chord iteration with an internally generated full Jacobian or functional iteration with no Jacobian.
• nsteps : int Maximum number of (internally defined) steps allowed during one call to the solver.
• first_step : float
• min_step : float
• max_step : float Limits for the step sizes used by the integrator.
• order : int Maximum order used by the integrator, order <= 12 for Adams, <= 5 for BDF.

“zvode”

Complex-valued Variable-coefficient Ordinary Differential Equation solver, with fixed-leading-coefficient implementation. It provides implicit Adams method (for non-stiff problems) and a method based on backward differentiation formulas (BDF) (for stiff problems).

Source: http://www.netlib.org/ode/zvode.f
**Warning:** This integrator is not re-entrant. You cannot have two `ode` instances using the “zvode” integrator at the same time.

This integrator accepts the same parameters in `set_integrator` as the “vode” solver.

**Note:** When using ZVODE for a stiff system, it should only be used for the case in which the function $f$ is analytic, that is, when each $f(i)$ is an analytic function of each $y(j)$. Analyticity means that the partial derivative $df(i)/dy(j)$ is a unique complex number, and this fact is critical in the way ZVODE solves the dense or banded linear systems that arise in the stiff case. For a complex stiff ODE system in which $f$ is not analytic, ZVODE is likely to have convergence failures, and for this problem one should instead use DVODE on the equivalent real system (in the real and imaginary parts of $y$).

“lsoda”

Real-valued Variable-coefficient Ordinary Differential Equation solver, with fixed-leading-coefficient implementation. It provides automatic method switching between implicit Adams method (for non-stiff problems) and a method based on backward differentiation formulas (BDF) (for stiff problems).

Source: [http://www.netlib.org/odepack](http://www.netlib.org/odepack)

**Warning:** This integrator is not re-entrant. You cannot have two `ode` instances using the “lsoda” integrator at the same time.

This integrator accepts the following parameters in `set_integrator()` method of the `ode` class:

- `atol` : float or sequence absolute tolerance for solution
- `rtol` : float or sequence relative tolerance for solution
- `lband` : None or int
- `uband` : None or int Jacobian band width, $jac_{[i,j]} != 0$ for $i-lband <= j <= i+uband$. Setting these requires your `jac` routine to return the jacobian in packed format, $jac_{packed}[i-j+uband, j] = jac_{[i,j]}$.
- `with_jacobian` : bool Not used.
- `nsteps` : int Maximum number of (internally defined) steps allowed during one call to the solver.
- `first_step` : float
- `min_step` : float
- `max_step` : float Limits for the step sizes used by the integrator.
- `max_order_ns` : int Maximum order used in the nonstiff case (default 12).
- `max_order_s` : int Maximum order used in the stiff case (default 5).
- `max_hnil` : int Maximum number of messages reporting too small step size ($t + h = t$) (default 0)
- `ixpr` : int Whether to generate extra printing at method switches (default False).

“dopri5”

This is an explicit runge-kutta method of order (4)5 due to Dormand & Prince (with stepsize control and dense output).

Authors:

E. Hairer and G. Wanner Universite de Genève, Dept. de Mathematiques CH-1211 Genève 24, Switzerland e-mail: ernst.hairer@math.unige.ch, gerhard.wanner@math.unige.ch

This code is described in [HNW93].

This integrator accepts the following parameters in `set_integrator()` method of the `ode` class:

- `atol` : float or sequence absolute tolerance for solution
- `rtol` : float or sequence relative tolerance for solution
• nsteps : int Maximum number of (internally defined) steps allowed during one call to the solver.
• first_step : float
• max_step : float
• safety : float Safety factor on new step selection (default 0.9)
• ifactor : float
• dfactor : float Maximum factor to increase/decrease step size by in one step
• beta : float Beta parameter for stabilised step size control.
• verbosity : int Switch for printing messages (< 0 for no messages).

“dop853”

This is an explicit runge-kutta method of order 8(5,3) due to Dormand & Prince (with stepsize control and dense output).

Options and references the same as “dopri5”.

References

/HNW93/

Examples

A problem to integrate and the corresponding jacobian:

```python
>>> from scipy.integrate import ode
>>> >>> y0, t0 = [1.0j, 2.0], 0
>>> >>> def f(t, y, arg1):
...     return [1j*arg1*y[0] + y[1], -arg1*y[1]**2]
>>> def jac(t, y, arg1):
...     return [[1j*arg1, 1], [0, -arg1*2*y[1]]]
```

The integration:

```python
>>> r = ode(f, jac).set_integrator('zvode', method='bdf')
>>> r.set_initial_value(y0, t0).set_f_params(2.0).set_jac_params(2.0)
>>> t1 = 10
>>> dt = 1
>>> while r.successful() and r.t < t1:
...     print(r.t+dt, r.integrate(r.t+dt))
1 [-0.71038232+0.23749653j 0.40000271+0.j ]
2.0 [0.19098503-0.52359246j 0.22222356+0.j ]
3.0 [0.47153208+0.52701229j 0.15384681+0.j ]
4.0 [-0.61905937+0.30726255j 0.11764744+0.j ]
5.0 [0.02340997-0.61418799j 0.09523835+0.j ]
6.0 [0.58643071+0.339819j 0.08000018+0.j ]
7.0 [-0.52070105+0.44525141j 0.06896565+0.j ]
8.0 [-0.15986733-0.61234476j 0.06060616+0.j ]
9.0 [0.64850462+0.15048982j 0.05405414+0.j ]
10.0 [-0.38404699+0.56382299j 0.04878055+0.j ]
```

 Attributes

 t [float] Current time.
 y [ndarray] Current variable values.

 Methods
get_return_code()  
Extracts the return code for the integration to enable better control if the integration fails.

integrate(t[, step, relax])  
Find y=y(t), set y as an initial condition, and return y.

set_f_params(*args)  
Set extra parameters for user-supplied function f.

set_initial_value(y[, t])  
Set initial conditions y(t) = y.

set_integrator(name, **integrator_params)  
Set integrator by name.

set_jac_params(*args)  
Set extra parameters for user-supplied function jac.

set_solout(solout)  
Set callable to be called at every successful integration step.

successful()  
Check if integration was successful.

scipy.integrate.ode.get_return_code

ode.get_return_code()  
Extracts the return code for the integration to enable better control if the integration fails.

In general, a return code > 0 implies success while a return code < 0 implies failure.

Notes  
This section describes possible return codes and their meaning, for available integrators that can be selected by set_integrator method.

“vode”

<table>
<thead>
<tr>
<th>Return Code</th>
<th>Message</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Integration successful.</td>
</tr>
<tr>
<td>-1</td>
<td>Excess work done on this call. (Perhaps wrong MF.)</td>
</tr>
<tr>
<td>-2</td>
<td>Excess accuracy requested. (Tolerances too small.)</td>
</tr>
<tr>
<td>-3</td>
<td>Illegal input detected. (See printed message.)</td>
</tr>
<tr>
<td>-4</td>
<td>Repeated error test failures. (Check all input.)</td>
</tr>
<tr>
<td>-5</td>
<td>Repeated convergence failures. (Perhaps bad Jacobian supplied or wrong choice of MF or tolerances.)</td>
</tr>
<tr>
<td>-6</td>
<td>Error weight became zero during problem. (Solution component i vanished, and ATOL or ATOL(i) = 0.)</td>
</tr>
</tbody>
</table>

“zvode”

<table>
<thead>
<tr>
<th>Return Code</th>
<th>Message</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Integration successful.</td>
</tr>
<tr>
<td>-1</td>
<td>Excess work done on this call. (Perhaps wrong MF.)</td>
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<tr>
<td>-2</td>
<td>Excess accuracy requested. (Tolerances too small.)</td>
</tr>
<tr>
<td>-3</td>
<td>Illegal input detected. (See printed message.)</td>
</tr>
<tr>
<td>-4</td>
<td>Repeated error test failures. (Check all input.)</td>
</tr>
<tr>
<td>-5</td>
<td>Repeated convergence failures. (Perhaps bad Jacobian supplied or wrong choice of MF or tolerances.)</td>
</tr>
<tr>
<td>-6</td>
<td>Error weight became zero during problem. (Solution component i vanished, and ATOL or ATOL(i) = 0.)</td>
</tr>
</tbody>
</table>
"dopri5"

<table>
<thead>
<tr>
<th>Return Code</th>
<th>Message</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Integration successful.</td>
</tr>
<tr>
<td>2</td>
<td>Integration successful (interrupted by solout).</td>
</tr>
<tr>
<td>-1</td>
<td>Input is not consistent.</td>
</tr>
<tr>
<td>-2</td>
<td>Larger nsteps is needed.</td>
</tr>
<tr>
<td>-3</td>
<td>Step size becomes too small.</td>
</tr>
<tr>
<td>-4</td>
<td>Problem is probably stiff (interrupted).</td>
</tr>
</tbody>
</table>

"dop853"

<table>
<thead>
<tr>
<th>Return Code</th>
<th>Message</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Integration successful.</td>
</tr>
<tr>
<td>2</td>
<td>Integration successful (interrupted by solout).</td>
</tr>
<tr>
<td>-1</td>
<td>Input is not consistent.</td>
</tr>
<tr>
<td>-2</td>
<td>Larger nsteps is needed.</td>
</tr>
<tr>
<td>-3</td>
<td>Step size becomes too small.</td>
</tr>
<tr>
<td>-4</td>
<td>Problem is probably stiff (interrupted).</td>
</tr>
</tbody>
</table>

"lsoda"

<table>
<thead>
<tr>
<th>Return Code</th>
<th>Message</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Integration successful.</td>
</tr>
<tr>
<td>-1</td>
<td>Excess work done on this call (perhaps wrong Dfun type).</td>
</tr>
<tr>
<td>-2</td>
<td>Excess accuracy requested (tolerances too small).</td>
</tr>
<tr>
<td>-3</td>
<td>Illegal input detected (internal error).</td>
</tr>
<tr>
<td>-4</td>
<td>Repeated error test failures (internal error).</td>
</tr>
<tr>
<td>-5</td>
<td>Repeated convergence failures (perhaps bad Jacobian or tolerances).</td>
</tr>
<tr>
<td>-6</td>
<td>Error weight became zero during problem.</td>
</tr>
<tr>
<td>-7</td>
<td>Internal workspace insufficient to finish (internal error).</td>
</tr>
</tbody>
</table>

**scipy.integrate.ode.integrate**

**ode.integrate**(t, step=False, relax=False)

Find y=y(t), set y as an initial condition, and return y.

**Parameters**

- **t** [float] The endpoint of the integration step.
- **step** [bool] If True, and if the integrator supports the step method, then perform a single integration step and return. This parameter is provided in order to expose internals of the implementation, and should not be changed from its default value in most cases.
- **relax** [bool] If True and if the integrator supports the run_relax method, then integrate until t_1 >= t and return. relax is not referenced if step=True. This parameter is provided in order to expose internals of the implementation, and should not be changed from its default value in most cases.

**Returns**

- **y** [float] The integrated value at t
scipy.integrate.ode.set_f_params

ode.set_f_params(*args)
Set extra parameters for user-supplied function f.

scipy.integrate.ode.set_initial_value

ode.set_initial_value(y, t=0.0)
Set initial conditions y(t) = y.

scipy.integrate.ode.set_integrator

ode.set_integrator(name, **integrator_params)
Set integrator by name.

Parameters
name [str] Name of the integrator.
integrator_params
Additional parameters for the integrator.

scipy.integrate.ode.set_jac_params

ode.set_jac_params(*args)
Set extra parameters for user-supplied function jac.

scipy.integrate.ode.set_solout

ode.set_solout(solout)
Set callable to be called at every successful integration step.

Parameters
solout [callable] solout(t, y) is called at each internal integrator step, t is a scalar providing the current independent position y is the current soloution y.shape == (n,) solout should return -1 to stop integration otherwise it should return None or 0

scipy.integrate.ode.successful

ode.successful()
Check if integration was successful.

scipy.integrate.complex_ode

class scipy.integrate.complex_ode(f, jac=None)
A wrapper of ode for complex systems.
This functions similarly as ode, but re-maps a complex-valued equation system to a real-valued one before using the integrators.

Parameters
f [callable f(t, y, *f_args)] Rhs of the equation. t is a scalar, y.shape == (n,). f_args is set by calling set_f_params(*args).
jac [callable jac(t, y, *jac_args)] Jacobian of the rhs, jac[i,j] = df[i] / dy[j]. jac_args is set by calling set_f_params(*args).
Examples
For usage examples, see `ode`.

Attributes
- `t` [float] Current time.
- `y` [ndarray] Current variable values.

Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>get_return_code()</code></td>
<td>Extracts the return code for the integration to enable better control if the integration fails.</td>
</tr>
<tr>
<td><code>integrate(t[, step, relax])</code></td>
<td>Find $y = y(t)$, set $y$ as an initial condition, and return $y$.</td>
</tr>
<tr>
<td><code>set_f_params(*args)</code></td>
<td>Set extra parameters for user-supplied function $f$.</td>
</tr>
<tr>
<td><code>set_initial_value(y[, t])</code></td>
<td>Set initial conditions $y(t) = y$.</td>
</tr>
<tr>
<td><code>set_integrator(name, **integrator_params)</code></td>
<td>Set integrator by name.</td>
</tr>
<tr>
<td><code>set_jac_params(*args)</code></td>
<td>Set extra parameters for user-supplied function $jac$.</td>
</tr>
<tr>
<td><code>set_solout(solout)</code></td>
<td>Set callable to be called at every successful integration step.</td>
</tr>
<tr>
<td><code>successful()</code></td>
<td>Check if integration was successful.</td>
</tr>
</tbody>
</table>

`scipy.integrate.complex_ode.get_return_code`

Extracts the return code for the integration to enable better control if the integration fails.

In general, a return code $> 0$ implies success while a return code $< 0$ implies failure.

Notes
This section describes possible return codes and their meaning, for available integrators that can be selected by `set_integrator` method.

“vode”

<table>
<thead>
<tr>
<th>Return Code</th>
<th>Message</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Integration successful.</td>
</tr>
<tr>
<td>-1</td>
<td>Excess work done on this call. (Perhaps wrong MF.)</td>
</tr>
<tr>
<td>-2</td>
<td>Excess accuracy requested. (Tolerances too small.)</td>
</tr>
<tr>
<td>-3</td>
<td>Illegal input detected. (See printed message.)</td>
</tr>
<tr>
<td>-4</td>
<td>Repeated error test failures. (Check all input.)</td>
</tr>
<tr>
<td>-5</td>
<td>Repeated convergence failures. (Perhaps bad Jacobian supplied or wrong choice of MF or tolerances.)</td>
</tr>
<tr>
<td>-6</td>
<td>Error weight became zero during problem. (Solution component $i$ vanished, and ATOL or ATOL($i$) = 0.)</td>
</tr>
</tbody>
</table>

“zvode”
<table>
<thead>
<tr>
<th>Return Code</th>
<th>Message</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Integration successful.</td>
</tr>
<tr>
<td>-1</td>
<td>Excess work done on this call. (Perhaps wrong MF.)</td>
</tr>
<tr>
<td>-2</td>
<td>Excess accuracy requested. (Tolerances too small.)</td>
</tr>
<tr>
<td>-3</td>
<td>Illegal input detected. (See printed message.)</td>
</tr>
<tr>
<td>-4</td>
<td>Repeated error test failures. (Check all input.)</td>
</tr>
<tr>
<td>-5</td>
<td>Repeated convergence failures. (Perhaps bad Jacobian supplied or wrong choice of MF or tolerances.)</td>
</tr>
<tr>
<td>-6</td>
<td>Error weight became zero during problem. (Solution component i vanished, and ATOL or ATOL(i) = 0.)</td>
</tr>
</tbody>
</table>

“dopri5”

<table>
<thead>
<tr>
<th>Return Code</th>
<th>Message</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Integration successful.</td>
</tr>
<tr>
<td>2</td>
<td>Integration successful (interrupted by solout).</td>
</tr>
<tr>
<td>-1</td>
<td>Input is not consistent.</td>
</tr>
<tr>
<td>-2</td>
<td>Larger nsteps is needed.</td>
</tr>
<tr>
<td>-3</td>
<td>Step size becomes too small.</td>
</tr>
<tr>
<td>-4</td>
<td>Problem is probably stiff (interrupted).</td>
</tr>
</tbody>
</table>

“dop853”

<table>
<thead>
<tr>
<th>Return Code</th>
<th>Message</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Integration successful.</td>
</tr>
<tr>
<td>2</td>
<td>Integration successful (interrupted by solout).</td>
</tr>
<tr>
<td>-1</td>
<td>Input is not consistent.</td>
</tr>
<tr>
<td>-2</td>
<td>Larger nsteps is needed.</td>
</tr>
<tr>
<td>-3</td>
<td>Step size becomes too small.</td>
</tr>
<tr>
<td>-4</td>
<td>Problem is probably stiff (interrupted).</td>
</tr>
</tbody>
</table>

“lsoda”

<table>
<thead>
<tr>
<th>Return Code</th>
<th>Message</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Integration successful.</td>
</tr>
<tr>
<td>-1</td>
<td>Excess work done on this call (perhaps wrong Dfun type).</td>
</tr>
<tr>
<td>-2</td>
<td>Excess accuracy requested (tolerances too small).</td>
</tr>
<tr>
<td>-3</td>
<td>Illegal input detected (internal error).</td>
</tr>
<tr>
<td>-4</td>
<td>Repeated error test failures (internal error).</td>
</tr>
<tr>
<td>-5</td>
<td>Repeated convergence failures (perhaps bad Jacobian or tolerances).</td>
</tr>
<tr>
<td>-6</td>
<td>Error weight became zero during problem.</td>
</tr>
<tr>
<td>-7</td>
<td>Internal workspace insufficient to finish (internal error).</td>
</tr>
</tbody>
</table>

`scipy.integrate.complex_ode.integrate`

`complex_ode.integrate(t, step=False, relax=False)`

Find y=y(t), set y as an initial condition, and return y.

**Parameters**

- `t` [float] The endpoint of the integration step.
step  [bool] If True, and if the integrator supports the step method, then perform a single integration step and return. This parameter is provided in order to expose internals of the implementation, and should not be changed from its default value in most cases.

relax  [bool] If True and if the integrator supports the run_relax method, then integrate until \( t_1 \geq t \) and return. relax is not referenced if step=True. This parameter is provided in order to expose internals of the implementation, and should not be changed from its default value in most cases.

Returns

y  [float] The integrated value at \( t \)

```python
scipy.integrate.complex_ode.set_f_params
c
complex_ode.set_f_params(*args)
    Set extra parameters for user-supplied function f.
```

```python
scipy.integrate.complex_ode.set_initial_value
c
complex_ode.set_initial_value(y, t=0.0)
    Set initial conditions \( y(t) = y \).
```

```python
scipy.integrate.complex_ode.set_integrator
c
complex_ode.set_integrator(name, **integrator_params)
    Set integrator by name.

Parameters

name  [str] Name of the integrator

integrator_params
    Additional parameters for the integrator.
```

```python
scipy.integrate.complex_ode.set_jac_params
c
complex_ode.set_jac_params(*args)
    Set extra parameters for user-supplied function jac.
```

```python
scipy.integrate.complex_ode.set_solout
c
complex_ode.set_solout(solout)
    Set callable to be called at every successful integration step.

Parameters

solout  [callable] solout(t, y) is called at each internal integrator step, \( t \) is a scalar providing the current independent position \( y \) is the current solution \( y \). shape == (n,) solout should return -1 to stop integration otherwise it should return None or 0
```

```python
scipy.integrate.complex_ode.successful
c
complex_ode.successful()
    Check if integration was successful.
```
6.6.4 Solving boundary value problems for ODE systems

`solve_bvp` function

```python
scipy.integrate.solve_bvp
```

This function numerically solves a first order system of ODEs subject to two-point boundary conditions:

\[
\frac{dy}{dx} = f(x, y, p) + S \cdot \frac{y}{x-a}, \quad a < x < b
\]

\[
bc(y(a), y(b), p) = 0
\]

Here \(x\) is a 1-dimensional independent variable, \(y(x)\) is a \(n\)-dimensional vector-valued function and \(p\) is a \(k\)-dimensional vector of unknown parameters which is to be found along with \(y(x)\). For the problem to be determined there must be \(n + k\) boundary conditions, i.e. \(bc\) must be \((n + k)\)-dimensional function.

The last singular term in the right-hand side of the system is optional. It is defined by an \(n\)-by-\(n\) matrix \(S\), such that the solution must satisfy \(S \cdot y(a) = 0\). This condition will be forced during iterations, so it must not contradict boundary conditions. See \cite{2} for the explanation how this term is handled when solving BVPs numerically.

Problems in a complex domain can be solved as well. In this case \(y\) and \(p\) are considered to be complex, and \(f\) and \(bc\) are assumed to be complex-valued functions, but \(x\) stays real. Note that \(f\) and \(bc\) must be complex differentiable (satisfy Cauchy-Riemann equations \cite{4}), otherwise you should rewrite your problem for real and imaginary parts separately. To solve a problem in a complex domain, pass an initial guess for \(y\) with a complex data type (see below).

**Parameters**

- **fun** [callable] Right-hand side of the system. The calling signature is `fun(x, y)`, or `fun(x, y, p)` if parameters are present. All arguments are `ndarray`: \(x\) with shape \((m,)\), \(y\) with shape \((n, m)\), meaning that \(y[:, i]\) corresponds to \(x[i]\), and \(p\) with shape \((k,)\). The return value must be an `ndarray` with shape \((n, m)\) and with the same layout as \(y\).

- **bc** [callable] Function evaluating residuals of the boundary conditions. The calling signature is `bc(ya, yb)`, or `bc(ya, yb, p)` if parameters are present. All arguments are `ndarray`: \(ya\) and \(yb\) with shape \((n,)\), and \(p\) with shape \((k,)\). The return value must be an `ndarray` with shape \((n + k,)\).

- **x** [array_like, shape \((m,)\)] Initial mesh. Must be a strictly increasing sequence of real numbers with \(x[0]=a\) and \(x[-1]=b\).

- **y** [array_like, shape \((n, m)\)] Initial guess for the function values at the mesh nodes, \(i\)-th column corresponds to \(x[i]\). For problems in a complex domain pass \(y\) with a complex data type (even if the initial guess is purely real).

- **p** [array_like with shape \((k,)\) or None, optional] Initial guess for the unknown parameters. If None (default), it is assumed that the problem doesn’t depend on any parameters.

- **S** [array_like with shape \((n, n)\) or None] Matrix defining the singular term. If None (default), the problem is solved without the singular term.

- **fun_jac** [callable or None, optional] Function computing derivatives of \(f\) with respect to \(y\) and \(p\). The calling signature is `fun_jac(x, y)`, or `fun_jac(x, y, p)` if parameters are present. The return must contain 1 or 2 elements in the following order:

```python
```
df_dy : array_like with shape (n, n, m) where an element (i, j, q) equals to \[\frac{d f_i(x_q, y_q, p)}{d (y_q)_j}\].

df_dp : array_like with shape (n, k, m) where an element (i, j, q) equals to \[\frac{d f_i(x_q, y_q, p)}{d p_j}\].

Here q numbers nodes at which x and y are defined, whereas i and j number vector components. If the problem is solved without unknown parameters df_dp should not be returned.

If fun_jac is None (default), the derivatives will be estimated by the forward finite differences.

bc_jac [callable or None, optional] Function computing derivatives of bc with respect to ya, yb and p. The calling signature is bc_jac(ya, yb), or bc_jac(ya, yb, p) if parameters are present. The return must contain 2 or 3 elements in the following order:

dbc_dya : array_like with shape (n, n) where an element (i, j) equals to \[\frac{d bc_i(ya, yb, p)}{d ya_j}\].

dbc_dyb : array_like with shape (n, n) where an element (i, j) equals to \[\frac{d bc_i(ya, yb, p)}{d yb_j}\].

dbc_dp : array_like with shape (n, k) where an element (i, j) equals to \[\frac{d bc_i(ya, yb, p)}{d p_j}\].

If the problem is solved without unknown parameters dbc_dp should not be returned.

If bc_jac is None (default), the derivatives will be estimated by the forward finite differences.

tol [float, optional] Desired tolerance of the solution. If we define \(r = y' - f(x, y)\) where y is the found solution, then the solver tries to achieve on each mesh interval \(\text{norm}(r / (1 + \text{abs}(f)) < \text{tol}\), where norm is estimated in a root mean squared sense (using a numerical quadrature formula). Default is 1e-3.

max_nodes [int, optional] Maximum allowed number of the mesh nodes. If exceeded, the algorithm terminates. Default is 1000.

verbose [{0, 1, 2}, optional] Level of algorithm’s verbosity:

• 0 (default) : work silently.
• 1 : display a termination report.
• 2 : display progress during iterations.

Returns

Bunch object with the following fields defined:

sol [PPoly] Found solution for y as scipy.interpolate.PPoly instance, a C1 continuous cubic spline.

p [ndarray or None, shape (k,)] Found parameters. None, if the parameters were not present in the problem.

x [ndarray, shape (m,)] Nodes of the final mesh.

y [ndarray, shape (n, m)] Solution values at the mesh nodes.

yp [ndarray, shape (n, m)] Solution derivatives at the mesh nodes.

rms_residuals [ndarray, shape (m - 1,)] RMS values of the relative residuals over each mesh interval (see the description of tol parameter).

niter [int] Number of completed iterations.

status [int] Reason for algorithm termination:

• 0: The algorithm converged to the desired accuracy.
• 1: The maximum number of mesh nodes is exceeded.
• 2: A singular Jacobian encountered when solving the collocation system.

message [string] Verbal description of the termination reason.

success [bool] True if the algorithm converged to the desired accuracy (status=0).
Notes
This function implements a 4-th order collocation algorithm with the control of residuals similar to [1].
A collocation system is solved by a damped Newton method with an affine-invariant criterion function as described in [3].

Note that in [1] integral residuals are defined without normalization by interval lengths. So their definition is different by a multiplier of \( h^{0.5} \) (\( h \) is an interval length) from the definition used here.

New in version 0.18.0.

References
[1], [2], [3], [4]

Examples
In the first example we solve Bratu’s problem:

\[
\begin{align*}
    y'''' + k \cdot \exp(y) &= 0 \\
    y(0) &= y(1) = 0
\end{align*}
\]

for \( k = 1 \).

We rewrite the equation as a first order system and implement its right-hand side evaluation:

\[
\begin{align*}
    y_1' &= y_2 \\
    y_2' &= -\exp(y_1)
\end{align*}
\]

```python
>>> def fun(x, y):
...     return np.vstack((y[1], -np.exp(y[0])))
```

Implement evaluation of the boundary condition residuals:

```python
>>> def bc(ya, yb):
...     return np.array([ya[0], yb[0]])
```

Define the initial mesh with 5 nodes:

```python
>>> x = np.linspace(0, 1, 5)
```

This problem is known to have two solutions. To obtain both of them we use two different initial guesses for \( y \). We denote them by subscripts a and b.

```python
>>> y_a = np.zeros((2, x.size))
>>> y_b = np.zeros((2, x.size))
>>> y_b[0] = 3
```

Now we are ready to run the solver.

```python
>>> from scipy.integrate import solve_bvp
>>> res_a = solve_bvp(fun, bc, x, y_a)
>>> res_b = solve_bvp(fun, bc, x, y_b)
```

Let’s plot the two found solutions. We take an advantage of having the solution in a spline form to produce a smooth plot.

```python
>>> x_plot = np.linspace(0, 1, 100)
>>> y_plot_a = res_a.sol(x_plot)[0]
>>> y_plot_b = res_b.sol(x_plot)[0]
```

(continues on next page)
We see that the two solutions have similar shape, but differ in scale significantly.

In the second example we solve a simple Sturm-Liouville problem:

\[
y'' + k^2 y = 0
\]
\[
y(0) = y(1) = 0
\]

It is known that a non-trivial solution \( y = A \sin(k \times x) \) is possible for \( k = \pi \times n \), where \( n \) is an integer. To establish the normalization constant \( A = 1 \) we add a boundary condition:

\[
y'(0) = k
\]

Again we rewrite our equation as a first order system and implement its right-hand side evaluation:

\[
y_1' = y_2
\]
\[
y_2' = -k^2 y_1
\]

```python
>>> def fun(x, y, p):
...     k = p[0]
...     return np.vstack((y[1], -k**2 * y[0]))
```

Note that parameters \( p \) are passed as a vector (with one element in our case).

Implement the boundary conditions:
>>> def bc(ya, yb, p):
    ...     k = p[0]
    ...     return np.array([ya[0], yb[0], ya[1] - k])

Setup the initial mesh and guess for y. We aim to find the solution for k = 2 * pi, to achieve that we set values of y to approximately follow sin(2 * pi * x):

>>> x = np.linspace(0, 1, 5)
>>> y = np.zeros((2, x.size))
>>> y[0, 1] = 1
>>> y[0, 3] = -1

Run the solver with 6 as an initial guess for k.

>>> sol = solve_bvp(fun, bc, x, y, p=[6])

We see that the found k is approximately correct:

>>> sol.p[0]
6.28329460046

And finally plot the solution to see the anticipated sinusoid:

>>> x_plot = np.linspace(0, 1, 100)
>>> y_plot = sol.sol(x_plot)[0]
>>> plt.plot(x_plot, y_plot)
>>> plt.xlabel("x")
>>> plt.ylabel("y")
>>> plt.show()

6.7 Interpolation (scipy.interpolate)

Sub-package for objects used in interpolation.
As listed below, this sub-package contains spline functions and classes, one-dimensional and multi-dimensional (univariate and multivariate) interpolation classes, Lagrange and Taylor polynomial interpolators, and wrappers for FITPACK and DFITPACK functions.

### 6.7.1 Univariate interpolation

- `interp1d(x, y[, kind, axis, copy, ...])`
  - Interpolate a 1-D function.
- `BarycentricInterpolator(xi[, yi, axis])`
  - The interpolating polynomial for a set of points.
- `KroghInterpolator(xi, yi[, axis])`
  - Interpolating polynomial for a set of points.
- `PchipInterpolator(x, y[, axis, extrapolate])`
  - PCHIP 1-d monotonic cubic interpolation.
- `barycentric_interpolate(xi, yi, x[, axis])`
  - Convenience function for polynomial interpolation.
- `krogh_interpolate(xi, yi, x[, der, axis])`
  - Convenience function for polynomial interpolation.
- `pchip_interpolate(xi, yi, x[, der, axis])`
  - Convenience function for pchip interpolation.
- `Akima1DInterpolator(x, y[, axis])`
  - Akima interpolator
- `CubicSpline(x, y[, axis, bc_type, extrapolate])`
  - Cubic spline data interpolator.
- `PPoly(c, x[, extrapolate, axis])`
  - Piecewise polynomial in terms of coefficients and breakpoints
- `BPoly(c, x[, extrapolate, axis])`
  - Piecewise polynomial in terms of coefficients and breakpoints

#### scipy.interpolate.interp1d

**class scipy.interpolate.interp1d(x, y, kind='linear', axis=-1, copy=True, bounds_error=None, fill_value=None, assume_sorted=False)**

Interpolate a 1-D function.

- `x` and `y` are arrays of values used to approximate some function f: y = f(x). This class returns a function whose call method uses interpolation to find the value of new points.

Note that calling `interp1d` with NaNs present in input values results in undefined behaviour.

**Parameters**

- `x` ([N,] array_like) A 1-D array of real values.
- `y` [(...,N,...) array_like] A N-D array of real values. The length of y along the interpolation axis must be equal to the length of x.
- `kind` [str or int, optional] Specifies the kind of interpolation as a string ('linear', 'nearest', 'zero', 'slinear', 'quadratic', 'cubic', 'previous', 'next', where 'zero', 'slinear', 'quadratic' and 'cubic' refer to a spline interpolation of zeroth, first, second or third order; 'previous' and 'next' simply return the previous or next value of the point) or as an integer specifying the order of the spline interpolator to use. Default is 'linear'.
- `axis` [int, optional] Specifies the axis of y along which to interpolate. Interpolation defaults to the last axis of y.
- `copy` [bool, optional] If True, the class makes internal copies of x and y. If False, references to x and y are used. The default is to copy.
- `bounds_error` [bool, optional] If True, a ValueError is raised any time interpolation is attempted on a value outside of the range of x (where extrapolation is necessary). If False, out of bounds values are assigned fill_value. By default, an error is raised unless fill_value = "extrapolate".
- `fill_value` [array-like or (array-like, array_like) or “extrapolate”, optional]
- if a `ndarray` (or float), this value will be used to fill in for requested points outside of the data range. If not provided, then the default is NaN. The array-like must broadcast properly to the dimensions of the non-interpolation axes.

- If a two-element tuple, then the first element is used as a fill value for \( x_{\text{new}} < x[0] \) and the second element is used for \( x_{\text{new}} > x[-1] \). Anything that is not a 2-element tuple (e.g., list or `ndarray`, regardless of shape) is taken to be a single array-like argument meant to be used for both bounds as `below`, `above`
  
  New in version 0.17.0.

- If “extrapolate”, then points outside the data range will be extrapolated.
  
  New in version 0.17.0.

```
assume_sorted
```

[bool, optional] If False, values of \( x \) can be in any order and they are sorted first. If True, \( x \) has to be an array of monotonically increasing values.

See also:

- `splev, splrep`

`UnivariateSpline`

An object-oriented wrapper of the FITPACK routines.

`interp2d`

2-D interpolation

```
import matplotlib.pyplot as plt
from scipy import interpolate

x = np.arange(0, 10)
y = np.exp(-x/3.0)
f = interpolate.interp1d(x, y)

xnew = np.arange(0, 9, 0.1)
ynew = f(xnew)  # use interpolation function returned by `interp1d`
plt.plot(x, y, 'o', xnew, ynew, '-')
plt.show()
```

Attributes

- `dtype`
- `fill_value`

Methods

```
__call__(x)
```

Evaluate the interpolant

**scipy.interpolate.interp1d.__call__**

interp1d.__call__(x)

Evaluate the interpolant

**Parameters**

- \( x \) [array_like] Points to evaluate the interpolant at.

**Returns**

- \( y \) [array_like] Interpolated values. Shape is determined by replacing the inter-
scipy.interpolate.BarycentricInterpolator

class scipy.interpolate.BarycentricInterpolator(xi, yi=None, axis=0)
The interpolating polynomial for a set of points.

Constructs a polynomial that passes through a given set of points. Allows evaluation of the polynomial, efficient changing of the y values to be interpolated, and updating by adding more x values. For reasons of numerical stability, this function does not compute the coefficients of the polynomial.

The values yi need to be provided before the function is evaluated, but none of the preprocessing depends on them, so rapid updates are possible.

Parameters

- **xi** : [array_like] 1-d array of x coordinates of the points the polynomial should pass through.
- **yi** : [array_like, optional] The y coordinates of the points the polynomial should pass through. If None, the y values will be supplied later via the set_y method.
- **axis** : [int, optional] Axis in the yi array corresponding to the x-coordinate values.

Notes

This class uses a “barycentric interpolation” method that treats the problem as a special case of rational function interpolation. This algorithm is quite stable, numerically, but even in a world of exact computation, unless the x coordinates are chosen very carefully - Chebyshev zeros (e.g. \cos(\pi i/n)) are a good choice - polynomial interpolation itself is a very ill-conditioned process due to the Runge phenomenon.

Based on Berrut and Trefethen 2004, “Barycentric Lagrange Interpolation”.

Attributes

- **dtype**

Methods
SciPy Reference Guide, Release 1.2.0

__call__(x)  
Evaluate the interpolating polynomial at the points x

add_xi(xi, yi)  
Add more x values to the set to be interpolated

set_yi(yi[, axis])  
Update the y values to be interpolated

**scipy.interpolate.BarycentricInterpolator.__call__**

BarycentricInterpolator.__call__(x)  
Evaluate the interpolating polynomial at the points x

**Parameters**

- x  
  [array_like] Points to evaluate the interpolant at.

**Returns**

- y  
  [array_like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

**Notes**

Currently the code computes an outer product between x and the weights, that is, it constructs an intermediate array of size N by len(x), where N is the degree of the polynomial.

**scipy.interpolate.BarycentricInterpolator.add_xi**

BarycentricInterpolator.add_xi(xi, yi=None)  
Add more x values to the set to be interpolated

The barycentric interpolation algorithm allows easy updating by adding more points for the polynomial to pass through.

**Parameters**

- xi  
  [array_like] The x coordinates of the points that the polynomial should pass through.

- yi  
  [array_like, optional] The y coordinates of the points the polynomial should pass through. Should have shape (xi.size, R); if R > 1 then the polynomial is vector-valued. If yi is not given, the y values will be supplied later. yi should be given if and only if the interpolator has y values specified.

**scipy.interpolate.BarycentricInterpolator.set_yi**

BarycentricInterpolator.set_yi(yi, axis=None)  
Update the y values to be interpolated

The barycentric interpolation algorithm requires the calculation of weights, but these depend only on the xi. The yi can be changed at any time.

**Parameters**

- yi  
  [array_like] The y coordinates of the points the polynomial should pass through. If None, the y values will be supplied later.

- axis  
  [int, optional] Axis in the yi array corresponding to the x-coordinate values.

**scipy.interpolate.KroghInterpolator**

class scipy.interpolate.KroghInterpolator(xi, yi, axis=0)  
Interpolating polynomial for a set of points.

The polynomial passes through all the pairs (xi, yi). One may additionally specify a number of derivatives at each point xi; this is done by repeating the value xi and specifying the derivatives as successive yi values.
Allows evaluation of the polynomial and all its derivatives. For reasons of numerical stability, this function does not compute the coefficients of the polynomial, although they can be obtained by evaluating all the derivatives.

**Parameters**

- **xi** [array_like, length N] Known x-coordinates. Must be sorted in increasing order.
- **yi** [array_like] Known y-coordinates. When an xi occurs two or more times in a row, the corresponding yi’s represent derivative values.
- **axis** [int, optional] Axis in the yi array corresponding to the x-coordinate values.

**Notes**

Be aware that the algorithms implemented here are not necessarily the most numerically stable known. Moreover, even in a world of exact computation, unless the x coordinates are chosen very carefully - Chebyshev zeros (e.g. cos(i*pi/n)) are a good choice - polynomial interpolation itself is a very ill-conditioned process due to the Runge phenomenon. In general, even with well-chosen x values, degrees higher than about thirty cause problems with numerical instability in this code.

Based on [1].

**References**

[1]

**Examples**

To produce a polynomial that is zero at 0 and 1 and has derivative 2 at 0, call

```python
>>> from scipy.interpolate import KroghInterpolator
>>> KroghInterpolator([0,0,1],[0,2,0])
```

This constructs the quadratic 2*X**2-2*X. The derivative condition is indicated by the repeated zero in the xi array; the corresponding yi values are 0, the function value, and 2, the derivative value.

For another example, given xi, yi, and a derivative ypi for each point, appropriate arrays can be constructed as:

```python
>>> xi = np.linspace(0, 1, 5)
>>> yi, ypi = np.random.randn(2, 5)
>>> xi_k, yi_k = np.repeat(xi, 2), np.ravel(np.dstack((yi,ypi)))
>>> KroghInterpolator(xi_k, yi_k)
```

To produce a vector-valued polynomial, supply a higher-dimensional array for yi:

```python
>>> KroghInterpolator([0,1],[[2,3],[4,5]])
```

This constructs a linear polynomial giving (2,3) at 0 and (4,5) at 1.

**Attributes**

- **dtype**

**Methods**

- **__call__(x)** Evaluate the interpolant
- **derivative(x[, der])** Evaluate one derivative of the polynomial at the point x
- **derivatives(x[, der])** Evaluate many derivatives of the polynomial at the point x
scipy.interpolate.KroghInterpolator.__call__
KroghInterpolator.__call__(x)
Evaluate the interpolant

Parameters
  x [array_like] Points to evaluate the interpolant at.

Returns
  y [array_like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

scipy.interpolate.KroghInterpolator.derivative
KroghInterpolator.derivative(x, der=1)
Evaluate one derivative of the polynomial at the point x

Parameters
  x [array_like] Point or points at which to evaluate the derivatives
der [integer, optional] Which derivative to extract. This number includes the function value as 0th derivative.

Returns
  d [ndarray] Derivative interpolated at the x-points. Shape of d is determined by replacing the interpolation axis in the original array with the shape of x.

Notes
This is computed by evaluating all derivatives up to the desired one (using self.derivatives()) and then discarding the rest.

scipy.interpolate.KroghInterpolator.derivatives
KroghInterpolator.derivatives(x, der=None)
Evaluate many derivatives of the polynomial at the point x

Produce an array of all derivative values at the point x.

Parameters
  x [array_like] Point or points at which to evaluate the derivatives
der [int or None, optional] How many derivatives to extract; None for all potentially nonzero derivatives (that is a number equal to the number of points). This number includes the function value as 0th derivative.

Returns
  d [ndarray] Array with derivatives; d[j] contains the j-th derivative. Shape of d[j] is determined by replacing the interpolation axis in the original array with the shape of x.

Examples
>>> from scipy.interpolate import KroghInterpolator
>>> KroghInterpolator([0,0,0],[1,2,3]).derivatives(0)
array([[1., 1.],
       [2., 2.],
       [3., 3.]])
>>> KroghInterpolator([0,0,0],[1,2,3]).derivatives([0,0])
array([[1.0, 1.0],
       [2.0, 2.0],
       [3.0, 3.0]])
scipy.interpolate.PchipInterpolator

class scipy.interpolate.PchipInterpolator(x, y, axis=0, extrapolate=None)

PCHIP 1-d monotonic cubic interpolation.

x and y are arrays of values used to approximate some function f, with y = f(x). The interpolant uses monotonic cubic splines to find the value of new points. (PCHIP stands for Piecewise Cubic Hermite Interpolating Polynomial).

Parameters

- x [ndarray] A 1-D array of monotonically increasing real values. x cannot include duplicate values (otherwise f is overspecified)
- y [ndarray] A 1-D array of real values. y’s length along the interpolation axis must be equal to the length of x. If N-D array, use axis parameter to select correct axis.
- axis [int, optional] Axis in the y array corresponding to the x-coordinate values.
- extrapolate [bool, optional] Whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs.

See also:

Akima1DInterpolator, CubicSpline, BPoly

Notes

The interpolator preserves monotonicity in the interpolation data and does not overshoot if the data is not smooth.

The first derivatives are guaranteed to be continuous, but the second derivatives may jump at x_k.

Determines the derivatives at the points x_k, f'_k, by using PCHIP algorithm [1].

Let h_k = x_{k+1} - x_k, and d_k = (y_{k+1} - y_k)/h_k are the slopes at internal points x_k. If the signs of d_k and d_{k-1} are different or either of them equals zero, then f'_k = 0. Otherwise, it is given by the weighted harmonic mean

\[
\frac{w_1 + w_2}{f'_k} = \frac{w_1}{d_{k-1}} + \frac{w_2}{d_k}
\]

where \(w_1 = 2h_k + h_{k-1}\) and \(w_2 = h_k + 2h_{k-1}\).

The end slopes are set using a one-sided scheme [2].

References

[1], [2]

Attributes

- axis
cextrapolate

x

Methods

- __call__([x, nu, extrapolate]) Evaluate the piecewise polynomial or its derivative.
- derivative([nu]) Construct a new piecewise polynomial representing the derivative.
- antiderivative([nu]) Construct a new piecewise polynomial representing the antiderivative.
- roots() Return the roots of the interpolated function.
**scipy.interpolate.PchipInterpolator.__call__**

PchipInterpolator.__call__(x, nu=0, extrapolate=None)

Evaluate the piecewise polynomial or its derivative.

**Parameters**

- **x** [array_like] Points to evaluate the interpolant at.
- **nu** [int, optional] Order of derivative to evaluate. Must be non-negative.
- **extrapolate** [{bool, ‘periodic’, None}, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If ‘periodic’, periodic extrapolation is used. If None (default), use self.extrapolate.

**Returns**

- **y** [array_like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

**Notes**

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, \([a, b)\), except for the last interval which is closed \([a, b]\).

**scipy.interpolate.PchipInterpolator.derivative**

PchipInterpolator.derivative(nu=1)

Construct a new piecewise polynomial representing the derivative.

**Parameters**

- **nu** [int, optional] Order of derivative to evaluate. Default is 1, i.e. compute the first derivative. If negative, the antiderivative is returned.

**Returns**

- **bp** [BPoly] Piecewise polynomial of order \(k - nu\) representing the derivative of this polynomial.

**scipy.interpolate.PchipInterpolator.antiderivative**

PchipInterpolator.antiderivative(nu=1)

Construct a new piecewise polynomial representing the antiderivative.

**Parameters**

- **nu** [int, optional] Order of antiderivative to evaluate. Default is 1, i.e. compute the first integral. If negative, the derivative is returned.

**Returns**

- **bp** [BPoly] Piecewise polynomial of order \(k + nu\) representing the antiderivative of this polynomial.

**Notes**

If antiderivative is computed and self.extrapolate='periodic', it will be set to False for the returned instance. This is done because the antiderivative is no longer periodic and its correct evaluation outside of the initially given x interval is difficult.

**scipy.interpolate.PchipInterpolator.roots**

PchipInterpolator.roots()

Return the roots of the interpolated function.
scipy.interpolate.barycentric_interpolate

scipy.interpolate.barycentric_interpolate(xi, yi, x, axis=0)

Convenience function for polynomial interpolation.

Constructs a polynomial that passes through a given set of points, then evaluates the polynomial. For reasons of numerical stability, this function does not compute the coefficients of the polynomial.

This function uses a “barycentric interpolation” method that treats the problem as a special case of rational function interpolation. This algorithm is quite stable, numerically, but even in a world of exact computation, unless the \(x\) coordinates are chosen very carefully - Chebyshev zeros (e.g. \(\cos(i\pi/n)\)) are a good choice - polynomial interpolation itself is a very ill-conditioned process due to the Runge phenomenon.

**Parameters**

- `xi` : [array_like] 1-d array of \(x\) coordinates of the points the polynomial should pass through.
- `yi` : [array_like] The \(y\) coordinates of the points the polynomial should pass through.
- `x` : [scalar or array_like] Points to evaluate the interpolator at.
- `axis` : [int, optional] Axis in the `yi` array corresponding to the \(x\)-coordinate values.

**Returns**

- `y` : [scalar or array_like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of `x`.

**See also:**

BarycentricInterpolator

**Notes**

Construction of the interpolation weights is a relatively slow process. If you want to call this many times with the same `xi` (but possibly varying `yi` or `x`) you should use the class BarycentricInterpolator. This is what this function uses internally.

scipy.interpolate.krogh_interpolate

scipy.interpolate.krogh_interpolate(xi, yi, x, der=0, axis=0)

Convenience function for polynomial interpolation.

See KroghInterpolator for more details.

**Parameters**

- `xi` : [array_like] Known \(x\)-coordinates.
- `yi` : [array_like] Known \(y\)-coordinates, of shape `(xi.size, R)`. Interpreted as vectors of length \(R\), or scalars if \(R=1\).
- `x` : [array_like] Point or points at which to evaluate the derivatives.
- `der` : [int or list, optional] How many derivatives to extract; None for all potentially nonzero derivatives (that is a number equal to the number of points), or a list of derivatives to extract. This number includes the function value as 0th derivative.
- `axis` : [int, optional] Axis in the `yi` array corresponding to the \(x\)-coordinate values.

**Returns**

- `d` : [ndarray] If the interpolator’s values are \(R\)-dimensional then the returned array will be the number of derivatives by \(N\) by \(R\). If \(x\) is a scalar, the middle dimension will be dropped; if the `yi` are scalars then the last dimension will be dropped.

**See also:**

KroghInterpolator
Notes
Construction of the interpolating polynomial is a relatively expensive process. If you want to evaluate it repeatedly consider using the class KroghInterpolator (which is what this function uses).

**scipy.interpolate.pchip_interpolate**

*scipy.interpolate.pchip_interpolate(xi, yi, x, der=0, axis=0)*

Convenience function for pchip interpolation. `xi` and `yi` are arrays of values used to approximate some function `f`, with `yi = f(xi)`. The interpolant uses monotonic cubic splines to find the value of new points `x` and the derivatives there.

See `PchipInterpolator` for details.

**Parameters**

- `xi`  
  [array_like] A sorted list of x-coordinates, of length N.

- `yi`  
  [array_like] A 1-D array of real values. `yi`'s length along the interpolation axis must be equal to the length of `xi`. If N-D array, use axis parameter to select correct axis.

- `x`  
  [scalar or array_like] Of length M.

- `der`  
  [int or list, optional] Derivatives to extract. The 0-th derivative can be included to return the function value.

- `axis`  
  [int, optional] Axis in the `yi` array corresponding to the x-coordinate values.

**Returns**

- `y`  
  [scalar or array_like] The result, of length R or length M or M by R,

See also:

`PchipInterpolator`

**scipy.interpolate.Akima1DInterpolator**

*class scipy.interpolate.Akima1DInterpolator(x, y, axis=0)*

Akima interpolator

Fit piecewise cubic polynomials, given vectors `x` and `y`. The interpolation method by Akima uses a continuously differentiable sub-spline built from piecewise cubic polynomials. The resultant curve passes through the given data points and will appear smooth and natural.

**Parameters**

- `x`  
  [ndarray, shape (m,)] 1-D array of monotonically increasing real values.

- `y`  
  [ndarray, shape (m, ...)] N-D array of real values. The length of `y` along the first axis must be equal to the length of `x`.

- `axis`  
  [int, optional] Specifies the axis of `y` along which to interpolate. Interpolation defaults to the first axis of `y`.

See also:

`PchipInterpolator`, `CubicSpline`, `PPoly`

**Notes**

New in version 0.14.

Use only for precise data, as the fitted curve passes through the given points exactly. This routine is useful for plotting a pleasingly smooth curve through a few given points for purposes of plotting.
References


Attributes

axis
c
extrap

Methods

__call__(x[, nu, extrapolate]) Evaluate the piecewise polynomial or its derivative.
derivative([nu]) Construct a new piecewise polynomial representing the derivative.
antiderivative([nu]) Construct a new piecewise polynomial representing the antiderivative.

roots([discontinuity, extrapolate]) Find real roots of the the piecewise polynomial.

scipy.interpolate.Akima1DInterpolator.__call__

Akima1DInterpolator.__call__(x, nu=0, extrapolate=None)

Evaluate the piecewise polynomial or its derivative.

Parameters

x [array_like] Points to evaluate the interpolant at.
nu [int, optional] Order of derivative to evaluate. Must be non-negative.
extrap [bool, ‘periodic’, None], optional If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If ‘periodic’, periodic extrapolation is used. If None (default), use self.extrapolate.

Returns

y [array_like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, [a, b), except for the last interval which is closed [a, b].

scipy.interpolate.Akima1DInterpolator.derivative

Akima1DInterpolator.derivative(nu=1)

Construct a new piecewise polynomial representing the derivative.

Parameters

nu [int, optional] Order of derivative to evaluate. Default is 1, i.e. compute the first derivative. If negative, the antiderivative is returned.

Returns

pp [PPoly] Piecewise polynomial of order k2 = k - n representing the derivative of this polynomial.
Notes
Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, \([a, b)\), except for the last interval which is closed \([a, b]\).

scipy.interpolate.Akima1DInterpolator.antiderivative
Akima1DInterpolator.antiderivative\((nu=1)\)
Construct a new piecewise polynomial representing the antiderivative.

Antiderivative is also the indefinite integral of the function, and derivative is its inverse operation.

Parameters
nu [int, optional] Order of antiderivative to evaluate. Default is 1, i.e. compute the first integral. If negative, the derivative is returned.

Returns
pp [PPoly] Piecewise polynomial of order \(k_2 = k + n\) representing the antiderivative of this polynomial.

Notes
The antiderivative returned by this function is continuous and continuously differentiable to order \(n-1\), up to floating point rounding error.

If antiderivative is computed and self.extrapolate='periodic', it will be set to False for the returned instance. This is done because the antiderivative is no longer periodic and its correct evaluation outside of the initially given x interval is difficult.

scipy.interpolate.Akima1DInterpolator.roots
Akima1DInterpolator.roots\((discontinuity=True, extrapolate=None)\)
Find real roots of the piecewise polynomial.

Parameters
discontinuity [bool, optional] Whether to report sign changes across discontinuities at breakpoints as roots.
extrapolate [{bool, ‘periodic’, None}, optional] If bool, determines whether to return roots from the polynomial extrapolated based on first and last intervals, ‘periodic’ works the same as False. If None (default), use self.extrapolate.

Returns
roots [ndarray] Roots of the polynomial(s).
If the PPoly object describes multiple polynomials, the return value is an object array whose each element is an ndarray containing the roots.

See also:
PPoly.solve

scipy.interpolate.CubicSpline
CubicSpline\((x, y, axis=0, bc_type='not-a-knot', extrapolate=None)\)
Cubic spline data interpolator.

Interpolate data with a piecewise cubic polynomial which is twice continuously differentiable \([1]\). The result is represented as a PPoly instance with breakpoints matching the given data.

Parameters
x  [array_like, shape (n,)] 1-d array containing values of the independent variable. Values must be real, finite and in strictly increasing order.

y  [array_like] Array containing values of the dependent variable. It can have arbitrary number of dimensions, but the length along axis (see below) must match the length of x. Values must be finite.

axis  [int, optional] Axis along which y is assumed to be varying. Meaning that for x[i] the corresponding values are np.take(y, i, axis=axis). Default is 0.

bc_type  [string or 2-tuple, optional] Boundary condition type. Two additional equations, given by the boundary conditions, are required to determine all coefficients of polynomials on each segment [2]. If bc_type is a string, then the specified condition will be applied at both ends of a spline. Available conditions are:
- ‘not-a-knot’ (default): The first and second segment at a curve end are the same polynomial. It is a good default when there is no information on boundary conditions.
- ‘periodic’: The interpolated functions is assumed to be periodic of period x[-1] - x[0]. The first and last value of y must be identical: y[0] == y[-1]. This boundary condition will result in y'[0] == y'[-1] and y''[0] == y''[-1].
- ‘clamped’: The first derivative at curves ends are zero. Assuming a 1D y, bc_type=((1, 0.0), (1, 0.0)) is the same condition.
- ‘natural’: The second derivative at curve ends are zero. Assuming a 1D y, bc_type=((2, 0.0), (2, 0.0)) is the same condition.

If bc_type is a 2-tuple, the first and the second value will be applied at the curve start and end respectively. The tuple values can be one of the previously mentioned strings (except ‘periodic’) or a tuple (order, deriv_values) allowing to specify arbitrary derivatives at curve ends:
- order: the derivative order, 1 or 2.
- deriv_value: array_like containing derivative values, shape must be the same as y, excluding axis dimension. For example, if y is 1D, then deriv_value must be a scalar. If y is 3D with the shape (n0, n1, n2) and axis=2, then deriv_value must be 2D and have the shape (n0, n1).

extrapolate  [{bool, ‘periodic’, None}, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If ‘periodic’, periodic extrapolation is used. If None (default), extrapolate is set to ‘periodic’ for bc_type=’periodic’ and to True otherwise.

See also:
Akima1DInterpolator, PchipInterpolator, PPoly

Notes
Parameters bc_type and interpolate work independently, i.e. the former controls only construction of a spline, and the latter only evaluation.

When a boundary condition is ‘not-a-knot’ and n = 2, it is replaced by a condition that the first derivative is equal to the linear interpolant slope. When both boundary conditions are ‘not-a-knot’ and n = 3, the solution is sought as a parabola passing through given points.

When ‘not-a-knot’ boundary conditions is applied to both ends, the resulting spline will be the same as returned by splrep (with s=0) and InterpolatedUnivariateSpline, but these two methods use a representation in B-spline basis.

New in version 0.18.0.

References
[1], [2]
Examples
In this example the cubic spline is used to interpolate a sampled sinusoid. You can see that the spline continuity property holds for the first and second derivatives and violates only for the third derivative.

```python
from scipy.interpolate import CubicSpline
import matplotlib.pyplot as plt

x = np.arange(10)
y = np.sin(x)
xs = np.arange(-0.5, 9.6, 0.1)
fig, ax = plt.subplots(figsize=(6.5, 4))
ax.plot(x, y, 'o', label='data')
ax.plot(xs, np.sin(xs), label='true')
ax.plot(xs, cs(xs), label='S')
ax.plot(xs, cs(xs, 1), label='S''')
ax.plot(xs, cs(xs, 2), label='S''')
ax.plot(xs, cs(xs, 3), label='S''''')
ax.set_xlim(-0.5, 9.5)
ax.legend(loc='lower left', ncol=2)
plt.show()
```

In the second example, the unit circle is interpolated with a spline. A periodic boundary condition is used. You can see that the first derivative values, ds/dx=0, ds/dy=1 at the periodic point (1, 0) are correctly computed. Note that a circle cannot be exactly represented by a cubic spline. To increase precision, more breakpoints would be required.

```python
theta = 2 * np.pi * np.linspace(0, 1, 5)
y = np.c_[np.cos(theta), np.sin(theta)]
```
The third example is the interpolation of a polynomial y = x**3 on the interval 0 <= x <= 1. A cubic spline can represent this function exactly. To achieve that we need to specify values and first derivatives at endpoints of the interval. Note that y' = 3 * x**2 and thus y'(0) = 0 and y'(1) = 3.

```python
>>> cs = CubicSpline([0, 1], [0, 1], bc_type=((1, 0), (1, 3)))
>>> x = np.linspace(0, 1)
>>> np.allclose(x**3, cs(x))
True
```

**Attributes**

- `x` (ndarray, shape (n,)) Breakpoints. The same x which was passed to the constructor.
- `c` (ndarray, shape (4, n-1, ...)) Coefficients of the polynomials on each segment. The trailing dimensions match the dimensions of y, excluding axis. For example, if y is 1-d, then c[k, i] is a coefficient for (x-x[i])**((3-k) on the segment between x[i] and x[i+1].
axis

[int] Interpolation axis. The same axis which was passed to the constructor.

Methods

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**scipy.interpolate.CubicSpline.__call__**

CubicSpline.__call__(x, nu=0, extrapolate=None)

Evaluate the piecewise polynomial or its derivative.

**Parameters**

- **x** [array_like] Points to evaluate the interpolant at.
- **nu** [int, optional] Order of derivative to evaluate. Must be non-negative.
- **extrapolate** [[bool, ‘periodic’, None], optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If ‘periodic’, periodic extrapolation is used. If None (default), use self.extrapolate.

**Returns**

- **y** [array_like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

**Notes**

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, \([a, b)\), except for the last interval which is closed \([a, b]\).

**scipy.interpolate.CubicSpline.derivative**

CubicSpline.derivative(nu=1)

Construct a new piecewise polynomial representing the derivative.

**Parameters**

- **nu** [int, optional] Order of derivative to evaluate. Default is 1, i.e. compute the first derivative. If negative, the antiderivative is returned.

**Returns**

- **pp** [PPoly] Piecewise polynomial of order \(k2 = k - n\) representing the derivative of this polynomial.

**Notes**

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, \([a, b)\), except for the last interval which is closed \([a, b]\).

**scipy.interpolate.CubicSpline.antiderivative**

CubicSpline.antiderivative(nu=1)

Construct a new piecewise polynomial representing the antiderivative.

Antiderivative is also the indefinite integral of the function, and derivative is its inverse operation.
Parameters

\( \nu \) [int, optional] Order of antiderivative to evaluate. Default is 1, i.e. compute the first integral. If negative, the derivative is returned.

Returns

\( pp \) [PPoly] Piecewise polynomial of order \( k_2 = k + n \) representing the antiderivative of this polynomial.

Notes

The antiderivative returned by this function is continuous and continuously differentiable to order \( n-1 \), up to floating point rounding error.

If antiderivative is computed and \texttt{self.extrapolate='periodic'}, it will be set to False for the returned instance. This is done because the antiderivative is no longer periodic and its correct evaluation outside of the initially given \( x \) interval is difficult.

\texttt{scipy.interpolate.CubicSpline.integrate}

\texttt{CubicSpline.integrate}(a, b, extrapolate=None)

Compute a definite integral over a piecewise polynomial.

Parameters

\( a \) [float] Lower integration bound
\( b \) [float] Upper integration bound
extrapolate [{bool, ‘periodic’, None}, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If ‘periodic’, periodic extrapolation is used. If None (default), use \texttt{self.extrapolate}.

Returns

\( ig \) [array_like] Definite integral of the piecewise polynomial over \([a, b]\)

\texttt{scipy.interpolate.CubicSpline.roots}

\texttt{CubicSpline.roots}(discontinuity=True, extrapolate=None)

Find real roots of the piecewise polynomial.

Parameters

discontinuity [bool, optional] Whether to report sign changes across discontinuities at breakpoints as roots.
extrapolate [{bool, ‘periodic’, None}, optional] If bool, determines whether to return roots from the polynomial extrapolated based on first and last intervals, ‘periodic’ works the same as False. If None (default), use \texttt{self.extrapolate}.

Returns

\( roots \) [ndarray] Roots of the polynomial(s).
If the \texttt{PPoly} object describes multiple polynomials, the return value is an object array whose each element is an \texttt{ndarray} containing the roots.

See also:

\texttt{PPoly.solve}
class scipy.interpolate.PPoly(c, x, extrapolate=None, axis=0)
Piecewise polynomial in terms of coefficients and breakpoints

The polynomial between \(x[i]\) and \(x[i + 1]\) is written in the local power basis:

\[
S = \sum(c[m, i] \times (xp - x[i])**(k-m) \text{ for } m \in \text{range}(k+1))
\]

where \(k\) is the degree of the polynomial.

Parameters
- \(c\) [ndarray, shape (k, m, …)] Polynomial coefficients, order \(k\) and \(m\) intervals
- \(x\) [ndarray, shape (m+1,)] Polynomial breakpoints. Must be sorted in either increasing or decreasing order.
- \(extrapolate\) [bool or ‘periodic’, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If ‘periodic’, periodic extrapolation is used. Default is True.
- \(axis\) [int, optional] Interpolation axis. Default is zero.

See also:
BPoly

piecewise polynomials in the Bernstein basis

Notes
High-order polynomials in the power basis can be numerically unstable. Precision problems can start to appear for orders larger than 20-30.

Attributes
- \(x\) [ndarray] Breakpoints.
- \(c\) [ndarray] Coefficients of the polynomials. They are reshaped to a 3-dimensional array with the last dimension representing the trailing dimensions of the original coefficient array.
- \(axis\) [int] Interpolation axis.

Methods

- \(--call--(x[, \text{nu, extrapolate}])\) Evaluate the piecewise polynomial or its derivative.
- \(\text{derivative}([\text{nu}])\) Construct a new piecewise polynomial representing the derivative.
- \(\text{antiderivative}([\text{nu}])\) Construct a new piecewise polynomial representing the antiderivative.
- \(\text{integrate}(a, b[, \text{extrapolate}])\) Compute a definite integral over a piecewise polynomial.
- \(\text{solve}([y, \text{discontinuity, extrapolate}])\) Find real solutions of the the equation \(\text{pp}(x) = y\).
- \(\text{roots}([\text{discontinuity, extrapolate}])\) Find real roots of the the piecewise polynomial.
- \(\text{extend}(c, x[, \text{right}])\) Add additional breakpoints and coefficients to the polynomial.
- \(\text{from_spline}(tck[, \text{extrapolate}])\) Construct a piecewise polynomial from a spline
- \(\text{from_bernstein_basis}(bp[, \text{extrapolate}])\) Construct a piecewise polynomial in the power basis from a polynomial in Bernstein basis.

Continued on next page
Table 40 – continued from previous page

construct_fast(c, x[, extrapolate, axis]) Construct the piecewise polynomial without making checks.

scipy.interpolate.PPoly.__call__
P Poly._call_(x, nu=0, extrapolate=None)
   Evaluate the piecewise polynomial or its derivative.

   Parameters
   x       [array_like] Points to evaluate the interpolant at.
   nu      [int, optional] Order of derivative to evaluate. Must be non-negative.
   extrapolate
     [{bool, ‘periodic’, None}, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If ‘periodic’, periodic extrapolation is used. If None (default), use self.extrapolate.

   Returns
   y       [array_like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

   Notes
   Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, [a, b), except for the last interval which is closed [a, b].

scipy.interpolate.PPoly.derivative
P Poly.derivative(nu=1)
   Construct a new piecewise polynomial representing the derivative.

   Parameters
   nu       [int, optional] Order of derivative to evaluate. Default is 1, i.e. compute the first derivative. If negative, the antiderivative is returned.

   Returns
   pp       [PPoly] Piecewise polynomial of order k2 = k - n representing the derivative of this polynomial.

   Notes
   Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, [a, b), except for the last interval which is closed [a, b].

scipy.interpolate.PPoly.antiderivative
P Poly.antiderivative(nu=1)
   Construct a new piecewise polynomial representing the antiderivative.

   Antiderivative is also the indefinite integral of the function, and derivative is its inverse operation.

   Parameters
   nu       [int, optional] Order of antiderivative to evaluate. Default is 1, i.e. compute the first integral. If negative, the derivative is returned.

   Returns
   pp       [PPoly] Piecewise polynomial of order k2 = k + n representing the antiderivative of this polynomial.
Notes

The antiderivative returned by this function is continuous and continuously differentiable to order n-1, up to floating point rounding error.

If antiderivative is computed and `self.extrapolate='periodic'`, it will be set to False for the returned instance. This is done because the antiderivative is no longer periodic and its correct evaluation outside of the initially given x interval is difficult.

```
scipy.interpolate.PPoly.integrate
PPoly.integrate(a, b, extrapolate=None)

Compute a definite integral over a piecewise polynomial.
```

**Parameters**

- `a` [float] Lower integration bound
- `b` [float] Upper integration bound
- `extrapolate` [{bool, ‘periodic’, None}, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If ‘periodic’, periodic extrapolation is used. If None (default), use `self.extrapolate`.

**Returns**

- `ig` [array_like] Definite integral of the piecewise polynomial over [a, b]

```
scipy.interpolate.PPoly.solve
PPoly.solve(y=0.0, discontinuity=True, extrapolate=None)

Find real solutions of the the equation pp(x) == y.
```

**Parameters**

- `y` [float, optional] Right-hand side. Default is zero.
- `discontinuity` [bool, optional] Whether to report sign changes across discontinuities at breakpoints as roots.
- `extrapolate` [{bool, ‘periodic’, None}, optional] If bool, determines whether to return roots from the polynomial extrapolated based on first and last intervals, ‘periodic’ works the same as False. If None (default), use `self.extrapolate`.

**Returns**

- `roots` [ndarray] Roots of the polynomial(s).
  If the PPoly object describes multiple polynomials, the return value is an object array whose each element is an ndarray containing the roots.

Notes

This routine works only on real-valued polynomials.

If the piecewise polynomial contains sections that are identically zero, the root list will contain the start point of the corresponding interval, followed by a `nan` value.

If the polynomial is discontinuous across a breakpoint, and there is a sign change across the breakpoint, this is reported if the `discont` parameter is True.

**Examples**

Finding roots of `[x**2 - 1, (x - 1)**2]` defined on intervals [-2, 1], [1, 2]:

```python
>>> from scipy.interpolate import PPoly
>>> pp = PPoly(np.array([[1, -4, 3], [1, 0, 0]]).T, [-2, 1, 2])
>>> pp.roots()
array([-1., 1.])
```
scipy.interpolate.PPoly.roots

PPoly.roots(discontinuity=True, extrapolate=None)
Find real roots of the the piecewise polynomial.

Parameters

- discontinuity
  [bool, optional] Whether to report sign changes across discontinuities at breakpoints as roots.
- extrapolate
  [{bool, 'periodic', None}, optional] If bool, determines whether to return roots from the polynomial extrapolated based on first and last intervals, ‘periodic’ works the same as False. If None (default), use self.extrapolate.

Returns

- roots [ndarray] Roots of the polynomial(s).
  If the PPoly object describes multiple polynomials, the return value is an object array whose each element is an ndarray containing the roots.

See also:
PPoly.solve

scipy.interpolate.PPoly.extend

PPoly.extend(c, x, right=None)
Add additional breakpoints and coefficients to the polynomial.

Parameters

- c [ndarray, size (k, m, …)] Additional coefficients for polynomials in intervals. Note that the first additional interval will be formed using one of the self.x end points.
- x [ndarray, size (m,)] Additional breakpoints. Must be sorted in the same order as self.x and either to the right or to the left of the current breakpoints.
- right Deprecated argument. Has no effect.
  Deprecated since version 0.19.

scipy.interpolate.PPoly.from_spline

classmethod PPoly.from_spline(tck, extrapolate=None)
Construct a piecewise polynomial from a spline

Parameters

- tck A spline, as returned by splrep or a BSpline object.
- extrapolate [bool or ‘periodic’, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If ‘periodic’, periodic extrapolation is used. Default is True.

scipy.interpolate.PPoly.from_bernstein_basis

classmethod PPoly.from_bernstein_basis(bp, extrapolate=None)
Construct a piecewise polynomial in the power basis from a polynomial in Bernstein basis.

Parameters

- bp [BPoly] A Bernstein basis polynomial, as created by BPoly
- extrapolate [bool or ‘periodic’, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If ‘periodic’, periodic extrapolation is used. Default is True.
scipy.interpolate.PPoly.construct_fast

**classmethod** PPoly.construct_fast(c, x, extrapolate=None, axis=0)

Construct the piecewise polynomial without making checks.

Takes the same parameters as the constructor. Input arguments c and x must be arrays of the correct shape and type. The c array can only be of dtypes float and complex, and x array must have dtype float.

scipy.interpolate.BPoly

**class** scipy.interpolate.BPoly(c, x, extrapolate=None, axis=0)

Piecewise polynomial in terms of coefficients and breakpoints.

The polynomial between \( x[i] \) and \( x[i+1] \) is written in the Bernstein polynomial basis:

\[
S = \sum (c[a, i] \cdot b(a, k; x) \text{ for } a \text{ in range}(k+1))
\]

where \( k \) is the degree of the polynomial, and:

\[
b(a, k; x) = \binom{k}{a} \cdot t^a \cdot (1 - t)^{k - a},
\]

with \( t = (x - x[i]) / (x[i+1] - x[i]) \) and \( \binom{\cdot}{\cdot} \) is the binomial coefficient.

**Parameters**

- \( c \) : [ndarray, shape (k, m, ...)] Polynomial coefficients, order \( k \) and \( m \) intervals
- \( x \) : [ndarray, shape (m+1,)] Polynomial breakpoints. Must be sorted in either increasing or decreasing order.
- \( \text{extrapolate} \) : [bool, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. Default is True.
- \( \text{axis} \) : [int, optional] Interpolation axis. Default is zero.

**See also:**

PPoly

piecewise polynomials in the power basis

**Notes**

Properties of Bernstein polynomials are well documented in the literature. Here’s a non-exhaustive list:

**Examples**

```python
>>> from scipy.interpolate import BPoly
>>> x = [0, 1]
>>> c = [[1], [2], [3]]
>>> bp = BPoly(c, x)
```

This creates a 2nd order polynomial

\[
B(x) = 1 \times b_{0,2}(x) + 2 \times b_{1,2}(x) + 3 \times b_{2,2}(x)
\]

\[
= 1 \times (1 - x)^2 + 2 \times 2x(1 - x) + 3 \times x^2
\]

**Attributes**

- \( x \) : [ndarray] Breakpoints.
c  [ndarray] Coefficients of the polynomials. They are reshaped to a 3-dimensional array with the last dimension representing the trailing dimensions of the original coefficient array.

axis  [int] Interpolation axis.

Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
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<tr>
<td><strong>call</strong>(x, nu, extrapolate)</td>
<td>Evaluate the piecewise polynomial or its derivative.</td>
</tr>
<tr>
<td>extend(c, x, right)</td>
<td>Add additional breakpoints and coefficients to the polynomial.</td>
</tr>
<tr>
<td>derivative(nu)</td>
<td>Construct a new piecewise polynomial representing the derivative.</td>
</tr>
<tr>
<td>antiderivative(nu)</td>
<td>Construct a new piecewise polynomial representing the antiderivative.</td>
</tr>
<tr>
<td>integrate(a, b, extrapolate)</td>
<td>Compute a definite integral over a piecewise polynomial.</td>
</tr>
<tr>
<td>construct_fast(c, x, extrapolate, axis)</td>
<td>Construct the piecewise polynomial without making checks.</td>
</tr>
<tr>
<td>from_power_basis(pp, extrapolate)</td>
<td>Construct a piecewise polynomial in Bernstein basis from a power basis polynomial.</td>
</tr>
<tr>
<td>from_derivatives(xi, yi, orders, extrapolate)</td>
<td>Construct a piecewise polynomial in the Bernstein basis, compatible with the specified values and derivatives at breakpoints.</td>
</tr>
</tbody>
</table>

scipy.interpolate.BPoly.__call__

scipy.interpolate.BPoly.__call__(x, nu=0, extrapolate=None)
Evaluate the piecewise polynomial or its derivative.

Parameters

x  [array_like] Points to evaluate the interpolant at.

nu  [int, optional] Order of derivative to evaluate. Must be non-negative.

extrapolate [(bool, ‘periodic’, None), optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If ‘periodic’, periodic extrapolation is used. If None (default), use self.extrapolate.

Returns

y  [array_like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

Notes
Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, [a, b), except for the last interval which is closed [a, b).

scipy.interpolate.BPoly.extend

scipy.interpolate.BPoly.extend(c, x, right=None)
Add additional breakpoints and coefficients to the polynomial.

Parameters

c  [ndarray, size (k, m, ...)] Additional coefficients for polynomials in intervals. Note that the first additional interval will be formed using one of the self.x end points.
Additional breakpoints. Must be sorted in the same order as `self.x` and either to the right or to the left of the current breakpoints.

`right`  
Deprecated argument. Has no effect.

Deprecated since version 0.19.

**scipy.interpolate.BPoly.derivative**  
`BPoly.derivative(nu=1)`  
Construct a new piecewise polynomial representing the derivative.

**Parameters**  
- `nu`  
  [int, optional] Order of derivative to evaluate. Default is 1, i.e. compute the first derivative. If negative, the antiderivative is returned.

**Returns**  
- `bp`  
  [BPoly] Piecewise polynomial of order \( k - nu \) representing the derivative of this polynomial.

**scipy.interpolate.BPoly.antiderivative**  
`BPoly.antiderivative(nu=1)`  
Construct a new piecewise polynomial representing the antiderivative.

**Parameters**  
- `nu`  
  [int, optional] Order of antiderivative to evaluate. Default is 1, i.e. compute the first integral. If negative, the derivative is returned.

**Returns**  
- `bp`  
  [BPoly] Piecewise polynomial of order \( k + nu \) representing the antiderivative of this polynomial.

**Notes**  
If antiderivative is computed and `self.extrapolate='periodic'`, it will be set to False for the returned instance. This is done because the antiderivative is no longer periodic and its correct evaluation outside of the initially given x interval is difficult.

**scipy.interpolate.BPoly.integrate**  
`BPoly.integrate(a, b, extrapolate=None)`  
Compute a definite integral over a piecewise polynomial.

**Parameters**  
- `a`  
  [float] Lower integration bound
- `b`  
  [float] Upper integration bound
- `extrapolate`  
  [{bool, ‘periodic’, None}, optional] Whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If ‘periodic’, periodic extrapolation is used. If None (default), use `self.extrapolate`.

**Returns**  
- `array_like`  
  Definite integral of the piecewise polynomial over `[a, b]`

**scipy.interpolate.BPoly.construct_fast**  
`classmethod BPoly.construct_fast(c, x, extrapolate=None, axis=0)`  
Construct the piecewise polynomial without making checks.

Takes the same parameters as the constructor. Input arguments `c` and `x` must be arrays of the correct shape and type. The `c` array can only be of dtypes float and complex, and `x` array must have dtype float.
scipy.interpolate.BPoly.from_power_basis

```python
classmethod BPoly.from_power_basis(pp, extrapolate=None)
```

Construct a piecewise polynomial in Bernstein basis from a power basis polynomial.

**Parameters**

- `pp`: [PPoly] A piecewise polynomial in the power basis.
- `extrapolate`: [bool or ‘periodic’, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If ‘periodic’, periodic extrapolation is used. Default is True.

scipy.interpolate.BPoly.from_derivatives

```python
classmethod BPoly.from_derivatives(xi, yi, orders=None, extrapolate=None)
```

Construct a piecewise polynomial in the Bernstein basis, compatible with the specified values and derivatives at breakpoints.

**Parameters**

- `xi`: [array_like] sorted 1D array of x-coordinates.
- `yi`: [array_like or list of array_likes] `yi[i][j]` is the j-th derivative known at `xi[i]`.
- `orders`: [None or int or array_like of ints. Default: None.] Specifies the degree of local polynomials. If not None, some derivatives are ignored.
- `extrapolate`: [bool or ‘periodic’, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If ‘periodic’, periodic extrapolation is used. Default is True.

**Notes**

If k derivatives are specified at a breakpoint x, the constructed polynomial is exactly k times continuously differentiable at x, unless the `order` is provided explicitly. In the latter case, the smoothness of the polynomial at the breakpoint is controlled by the `order`.

Deduces the number of derivatives to match at each end from `order` and the number of derivatives available. If possible it uses the same number of derivatives from each end; if the number is odd it tries to take the extra one from `y2`. In any case if not enough derivatives are available at one end or another it draws enough to make up the total from the other end.

If the order is too high and not enough derivatives are available, an exception is raised.

**Examples**

```python
>>> from scipy.interpolate import BPoly
>>> BPoly.from_derivatives([0, 1], [[1], [2], [3, 4]])

Creates a polynomial \(f(x)\) of degree 3, defined on \([0, 1]\) such that \(f(0) = 1, \; df/dx(0) = 2, \; f(1) = 3, \; df/dx(1) = 4\).

```python
>>> BPoly.from_derivatives([0, 1, 2], [[0, 1], [0], [2]])

Creates a piecewise polynomial \(f(x)\), such that \(f(0) = f(1) = 0, \; f(2) = 2, \; \;\) and \(df/dx(0) = 1\). Based on the number of derivatives provided, the order of the local polynomials is 2 on \([0, 1]\) and 1 on \([1, 2]\). Notice that no restriction is imposed on the derivatives at \(x = 1\) and \(x = 2\).

Indeed, the explicit form of the polynomial is:

\[
f(x) = \begin{cases} 
  x \times (1 - x), & 0 < x < 1 \\
  2 \times (x - 1), & 1 < x < 2 
\end{cases}
\]
So that $f'(1-0) = -1$ and $f'(1+0) = 2$

### 6.7.2 Multivariate interpolation

Unstructured data:

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<td><code>griddata(points, values, xi[, method, ...])</code></td>
<td>Interpolate unstructured D-dimensional data.</td>
</tr>
<tr>
<td><code>LinearNDInterpolator(points, values[, ...])</code></td>
<td>Piecewise linear interpolant in N dimensions.</td>
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<tr>
<td><code>NearestNDInterpolator(x, y)</code></td>
<td>Nearest-neighbour interpolation in N dimensions.</td>
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<tr>
<td><code>CloughTocher2DInterpolator(points, values[, tol])</code></td>
<td>Piecewise cubic, C1 smooth, curvature-minimizing interpolant in 2D.</td>
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<tr>
<td><code>Rbf(*args)</code></td>
<td>A class for radial basis function approximation/interpolation of n-dimensional scattered data.</td>
</tr>
<tr>
<td><code>interp2d(x, y, z[, kind, copy, ...])</code></td>
<td>Interpolate over a 2-D grid.</td>
</tr>
</tbody>
</table>

**scipy.interpolate.griddata**

Interpolate unstructured D-dimensional data.

**Parameters**

- **points** [ndarray of floats, shape (n, D)] Data point coordinates. Can either be an array of shape (n, D), or a tuple of `ndim` arrays.
- **values** [ndarray of float or complex, shape (n,)] Data values.
- **xi** [2-D ndarray of float or tuple of 1-D array, shape (M, D)] Points at which to interpolate data.
- **method** [{'linear', 'nearest', 'cubic'}, optional] Method of interpolation. One of
  - **nearest** return the value at the data point closest to the point of interpolation. See `NearestNDInterpolator` for more details.
  - **linear** tessellate the input point set to n-dimensional simplices, and interpolate linearly on each simplex. See `LinearNDInterpolator` for more details.
  - **cubic** (1-D) return the value determined from a cubic spline.
  - **cubic** (2-D) return the value determined from a piecewise cubic, continuously differentiable (C1), and approximately curvature-minimizing polynomial surface. See `CloughTocher2DInterpolator` for more details.
- **fill_value** [float, optional] Value used to fill in for requested points outside of the convex hull of the input points. If not provided, then the default is `nan`. This option has no effect for the ‘nearest’ method.
- **rescale** [bool, optional] Rescale points to unit cube before performing interpolation. This is useful if some of the input dimensions have incommensurable units and differ by many orders of magnitude. New in version 0.14.0.

**Returns**

- **ndarray** Array of interpolated values.

**Notes**

New in version 0.9.
Examples
Suppose we want to interpolate the 2-D function

```python
def func(x, y):
    ...  return x*(1-x)*np.cos(4*np.pi*x) * np.sin(4*np.pi*y**2)**2
```
on a grid in [0, 1]x[0, 1]

```python
>>> grid_x, grid_y = np.mgrid[0:1:100j, 0:1:200j]
```

but we only know its values at 1000 data points:

```python
>>> points = np.random.rand(1000, 2)
>>> values = func(points[:,0], points[:,1])
```

This can be done with `griddata`—below we try out all of the interpolation methods:

```python
>>> from scipy.interpolate import griddata
>>> grid_z0 = griddata(points, values, (grid_x, grid_y), method='nearest')
>>> grid_z1 = griddata(points, values, (grid_x, grid_y), method='linear')
>>> grid_z2 = griddata(points, values, (grid_x, grid_y), method='cubic')
```

One can see that the exact result is reproduced by all of the methods to some degree, but for this smooth function the piecewise cubic interpolant gives the best results:

```python
>>> import matplotlib.pyplot as plt
>>> plt.imshow(func(grid_x, grid_y).T, extent=(0,1,0,1), origin='lower')
>>> plt.plot(points[:,0], points[:,1], 'k.', ms=1)
>>> plt.title('Original')
>>> plt.subplot(222)
>>> plt.imshow(grid_z0.T, extent=(0,1,0,1), origin='lower')
>>> plt.title('Nearest')
>>> plt.subplot(223)
>>> plt.imshow(grid_z1.T, extent=(0,1,0,1), origin='lower')
>>> plt.title('Linear')
>>> plt.subplot(224)
>>> plt.imshow(grid_z2.T, extent=(0,1,0,1), origin='lower')
>>> plt.title('Cubic')
>>> plt.gcf().set_size_inches(6, 6)
>>> plt.show()
```

**scipy.interpolate.LinearNDInterpolator**

```python
class scipy.interpolate.LinearNDInterpolator(points, values, fill_value=np.nan, rescale=False)
```
Piecewise linear interpolant in N dimensions.

New in version 0.9.

**Parameters**

- `points`: [ndarray of floats, shape (npoints, ndims); or Delaunay] Data point coordinates, or a precomputed Delaunay triangulation.
- `values`: [ndarray of float or complex, shape (npoints, ...)] Data values.
6.7. Interpolation (scipy.interpolate)
fill_value
[float, optional] Value used to fill in for requested points outside of the convex hull of the input points. If not provided, then the default is nan.

rescale
[bool, optional] Rescale points to unit cube before performing interpolation. This is useful if some of the input dimensions have incommensurable units and differ by many orders of magnitude.

Notes
The interpolant is constructed by triangulating the input data with Qhull [1], and on each triangle performing linear barycentric interpolation.

References
[1]

Methods
__call__(xi) Evaluate interpolator at given points.

scipy.interpolate.NearestNDInterpolator

class scipy.interpolate.NearestNDInterpolator(x, y)
Nearest-neighbour interpolation in N dimensions.
New in version 0.9.

Parameters
x [(Npoints, Ndims) ndarray of floats] Data point coordinates.
y [(Npoints,) ndarray of float or complex] Data values.
rescale [boolean, optional] Rescale points to unit cube before performing interpolation. This is useful if some of the input dimensions have incommensurable units and differ by many orders of magnitude.
New in version 0.14.0.
tree__options [dict, optional] Options passed to the underlying cKDTree.
New in version 0.17.0.

Notes
Uses scipy.spatial.cKDTree

Methods
__call__(*args) Evaluate interpolator at given points.

scipy.interpolate.NearestNDInterpolator.__call__
NearestNDInterpolator.__call__(*args)
Evaluate interpolator at given points.

Parameters
xi [ndarray of float, shape (..., ndim)] Points where to interpolate data at.

scipy.interpolate.CloughTocher2DInterpolator

class scipy.interpolate.CloughTocher2DInterpolator(points, values, tol=1e-6)
Piecewise cubic, C1 smooth, curvature-minimizing interpolant in 2D.
New in version 0.9.

Parameters
points [ndarray of floats, shape (npoints, ndims); or Delaunay] Data point coordinates, or a precomputed Delaunay triangulation.
values [ndarray of float or complex, shape (npoints, ...)] Data values.
fill_value [float, optional] Value used to fill in for requested points outside of the convex hull of the input points. If not provided, then the default is \texttt{nan}.
maxiter [int, optional] Maximum number of iterations in gradient estimation.
rescale [bool, optional] Rescale points to unit cube before performing interpolation. This is useful if some of the input dimensions have incommensurable units and differ by many orders of magnitude.

Notes
The interpolant is constructed by triangulating the input data with Qhull \cite{1}, and constructing a piecewise cubic interpolating Bezier polynomial on each triangle, using a Clough-Tocher scheme \cite{CT}. The interpolant is guaranteed to be continuously differentiable.

The gradients of the interpolant are chosen so that the curvature of the interpolating surface is approximatively minimized. The gradients necessary for this are estimated using the global algorithm described in \cite{Nielson83,Renka84}.

References
\cite{1}, \cite{CT}, \cite{Nielson83}, \cite{Renka84}

Methods

\_\_call\_\_(xi) Evaluate interpolator at given points.

\texttt{scipy.interpolate.Rbf}

class \texttt{scipy.interpolate.Rbf(*args)}
A class for radial basis function approximation/interpolation of n-dimensional scattered data.

Parameters

*args [arrays] x, y, z, ..., d, where x, y, z, ... are the coordinates of the nodes and d is the array of values at the nodes
function [str or callable, optional] The radial basis function, based on the radius, r, given by the norm (default is Euclidean distance); the default is ‘multiquadric’:

\begin{verbatim}
'multiquadric': sqrt((r/self.epsilon)**2 + 1)
'inverse': 1.0/sqrt((r/self.epsilon)**2 + 1)
'gaussian': exp(-(r/self.epsilon)**2)
'linear': r
'cubic': r**3
'quintic': r**5
'thin_plate': r**2 * log(r)
\end{verbatim}

If callable, then it must take 2 arguments (self, r). The epsilon parameter will be available as self.epsilon. Other keyword arguments passed in will be available as well.

epsilon [float, optional] Adjustable constant for gaussian or multiquadrics functions - defaults to approximate average distance between nodes (which is a good start).
smooth [float, optional] Values greater than zero increase the smoothness of the approximation. 0 is for interpolation (default), the function will always go through the nodal points in this case.
norm [str, callable, optional] A function that returns the ‘distance’ between two points, with inputs as arrays of positions (x, y, z, ...), and an output as an array of distance.

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E.g., the default: ‘euclidean’, such that the result is a matrix of the distances from each point in \( x_1 \) to each point in \( x_2 \). For more options, see documentation of \texttt{scipy.spatial.distances.cdist}.

**Examples**

```python
>>> from scipy.interpolate import Rbf

```from scipy.interpolate import Rbf
```

```python
>>> x, y, z, d = np.random.rand(4, 50)
```from scipy.interpolate import Rbf
```

```python
>>> rbf = Rbf(x, y, z, d)  # radial basis function interpolator instance
```from scipy.interpolate import Rbf
```

```python
>>> xi = yi = zi = np.linspace(0, 1, 20)
```from scipy.interpolate import Rbf
```

```python
>>> di = rbf(xi, yi, zi)  # interpolated values
```from scipy.interpolate import Rbf
```

```python
>>> di.shape
(20,)
```from scipy.interpolate import Rbf
```

**Attributes**

- \( N \) [int] The number of data points (as determined by the input arrays).
- \( di \) [ndarray] The 1-D array of data values at each of the data coordinates \( x_i \).
- \( xi \) [ndarray] The 2-D array of data coordinates.
- \( function \) [str or callable] The radial basis function. See description under Parameters.
- \( epsilon \) [float] Parameter used by gaussian or multiquadrics functions. See Parameters.
- \( smooth \) [float] Smoothing parameter. See description under Parameters.
- \( norm \) [str or callable] The distance function. See description under Parameters.
- \( nodes \) [ndarray] A 1-D array of node values for the interpolation.
- \( A \) [internal property, do not use]

**Methods**

```
__call__(*args)
```

Call self as a function.

```python
scipy.interpolate.Rbf.__call__
```from scipy.interpolate import Rbf
```

```
Rbf.__call__(*args)
```

Call self as a function.

**scipy.interpolate.interp2d**

```python
class scipy.interpolate.interp2d(x, y, z, kind='linear', copy=True, bounds_error=False, fill_value=nan)
```from scipy.interpolate import interp2d
```

Interpolate over a 2-D grid.

\( x, y \) and \( z \) are arrays of values used to approximate some function \( f: z = f(x, y) \). This class returns a function whose call method uses spline interpolation to find the value of new points.

If \( x \) and \( y \) represent a regular grid, consider using RectBivariateSpline.

Note that calling \texttt{interp2d} with NaNs present in input values results in undefined behaviour.

**Parameters**

- \( x, y \) [array_like] Arrays defining the data point coordinates.
  If the points lie on a regular grid, \( x \) can specify the column coordinates and \( y \) the row coordinates, for example:
  ```python
  >>> x = [0,1,2]; y = [0,3]; z = [[1,2,3], [4,5,6]]
  ```from scipy.interpolate import interp2d
```

Otherwise, \( x \) and \( y \) must specify the full coordinates for each point, for example:
```
>>> x = [0,1,2,0,1,2]; y = [0,0,0,3,3,3]; z = [1,2,3,4,5,6]
```from scipy.interpolate import interp2d
```

If \( x \) and \( y \) are multi-dimensional, they are flattened before use.
z [array_like] The values of the function to interpolate at the data points. If z is a multi-dimensional array, it is flattened before use. The length of a flattened z array is either len(x)*len(y) if x and y specify the column and row coordinates or len(z) == len(x) == len(y) if x and y specify coordinates for each point.

kind [{'linear', 'cubic', 'quintic'}, optional] The kind of spline interpolation to use. Default is 'linear'.

copy [bool, optional] If True, the class makes internal copies of x, y and z. If False, references may be used. The default is to copy.

bounds_error [bool, optional] If True, when interpolated values are requested outside of the domain of the input data (x,y), a ValueError is raised. If False, then fill_value is used.

fill_value [number, optional] If provided, the value to use for points outside of the interpolation domain. If omitted (None), values outside the domain are extrapolated.

See also:

RectBivariateSpline
Much faster 2D interpolation if your input data is on a grid

bisplrep, bisplev

BivariateSpline
a more recent wrapper of the FITPACK routines

interp1d
one dimension version of this function

Notes
The minimum number of data points required along the interpolation axis is (k+1)**2, with k=1 for linear, k=3 for cubic and k=5 for quintic interpolation.

The interpolator is constructed by bisplrep, with a smoothing factor of 0. If more control over smoothing is needed, bisplrep should be used directly.

Examples
Construct a 2-D grid and interpolate on it:

```python
>>> from scipy import interpolate
>>> x = np.arange(-5.01, 5.01, 0.25)
>>> y = np.arange(-5.01, 5.01, 0.25)
>>> xx, yy = np.meshgrid(x, y)
>>> z = np.sin(xx**2+yy**2)
>>> f = interpolate.interp2d(x, y, z, kind='cubic')
```

Now use the obtained interpolation function and plot the result:

```python
>>> import matplotlib.pyplot as plt
>>> xnew = np.arange(-5.01, 5.01, 1e-2)
>>> ynew = np.arange(-5.01, 5.01, 1e-2)
>>> znew = f(xnew, ynew)
>>> plt.plot(x, z[0, :], 'ro-', xnew, znew[0, :], 'b-')
>>> plt.show()
```
Methods

__call__(x, y[, dx, dy, assume_sorted]) Interpolate the function.

scipy.interpolate.interp2d.__call__
interp2d.__call__(x, y, dx=0, dy=0, assume_sorted=False)
Interpolate the function.

Parameters

x [1D array] x-coordinates of the mesh on which to interpolate.
y [1D array] y-coordinates of the mesh on which to interpolate.
dx [int >= 0, < kx] Order of partial derivatives in x.
dy [int >= 0, < ky] Order of partial derivatives in y.
assume_sorted [bool, optional] If False, values of x and y can be in any order and they are sorted first. If True, x and y have to be arrays of monotonically increasing values.

Returns

z [2D array with shape (len(y), len(x))] The interpolated values.

For data on a grid:

interpn(points, values, xi[, method, ...]) Multidimensional interpolation on regular grids.

RegularGridInterpolator(points, values[, ...]) Interpolation on a regular grid in arbitrary dimensions

RectBivariateSpline(x, y, z[, bbox, kx, ky, s]) Bivariate spline approximation over a rectangular mesh.

scipy.interpolate.interpn

scipy.interpolate.interpn(points, values, xi, method='linear', bounds_error=True, fill_value=nan)
Multidimensional interpolation on regular grids.

Parameters

points [tuple of ndarray of float, with shapes (m1, ), ..., (mn, )] The points defining the regular grid in n dimensions.
values [array_like, shape (m1, ..., mn, ...)] The data on the regular grid in n dimensions.
xi [ndarray of shape (...), ndim] The coordinates to sample the gridded data at.
method [str, optional] The method of interpolation to perform. Supported are “linear” and
See also:

**NearestNDInterpolator**

Nearest neighbour interpolation on unstructured data in N dimensions

**LinearNDInterpolator**

Piecewise linear interpolant on unstructured data in N dimensions

**RegularGridInterpolator**

Linear and nearest-neighbor Interpolation on a regular grid in arbitrary dimensions

**RectBivariateSpline**

Bivariate spline approximation over a rectangular mesh

**Notes**

New in version 0.14.

```python
scipy.interpolate.RegularGridInterpolator
```

```python
class scipy.interpolate.RegularGridInterpolator(points, values, method='linear', bounds_error=True, fill_value=nan)
```

Interpolation on a regular grid in arbitrary dimensions

The data must be defined on a regular grid; the grid spacing however may be uneven. Linear and nearest-neighbour interpolation are supported. After setting up the interpolator object, the interpolation method (linear or nearest) may be chosen at each evaluation.

**Parameters**

- **points**
  [tuple of ndarray of float, with shapes (m1, ), ..., (mn, )] The points defining the regular grid in n dimensions.
- **values**
  [array_like, shape (m1, ..., mn, ...)] The data on the regular grid in n dimensions.
- **method**
  [str, optional] The method of interpolation to perform. Supported are “linear” and “nearest”. This parameter will become the default for the object’s __call__ method. Default is “linear”.
- **bounds_error**
  [bool, optional] If True, when interpolated values are requested outside of the domain of the input data, a ValueError is raised. If False, then fill_value is used.
- **fill_value**
  [number, optional] If provided, the value to use for points outside of the interpolation domain. If None, values outside the domain are extrapolated.

See also:

**NearestNDInterpolator**

Nearest neighbour interpolation on unstructured data in N dimensions

**LinearNDInterpolator**

Piecewise linear interpolant on unstructured data in N dimensions

**Notes**

Contrary to LinearNDInterpolator and NearestNDInterpolator, this class avoids expensive triangulation of the input data by taking advantage of the regular grid structure.

If any of points have a dimension of size 1, linear interpolation will return an array of nan values. Nearest-neighbor interpolation will work as usual in this case.
New in version 0.14.

References
[1], [2], [3]

Examples
Evaluate a simple example function on the points of a 3D grid:

```python
>>> from scipy.interpolate import RegularGridInterpolator
>>> def f(x, y, z):
...     return 2 * x**3 + 3 * y**2 - z
>>> x = np.linspace(1, 4, 11)
>>> y = np.linspace(4, 7, 22)
>>> z = np.linspace(7, 9, 33)
>>> data = f(*np.meshgrid(x, y, z, indexing='ij', sparse=True))
```
data is now a 3D array with $data[i,j,k] = f(x[i], y[j], z[k])$. Next, define an interpolating function from this data:

```python
>>> my_interpolating_function = RegularGridInterpolator((x, y, z), data)
```
Evaluate the interpolating function at the two points $(x,y,z) = (2.1, 6.2, 8.3)$ and $(3.3, 5.2, 7.1)$:

```python
>>> pts = np.array([[2.1, 6.2, 8.3], [3.3, 5.2, 7.1]])
>>> my_interpolating_function(pts)
array([ 125.80469388, 146.30069388])
```
which is indeed a close approximation to $[f(2.1, 6.2, 8.3), f(3.3, 5.2, 7.1)]$.

Methods

```
scipy.interpolate.RegularGridInterpolator.__call__(xi[, method])

Interpolation at coordinates
```

```
Parameters
xi [ndarray of shape (..., ndim)] The coordinates to sample the gridded data at
method [str] The method of interpolation to perform. Supported are “linear” and
“nearest”.
```

```
scipy.interpolate.RectBivariateSpline

class scipy.interpolate.RectBivariateSpline(x, y, z, bbox=[None, None, None, None], kx=3, ky=3, s=0)

Bivariate spline approximation over a rectangular mesh.
Can be used for both smoothing and interpolating data.
```

```
Parameters
x, y [array_like] 1-D arrays of coordinates in strictly ascending order.
z [array_like] 2-D array of data with shape (x.size, y.size).
bbox [array_like, optional] Sequence of length 4 specifying the boundary of the rectangular approximation domain. By default, bbox=[min(x,tx), max(x,tx), min(y, ty), max(y,ty)].
```
SciPy Reference Guide, Release 1.2.0

kx, ky  [ints, optional] Degrees of the bivariate spline. Default is 3.
s  [float, optional] Positive smoothing factor defined for estimation condition:
\[
\sum((w[i]*(z[i]-s(x[i], y[i])))**2, axis=0) <= s
\]
Default is s=0, which is for interpolation.

See also:

SmoothBivariateSpline
  a smoothing bivariate spline for scattered data
bisplrep
  an older wrapping of FITPACK
bisplev
  an older wrapping of FITPACK
UnivariateSpline
  a similar class for univariate spline interpolation

Methods

Callable(x, y[, dx, dy, grid])  Evaluate the spline or its derivatives at given positions.
en(xi, yi[, dx, dy])  Evaluate the spline at points
get_coeffs()  Return spline coefficients.
get_knots()  Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively.
get_residual()  Return weighted sum of squared residuals of the spline approximation:
\[
\sum ((w[i]*(z[i]-s(x[i],y[i])))**2, axis=0)
\]
integral(xa, xb, ya, yb)  Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

scipy.interpolate.RectBivariateSpline.__call__
RectBivariateSpline.__call__(x, y, dx=0, dy=0, grid=True)
  Evaluate the spline or its derivatives at given positions.

Parameters

x, y  [array_like] Input coordinates.
If grid is False, evaluate the spline at points (x[i], y[i]), i=0, ..., len(x)-1. Standard Numpy broadcasting is obeyed.
If grid is True: evaluate spline at the grid points defined by the coordinate arrays x, y. The arrays must be sorted to increasing order.
Note that the axis ordering is inverted relative to the output of meshgrid.
dx  [int] Order of x-derivative
New in version 0.14.0.
dy  [int] Order of y-derivative
New in version 0.14.0.
grid  [bool] Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.
New in version 0.14.0.
scipy.interpolate.RectBivariateSpline.ev
RectBivariateSpline.ev(xi, yi, dx=0, dy=0)
Evaluate the spline at points

Returns the interpolated value at (xi[i], yi[i]), i=0,...,len(xi)-1.

Parameters
xi, yi [array_like] Input coordinates. Standard Numpy broadcasting is obeyed.
dx [int, optional] Order of x-derivative
New in version 0.14.0.
dy [int, optional] Order of y-derivative
New in version 0.14.0.

scipy.interpolate.RectBivariateSpline.get_coeffs
RectBivariateSpline.get_coeffs()
Return spline coefficients.

scipy.interpolate.RectBivariateSpline.get_knots
RectBivariateSpline.get_knots()
Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

scipy.interpolate.RectBivariateSpline.get_residual
RectBivariateSpline.get_residual()
Return weighted sum of squared residuals of the spline approximation: \( \sum (w[i] * (z[i] - s(x[i], y[i])))^2 \) axis=0)

scipy.interpolate.RectBivariateSpline.integral
RectBivariateSpline.integral(xa, xb, ya, yb)
Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

Parameters
xa, xb [float] The end-points of the x integration interval.
ya, yb [float] The end-points of the y integration interval.

Returns
integ [float] The value of the resulting integral.

See also:
scipy.ndimage.map_coordinates
Tensor product polynomials:

\( NdPPoly(c, x[, extrapolate]) \)
Piecewise tensor product polynomial

scipy.interpolate.NdPPoly
class scipy.interpolate.NdPPoly(c, x, extrapolate=None)
Piecewise tensor product polynomial

The value at point \( xp = (x', y', z', ...) \) is evaluated by first computing the interval indices \( i \) such that:

\[
\begin{align*}
x[0][i[0]] &\leq x' < x[0][i[0]+1] \\
x[1][i[1]] &\leq y' < x[1][i[1]+1] \\
\end{align*}
\]

... and then computing:
```plaintext
S = sum(c[k0-m0-1,...,kn-mn-1,i[0],...,i[n]]
    * (xp[0] - x[0][i[0]])**m0
    * ...
    * (xp[n] - x[n][i[n]])**mn
    for m0 in range(k[0]+1)
    ...
    for mn in range(k[n]+1))
```

where \( k[j] \) is the degree of the polynomial in dimension \( j \). This representation is the piecewise multivariate power basis.

**Parameters**
- \( c \) ([ndarray, shape (k0, ..., kn, m0, ..., mn, ...)]) Polynomial coefficients, with polynomial order \( kj \) and \( mj+1 \) intervals for each dimension \( j \).
- \( x \) ([ndim-tuple of ndarrays, shapes (mj+1,)] Polynomial breakpoints for each dimension. These must be sorted in increasing order.
- \( \text{extrapolate} \) [bool, optional] Whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. Default: True.

**See also:**
- `PPoly`
  piecewise polynomials in 1D

**Notes**
High-order polynomials in the power basis can be numerically unstable.

**Attributes**
- \( x \) [tuple of ndarrays] Breakpoints.
- \( c \) [ndarray] Coefficients of the polynomials.

**Methods**
- `__call__(x[, nu, extrapolate])` Evaluate the piecewise polynomial or its derivative
- `construct_fast(c, x[, extrapolate])` Construct the piecewise polynomial without making checks.

**scipy.interpolate.NdPPoly.__call__**

NdPPoly.__call__(x, nu=None, extrapolate=None)
Evaluate the piecewise polynomial or its derivative

**Parameters**
- \( x \) [array-like] Points to evaluate the interpolant at.
- \( nu \) [tuple, optional] Orders of derivatives to evaluate. Each must be non-negative.
- \( \text{extrapolate} \) [bool, optional] Whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs.

**Returns**
- \( y \) [array-like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of \( x \).
Notes
Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not
differentiable at the breakpoints. The polynomial intervals are considered half-open, [a, b),
except for the last interval which is closed [a, b].

\texttt{scipy.interpolate.NdPPoly.construct_fast}
\begin{verbatim}
classmethod NdPPoly.construct_fast(c, x, extrapolate=None)
Construct the piecewise polynomial without making checks.
Takes the same parameters as the constructor. Input arguments c and x must be arrays of the
correct shape and type. The c array can only be of dtypes float and complex, and x array must
have dtype float.
\end{verbatim}

6.7.3 1-D Splines

\begin{verbatim}
BSpline(t, c, k[, extrapolate, axis])
Univariate spline in the B-spline basis.
make_interp_spline(x, y[, k, t, bc_type, ...])
Compute the (coefficients of) interpolating B-
spline.
make_lsq_spline(x, y, t[, k, w, axis, ...])
Compute the (coefficients of) an LSQ B-spline.
\end{verbatim}

\texttt{scipy.interpolate.BSpline}
\begin{verbatim}
class scipy.interpolate.BSpline(t, c, k, extrapolate=True, axis=0)
Univariate spline in the B-spline basis.
S(x) = \sum_{j=0}^{n-1} c_j B_{j;k}(x)
where B_{j;k;t} are B-spline basis functions of degree k and knots t.
\end{verbatim}

Parameters
\begin{itemize}
\item \texttt{t} [ndarray, shape (\text{n+k+1,})] knots
\item \texttt{c} [ndarray, shape (\geq n, ...)] spline coefficients
\item \texttt{k} [int] B-spline order
\item \texttt{extrapolate} [bool or ‘periodic’, optional] whether to extrapolate beyond the base interval, \texttt{t[k]}
.. \texttt{t[n]}, or to return nans. If True, extrapolates the first and last polynomial
pieces of b-spline functions active on the base interval. If ‘periodic’, periodic ex-
trapolation is used. Default is True.
\item \texttt{axis} [int, optional] Interpolation axis. Default is zero.
\end{itemize}

Notes
B-spline basis elements are defined via
\begin{align*}
B_{i,0}(x) &= 1, \text{if } t_i \leq x < t_{i+1}, \text{otherwise } 0, \\
B_{i,k}(x) &= \frac{x-t_i}{t_{i+k}-t_i}B_{i,k-1}(x) + \frac{t_{i+k+1}-x}{t_{i+k+1}-t_{i+1}}B_{i+1,k-1}(x)
\end{align*}

Implementation details
\begin{itemize}
\item At least \text{k+1} coefficients are required for a spline of degree \text{k}, so that \text{n} >= \text{k+1}. Additional
coefficients, \text{c[j]} with \text{j > n}, are ignored.
\item B-spline basis elements of degree \text{k} form a partition of unity on the base interval, \text{t[k]} <= \text{x} <=
\text{t[n]}.
\end{itemize}

References
[1], [2]
Examples
Translating the recursive definition of B-splines into Python code, we have:

```python
>>> def B(x, k, i, t):
...     if k == 0:
...         return 1.0 if t[i] <= x < t[i+1] else 0.0
...     if t[i+k] == t[i+1]:
...         c1 = 0.0
...     else:
...         c1 = (x - t[i])/(t[i+k] - t[i]) * B(x, k-1, i, t)
...     if t[i+k+1] == t[i+1]:
...         c2 = 0.0
...     else:
...         c2 = (t[i+k+1] - x)/(t[i+k+1] - t[i+1]) * B(x, k-1, i+1, t)
...     return c1 + c2
```

```python
>>> def bspline(x, t, c, k):
...     n = len(t) - k - 1
...     assert (n >= k+1) and (len(c) == n)
...     return sum(c[i] * B(x, k, i, t) for i in range(n))
```

Note that this is an inefficient (if straightforward) way to evaluate B-splines — this spline class does it in an equivalent, but much more efficient way.

Here we construct a quadratic spline function on the base interval $2 \leq x \leq 4$ and compare with the naive way of evaluating the spline:

```python
>>> from scipy.interpolate import BSpline
>>> k = 2
>>> t = [0, 1, 2, 3, 4, 5, 6]
>>> c = [-1, 2, 0, -1]
>>> spl = BSpline(t, c, k)
>>> spl(2.5)
array(1.375)
>>> bspline(2.5, t, c, k)
1.375
```

Note that outside of the base interval results differ. This is because `BSpline` extrapolates the first and last polynomial pieces of b-spline functions active on the base interval.

```python
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots()
>>> xx = np.linspace(1.5, 4.5, 50)
>>> ax.plot(xx, [bspline(x, t, c, k) for x in xx], 'r-', lw=3, label='naive')
>>> ax.plot(xx, spl(xx), 'b-', lw=4, alpha=0.7, label='BSpline')
>>> ax.grid(True)
>>> ax.legend(loc='best')
>>> plt.show()
```

Attributes

- `t` [ndarray] knot vector
- `c` [ndarray] spline coefficients
- `k` [int] spline degree
extrapolate
   [bool] If True, extrapolates the first and last polynomial pieces of b-spline functions
       active on the base interval.
axis
   [int] Interpolation axis.
tck
   [tuple] Equivalent to (self.t, self.c, self.k) (read-only).

Methods
__call__(x[, nu, extrapolate]) Evaluate a spline function.

basis_element(t[, extrapolate]) Return a B-spline basis element B(x | t[0], ..., t[k+1]).
derivative([nu]) Return a b-spline representing the derivative.
antiderivative([nu]) Return a b-spline representing the antiderivative.
integrate(a, b[, extrapolate]) Compute a definite integral of the spline.
construct_fast(t, c, k[, extrapolate, axis]) Construct a spline without making checks.

scipy.interpolate.BSpline.__call__
BSpline.__call__(x, nu=0, extrapolate=None)
   Evaluate a spline function.

Parameters
x
   [array_like] points to evaluate the spline at.
nu: int, optional
   derivative to evaluate (default is 0).
extrapolate
   [bool or ‘periodic’, optional] whether to extrapolate based on the first and last
       intervals or return nans. If ‘periodic’, periodic extrapolation is used. Default
       is self.extrapolate.

Returns
y
   [array_like] Shape is determined by replacing the interpolation axis in the
       coefficient array with the shape of x.

scipy.interpolate.BSpline.basis_element
classmethod BSpline.basis_element(t, extrapolate=True)
   Return a B-spline basis element B(x | t[0], ..., t[k+1]).

Parameters
t
   [ndarray, shape (k+1,)] internal knots
extrapolate
   [bool or ‘periodic’, optional] whether to extrapolate beyond the base interval.
Examples
Construct a cubic b-spline:

```python
>>> from scipy.interpolate import BSpline
>>> b = BSpline.basis_element([0, 1, 2, 3, 4])
>>> k = b.k
>>> np.sort(b.t[k:-k])
array([ 0., 1., 2., 3., 4.])
>>> k
3
```

Construct a second order b-spline on [0, 1, 1, 2], and compare to its explicit form:

```python
>>> t = [-1, 0, 1, 1, 2]
>>> b = BSpline.basis_element(t[1:])
>>> def f(x):
...     return np.where(x < 1, x*x, (2. - x)**2)

>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots()
>>> x = np.linspace(0, 2, 51)
>>> ax.plot(x, b(x), 'g', lw=3)
>>> ax.plot(x, f(x), 'r', lw=8, alpha=0.4)
>>> ax.grid(True)
>>> plt.show()
```

\texttt{scipy.interpolate.BSpline.derivative}

\texttt{BSpline.derivative(\textit{nu}=1)}

Return a b-spline representing the derivative.

**Parameters**

- \texttt{nu} [int, optional] Derivative order. Default is 1.

**Returns**

- \texttt{b} [BSpline object] A new instance representing the derivative.
**scipy.interpolate.BSpline.antiderivative**

BSpline.antiderivative(nu=1)

Return a b-spline representing the antiderivative.

**Parameters**

- **nu** [int, optional] Antiderivative order. Default is 1.

**Returns**

- **b** [BSpline object] A new instance representing the antiderivative.

**See also:**

*splder, splantider*

**Notes**

If antiderivative is computed and self.extrapolate='periodic', it will be set to False for the returned instance. This is done because the antiderivative is no longer periodic and its correct evaluation outside of the initially given x interval is difficult.

**scipy.interpolate.BSpline.integrate**

BSpline.integrate(a, b, extrapolate=None)

Compute a definite integral of the spline.

**Parameters**

- **a** [float] Lower limit of integration.
- **b** [float] Upper limit of integration.
- **extrapolate** [bool or 'periodic', optional] whether to extrapolate beyond the base interval, \( t[k] .. t[-k-1] \), or take the spline to be zero outside of the base interval. If ‘periodic’, periodic extrapolation is used. If None (default), use self.extrapolate.

**Returns**

- **I** [array_like] Definite integral of the spline over the interval \([a, b]\).

**Examples**

Construct the linear spline \( x \) if \( x < 1 \) else \( 2 - x \) on the base interval \([0, 2]\), and integrate it:

```python
>>> from scipy.interpolate import BSpline
>>> b = BSpline.basis_element([0, 1, 2])
>>> b.integrate(0, 1)
array(0.5)
```

If the integration limits are outside of the base interval, the result is controlled by the extrapolate parameter:

```python
>>> b.integrate(-1, 1)
array(0.0)
>>> b.integrate(-1, 1, extrapolate=False)
array(0.5)
```

```python
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots()
>>> ax.grid(True)
(continues on next page)```
```python
>>> ax.axvline(0, c='r', lw=5, alpha=0.5)  # base interval
>>> ax.axvline(2, c='r', lw=5, alpha=0.5)
>>> xx = [-1, 1, 2]
>>> ax.plot(xx, b(xx))
>>> plt.show()
```

![Plot of axvline example](image)

**scipy.interpolate.BSpline.construct_fast**

```python
classmethod BSpline.construct_fast(t, c, k, extrapolate=True, axis=0)
```

Construct a spline without making checks. Accepts same parameters as the regular constructor. Input arrays `t` and `c` must of correct shape and dtype.

**scipy.interpolate.make_interp_spline**

```python
scipy.interpolate.make_interp_spline(x, y, k=3, t=None, bc_type=None, axis=0, check_finite=True)
```

Compute the (coefficients of) interpolating B-spline.

**Parameters**

- **x**  
  [array_like, shape (n,)] Abscissas.
- **y**  
  [array_like, shape (n, ...)] Ordinates.
- **k**  
  [int, optional] B-spline degree. Default is cubic, k=3.
- **t**  
  [array_like, shape (nt + k + 1,), optional] Knots. The number of knots needs to agree with the number of datapoints and the number of derivatives at the edges. Specifically, `nt - n` must equal `len(deriv_l) + len(deriv_r)`.
- **bc_type**  
  [2-tuple or None] Boundary conditions. Default is None, which means choosing the boundary conditions automatically. Otherwise, it must be a length-two tuple where the first element sets the boundary conditions at `x[0]` and the second element sets the boundary conditions at `x[-1]`. Each of these must be an iterable of pairs `(order, value)` which gives the values of derivatives of specified orders at the given edge of the interpolation interval. Alternatively, the following string aliases are recognized:
  - "clamped": The first derivatives at the ends are zero. This is
equivalent to bc_type=((1, 0.0), (1, 0.0)).

- "natural": The second derivatives at ends are zero. This is equivalent to bc_type=((2, 0.0), (2, 0.0)).
- "not-a-knot" (default): The first and second segments are the same polynomial. This is equivalent to having bc_type=None.

axis [int, optional] Interpolation axis. Default is 0.

check_finite [bool, optional] Whether to check that the input arrays contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default is True.

Returns

b [a BSpline object of the degree k and with knots t.]

See also:

BSpline

base class representing the B-spline objects

CubicSpline

a cubic spline in the polynomial basis

make_lsq_spline

a similar factory function for spline fitting

UnivariateSpline

a wrapper over FITPACK spline fitting routines

splrep

a wrapper over FITPACK spline fitting routines

Examples

Use cubic interpolation on Chebyshev nodes:

```python
>>> def cheb_nodes(N):
...     jj = 2.*np.arange(N) + 1
...     x = np.cos(np.pi * jj / 2 / N)[:-1]
...     return x
```

```python
>>> x = cheb_nodes(20)
>>> y = np.sqrt(1 - x**2)
```

```python
from scipy.interpolate import BSpline, make_interp_spline
>>> b = make_interp_spline(x, y)
>>> np.allclose(b(x), y)
True
```

Note that the default is a cubic spline with a not-a-knot boundary condition

```python
>>> b.k
3
```

Here we use a ‘natural’ spline, with zero 2nd derivatives at edges:
Interpolation of parametric curves is also supported. As an example, we compute a discretization of a snail curve in polar coordinates:

```python
>>> phi = np.linspace(0, 2.*np.pi, 40)
>>> r = 0.3 + np.cos(phi)
>>> x, y = r*np.cos(phi), r*np.sin(phi)  # convert to Cartesian coordinates

Build an interpolating curve, parameterizing it by the angle:

```python
>>> from scipy.interpolate import make_interp_spline
>>> spl = make_interp_spline(phi, np.c_[x, y])
```

Evaluate the interpolant on a finer grid (note that we transpose the result to unpack it into a pair of x- and y-arrays):

```python
>>> phi_new = np.linspace(0, 2.*np.pi, 100)
>>> x_new, y_new = spl(phi_new).T
```

Plot the result:

```python
>>> import matplotlib.pyplot as plt
>>> plt.plot(x, y, 'o')
>>> plt.plot(x_new, y_new, '-')
>>> plt.show()
```
scipy.interpolate.make_lsq_spline

scipy.interpolate.make_lsq_spline(x, y, t, k=3, w=None, axis=0, check_finite=True)

Compute the (coefficients of) an LSQ B-spline.

The result is a linear combination

\[ S(x) = \sum_j c_j B_j(x; t) \]

of the B-spline basis elements, \( B_j(x; t) \), which minimizes

\[ \sum_j (w_j \times (S(x_j) - y_j))^2 \]

**Parameters**

- **x** [array_like, shape (m,)] Abscissas.
- **y** [array_like, shape (m, ...)] Ordinates.
- **t** [array_like, shape (n + k + 1,)] Knots. Knots and data points must satisfy Schoenberg-Whitney conditions.
- **k** [int, optional] B-spline degree. Default is cubic, k=3.
- **w** [array_like, shape (n,), optional] Weights for spline fitting. Must be positive. If None, then weights are all equal. Default is None.
- **axis** [int, optional] Interpolation axis. Default is zero.
- **check_finite** [bool, optional] Whether to check that the input arrays contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default is True.

**Returns**

- **b** [a BSpline object of the degree k with knots t.]

See also:

- BSpline
  base class representing the B-spline objects
- make_interp_spline
  a similar factory function for interpolating splines
- LSQUnivariateSpline
  a FITPACK-based spline fitting routine
- splrep
  a FITPACK-based fitting routine

**Notes**

The number of data points must be larger than the spline degree \( k \).

Knots \( t \) must satisfy the Schoenberg-Whitney conditions, i.e., there must be a subset of data points \( x[j] \) such that \( t[j] < x[j] < t[j+k+1] \), for \( j=0, 1, \ldots, n-k-2 \).
Examples

Generate some noisy data:

```python
>>> x = np.linspace(-3, 3, 50)
>>> y = np.exp(-x**2) + 0.1 * np.random.randn(50)
```

Now fit a smoothing cubic spline with a pre-defined internal knots. Here we make the knot vector (k+1)-regular by adding boundary knots:

```python
>>> from scipy.interpolate import make_lsq_spline, BSpline
>>> t = [-1, 0, 1]
>>> k = 3
>>> t = np.r_[(x[0],)*(k+1),
...          t,
...          (x[-1],)*(k+1)]
>>> spl = make_lsq_spline(x, y, t, k)
```

For comparison, we also construct an interpolating spline for the same set of data:

```python
>>> from scipy.interpolate import make_interp_spline
>>> spl_i = make_interp_spline(x, y)
```

Plot both:

```python
>>> import matplotlib.pyplot as plt
>>> xs = np.linspace(-3, 3, 100)
>>> plt.plot(x, y, 'ro', ms=5)
>>> plt.plot(xs, spl(xs), 'g-', lw=3, label='LSQ spline')
>>> plt.plot(xs, spl_i(xs), 'b-', lw=3, alpha=0.7, label='interp spline')
>>> plt.legend(loc='best')
>>> plt.show()
```

**NaN handling:** If the input arrays contain `nan` values, the result is not useful since the underlying spline fitting routines cannot deal with `nan`. A workaround is to use zero weights for not-a-number data points:
```python
>>> y[8] = np.nan
>>> w = np.isnan(y)
>>> y[w] = 0.
>>> tck = make_lsq_spline(x, y, t, w=-w)
```

Notice the need to replace a `nan` by a numerical value (precise value does not matter as long as the corresponding weight is zero.)

Functional interface to FITPACK routines:

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<td><code>splprep</code></td>
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<td>Evaluate a B-spline or its derivatives.</td>
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<td><code>sproot</code></td>
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<td>Compute the spline representation of the derivative of a given spline.</td>
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<td>Compute the spline for the antiderivative (integral) of a given spline.</td>
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<tr>
<td><code>insert</code></td>
<td>Insert knots into a B-spline.</td>
</tr>
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</table>

`scipy.interpolate.splrep`

`scipy.interpolate.splrep(x, y, w=None, xb=None, xe=None, k=3, task=0, s=None, t=None, full_output=0, per=0, quiet=1)`

Find the B-spline representation of 1-D curve.

Given the set of data points \((x[i], y[i])\) determine a smooth spline approximation of degree \(k\) on the interval \(xb <= x <= xe\).

**Parameters**

- `x, y` [array_like] The data points defining a curve \(y = f(x)\).
- `w` [array_like, optional] Strictly positive rank-1 array of weights the same length as \(x\) and \(y\). The weights are used in computing the weighted least-squares spline fit. If the errors in the \(y\) values have standard-deviation given by the vector \(d\), then \(w\) should be \(1/d\). Default is ones(len(x)).
- `xb, xe` [float, optional] The interval to fit. If None, these default to \(x[0] \text{ and } x[-1]\) respectively.
- `k` [int, optional] The degree of the spline fit. It is recommended to use cubic splines. Even values of \(k\) should be avoided especially with small \(s\) values. 1 <= \(k\) <= 5
- `task` [{1, 0, -1}, optional] If `task=-1` find \(t\) and \(c\) for a given set of knots, \(t\). There must have been a previous call with `task=0` or `task=1` for the same set of data (\(t\) will be stored an used internally) If `task=-1` find the weighted least square spline for a given set of knots, \(t\). These should be interior knots as knots on the ends will be added automatically.
- `s` [float, optional] A smoothing condition. The amount of smoothness is determined by satisfying the conditions: \(\sum((w * (y - g))^2, axis=0) <= s\) where \(g(x)\) is the smoothed interpolation of \((x,y)\). The user can use \(s\) to control the tradeoff between closeness and smoothness of fit. Larger \(s\) means more smoothing while smaller values of \(s\) indicate less smoothing. Recommended values of \(s\) depend on
the weights, w. If the weights represent the inverse of the standard-deviation of
y, then a good s value should be found in the range \((m - \sqrt{2m}, m + \sqrt{2m})\)
where \(m\) is the number of datapoints in x, y, and w. default : \(s = m - \sqrt{2m}\) if
weights are supplied. \(s = 0.0\) (interpolating) if no weights are supplied.

t
[array_like, optional] The knots needed for task=-1. If given then task is auto-
matically set to -1.

full_output
[bool, optional] If non-zero, then return optional outputs.

per
[bool, optional] If non-zero, data points are considered periodic with period \(x[m-1] - x[0]\)
and a smooth periodic spline approximation is returned. Values of \(y[m-1]\)
and \(w[m-1]\) are not used.

quiet
[bool, optional] Non-zero to suppress messages. This parameter is deprecated; use
standard Python warning filters instead.

Returns

tck
[tuple] A tuple (t,c,k) containing the vector of knots, the B-spline coefficients, and
the degree of the spline.

fp
[array, optional] The weighted sum of squared residuals of the spline approximation.

ier
[int, optional] An integer flag about splrep success. Success is indicated if ier<=0.
If ier in \([1,2,3]\) an error occurred but was not raised. Otherwise an error is raised.

msg
[str, optional] A message corresponding to the integer flag, ier.

See also:

UnivariateSpline, BivariateSpline, splprep, spline, sproot, splaln, splint, bisplrep, bisplev,
BSpline, make_interp_spline

Notes

See splev for evaluation of the spline and its derivatives. Uses the FORTRAN routine curfit from
FITPACK.

The user is responsible for assuring that the values of \(x\) are unique. Otherwise, splrep will not return
sensible results.

If provided, knots \(t\) must satisfy the Schoenberg-Whitney conditions, i.e., there must be a subset of
data points \(x[j]\) such that \(t[j] < x[j] < t[j+k+1]\), for \(j=0, 1, \ldots, n-k-2\).

This routine zero-pads the coefficients array \(c\) to have the same length as the array of knots \(t\) (the
trailing \(k + 1\) coefficients are ignored by the evaluation routines, splev and BSpline.) This is in
contrast with splprep, which does not zero-pad the coefficients.

References

Based on algorithms described in [1], [2], [3], and [4]:

[1], [2], [3], [4]

Examples

```python
>>> import matplotlib.pyplot as plt
>>> from scipy.interpolate import splrep, splev
>>> x = np.linspace(0, 10, 10)
>>> y = np.sin(x)
>>> spl = splrep(x, y)
>>> x2 = np.linspace(0, 10, 200)
>>> y2 = splev(x2, spl)
>>> plt.plot(x, y, 'o', x2, y2)
>>> plt.show()
```
scipy.interpolate.splprep

scipy.interpolate.splprep(x, w=None, u=None, ub=None, ue=None, k=3, task=0, s=None, t=None, full_output=0, nest=None, per=0, quiet=1)

Find the B-spline representation of an N-dimensional curve.

Given a list of N rank-1 arrays, x, which represent a curve in N-dimensional space parametrized by u, find a smooth approximating spline curve g(u). Uses the FORTRAN routine parcur from FITPACK.

**Parameters**

- **x** [array_like] A list of sample vector arrays representing the curve.
- **w** [array_like, optional] Strictly positive rank-1 array of weights the same length as x[0]. The weights are used in computing the weighted least-squares spline fit. If the errors in the x values have standard-deviation given by the vector d, then w should be 1/d. Default is ones(len(x[0])).
- **u** [array_like, optional] An array of parameter values. If not given, these values are calculated automatically as M = len(x[0]), where
  - v[0] = 0
  - v[i] = v[i-1] + distance(x[i], x[i-1])
  - u[i] = v[i] / v[M-1]
- **ub, ue** [int, optional] The end-points of the parameters interval. Defaults to u[0] and u[-1].
- **k** [int, optional] Degree of the spline. Cubic splines are recommended. Even values of k should be avoided especially with a small s-value. 1 <= k <= 5, default is 3.
- **task** [int, optional] If task==0 (default), find t and c for a given smoothing factor, s. If task==1, find t and c for another value of the smoothing factor, s. There must have been a previous call with task==0 or task==1 for the same set of data. If task==1 find the weighted least square spline for a given set of knots, t.
- **s** [float, optional] A smoothing condition. The amount of smoothness is determined by satisfying the conditions: sum((w * (y - g))**2, axis=0) <= s, where g(x) is the smoothed interpolation of (x,y). The user can use s to control the trade-off between closeness and smoothness of fit. Larger s means more smoothing while smaller values of s indicate less smoothing. Recommended values of s depend on the weights, w. If the weights represent the inverse of the standard-deviation of y, then a good s value should be found in the range (m-sqrt(2*m),m+sqrt(2*m)), where m is the number of data points in x, y, and w.
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```
<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>t</td>
<td>[int, optional] The knots needed for task=-1.</td>
</tr>
<tr>
<td>full_output</td>
<td>[int, optional] If non-zero, then return optional outputs.</td>
</tr>
<tr>
<td>nest</td>
<td>[int, optional] An over-estimate of the total number of knots of the spline to help in determining the storage space. By default nest=m/2. Always large enough is nest=m+k+1.</td>
</tr>
<tr>
<td>per</td>
<td>[int, optional] If non-zero, data points are considered periodic with period x[m-1] - x[0] and a smooth periodic spline approximation is returned. Values of y[m-1] and w[m-1] are not used.</td>
</tr>
<tr>
<td>quiet</td>
<td>[int, optional] Non-zero to suppress messages. This parameter is deprecated; use standard Python warning filters instead.</td>
</tr>
</tbody>
</table>

Returns

- tck  [tuple] (t,c,k) a tuple containing the vector of knots, the B-spline coefficients, and the degree of the spline.
- u     [array] An array of the values of the parameter.
- fp    [float] The weighted sum of squared residuals of the spline approximation.
- ier   [int] An integer flag about splrep success. Success is indicated if ier<=0. If ier in [1,2,3] an error occurred but was not raised. Otherwise an error is raised.
- msg   [str] A message corresponding to the integer flag, ier. |

See also:

- splrep, splev, sproot, spalde, splint, bisplrep, bisplev, UnivariateSpline, BivariateSpline, BSpline, make_interp_spline

Notes

See splev for evaluation of the spline and its derivatives. The number of dimensions N must be smaller than 11.

The number of coefficients in the c array is k+1 less then the number of knots, len(t). This is in contrast with splrep, which zero-pads the array of coefficients to have the same length as the array of knots. These additional coefficients are ignored by evaluation routines, splev and BSpline.

References

[1], [2], [3]

Examples

Generate a discretization of a limacon curve in the polar coordinates:

```
>>> phi = np.linspace(0, 2*np.pi, 40)
>>> r = 0.5 + np.cos(phi)  # polar coords
>>> x, y = r * np.cos(phi), r * np.sin(phi)  # convert to cartesian
```

And interpolate:

```
>>> from scipy.interpolate import splprep, splev
>>> tck, u = splprep([x, y], s=0)
>>> new_points = splev(u, tck)
```

Notice that (i) we force interpolation by using s=0, (ii) the parameterization, u, is generated automatically. Now plot the result:

```
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots()
>>> ax.plot(x, y, 'ro')
>>> ax.plot(new_points[0], new_points[1], 'r-')
>>> plt.show()
```
scipy.interpolate.splev

scipy.interpolate.splev(x, tck, der=0, ext=0)

Evaluate a B-spline or its derivatives.

Given the knots and coefficients of a B-spline representation, evaluate the value of the smoothing polynomial and its derivatives. This is a wrapper around the FORTRAN routines splev and spder of FITPACK.

Parameters

- x : array_like
  An array of points at which to return the value of the smoothed spline or its derivatives. If tck was returned from splrep, then the parameter values, u should be given.

- tck : 3-tuple or a BSpline object
  If a tuple, then it should be a sequence of length 3 returned by splrep or splprep containing the knots, coefficients, and degree of the spline. (Also see Notes.)

- der : int, optional
  The order of derivative of the spline to compute (must be less than or equal to k).

- ext : int, optional
  Controls the value returned for elements of x not in the interval defined by the knot sequence.
  - if ext=0, return the extrapolated value.
  - if ext=1, return 0
  - if ext=2, raise a ValueError
  - if ext=3, return the boundary value.
  The default value is 0.

Returns

- y : ndarray or list of ndarrays
  An array of values representing the spline function evaluated at the points in x. If tck was returned from splprep, then this is a list of arrays representing the curve in N-dimensional space.

See also:

- splprep, splrep, sproot, splaln, splint, bisplrep, bisplev, BSpline

Notes

Manipulating the tck-tuples directly is not recommended. In new code, prefer using BSpline objects.
```python
scipy.interpolate.splint

Evaluate the definite integral of a B-spline between two given points.

**Parameters**

- `a, b` [float] The end-points of the integration interval.
- `tck` [tuple or a BSpline instance] If a tuple, then it should be a sequence of length 3, containing the vector of knots, the B-spline coefficients, and the degree of the spline (see `splev`).
- `full_output` [int, optional] Non-zero to return optional output.

**Returns**

- `integral` [float] The resulting integral.
- `wrk` [ndarray] An array containing the integrals of the normalized B-splines defined on the set of knots. (Only returned if `full_output` is non-zero)

**See also:**

`splprep, splrep, sproot, spalde, splev, bisplrep, bisplev, BSpline`

**Notes**

`splint` silently assumes that the spline function is zero outside the data interval `(a, b)`. Manipulating the tck-tuples directly is not recommended. In new code, prefer using the `BSpline` objects.

**References**

[1], [2]

---

```python
scipy.interpolate.sproot

Find the roots of a cubic B-spline.

Given the knots (`>=8`) and coefficients of a cubic B-spline return the roots of the spline.

**Parameters**

- `tck` [tuple or a BSpline object] If a tuple, then it should be a sequence of length 3, containing the vector of knots, the B-spline coefficients, and the degree of the spline. The number of knots must be `>= 8`, and the degree must be 3. The knots must be a monotonically increasing sequence.
- `mest` [int, optional] An estimate of the number of zeros (Default is 10).

**Returns**

- `zeros` [ndarray] An array giving the roots of the spline.

**See also:**

`splprep, splrep, splint, spalde, splev, bisplrep, bisplev, BSpline`

**Notes**

Manipulating the tck-tuples directly is not recommended. In new code, prefer using the `BSpline` objects.

---

6.7. Interpolation (`scipy.interpolate`) 647
References
[1], [2], [3]

scipy.interpolate.spalde

scipy.interpolate.spalde(x, tck)
Evaluate all derivatives of a B-spline.

Given the knots and coefficients of a cubic B-spline compute all derivatives up to order k at a point (or set of points).

Parameters
x [array_like] A point or a set of points at which to evaluate the derivatives. Note that t(k) <= x <= t(n-k+1) must hold for each x.
tck [tuple] A tuple (t, c, k), containing the vector of knots, the B-spline coefficients, and the degree of the spline (see splev).

Returns
results [{ndarray, list of ndarrays}] An array (or a list of arrays) containing all derivatives up to order k inclusive for each point x.

See also:
splprep, splrep, splint, sproot, splev, bisplrep, bisplev, BSpline

References
[1], [2], [3]

scipy.interpolate.splder

scipy.interpolate.splder(tck, n=1)
Compute the spline representation of the derivative of a given spline

Parameters
tck [BSpline instance or a tuple of (t, c, k)] Spline whose derivative to compute
n [int, optional] Order of derivative to evaluate. Default: 1

Returns
‘BSpline’ instance or tuple
Spline of order k2=k-n representing the derivative of the input spline. A tuple is returned iff the input argument tck is a tuple, otherwise a BSpline object is constructed and returned.

See also:
splantider, splev, spalde, BSpline

Notes
New in version 0.13.0.

Examples
This can be used for finding maxima of a curve:

```python
>>> from scipy.interpolate import splrep, splder, sproot
>>> x = np.linspace(0, 10, 70)
>>> y = np.sin(x)
>>> spl = splrep(x, y, k=4)
```
Now, differentiate the spline and find the zeros of the derivative. (NB: \texttt{sroot} only works for order 3 splines, so we fit an order 4 spline):

```
>>> dspl = splder(spl)
>>> sproot(dspl) / np.pi
array([ 0.50000001, 1.5 , 2.49999998])
```

This agrees well with roots $\pi/2 + n\pi$ of $\cos(x) = \sin'(x)$.

**\texttt{scipy.interpolate.splantider}**

\texttt{scipy.interpolate.splantider}(\texttt{tck, n=1})

Compute the spline for the antiderivative (integral) of a given spline.

**Parameters**

- \texttt{tck} [BSpline instance or a tuple of (t, c, k)] Spline whose antiderivative to compute
- \texttt{n} [int, optional] Order of antiderivative to evaluate. Default: 1

**Returns**

- BSpline instance or a tuple of (t2, c2, k2) Spline of order $k2=k+n$ representing the antiderivative of the input spline. A tuple is returned iff the input argument \texttt{tck} is a tuple, otherwise a BSpline object is constructed and returned.

**See also:**

- \texttt{splder}, \texttt{splev}, \texttt{spalde}, \texttt{BSpline}

**Notes**

The \texttt{splder} function is the inverse operation of this function. Namely, \texttt{splder(splantider(tck))} is identical to \texttt{tck}, modulo rounding error.

New in version 0.13.0.

**Examples**

```
>>> from scipy.interpolate import splrep, splder, splantider, splev
>>> x = np.linspace(0, np.pi/2, 70)
>>> y = 1 / np.sqrt(1 - 0.8*np.sin(x)**2)
>>> spl = splrep(x, y)
```

The derivative is the inverse operation of the antiderivative, although some floating point error accumulates:

```
>>> splev(1.7, spl), splev(1.7, splder(splantider(spl))))
(array(2.1565429877197317), array(2.1565429877201865))
```

Antiderivative can be used to evaluate definite integrals:

```
>>> ispl = splantider(spl)
>>> splev(np.pi/2, ispl) - splev(0, ispl)
2.2572053588768486
```

This is indeed an approximation to the complete elliptic integral $K(m) = \int_0^{\pi/2} [1 - m \sin^2 x]^{-1/2} dx$:

```
>>> from scipy.special import ellipk
>>> ellipk(0.8)
2.2572053268208538
```
scipy.interpolate.insert

scipy.interpolate.insert(x, tck, m=1, per=0)

Insert knots into a B-spline.

Given the knots and coefficients of a B-spline representation, create a new B-spline with a knot inserted m times at point x. This is a wrapper around the FORTRAN routine insert of FITPACK.

Parameters

- **x (u)**: [array_like] A 1-D point at which to insert a new knot(s). If tck was returned from splprep, then the parameter values, u should be given.
- **tck**: [a BSpline instance or a tuple] If tuple, then it is expected to be a tuple (t,c,k) containing the vector of knots, the B-spline coefficients, and the degree of the spline.
- **m**: [int, optional] The number of times to insert the given knot (its multiplicity). Default is 1.
- **per**: [int, optional] If non-zero, the input spline is considered periodic.

Returns

BSpline instance or a tuple

A new B-spline with knots t, coefficients c, and degree k. \( t(k+1) \leq x \leq t(n-k) \), where k is the degree of the spline. In case of a periodic spline (per \( \neq 0 \)) there must be either at least k interior knots \( t(j) \) satisfying \( t(k+1) < t(j) \leq x \) or at least k interior knots \( t(j) \) satisfying \( x < t(j) < t(n-k) \). A tuple is returned if the input argument tck is a tuple, otherwise a BSpline object is constructed and returned.

Notes

Based on algorithms from [1] and [2].

Manipulating the tck-tuples directly is not recommended. In new code, prefer using the BSpline objects.

References

[1], [2]

Object-oriented FITPACK interface:

- **UnivariateSpline**(x, y[, w, bbox, k, s, ext, ...]) One-dimensional smoothing spline fit to a given set of data points.
- **InterpolatedUnivariateSpline**(x, y[, w, ...]) One-dimensional interpolating spline for a given set of data points.
- **LSQUnivariateSpline**(x, y, t[, w, bbox, k, ...]) One-dimensional spline with explicit internal knots.

### 6.7.4 2-D Splines

For data on a grid:

- **RectBivariateSpline**(x, y, z[, bbox, kx, ky, s]) Bivariate spline approximation over a rectangular mesh.
- **RectSphereBivariateSpline**(u, v, r[, s, ...]) Bivariate spline approximation over a rectangular mesh on a sphere.
scipy.interpolate.RectSphereBivariateSpline

class scipy.interpolate.RectSphereBivariateSpline(u, v, r, s=0.0, pole_continuity=False, pole_values=None, pole_exact=False, pole_flat=False)

Bivariate spline approximation over a rectangular mesh on a sphere.

Can be used for smoothing data.

New in version 0.11.0.

Parameters

u [array_like] 1-D array of latitude coordinates in strictly ascending order. Coordinates must be given in radians and lie within the interval (0, pi).

v [array_like] 1-D array of longitude coordinates in strictly ascending order. Coordinates must be given in radians. First element (v[0]) must lie within the interval [-pi, pi). Last element (v[-1]) must satisfy v[-1] <= v[0] + 2*pi.

r [array_like] 2-D array of data with shape (u.size, v.size).

s [float, optional] Positive smoothing factor defined for estimation condition (s=0 is for interpolation).

pole_continuity [bool or (bool, bool), optional] Order of continuity at the poles u=0 (pole_continuity[0]) and u=pi (pole_continuity[1]). The order of continuity at the pole will be 1 or 0 when this is True or False, respectively. Defaults to False.

pole_values [float or (float, float), optional] Data values at the poles u=0 and u=pi. Either the whole parameter or each individual element can be None. Defaults to None.

pole_exact [bool or (bool, bool), optional] Data value exactness at the poles u=0 and u=pi. If True, the value is considered to be the right function value, and it will be fitted exactly. If False, the value will be considered to be a data value just like the other data values. Defaults to False.

pole_flat [bool or (bool, bool), optional] For the poles at u=0 and u=pi, specify whether or not the approximation has vanishing derivatives. Defaults to False.

See also:

RectBivariateSpline

bivariate spline approximation over a rectangular mesh

Notes

Currently, only the smoothing spline approximation (iopt[0] = 0 and iopt[0] = 1 in the FITPACK routine) is supported. The exact least-squares spline approximation is not implemented yet.

When actually performing the interpolation, the requested v values must lie within the same length 2pi interval that the original v values were chosen from.

For more information, see the FITPACK site about this function.

Examples

Suppose we have global data on a coarse grid

```python
>>> lats = np.linspace(10, 170, 9) * np.pi / 180.
>>> lons = np.linspace(0, 350, 18) * np.pi / 180.
>>> data = np.dot(np.atleast_2d(90. - np.linspace(-80., 80., 18)).T,
...               np.atleast_2d(180. - np.abs(np.linspace(0., 350., 9))).T)
```
We want to interpolate it to a global one-degree grid

```python
>>> new_lats = np.linspace(1, 180, 180) * np.pi / 180
>>> new_lons = np.linspace(1, 360, 360) * np.pi / 180
>>> new_lats, new_lons = np.meshgrid(new_lats, new_lons)
```

We need to set up the interpolator object

```python
>>> from scipy.interpolate import RectSphereBivariateSpline
>>> lut = RectSphereBivariateSpline(lats, lons, data)
```

Finally we interpolate the data. The `RectSphereBivariateSpline` object only takes 1-D arrays as input, therefore we need to do some reshaping.

```python
>>> data_interp = lut.ev(new_lats.ravel(),
...                       new_lons.ravel()).reshape((360, 180)).T
```

Looking at the original and the interpolated data, one can see that the interpolant reproduces the original data very well:

```python
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(211)
>>> ax1.imshow(data, interpolation='nearest')
>>> ax2 = fig.add_subplot(212)
>>> ax2.imshow(data_interp, interpolation='nearest')
>>> plt.show()
```

Choosing the optimal value of $s$ can be a delicate task. Recommended values for $s$ depend on the accuracy of the data values. If the user has an idea of the statistical errors on the data, she can also find a proper estimate for $s$. By assuming that, if she specifies the right $s$, the interpolator will use a spline $f(u,v)$ which exactly reproduces the function underlying the data, she can evaluate $\sum((r(i, j)-s(u(i),v(j)))^2)$ to find a good estimate for this $s$. For example, if she knows that the statistical errors on her $r(i,j)$-values are not greater than 0.1, she may expect that a good $s$ should have a value not larger than $u.size * v.size * (0.1)^2$. 

![Original data](image1)

![Interpolated data](image2)
If nothing is known about the statistical error in $r(i,j)$, $s$ must be determined by trial and error. The best is then to start with a very large value of $s$ (to determine the least-squares polynomial and the corresponding upper bound $fp0$ for $s$) and then to progressively decrease the value of $s$ (say by a factor 10 in the beginning, i.e. $s = fp0 / 10$, $fp0 / 100$, ... and more carefully as the approximation shows more detail) to obtain closer fits.

The interpolation results for different values of $s$ give some insight into this process:

```python
>>> fig2 = plt.figure()
>>> s = [3e9, 2e9, 1e9, 1e8]
>>> for ii in range(len(s)):
...     lut = RectSphereBivariateSpline(lats, lons, data, s=s[ii])
...     data_interp = lut.ev(new_lats.ravel(),
...                         new_lons.ravel()).reshape((360, 180)).T
...     ax = fig2.add_subplot(2, 2, ii+1)
...     ax.imshow(data_interp, interpolation='nearest')
...     ax.set_title("s = %g" % s[ii])
>>> plt.show()
```

### Methods

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<td>Return a tuple $(tx,ty)$ where $tx,ty$ contain knots positions of the spline with respect to $x$-, $y$-variable, respectively.</td>
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### scipy.interpolate.RectSphereBivariateSpline.__call__

**RectSphereBivariateSpline.__call__**(theta, phi[, dtheta=0, dphi=0, grid=True))

Evaluate the spline or its derivatives at given positions.
Parameters

theta, phi
[array_like] Input coordinates.
If grid is False, evaluate the spline at points (theta[i], phi[i]), i=0, .. , len(x)-1. Standard Numpy broadcasting is obeyed.
If grid is True: evaluate spline at the grid points defined by the coordinate arrays theta, phi. The arrays must be sorted to increasing order.

dtheta [int, optional] Order of theta-derivative
New in version 0.14.0.
dphi [int] Order of phi-derivative
New in version 0.14.0.
grid [bool] Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.
New in version 0.14.0.

scipy.interpolate.RectSphereBivariateSpline.ev
RectSphereBivariateSpline.ev(theta, phi, dtheta=0, dphi=0)
Evaluate the spline at points

Returns the interpolated value at (theta[i], phi[i]), i=0,...,len(theta)-1.

Parameters

theta, phi
dtheta [int, optional] Order of theta-derivative
New in version 0.14.0.
dphi [int, optional] Order of phi-derivative
New in version 0.14.0.

scipy.interpolate.RectSphereBivariateSpline.get_coeffs
RectSphereBivariateSpline.get_coeffs()
Return spline coefficients.

scipy.interpolate.RectSphereBivariateSpline.get_knots
RectSphereBivariateSpline.get_knots()
Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

scipy.interpolate.RectSphereBivariateSpline.get_residual
RectSphereBivariateSpline.get_residual()
Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

For unstructured data:

| BivariateSpline | Base class for bivariate splines. |
| SmoothBivariateSpline(x, y, z[, w, bbox, ...]) | Smooth bivariate spline approximation. |
| SmoothSphereBivariateSpline(theta, phi, r[, ...]) | Smooth bivariate spline approximation in spherical coordinates. |
| LSQBivariateSpline(x, y, z, tx, ty[, w, ...]) | Weighted least-squares bivariate spline approximation. |
| LSQSphereBivariateSpline(theta, phi, r, tt, tp) | Weighted least-squares bivariate spline approximation in spherical coordinates. |
scipy.interpolate.BivariateSpline

class scipy.interpolate.BivariateSpline

Base class for bivariate splines.

This describes a spline \( s(x, y) \) of degrees \( kx \) and \( ky \) on the rectangle \([xb, xe] \times [yb, ye]\) calculated from a given set of data points \((x, y, z)\).

This class is meant to be subclassed, not instantiated directly. To construct these splines, call either SmoothBivariateSpline or LSQBivariateSpline.

See also:

UnivariateSpline

a similar class for univariate spline interpolation

SmoothBivariateSpline

to create a BivariateSpline through the given points

LSQBivariateSpline

to create a BivariateSpline using weighted least-squares fitting

SphereBivariateSpline

bivariate spline interpolation in spherical coordinates

bisplrep

older wrapping of FITPACK

bisplev

older wrapping of FITPACK

Methods

__call__(x, y[, dx, dy, grid]) Evaluate the spline or its derivatives at given positions.

\( \text{ev}(xi, yi[, dx, dy]) \) Evaluate the spline at points

get_coeffs() Return spline coefficients.

get_knots() Return a tuple \((tx,ty)\) where \(tx,ty\) contain knots positions of the spline with respect to \(x-, y\)-variable, respectively.

get_residual() Return weighted sum of squared residuals of the spline approximation:

\[
\text{sum} \left( \frac{(w[i] \cdot (z[i] - s(x[i],y[i])))^2}{\text{axis}=0} \right)
\]

integral(xa, xb, ya, yb) Evaluate the integral of the spline over area \([xa,xb] \times [ya,yb]\).

scipy.interpolate.BivariateSpline.__call__

BivariateSpline.__call__(x, y, dx=0, dy=0, grid=True)

Evaluate the spline or its derivatives at given positions.

Parameters

\( x, y \) [array_like] Input coordinates.

If \( grid \) is False, evaluate the spline at points \((x[i], y[i]), i=0, \ldots, \text{len}(x)-1\). Standard Numpy broadcasting is obeyed.

If \( grid \) is True: evaluate spline at the grid points defined by the coordinate
arrays $x, y$. The arrays must be sorted to increasing order. Note that the axis ordering is inverted relative to the output of meshgrid.

- $dx$ [int] Order of x-derivative  
  New in version 0.14.0.
- $dy$ [int] Order of y-derivative  
  New in version 0.14.0.
- $grid$ [bool] Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.  
  New in version 0.14.0.

**scipy.interpolate.BivariateSpline.ev**

BivariateSpline.ev($xi, yi, dx=0, dy=0$)

Evaluate the spline at points

Returns the interpolated value at ($xi[i], yi[i]$), $i=0,...,\text{len}(xi)-1$.

**Parameters**

- $dx$ [int, optional] Order of x-derivative  
  New in version 0.14.0.
- $dy$ [int, optional] Order of y-derivative  
  New in version 0.14.0.

**scipy.interpolate.BivariateSpline.get_coeffs**

BivariateSpline.get_coeffs()

Return spline coefficients.

**scipy.interpolate.BivariateSpline.get_knots**

BivariateSpline.get_knots()

Return a tuple ($tx, ty$) where $tx, ty$ contain knots positions of the spline with respect to $x$, $y$ variable, respectively. The position of interior and additional knots are given as $t[k+1:-k-1]$ and $t[:k+1]=b, t[-k-1:]=e$, respectively.

**scipy.interpolate.BivariateSpline.get_residual**

BivariateSpline.get_residual()

Return weighted sum of squared residuals of the spline approximation: $\sum (w[i]*(z[i]-s(x[i],y[i])))^2, axis=0)$

**scipy.interpolate.BivariateSpline.integral**

BivariateSpline.integral($xa, xb, ya, yb$)

Evaluate the integral of the spline over area $[xa,xb] \times [ya,yb]$.

**Parameters**

- $xa, xb$ [float] The end-points of the x integration interval.
- $ya, yb$ [float] The end-points of the y integration interval.

**Returns**

- $\text{integ}$ [float] The value of the resulting integral.

**scipy.interpolate.SmoothBivariateSpline**

class scipy.interpolate.SmoothBivariateSpline($x, y, z, w=None, bbox=[None, None, None, None], kx=3, ky=3, s=None, eps=None$)

Smooth bivariate spline approximation.

**Parameters**

- $x, y, z$ [array_like] 1-D sequences of data points (order is not important).
w array_like, optional] Positive 1-D sequence of weights, of same length as x, y and z.
bbox array_like, optional] Sequence of length 4 specifying the boundary of the rectangular approximation domain. By default, bbox=[min(x,tx),max(x,tx), min(y,ty),max(y,ty)].
kx, ky ints, optional] Degrees of the bivariate spline. Default is 3.
s float, optional] Positive smoothing factor defined for estimation condition: \( \text{sum}((w[i]*(z[i]-s(x[i], y[i])))**2, axis=0) \leq s \) Default \( s=len(w) \) which should be a good value if \( 1/w[i] \) is an estimate of the standard deviation of \( z[i] \).
eps float, optional] A threshold for determining the effective rank of an overdetermined linear system of equations. \( eps \) should have a value between 0 and 1, the default is 1e-16.

See also:
bisplrep an older wrapping of FITPACK
bisplev an older wrapping of FITPACK
UnivariateSpline a similar class for univariate spline interpolation
LSQUnivariateSpline to create a BivariateSpline using weighted

Notes
The length of \( x, y \) and \( z \) should be at least \( (kx+1) \cdot (ky+1) \).

Methods

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If `grid` is True: evaluate spline at the grid points defined by the coordinate arrays `x`, `y`. The arrays must be sorted to increasing order.

Note that the axis ordering is inverted relative to the output of meshgrid.

- `dx` [int] Order of x-derivative
  - New in version 0.14.0.
- `dy` [int] Order of y-derivative
  - New in version 0.14.0.
- `grid` [bool] Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.
  - New in version 0.14.0.

```python
scipy.interpolate.SmoothBivariateSpline.ev
```

`SmoothBivariateSpline.ev(xi, yi, dx=0, dy=0)`

Evaluate the spline at points

Returns the interpolated value at `(xi[i], yi[i]), i=0,...,len(xi)-1.`

**Parameters**

- `dx` [int, optional] Order of x-derivative
  - New in version 0.14.0.
- `dy` [int, optional] Order of y-derivative
  - New in version 0.14.0.

```python
scipy.interpolate.SmoothBivariateSpline.get_coeffs
```

`SmoothBivariateSpline.get_coeffs()`

Return spline coefficients.

```python
scipy.interpolate.SmoothBivariateSpline.get_knots
```

`SmoothBivariateSpline.get_knots()`

Return a tuple `(tx,ty)` where `tx,ty` contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as `t[k+1:-k-1]` and `t[:k+1]=b, t[-k-1:]=e`, respectively.

```python
scipy.interpolate.SmoothBivariateSpline.get_residual
```

`SmoothBivariateSpline.get_residual()`

Return weighted sum of squared residuals of the spline approximation: `sum ((w[i]*(zi-s(x[i],y[i])))**2,axis=0)`

```python
scipy.interpolate.SmoothBivariateSpline.integral
```

`SmoothBivariateSpline.integral(xa, xb, ya, yb)`

Evaluate the integral of the spline over area `[xa,xb] x [ya,yb].`

**Parameters**

- `xa, xb` [float] The end-points of the x integration interval.
- `ya, yb` [float] The end-points of the y integration interval.

**Returns**

- `integ` [float] The value of the resulting integral.

```python
class scipy.interpolate.SmoothSphereBivariateSpline
```

`scipy.interpolate.SmoothSphereBivariateSpline(theta, phi, r, w=None, s=0.0, eps=1e-16)`

Smooth bivariate spline approximation in spherical coordinates.

- New in version 0.11.0.

**Parameters**
theta, phi, r
[array_like] 1-D sequences of data points (order is not important). Coordinates
must be given in radians. Theta must lie within the interval (0, pi), and phi must
lie within the interval (0, 2pi).
w [array_like, optional] Positive 1-D sequence of weights.
s [float, optional] Positive smoothing factor defined for estimation condi-
tion: sum((w(i)*(r(i) - s(theta(i), phi(i))))**2, axis=0) <= s Default
s=len(w) which should be a good value if 1/w[i] is an estimate of the standard
deviation of r[i].
eps [float, optional] A threshold for determining the effective rank of an over-
determined linear system of equations. eps should have a value between 0 and
1, the default is 1e-16.

Notes
For more information, see the FITPACK site about this function.

Examples
Suppose we have global data on a coarse grid (the input data does not have to be on a grid):

>>> theta = np.linspace(0., np.pi, 7)
>>> phi = np.linspace(0., 2*np.pi, 9)
>>> data = np.empty((theta.shape[0], phi.shape[0]))
>>> data[:,0], data[0,:], data[-1,:] = 0., 0., 0.
>>> data[1:-1,1], data[1:-1,-1] = 1., 1.
>>> data[1,1:-1], data[-2,1:-1] = 1., 1.
>>> data[2:-2,2], data[2:-2,-2] = 2., 2.
>>> data[2,2:-2], data[-3,2:-2] = 2., 2.
>>> data[3,3:-2] = 3.
>>> data = np.roll(data, 4, 1)

We need to set up the interpolator object

>>> lats, lons = np.meshgrid(theta, phi)
>>> from scipy.interpolate import SmoothSphereBivariateSpline
>>> lut = SmoothSphereBivariateSpline(lats.ravel(), lons.ravel(), ...
                 data.T.ravel(), s=3.5)

As a first test, we'll see what the algorithm returns when run on the input coordinates

>>> dataOrig = lut(theta, phi)

Finally we interpolate the data to a finer grid

>>> fine_lats = np.linspace(0., np.pi, 70)
>>> fine_lons = np.linspace(0., 2 * np.pi, 90)

>>> data_smth = lut(fine_lats, fine_lons)

>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(131)
>>> ax1.imshow(data, interpolation='nearest')
>>> ax2 = fig.add_subplot(132)
>>> ax2.imshow(dataOrig, interpolation='nearest')
>>> ax3 = fig.add_subplot(133)

(continues on next page)
```python
>>> ax3.imshow(data_smth, interpolation='nearest')
>>> plt.show()

Methods

__call__(theta, phi[, dtheta, dphi, grid]) Evaluate the spline or its derivatives at
given positions.

ev(theta, phi[, dtheta, dphi]) Evaluate the spline at points

g_coeffs() Return spline coefficients.

g_knots() Return a tuple (tx,ty) where tx,ty contain knots
positions of the spline with respect to x-, y-
variable, respectively.

g_residual() Return weighted sum of squared residuals of
the spline approximation:

scipy.interpolate.SmoothSphereBivariateSpline.__call__

Scipy.interpolate.SmoothSphereBivariateSpline.__call__ (theta, phi, dtheta=0, dphi=0, grid=True)

Evaluate the spline or its derivatives at given positions.

Parameters

theta, phi

[array_like] Input coordinates.
If grid is False, evaluate the spline at points (theta[i], phi[i]), i=0, ..
., len(x)-1. Standard Numpy broadcasting is obeyed.
If grid is True: evaluate spline at the grid points defined by the coordinate
arrays theta, phi. The arrays must be sorted to increasing order.

dtheta [int, optional] Order of theta-derivative
New in version 0.14.0.
dphi [int] Order of phi-derivative
New in version 0.14.0.
grid [bool] Whether to evaluate the results on a grid spanned by the input arrays,
or at points specified by the input arrays.
New in version 0.14.0.

**scipy.interpolate.SmoothSphereBivariateSpline.ev**

SmoothSphereBivariateSpline.ev(theta, phi, dtheta=0, dphi=0)

Evaluate the spline at points

Returns the interpolated value at (theta[i], phi[i]), i=0,...,len(theta)-1.

**Parameters**

- **theta**, **phi**
- **dtheta**
  - int, optional: Order of theta-derivative
  - New in version 0.14.0.
- **dphi**
  - int, optional: Order of phi-derivative
  - New in version 0.14.0.

**scipy.interpolate.SmoothSphereBivariateSpline.get_coeffs**

SmoothSphereBivariateSpline.get_coeffs()

Return spline coefficients.

**scipy.interpolate.SmoothSphereBivariateSpline.get_knots**

SmoothSphereBivariateSpline.get_knots()

Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

**scipy.interpolate.SmoothSphereBivariateSpline.get_residual**

SmoothSphereBivariateSpline.get_residual()

Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

**scipy.interpolate.LSQBivariateSpline**

class scipy.interpolate.LSQBivariateSpline(x, y, z, tx, ty, w=None, bbox=[None, None, None, None], kx=3, ky=3, eps=None)

Weighted least-squares bivariate spline approximation.

**Parameters**

- **x**, **y**, **z**
  - array_like: 1-D sequences of data points (order is not important).
- **tx**, **ty**
  - array_like: Strictly ordered 1-D sequences of knots coordinates.
- **w**
  - array_like, optional: Positive 1-D array of weights, of the same length as x, y and z.
- **bbox**
  - [(4,) array_like, optional]: Sequence of length 4 specifying the boundary of the rectangular approximation domain. By default, bbox=[min(x,tx), max(x,tx), min(y,ty), max(y,ty)].
- **kx**, **ky**
  - ints, optional: Degrees of the bivariate spline. Default is 3.
- **eps**
  - float, optional: A threshold for determining the effective rank of an over-determined linear system of equations. eps should have a value between 0 and 1, the default is 1e-16.

See also:

- **bisplrep**
  - an older wrapping of FITPACK
- **bisplev**
  - an older wrapping of FITPACK
UnivariateSpline

A similar class for univariate spline interpolation

SmoothBivariateSpline

Create a smoothing BivariateSpline

Notes
The length of x, y and z should be at least \((kx+1) \times (ky+1)\).

Methods

- \_\_call\_\_(x, y[, dx, dy, grid])
  Evaluate the spline or its derivatives at given positions.

- ev(xi, yi[, dx, dy])
  Evaluate the spline at points

- get_coeffs()
  Return spline coefficients.

- get_knots()
  Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively.

- get_residual()
  Return weighted sum of squared residuals of the spline approximation: \(\sum (w[i]*(z[i]-s(x[i],y[i])))**2, \text{axis}=0\)

- integral(xa, xb, ya, yb)
  Evaluate the integral of the spline over area \([xa,xb] \times [ya, yb]\).

scipy.interpolate.LSQBivariateSpline.__call__

LSQBivariateSpline.__call__ (x, y, dx=0, dy=0, grid=True)
Evaluate the spline or its derivatives at given positions.

Parameters

- x, y
  [array_like] Input coordinates.
  If grid is False, evaluate the spline at points \((x[i], y[i]), i=0, \ldots, len(x)-1\). Standard Numpy broadcasting is obeyed.
  If grid is True: evaluate spline at the grid points defined by the coordinate arrays x, y. The arrays must be sorted to increasing order.
  Note that the axis ordering is inverted relative to the output of meshgrid.

- dx
  [int] Order of x-derivative
  New in version 0.14.0.

- dy
  [int] Order of y-derivative
  New in version 0.14.0.

- grid
  [bool] Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.
  New in version 0.14.0.

scipy.interpolate.LSQBivariateSpline.ev

LSQBivariateSpline.ev(xi, yi, dx=0, dy=0)
Evaluate the spline at points

Returns the interpolated value at \((xi[i], yi[i]), i=0, \ldots, len(xi)-1\).

Parameters

- xi, yi

- dx
  [int, optional] Order of x-derivative
  New in version 0.14.0.

- dy
  [int, optional] Order of y-derivative
  New in version 0.14.0.
scipy.interpolate.LSQBivariateSpline.get_coeffs

Return spline coefficients.

scipy.interpolate.LSQBivariateSpline.get_knots

Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y- variable, respectively. The position of interior and additional knots are given as t[k+1:k-1] and t[k+1]=b, t[k-1]=e, respectively.

scipy.interpolate.LSQBivariateSpline.get_residual

Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2, axis=0)

scipy.interpolate.LSQBivariateSpline.integral

Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

Parameters

xa, xb  [float] The end-points of the x integration interval.

ya, yb  [float] The end-points of the y integration interval.

Returns

integ  [float] The value of the resulting integral.

scipy.interpolate.LSQSphereBivariateSpline

class scipy.interpolate.LSQSphereBivariateSpline(theta, phi, r, tt, tp, w=None, eps=1e-16)

Weighted least-squares bivariate spline approximation in spherical coordinates.

New in version 0.11.0.

Parameters

theta, phi, r  [array_like] 1-D sequences of data points (order is not important). Coordinates must be given in radians. Theta must lie within the interval (0, pi), and phi must lie within the interval (0, 2pi).

tt, tp  [array_like] Strictly ordered 1-D sequences of knots coordinates. Coordinates must satisfy 0 < tt[i] < pi, 0 < tp[i] < 2*pi.

w  [array_like, optional] Positive 1-D sequence of weights, of the same length as theta, phi and r.

eps  [float, optional] A threshold for determining the effective rank of an over-determined linear system of equations. eps should have a value between 0 and 1, the default is 1e-16.

Notes

For more information, see the FITPACK site about this function.

Examples

Suppose we have global data on a coarse grid (the input data does not have to be on a grid):

```python
>>> theta = np.linspace(0., np.pi, 7)
>>> phi = np.linspace(0., 2.*np.pi, 9)
>>> data = np.empty((theta.shape[0], phi.shape[0]))
>>> data[:,0], data[0,:], data[-1,:] = 0., 0., 0.
>>> data[1:-1,1], data[1:-1,-1] = 1., 1.
```
We need to set up the interpolator object. Here, we must also specify the coordinates of the knots to use.

```python
>>> lats, lons = np.meshgrid(theta, phi)
>>> knotst, knotsp = theta.copy(), phi.copy()
>>> knotst[0] += 0.0001
>>> knotst[-1] -= 0.0001
>>> knotsp[0] += 0.0001
>>> knotsp[-1] -= 0.0001
>>> from scipy.interpolate import LSQSphereBivariateSpline
>>> lut = LSQSphereBivariateSpline(lats.ravel(), lons.ravel(), ...
                                    data.T.ravel(), knotst, knotsp)
```

As a first test, we'll see what the algorithm returns when run on the input coordinates

```python
>>> data_orig = lut(theta, phi)
```

Finally we interpolate the data to a finer grid

```python
>>> fine_lats = np.linspace(0., np.pi, 70)
>>> fine_lons = np.linspace(0., 2*np.pi, 90)

>>> data_lsq = lut(fine_lats, fine_lons)
```

```python
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(131)
>>> ax1.imshow(data, interpolation='nearest')
>>> ax2 = fig.add_subplot(132)
>>> ax2.imshow(data_orig, interpolation='nearest')
>>> ax3 = fig.add_subplot(133)
>>> ax3.imshow(data_lsq, interpolation='nearest')
>>> plt.show()
```

Methods

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<th>Method</th>
<th>Description</th>
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<td><code>__call__</code></td>
<td>Evaluate the spline or its derivatives at given positions.</td>
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<tr>
<td><code>ev</code></td>
<td>Evaluate the spline at points</td>
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<tr>
<td><code>get_coeffs</code></td>
<td>Return spline coefficients.</td>
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<tr>
<td><code>get_knots</code></td>
<td>Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively.</td>
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<tr>
<td><code>get_residual</code></td>
<td>Return weighted sum of squared residuals of the spline approximation: <code>sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)</code></td>
</tr>
</tbody>
</table>
scipy.interpolate.LSQSphereBivariateSpline.__call__

LSQSphereBivariateSpline.__call__(theta, phi, dtheta=0, dphi=0, grid=True)

Evaluate the spline or its derivatives at given positions.

Parameters

- **theta**, **phi**
  - array_like: Input coordinates.
  - If grid is False, evaluate the spline at points \((\theta[i], \phi[i]), \ i=0, \ldots, \text{len}(x)-1\). Standard Numpy broadcasting is obeyed.
  - If grid is True: evaluate spline at the grid points defined by the coordinate arrays theta, phi. The arrays must be sorted to increasing order.

- **dtheta**
  - int, optional: Order of theta-derivative
    - New in version 0.14.0.

- **dphi**
  - int: Order of phi-derivative
    - New in version 0.14.0.

- **grid**
  - bool: Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.
    - New in version 0.14.0.

scipy.interpolate.LSQSphereBivariateSpline.ev

LSQSphereBivariateSpline.ev(theta, phi, dtheta=0, dphi=0)

Evaluate the spline at points

Returns the interpolated value at \((\theta[i], \phi[i]), \ i=0, \ldots, \text{len}(\theta)-1\).

Parameters

- **theta**, **phi**

- **dtheta**
  - int, optional: Order of theta-derivative
    - New in version 0.14.0.

- **dphi**
  - int, optional: Order of phi-derivative
    - New in version 0.14.0.

scipy.interpolate.LSQSphereBivariateSpline.get_coeffs

LSQSphereBivariateSpline.get_coeffs()

Return spline coefficients.

6.7. Interpolation (scipy.interpolate)
**scipy.interpolate.LSQSphereBivariateSpline.get_knots**

Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

**scipy.interpolate.LSQSphereBivariateSpline.get_residual**

Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]- s(x[i],y[i])))**2,axis=0)

**Low-level interface to FITPACK functions:**

<table>
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<tr>
<th>Function</th>
<th>Description</th>
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<tbody>
<tr>
<td>bisplrep(x, y, z[, w, xb, xe, yb, ye, kx, ky, ...])</td>
<td>Find a bivariate B-spline representation of a surface.</td>
</tr>
<tr>
<td>bisplev(x, y, tck[, dx, dy])</td>
<td>Evaluate a bivariate B-spline and its derivatives.</td>
</tr>
</tbody>
</table>

**scipy.interpolate.bisplrep**

Find a bivariate B-spline representation of a surface.

Given a set of data points (x[i], y[i], z[i]) representing a surface z=f(x,y), compute a B-spline representation of the surface. Based on the routine SURFIT from FITPACK.

**Parameters**

- x, y, z [ndarray] Rank-1 arrays of data points.
- w [ndarray, optional] Rank-1 array of weights. By default w=np.ones(len(x)).
- xb, xe [float, optional] End points of approximation interval in x. By default xb = x.min(), xe=x.max().
- yb, ye [float, optional] End points of approximation interval in y. By default yb=y.min(), ye = y.max().
- kx, ky [int, optional] The degrees of the spline (1 <= kx, ky <= 5). Third order (kx=ky=3) is recommended.
- task [int, optional] If task=0, find knots in x and y and coefficients for a given smoothing factor, s. If task=1, find knots and coefficients for another value of the smoothing factor, s. bisplrep must have been previously called with task=0 or task=1. If task=-1, find coefficients for a given set of knots tx, ty.
- s [float, optional] A non-negative smoothing factor. If weights correspond to the inverse of the standard-deviation of the errors in z, then a good s-value should be found in the range (m-sqrt(2*m),m+sqrt(2*m)) where m=len(x).
- eps [float, optional] A threshold for determining the effective rank of an overdetermined linear system of equations (0 < eps < 1). eps is not likely to need changing.
- tx, ty [ndarray, optional] Rank-1 arrays of the knots of the spline for task=-1
- full_output [int, optional] Non-zero to return optional outputs.
- nxest, nyest [int, optional] Over-estimates of the total number of knots. If None then nxest = max(kx+sqrt(m/2),2*kx+3), nyest = max(ky+sqrt(m/2),2*ky+3).
- quiet [int, optional] Non-zero to suppress printing of messages. This parameter is deprecated; use standard Python warning filters instead.

**Returns**
SciPy Reference Guide, Release 1.2.0

**tck**
[array_like] A list [tx, ty, c, kx, ky] containing the knots (tx, ty) and coefficients (c) of the bivariate B-spline representation of the surface along with the degree of the spline.

**fp**
[ndarray] The weighted sum of squared residuals of the spline approximation.

**ier**
[int] An integer flag about splrep success. Success is indicated if ier <= 0. If ier in [1,2,3] an error occurred but was not raised. Otherwise an error is raised.

**msg**
[str] A message corresponding to the integer flag, ier.

See also:
splprep, splrep, splint, sproot, splev, UnivariateSpline, BivariateSpline

Notes
See bisplev to evaluate the value of the B-spline given its tck representation.

References
[1], [2], [3]

scipy.interpolate.bisplev

**scipy.interpolate.bisplev(x, y, tck, dx=0, dy=0)**
Evaluate a bivariate B-spline and its derivatives.

Return a rank-2 array of spline function values (or spline derivative values) at points given by the cross-product of the rank-1 arrays x and y. In special cases, return an array or just a float if either x or y or both are floats. Based on BISPEV from FITPACK.

Parameters

- **x**, **y** [ndarray] Rank-1 arrays specifying the domain over which to evaluate the spline or its derivative.
- **tck** [tuple] A sequence of length 5 returned by bisplrep containing the knot locations, the coefficients, and the degree of the spline: [tx, ty, c, kx, ky].
- **dx**, **dy** [int, optional] The orders of the partial derivatives in x and y respectively.

Returns

- **vals** [ndarray] The B-spline or its derivative evaluated over the set formed by the cross-product of x and y.

See also:
splprep, splrep, splint, sproot, splev, UnivariateSpline, BivariateSpline

Notes
See bisplrep to generate the tck representation.

References
[1], [2], [3]

6.7.5 Additional tools

<table>
<thead>
<tr>
<th>Function</th>
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<td><code>lagrange(x, w)</code></td>
<td>Return a Lagrange interpolating polynomial.</td>
</tr>
<tr>
<td><code>approximate_taylor_polynomial(f, x, degree, ...)</code></td>
<td>Estimate the Taylor polynomial of f at x by polynomial fitting.</td>
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<tr>
<td><code>pade(an, m[, n])</code></td>
<td>Return Pade approximation to a polynomial as the ratio of two polynomials.</td>
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</table>

6.7. Interpolation (scipy.interpolate) 667
scipy.interpolate.lagrange

scipy.interpolate.lagrange(x, w)

Return a Lagrange interpolating polynomial.

Given two 1-D arrays x and w, returns the Lagrange interpolating polynomial through the points (x, w).

Warning: This implementation is numerically unstable. Do not expect to be able to use more than about 20 points even if they are chosen optimally.

Parameters

- x: [array_like] x represents the x-coordinates of a set of datapoints.
- w: [array_like] w represents the y-coordinates of a set of datapoints, i.e. f(x).

Returns

lagrange: [numpy.poly1d instance] The Lagrange interpolating polynomial.

Examples

Interpolate f(x) = x³ by 3 points.

```python
>>> from scipy.interpolate import lagrange
>>> x = np.array([0, 1, 2])
>>> y = x**3
>>> poly = lagrange(x, y)
```

Since there are only 3 points, Lagrange polynomial has degree 2. Explicitly, it is given by

\[
L(x) = 1 \times \frac{x(x - 2)}{-1} + 8 \times \frac{x(x - 1)}{2} = x(-2 + 3x)
\]

```python
>>> from numpy.polynomial.polynomial import Polynomial
>>> Polynomial(poly).coef
array([ 3., -2., 0.])
```

scipy.interpolate.approximate_taylor_polynomial

scipy.interpolate.approximate_taylor_polynomial(f, x, degree, scale, order=None)

Estimate the Taylor polynomial of f at x by polynomial fitting.

Parameters

- f: [callable] The function whose Taylor polynomial is sought. Should accept a vector of x values.
- x: [scalar] The point at which the polynomial is to be evaluated.
- degree: [int] The degree of the Taylor polynomial
- scale: [scalar] The width of the interval to use to evaluate the Taylor polynomial. Function values spread over a range this wide are used to fit the polynomial. Must be chosen carefully.
- order: [int or None, optional] The order of the polynomial to be used in the fitting; f will be evaluated order+1 times. If None, use degree.

Returns

p: [poly1d instance] The Taylor polynomial (translated to the origin, so that for example p(0)=f(x)).
Notes
The appropriate choice of “scale” is a trade-off; too large and the function differs from its Taylor polynomial too much to get a good answer, too small and round-off errors overwhelm the higher-order terms. The algorithm used becomes numerically unstable around order 30 even under ideal circumstances.

Choosing order somewhat larger than degree may improve the higher-order terms.

scipy.interpolate.pade

scipy.interpolate.pade(an, m, n=None)
Return Pade approximation to a polynomial as the ratio of two polynomials.

Parameters
m [int] The order of the returned approximating polynomial q.
n [int, optional] The order of the returned approximating polynomial p. By default, the order is len(an)-m.

Returns
p, q [Polynomial class] The Pade approximation of the polynomial defined by an is p(x)/q(x).

Examples
>>> from scipy.interpolate import pade
>>> e_exp = [1.0, 1.0, 1.0/2.0, 1.0/6.0, 1.0/24.0, 1.0/120.0]
>>> p, q = pade(e_exp, 2)

>>> e_exp.reverse()
>>> e_poly = np.poly1d(e_exp)

Compare e_poly(x) and the Pade approximation p(x)/q(x)

>>> e_poly(1)
2.7166666666666668

>>> p(1)/q(1)
2.7179487179487181

See also:
scipy.ndimage.map_coordinates, scipy.ndimage.spline_filter, scipy.signal.resample, scipy.signal.bspline, scipy.signal.gauss_spline, scipy.signal.qspline1d, scipy.signal.cspline1d, scipy.signal.qspline1d_eval, scipy.signal.cspline1d_eval, scipy.signal.qspline2d, scipy.signal.cspline2d.

Functions existing for backward compatibility (should not be used in new code):

<table>
<thead>
<tr>
<th>spleval(*args, **kwds)</th>
<th>spleval is deprecated! spleval is deprecated in scipy 0.19.0, use BSpline instead.</th>
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<tbody>
<tr>
<td>spline(*args, **kwds)</td>
<td>spline is deprecated! spline is deprecated in scipy 0.19.0, use Bspline class instead.</td>
</tr>
<tr>
<td>splmake(*args, **kwds)</td>
<td>splmake is deprecated! splmake is deprecated in scipy 0.19.0, use make_interp_spline instead.</td>
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<td><code>spltopp</code></td>
<td>*args, *<em>kwds</em></td>
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<tr>
<td><code>spltopp</code></td>
<td>deprecated! <code>spltopp</code> is deprecated in scipy 0.19.0, use PPoly.from_spline instead.</td>
</tr>
<tr>
<td><code>pchip</code></td>
<td>alias of <code>scipy.interpolate._cubic.PchipInterpolator</code></td>
</tr>
</tbody>
</table>

`scipy.interpolate.spleval`  

`scipy.interpolate.spleval(*args, **kwds)`  

`spleval` is deprecated! `spleval` is deprecated in scipy 0.19.0, use BSpline instead.  

Evaluate a fixed spline represented by the given tuple at the new x-values.  
The \(x_j\) values are the interior knot points. The approximation region is \(x_j[0]\) to \(x_j[-1]\). If \(N+1\) is the length of \(x_j\), then \(cvals\) should have length \(N+k\) where \(k\) is the order of the spline.

**Parameters**  

\((x_j, cvals, k)\)  
[[tuple]] Parameters that define the fixed spline.  
\(x_j\) [array_like] Interior knot points.  
\(cvals\) [array_like] Curvature.  
\(k\) [int] Order of the spline.  
\(xnew\) [array_like] Locations to calculate spline.  
\(deriv\) [int] Deriv.

**Returns**  

`spleval` [ndarray] If \(cvals\) represents more than one curve (\(cvals.ndim > 1\)) and/or \(xnew\) is \(N-d\), then the result is \(xnew.shape + cvals.shape[1:]\) providing the interpolation of multiple curves.

**Notes**  

Internally, an additional \(k-1\) knot points are added on either side of the spline.

`scipy.interpolate.spline`  

`scipy.interpolate.spline(*args, **kwds)`  

`spline` is deprecated! `spline` is deprecated in scipy 0.19.0, use Bspline class instead.  

Interpolate a curve at new points using a spline fit.

**Parameters**  

\(xk, yk\) [array_like] The x and y values that define the curve.  
\(xnew\) [array_like] The x values where spline should estimate the y values.  
\(order\) [int] Default is 3.  
\(kind\) [string] One of `{smootherest'}`.  
\(conds\) [Don’t know] Don’t know.

**Returns**  

`spline` [ndarray] An array of y values; the spline evaluated at the positions \(xnew\).
scipy.interpolate.splmake

**scipy.interpolate.splmake(*args, **kwds)**

`splmake` is deprecated! `splmake` is deprecated in scipy 0.19.0, use `make_interp_spline` instead.

Return a representation of a spline given data-points at internal knots

**Parameters**

- `xk` [array_like] The input array of x values of rank 1
- `yk` [array_like] The input array of y values of rank N. `yk` can be an N-d array to represent more than one curve, through the same `xk` points. The first dimension is assumed to be the interpolating dimension and is the same length of `xk`.
- `order` [int, optional] Order of the spline
- `conds` [optional] Conds

**Returns**

- `splmake` [tuple] Return a `(xk, cvals, k)` representation of a spline given data-points where the (internal) knots are at the data-points.

scipy.interpolate.spltopp

**scipy.interpolate.spltopp(*args, **kwds)**

`spltopp` is deprecated! `spltopp` is deprecated in scipy 0.19.0, use `PPoly.from_spline` instead.

Return a piece-wise polynomial object from a fixed-spline tuple.

scipy.interpolate.pchip

**scipy.interpolate.pchip**

alias of `scipy.interpolate._cubic.PchipInterpolator`

6.8 Input and output (scipy.io)

SciPy has many modules, classes, and functions available to read data from and write data to a variety of file formats.

See also:

- numpy-reference.routines.io (in Numpy)

6.8.1 MATLAB® files

<table>
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<th>Function</th>
<th>Description</th>
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<td><code>loadmat(file_name[, mdict, appendmat])</code></td>
<td>Load MATLAB file.</td>
</tr>
<tr>
<td><code>savemat(file_name, mdict[, appendmat, ...])</code></td>
<td>Save a dictionary of names and arrays into a MATLAB-style .mat file.</td>
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<td><code>whosmat(file_name[, appendmat])</code></td>
<td>List variables inside a MATLAB file.</td>
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</table>

6.8. Input and output (scipy.io)
scipy.io.loadmat

`scipy.io.loadmat(file_name, mdict=None, appendmat=True, **kwargs)`

Load MATLAB file.

**Parameters**

- `file_name` : [str] Name of the mat file (do not need .mat extension if appendmat==True). Can also pass open file-like object.
- `mdict` : [dict, optional] Dictionary in which to insert matfile variables.
- `appendmat` : [bool, optional] True to append the .mat extension to the end of the given filename, if not already present.
- `byte_order` : [str or None, optional] None by default, implying byte order guessed from mat file. Otherwise can be one of ('native', '=' , 'little', '<', 'BIG', '>').
- `mat_dtype` : [bool, optional] If True, return arrays in same dtype as would be loaded into MATLAB (instead of the dtype with which they are saved).
- `squeeze_me` : [bool, optional] Whether to squeeze unit matrix dimensions or not.
- `chars_as_strings` : [bool, optional] Whether to convert char arrays to string arrays.
- `matlab_compatible` : [bool, optional] Returns matrices as would be loaded by MATLAB (implies squeeze_me=False, chars_as_strings=False, mat_dtype=True, struct_as_record=True).
- `struct_as_record` : [bool, optional] Whether to load MATLAB structs as numpy record arrays, or as old-style numpy arrays with dtype=object. Setting this flag to False replicates the behavior of scipy version 0.7.x (returning numpy object arrays). The default setting is True, because it allows easier round-trip load and save of MATLAB files.
- `verify_compressed_data_integrity` : [bool, optional] Whether the length of compressed sequences in the MATLAB file should be checked, to ensure that they are not longer than we expect. It is advisable to enable this (the default) because overlong compressed sequences in MATLAB files generally indicate that the files have experienced some sort of corruption.
- `variable_names` : [None or sequence] If None (the default) - read all variables in file. Otherwise `variable_names` should be a sequence of strings, giving names of the MATLAB variables to read from the file. The reader will skip any variable with a name not in this sequence, possibly saving some read processing.

**Returns**

- `mat_dict` : [dict] dictionary with variable names as keys, and loaded matrices as values.

**Notes**

v4 (Level 1.0), v6 and v7 to 7.2 matfiles are supported.

You will need an HDF5 python library to read MATLAB 7.3 format mat files. Because scipy does not supply one, we do not implement the HDF5 / 7.3 interface here.

**Examples**
```python
>>> from os.path import dirname, join as pjoin
>>> import scipy.io as sio

Get the filename for an example .mat file from the tests/data directory.

```python
>>> data_dir = pjoin(dirname(sio.__file__), 'matlab', 'tests', 'data')
>>> mat_fname = pjoin(data_dir, 'testdouble_7.4_GLNX86.mat')
```

Load the .mat file contents.

```python
>>> mat_contents = sio.loadmat(mat_fname)
```

The result is a dictionary, one key/value pair for each variable:

```python
>>> sorted(mat_contents.keys())
['__globals__', '__header__', '__version__', 'testdouble']
```

By default SciPy reads MATLAB structs as structured NumPy arrays where the dtype fields are of type `object` and the names correspond to the MATLAB struct field names. This can be disabled by setting the optional argument `struct_as_record=False`.

Get the filename for an example .mat file that contains a MATLAB struct called `teststruct` and load the contents.

```python
>>> matstruct_fname = pjoin(data_dir, 'teststruct_7.4_GLNX86.mat')
>>> matstruct_contents = sio.loadmat(matstruct_fname)
>>> teststruct = matstruct_contents['teststruct']
>>> teststruct.dtype
dtype([('stringfield', 'O'), ('doublefield', 'O'), ('complexfield', 'O')])
```

The size of the structured array is the size of the MATLAB struct, not the number of elements in any particular field. The shape defaults to 2-D unless the optional argument `squeeze_me=True`, in which case all length 1 dimensions are removed.

```python
>>> teststruct.size
1
>>> teststruct.shape
(1, 1)
```

Get the ‘stringfield’ of the first element in the MATLAB struct.

```python
>>> teststruct[0, 0]['stringfield']
array(['Rats live on no evil star.'],
      dtype='<U26')
```

Get the first element of the ‘doublefield’.

```python
>>> teststruct['doublefield'][0, 0]
array([[ 1.41421356,  2.71828183,  3.14159265]])
```

Load the MATLAB struct, squeezing out length 1 dimensions, and get the item from the ‘complexfield’.
>>> matstruct_squeezed = sio.loadmat(matstruct_fname, squeeze_me=True)
>>> matstruct_squeezed['teststruct'].shape
()
>>> matstruct_squeezed['teststruct']['complexfield'].shape
()
>>> matstruct_squeezed['teststruct']['complexfield'].item()
array([[ 1.41421356+1.41421356j, 2.71828183+2.71828183j, 3.14159265+3.14159265j]])

scipy.io.savemat

Save a dictionary of names and arrays into a MATLAB-style .mat file. This saves the array objects in the given dictionary to a MATLAB- style .mat file.

Parameters

- **file_name** (str or file-like object) Name of the .mat file (.mat extension not needed if appendmat == True). Can also pass open file_like object.
- **mdict** (dict) Dictionary from which to save matfile variables.
- **appendmat** (bool, optional) True (the default) to append the .mat extension to the end of the given filename, if not already present.
- **format** ([{'5', '4'}, string, optional] '5' (the default) for MATLAB 5 and up (to 7.2), '4' for MATLAB 4 .mat files.
- **long_field_names** (bool, optional) False (the default) - maximum field name length in a structure is 31 characters which is the documented maximum length. True - maximum field name length in a structure is 63 characters which works for MATLAB 7.6+.
- **do_compression** (bool, optional) Whether or not to compress matrices on write. Default is False.
- **oned_as** ([‘row’, ‘column’], optional) If ‘column’, write 1-D numpy arrays as column vectors. If ‘row’, write 1-D numpy arrays as row vectors.

See also:
mio4.MatFile4Writer, mio5.MatFile5Writer

scipy.io.whosmat

List variables inside a MATLAB file.

Parameters

- **file_name** (str) Name of the mat file (do not need .mat extension if appendmat==True) Can also pass open file_like object.
- **appendmat** (bool, optional) True to append the .mat extension to the end of the given filename, if not already present.
- **byte_order** (str or None, optional) None by default, implying byte order guessed from mat file. Otherwise can be one of (‘native’, ‘=’, ‘little’, ‘<’, ‘BIG’, ‘>’).
**mat_dtype**

[bool, optional] If True, return arrays in same dtype as would be loaded into MATLAB (instead of the dtype with which they are saved).

**squeeze_me**

[bool, optional] Whether to squeeze unit matrix dimensions or not.

**chars_as_strings**

[bool, optional] Whether to convert char arrays to string arrays.

**matlab_compatible**

[bool, optional] Returns matrices as would be loaded by MATLAB (implies squeeze_me=False, chars_as_strings=False, mat_dtype=True, struct_as_record=True).

**struct_as_record**

[bool, optional] Whether to load MATLAB structs as numpy record arrays, or as old-style numpy arrays with dtype=object. Setting this flag to False replicates the behavior of scipy version 0.7.x (returning numpy object arrays). The default setting is True, because it allows easier round-trip load and save of MATLAB files.

---

**Returns**

**variables**

[list of tuples] A list of tuples, where each tuple holds the matrix name (a string), its shape (tuple of ints), and its data class (a string). Possible data classes are: int8, uint8, int16, uint16, int32, uint32, int64, uint64, single, double, cell, struct, object, char, sparse, function, opaque, logical, unknown.

**Notes**

v4 (Level 1.0), v6 and v7 to 7.2 matfiles are supported.

You will need an HDF5 python library to read matlab 7.3 format mat files. Because scipy does not supply one, we do not implement the HDF5 / 7.3 interface here.

New in version 0.12.0.

---

### 6.8.2 IDL® files

**readsav(file_name[, idict, python_dict, ...])** Read an IDL .sav file.

**scipy.io.readsav**

**scipy.io.readsav(file_name, idict=None, python_dict=False, uncompressed_file_name=None, verbose=False)**

Read an IDL .sav file.

**Parameters**

**file_name**

[str] Name of the IDL save file.

**idict**

[dict, optional] Dictionary in which to insert .sav file variables.

**python_dict**

[bool, optional] By default, the object return is not a Python dictionary, but a case-insensitive dictionary with item, attribute, and call access to variables. To get a standard Python dictionary, set this option to True.

**uncompressed_file_name**

[str, optional] This option only has an effect for .sav files written with the /compress option. If a file name is specified, compressed .sav files are uncompressed to this file. Otherwise, readsav will use the tempfile module to determine a temporary filename automatically, and will remove the temporary file upon successfully reading it in.
verbose [bool, optional] Whether to print out information about the save file, including the records read, and available variables.

Returns

idl_dict [AttrDict or dict] If python_dict is set to False (default), this function returns a case-insensitive dictionary with item, attribute, and call access to variables. If python_dict is set to True, this function returns a Python dictionary with all variable names in lowercase. If idict was specified, then variables are written to the dictionary specified, and the updated dictionary is returned.

6.8.3 Matrix Market files

<table>
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<td>mminfo(source)</td>
<td>Return size and storage parameters from Matrix Market file-like ‘source’.</td>
</tr>
<tr>
<td>mmread(source)</td>
<td>Reads the contents of a Matrix Market file-like ‘source’ into a matrix.</td>
</tr>
<tr>
<td>mmwrite(target, a[, comment, field, ...])</td>
<td>Writes the sparse or dense array a to Matrix Market file-like target.</td>
</tr>
</tbody>
</table>

scipy.io.mminfo

scipy.io.mminfo(source)
Return size and storage parameters from Matrix Market file-like ‘source’.

Parameters

source [str or file-like] Matrix Market filename (extension .mtx) or open file-like object

Returns

rows [int] Number of matrix rows.
cols [int] Number of matrix columns.
entries [int] Number of non-zero entries of a sparse matrix or rows*cols for a dense matrix.
format [str] Either ‘coordinate’ or ‘array’.

scipy.io.mmread

scipy.io.mmread(source)
Reads the contents of a Matrix Market file-like ‘source’ into a matrix.

Parameters

source [str or file-like] Matrix Market filename (extensions .mtx, .mtz.gz) or open file-like object.

Returns

a [ndarray or coo_matrix] Dense or sparse matrix depending on the matrix format in the Matrix Market file.

scipy.io.mmwrite

scipy.io.mmwrite(target, a[, comment=", field=None, precision=None, symmetry=None])
Writes the sparse or dense array a to Matrix Market file-like target.
Parameters

- **target** [str or file-like] Matrix Market filename (extension .mtx) or open file-like object.
- **a** [array like] Sparse or dense 2D array.
- **comment** [str, optional] Comments to be prepended to the Matrix Market file.
- **field** [None or str, optional] Either ‘real’, ‘complex’, ‘pattern’, or ‘integer’.
- **precision** [None or int, optional] Number of digits to display for real or complex values.
- **symmetry** [None or str, optional] Either ‘general’, ‘symmetric’, ‘skew-symmetric’, or ‘hermitian’. If symmetry is None the symmetry type of ‘a’ is determined by its values.

6.8.4 Unformatted Fortran files

### FortranFile(filename[, mode, header_dtype])

A file object for unformatted sequential files from Fortran code.

#### Parameters

- **filename** [file or str] Open file object or filename.
- **mode** [‘r’, ‘w’], optional] Read-write mode, default is ‘r’.
- **header_dtype** [dtype, optional] Data type of the header. Size and endiness must match the input/output file.

#### Notes

These files are broken up into records of unspecified types. The size of each record is given at the start (although the size of this header is not standard) and the data is written onto disk without any formatting. Fortran compilers supporting the BACKSPACE statement will write a second copy of the size to facilitate backwards seeking.

This class only supports files written with both sizes for the record. It also does not support the subrecords used in Intel and gfortran compilers for records which are greater than 2GB with a 4-byte header.

An example of an unformatted sequential file in Fortran would be written as:

```fortran
OPEN(1, FILE=myfilename, FORM='unformatted')
WRITE(1) myvariable
```

Since this is a non-standard file format, whose contents depend on the compiler and the endianness of the machine, caution is advised. Files from gfortran 4.8.0 and gfortran 4.1.2 on x86_64 are known to work.

Consider using Fortran direct-access files or files from the newer Stream I/O, which can be easily read by `numpy.fromfile`.

#### Examples

To create an unformatted sequential Fortran file:
```python
>>> from scipy.io import FortranFile
>>> f = FortranFile('test.unf', 'w')
>>> f.write_record(np.array([1, 2, 3, 4, 5], dtype=np.int32))
>>> f.write_record(np.linspace(0, 1, 20).reshape((5, 4)).T)
>>> f.close()
```

To read this file:

```python
>>> f = FortranFile('test.unf', 'r')
>>> print(f.read_ints(np.int32))
[1 2 3 4 5]
>>> print(f.read_reals(float).reshape((5, 4), order="F"))
[[0. 0.05263158 0.10526316 0.15789474]
 [0.21052632 0.26315789 0.31578947 0.36842105]
 [0.42105263 0.47368421 0.52631579 0.57894737]
 [0.63157895 0.68421053 0.73684211 0.78947368]
 [0.84210526 0.89473684 0.94736842 1.]]
```  

```fortran
integer :: a(5), i
double precision :: b(5,4)
open(1, file='test.unf', form='unformatted')
read(1) a
read(1) b
close(1)
write(*,*) a
do i = 1, 5
   write(*,*) b(i, :)
end do
```

Methods

- **close()** Closes the file.
- **read_ints([dtype])** Reads a record of a given type from the file, defaulting to an integer type (INTEGER*4 in Fortran).
- **read_reals([dtype])** Reads a record of a given type from the file, defaulting to a floating point number (REAL*8 in Fortran).
- **read_record(*dtypes, **kwargs)** Reads a record of a given type from the file.
- **write_record(*items)** Write a record (including sizes) to the file.

**scipy.io.FortranFile.close**

FortranFile.close()

Closes the file. It is unsupported to call any other methods off this object after closing it. Note that this class supports the ‘with’ statement in modern versions of Python, to call this automatically.

**scipy.io.FortranFile.read_ints**

FortranFile.read_ints(dtype='i4')

Reads a record of a given type from the file, defaulting to an integer type (INTEGER*4 in Fortran).

**Parameters**
**dtype**  [dtype, optional] Data type specifying the size and endiness of the data.

**Returns**

data  [ndarray] A one-dimensional array object.

**See also:**

*read_reals*, *read_record*

**scipy.io.FortranFile.read_reals**

FortranFile.read_reals(*dtype=’f8’*)

Reads a record of a given type from the file, defaulting to a floating point number (real*8 in Fortran).

**Parameters**

dtype  [dtype, optional] Data type specifying the size and endiness of the data.

**Returns**

data  [ndarray] A one-dimensional array object.

**See also:**

*read_ints*, *read_record*

**scipy.io.FortranFile.read_record**

FortranFile.read_record(*dtypes, **kwargs*)

Reads a record of a given type from the file.

**Parameters**

* dtypes  [dtypes, optional] Data type(s) specifying the size and endiness of the data.

**Returns**

data  [ndarray] A one-dimensional array object.

**See also:**

*read_reals*, *read_ints*

**Notes**

If the record contains a multi-dimensional array, you can specify the size in the dtype. For example:

```
INTEGER var(5,4)
```

can be read with:

```
read_record(’(4,5)i4’).T
```

Note that this function does **not** assume the file data is in Fortran column major order, so you need to (i) swap the order of dimensions when reading and (ii) transpose the resulting array.

Alternatively, you can read the data as a 1D array and handle the ordering yourself. For example:

```
read_record(’i4’).reshape(5, 4, order=’F’)
```

For records that contain several variables or mixed types (as opposed to single scalar or array types), give them as separate arguments:
double precision :: a
type :: b
write(1) a, b

record = f.read_record('i4', 'i4')
a = record[0]  # first number
b = record[1]  # second number

and if any of the variables are arrays, the shape can be specified as the third item in the relevant
dtype:

double precision :: a
type :: b(3,4)
write(1) a, b

record = f.read_record('i4', np.dtype((('i4', (4, 3)))))
a = record[0]
b = record[1].T

Numpy also supports a short syntax for this kind of type:

record = f.read_record('i4', '(3,3)<i4')

scipy.io.FortranFile.write_record
FortranFile.write_record(*items)
Write a record (including sizes) to the file.

Parameters

*items [array_like] The data arrays to write.

Notes

Writes data items to a file:

write_record(a.T, b.T, c.T, ...)
write(1) a, b, c, ...  

Note that data in multidimensional arrays is written in row-major order — to make them read
correctly by Fortran programs, you need to transpose the arrays yourself when writing them.

6.8.5 Netcdf

netcdf_file(filename[, mode, mmap, version, ...]) A file object for NetCDF data.

netcdf_variable(data, typecode, size, shape, ...) A data object for the netcdf module.

scipy.io.netcdf_file

class scipy.io.netcdf_file(filename, mode='r', mmap=None, version=1, maskandscale=False)
A file object for NetCDF data.

A netcdf_file object has two standard attributes: dimensions and variables. The values of both are
dictionaries, mapping dimension names to their associated lengths and variable names to variables,
respectively. Application programs should never modify these dictionaries.

All other attributes correspond to global attributes defined in the NetCDF file. Global file attributes
are created by assigning to an attribute of the `netcdf_file` object.

**Parameters**

- **filename** [string or file-like] string -> filename
- **mode** [‘r’, ‘w’, ‘a’], optional] read-write-append mode, default is ‘r’
- **mmap** [None or bool, optional] Whether to mmap `filename` when reading. Default is True when `filename` is a file name, False when `filename` is a file-like object. Note that when mmap is in use, data arrays returned refer directly to the mmapped data on disk, and the file cannot be closed as long as references to it exist.
- **version** [{1, 2}, optional] version of netcdf to read / write, where 1 means Classic format and 2 means 64-bit offset format. Default is 1. See here for more info.
- **maskandscale** [bool, optional] Whether to automatically scale and/or mask data based on attributes. Default is False.

**Notes**

The major advantage of this module over other modules is that it doesn’t require the code to be linked to the NetCDF libraries. This module is derived from pupynere.

NetCDF files are a self-describing binary data format. The file contains metadata that describes the dimensions and variables in the file. More details about NetCDF files can be found here. There are three main sections to a NetCDF data structure:

1. Dimensions
2. Variables
3. Attributes

The dimensions section records the name and length of each dimension used by the variables. The variables would then indicate which dimensions it uses and any attributes such as data units, along with containing the data values for the variable. It is good practice to include a variable that is the same name as a dimension to provide the values for that axes. Lastly, the attributes section would contain additional information such as the name of the file creator or the instrument used to collect the data.

When writing data to a NetCDF file, there is often the need to indicate the ‘record dimension’. A record dimension is the unbounded dimension for a variable. For example, a temperature variable may have dimensions of latitude, longitude and time. If one wants to add more temperature data to the NetCDF file as time progresses, then the temperature variable should have the time dimension flagged as the record dimension.

In addition, the NetCDF file header contains the position of the data in the file, so access can be done in an efficient manner without loading unnecessary data into memory. It uses the `mmap` module to create Numpy arrays mapped to the data on disk, for the same purpose.

Note that when `netcdf_file` is used to open a file with mmap=True (default for read-only), arrays returned by it refer to data directly on the disk. The file should not be closed, and cannot be cleanly closed when asked, if such arrays are alive. You may want to copy data arrays obtained from mmapped Netcdf file if they are to be processed after the file is closed, see the example below.

**Examples**

To create a NetCDF file:

```python
>>> from scipy.io import netcdf
>>> f = netcdf.netcdf_file('simple.nc', 'w')
>>> f.history = 'Created for a test'
>>> f.createDimension('time', 10)
```

(continues on next page)
```python
>>> time = f.createVariable('time', 'i', ('time',))
>>> time[:] = np.arange(10)
>>> time.units = 'days since 2008-01-01'
>>> f.close()
```

Note the assignment of `arange(10)` to `time[:]`. Exposing the slice of the time variable allows for the data to be set in the object, rather than letting `arange(10)` overwrite the `time` variable.

To read the NetCDF file we just created:

```python
>>> from scipy.io import netcdf
>>> f = netcdf.netcdf_file('simple.nc', 'r')
>>> print(f.history)
b'Created for a test'
>>> time = f.variables['time']
>>> print(time.units)
b'days since 2008-01-01'
>>> print(time.shape)
(10,)
>>> print(time[-1])
9
```

NetCDF files, when opened read-only, return arrays that refer directly to memory-mapped data on disk:

```python
>>> data = time[:]
>>> data.base.base
<mmap.mmap object at 0x7fe753763180>
```

If the data is to be processed after the file is closed, it needs to be copied to main memory:

```python
>>> data = time[:].copy()
>>> f.close()
>>> data.mean()
4.5
```

A NetCDF file can also be used as context manager:

```python
>>> from scipy.io import netcdf
>>> with netcdf.netcdf_file('simple.nc', 'r') as f:
...     print(f.history)
b'Created for a test'
```

**Methods**

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>close()</code></td>
<td>Closes the NetCDF file.</td>
</tr>
<tr>
<td><code>createDimension(name, length)</code></td>
<td>Adds a dimension to the Dimension section of the NetCDF data structure.</td>
</tr>
<tr>
<td><code>createVariable(name, type, dimensions)</code></td>
<td>Create an empty variable for the <code>netcdf_file</code> object, specifying its data type and the dimensions it uses.</td>
</tr>
<tr>
<td><code>flush()</code></td>
<td>Perform a sync-to-disk flush if the <code>netcdf_file</code> object is in write mode.</td>
</tr>
</tbody>
</table>
Table 74 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>sync()</code></td>
<td>Perform a sync-to-disk flush if the <code>netcdf_file</code> object is in write mode.</td>
</tr>
</tbody>
</table>

```python
scipy.io.netcdf_file.close
netcdf_file.close()
```

Closes the NetCDF file.

```python
scipy.io.netcdf_file.createDimension
netcdf_file.createDimension(name, length)
```

Adds a dimension to the Dimension section of the NetCDF data structure.

Note that this function merely adds a new dimension that the variables can reference. The values for the dimension, if desired, should be added as a variable using `createVariable`, referring to this dimension.

**Parameters**

- `name`  
  [str] Name of the dimension (Eg, ‘lat’ or ‘time’).
- `length`  
  [int] Length of the dimension.

**See also:**

`createVariable`

```python
scipy.io.netcdf_file.createVariable
netcdf_file.createVariable(name, type, dimensions)
```

Create an empty variable for the `netcdf_file` object, specifying its data type and the dimensions it uses.

**Parameters**

- `name`  
  [str] Name of the new variable.
- `type`  
  [dtype or str] Data type of the variable.
- `dimensions`  
  [sequence of str] List of the dimension names used by the variable, in the desired order.

**Returns**

- `variable`  
  [netcdf_variable] The newly created `netcdf_variable` object. This object has also been added to the `netcdf_file` object as well.

**See also:**

`createDimension`

**Notes**

Any dimensions to be used by the variable should already exist in the NetCDF data structure or should be created by `createDimension` prior to creating the NetCDF variable.

```python
scipy.io.netcdf_file.flush
netcdf_file.flush()
```

Perform a sync-to-disk flush if the `netcdf_file` object is in write mode.

**See also:**

`sync`

Identical function

6.8. Input and output (`scipy.io`)
scipy.io.netcdf_file.sync

netcdf_file.sync()

Perform a sync-to-disk flush if the netcdf_file object is in write mode.

See also:

sync

Identical function

scipy.io.netcdf_variable

class scipy.io.netcdf_variable(data, typecode, size, shape, dimensions, attributes=None, maskandscale=False)

A data object for the netcdf module.

netcdf_variable objects are constructed by calling the method netcdf_file.createVariable on the netcdf_file object. netcdf_variable objects behave much like array objects defined in numpy, except that their data resides in a file. Data is read by indexing and written by assigning to an indexed subset; the entire array can be accessed by the index [:] or (for scalars) by using the methods getValue and assignValue. netcdf_variable objects also have attribute shape with the same meaning as for arrays, but the shape cannot be modified. There is another read-only attribute dimensions, whose value is the tuple of dimension names.

All other attributes correspond to variable attributes defined in the NetCDF file. Variable attributes are created by assigning to an attribute of the netcdf_variable object.

Parameters

data [array_like] The data array that holds the values for the variable. Typically, this is initialized as empty, but with the proper shape.
typecode [dtype character code] Desired data-type for the data array.
size [int] Desired element size for the data array.
shape [sequence of ints] The shape of the array. This should match the lengths of the variable’s dimensions.
dimensions [sequence of strings] The names of the dimensions used by the variable. Must be in the same order of the dimension lengths given by shape.
attributes [dict, optional] Attribute values (any type) keyed by string names. These attributes become attributes for the netcdf_variable object.
maskandscale [bool, optional] Whether to automatically scale and/or mask data based on attributes. Default is False.

See also:

isrec, shape

Attributes

dimensions [list of str] List of names of dimensions used by the variable object.
isrec, shape

Properties

Methods
### `assignValue(value)`
Assign a scalar value to a `netcdf_variable` of length one.

### `getValue()`
Retrieve a scalar value from a `netcdf_variable` of length one.

### `itemsize()`
Return the itemsize of the variable.

### `typecode()`
Return the typecode of the variable.

---

**scipy.io.netcdf_variable.assignValue**

`netcdf_variable.assignValue(value)`

Assign a scalar value to a `netcdf_variable` of length one.

**Parameters**

- **value** [scalar] Scalar value (of compatible type) to assign to a length-one netcdf variable. This value will be written to file.

**Raises**

- **ValueError** If the input is not a scalar, or if the destination is not a length-one netcdf variable.

**scipy.io.netcdf_variable.getValue**

`netcdf_variable.getValue()`

Retrieve a scalar value from a `netcdf_variable` of length one.

**Raises**

- **ValueError** If the netcdf variable is an array of length greater than one, this exception will be raised.

**scipy.io.netcdf_variable.itemsize**

`netcdf_variable.itemsize()`

Return the itemsize of the variable.

**Returns**

- **itemsize** [int] The element size of the variable (eg, 8 for float64).

**scipy.io.netcdf_variable.typecode**

`netcdf_variable.typecode()`

Return the typecode of the variable.

**Returns**

- **typecode** [char] The character typecode of the variable (eg, ‘i’ for int).

---

**6.8.6 Harwell-Boeing files**

**`hb_read(path_or_open_file)`**
Read HB-format file.

**`hb_write(path_or_open_file, m[, hb_info])`**
Write HB-format file.

---

**scipy.io.hb_read**

**scipy.io.hb_read(path_or_open_file)**
Read HB-format file.

**Parameters**
path_or_open_file

[PATH-LIKE OR FILE-LIKE] If a file-like object, it is used as-is. Otherwise it is opened before reading.

Returns

data [SCIPY.SPARSE.CSC_MATRIX INSTANCE] The data read from the HB file as a sparse matrix.

Notes
At the moment not the full Harwell-Boeing format is supported. Supported features are:

- assembled, non-symmetric, real matrices
- integer for pointer/indices
- exponential format for float values, and int format

scipy.io.hb_write

scipy.io.hb_write(path_or_open_file, m, hb_info=None)
Write HB-format file.

Parameters

path_or_open_file [PATH-LIKE OR FILE-LIKE] If a file-like object, it is used as-is. Otherwise it is opened before writing.
m [SPARSE-MATRIX] The sparse matrix to write
hb_info [HBINFO] contains the meta-data for write

Returns

None

Notes
At the moment not the full Harwell-Boeing format is supported. Supported features are:

- assembled, non-symmetric, real matrices
- integer for pointer/indices
- exponential format for float values, and int format

6.8.7 Wav sound files (scipy.io.wavfile)

read(filename[, mmap])
Open a WAV file

write(filename, rate, data)
Write a numpy array as a WAV file.

WavFileWarning

scipy.io.wavfile.read

scipy.io.wavfile.read(filename, mmap=False)
Open a WAV file

Return the sample rate (in samples/sec) and data from a WAV file.

Parameters

filename [STRING OR OPEN FILE HANDLE] Input wav file.
mmap [BOOL, OPTIONAL] Whether to read data as memory-mapped. Only to be used on real files (Default: False).
New in version 0.12.0.
Returns

rate [int] Sample rate of wav file.
data [numpy array] Data read from wav file. Data-type is determined from the file; see Notes.

Notes
This function cannot read wav files with 24-bit data.

Common data types: [1]

<table>
<thead>
<tr>
<th>WAV format</th>
<th>Min</th>
<th>Max</th>
<th>NumPy dtype</th>
</tr>
</thead>
<tbody>
<tr>
<td>32-bit floating-point</td>
<td>-1.0</td>
<td>+1.0</td>
<td>float32</td>
</tr>
<tr>
<td>32-bit PCM</td>
<td>-2147483648</td>
<td>+2147483647</td>
<td>int32</td>
</tr>
<tr>
<td>16-bit PCM</td>
<td>-32768</td>
<td>+32767</td>
<td>int16</td>
</tr>
<tr>
<td>8-bit PCM</td>
<td>0</td>
<td>255</td>
<td>uint8</td>
</tr>
</tbody>
</table>

Note that 8-bit PCM is unsigned.

References
[1]

scipy.io.wavfile.write

scipy.io.wavfile.write(filename, rate, data)

Write a numpy array as a WAV file.

Parameters

filename [string or open file handle] Output wav file.
rate [int] The sample rate (in samples/sec).
data [ndarray] A 1-D or 2-D numpy array of either integer or float data-type.

Notes
- Writes a simple uncompressed WAV file.
- To write multiple-channels, use a 2-D array of shape (Nsamples, Nchannels).
- The bits-per-sample and PCM/float will be determined by the data-type.

Common data types: [1]

<table>
<thead>
<tr>
<th>WAV format</th>
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<th>Max</th>
<th>NumPy dtype</th>
</tr>
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</tr>
<tr>
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<td>0</td>
<td>255</td>
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</tr>
</tbody>
</table>

Note that 8-bit PCM is unsigned.

References
[1]

scipy.io.wavfile.WavFileWarning

exception scipy.io.wavfile.WavFileWarning
6.8.8 Arff files (scipy.io.arff)

loadarff(f)

Read an arff file.

MetaData(rel, attr)

Small container to keep useful information on a ARFF dataset.

ArffError

ParseArffError

scipy.io.arff.loadarff

scipy.io.arff.loadarff(f)

Read an arff file.

The data is returned as a record array, which can be accessed much like a dictionary of numpy arrays. For example, if one of the attributes is called ‘pressure’, then its first 10 data points can be accessed from the data record array like so: data['pressure'][0:10]

Parameters

f [file-like or str] File-like object to read from, or filename to open.

Returns

data [record array] The data of the arff file, accessible by attribute names.

meta [MetaData] Contains information about the arff file such as name and type of attributes, the relation (name of the dataset), etc...

Raises

ParseArffError

This is raised if the given file is not ARFF-formatted.

NotImplementedError

The ARFF file has an attribute which is not supported yet.

Notes

This function should be able to read most arff files. Not implemented functionality include:

- date type attributes
- string type attributes

It can read files with numeric and nominal attributes. It cannot read files with sparse data ({}) in the file). However, this function can read files with missing data ({} in the file), representing the data points as NaNs.

Examples

```python
>>> from scipy.io import arff
>>> from io import StringIO
>>> content = ""
... @relation foo
... @attribute width numeric
... @attribute height numeric
... @attribute color {red,green,blue,yellow,black}
... @data
... 5.0,3.25,blue
... 4.5,3.75,green
... 3.0,4.00,red
... ""
>>> f = StringIO(content)
```

(continues on next page)
>>> data, meta = arff.loadarff(f)
>>> data
array([(5.0, 3.25, 'blue'), (4.5, 3.75, 'green'), (3.0, 4.0, 'red')],
      dtype=[('width', '<f8'), ('height', '<f8'), ('color', '|S6')])
>>> meta
Dataset: foo
  width's type is numeric
  height's type is numeric
  color's type is nominal, range is ('red', 'green', 'blue', 'yellow', 'black')

scipy.io.arff.MetaData

class scipy.io.arff.MetaData(rel, attr)

Small container to keep useful information on a ARFF dataset.

Knows about attributes names and types.

Notes
Also maintains the list of attributes in order, i.e. doing for i in meta, where meta is an instance of
MetaData, will return the different attribute names in the order they were defined.

Examples

data, meta = loadarff('iris.arff')
# This will print the attributes names of the iris.arff dataset
for i in meta:
    print(i)
# This works too
meta.names()
# Getting attribute type
types = meta.types()

Methods

    names()    Return the list of attribute names.
    types()    Return the list of attribute types.

scipy.io.arff.MetaData.names
MetaData.names()
    Return the list of attribute names.

scipy.io.arff.MetaData.types
MetaData.types()
    Return the list of attribute types.

scipy.io.arff.ArffError

exception scipy.io.arff.ArffError

scipy.io.arff.ParseArffError

exception scipy.io.arff.ParseArffError

6.9 Linear algebra (scipy.linalg)

Linear algebra functions.
See also:

numpy.linalg for more linear algebra functions. Note that although scipy.linalg imports most of them, identically named functions from scipy.linalg may offer more or slightly differing functionality.

### 6.9.1 Basics

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>inv(a[, overwrite_a, check_finite])</code></td>
<td>Compute the inverse of a matrix.</td>
</tr>
<tr>
<td><code>solve(a, b[, sym_pos, lower, overwrite_a, ...])</code></td>
<td>Solves the linear equation set ( a \cdot x = b ) for the unknown ( x ) for square ( a ) matrix.</td>
</tr>
<tr>
<td><code>solve_banded(l_and_u, ab, b[, overwrite_ab, ...])</code></td>
<td>Solve the equation ( a \cdot x = b ) for ( x ), assuming ( a ) is banded matrix.</td>
</tr>
<tr>
<td><code>solveh_banded(ab, b[, overwrite_ab, ...])</code></td>
<td>Solve equation ( a \cdot x = b ).</td>
</tr>
<tr>
<td><code>solve_triangular(a, b[, trans, lower, ...])</code></td>
<td>Solve the equation ( a \cdot x = b ) for ( x ), assuming ( a ) is a triangular matrix.</td>
</tr>
<tr>
<td><code>solve_toeplitz(c_or_cr, b[, check_finite])</code></td>
<td>Solve a Toeplitz system using Levinson Recursion</td>
</tr>
<tr>
<td><code>det(a[, overwrite_a, check_finite])</code></td>
<td>Compute the determinant of a matrix</td>
</tr>
<tr>
<td><code>norm(a[, ord, axis, keepdims])</code></td>
<td>Matrix or vector norm.</td>
</tr>
<tr>
<td><code>lstsq(a, b[, cond, overwrite_a, ...])</code></td>
<td>Compute least-squares solution to equation ( A \cdot x = b ).</td>
</tr>
<tr>
<td><code>pinv(a[, cond, rcond, return_rank, check_finite])</code></td>
<td>Compute the (Moore-Penrose) pseudo-inverse of a matrix.</td>
</tr>
<tr>
<td><code>pinv2(a[, cond, rcond, return_rank, ...])</code></td>
<td>Compute the (Moore-Penrose) pseudo-inverse of a matrix.</td>
</tr>
<tr>
<td><code>pinvh(a[, cond, rcond, lower, return_rank, ...])</code></td>
<td>Compute the (Moore-Penrose) pseudo-inverse of a Hermitian matrix.</td>
</tr>
<tr>
<td><code>kron(a, b)</code></td>
<td>Kronecker product.</td>
</tr>
<tr>
<td><code>tril(m[, k])</code></td>
<td>Make a copy of a matrix with elements above the k-th diagonal zeroed.</td>
</tr>
<tr>
<td><code>triu(m[, k])</code></td>
<td>Make a copy of a matrix with elements below the k-th diagonal zeroed.</td>
</tr>
<tr>
<td><code>orthogonal_procrustes(A, B[, check_finite])</code></td>
<td>Compute the matrix solution of the orthogonal Procrustes problem.</td>
</tr>
<tr>
<td><code>matrix_balance(A[, permute, scale, ...])</code></td>
<td>Compute a diagonal similarity transformation for row/column balancing.</td>
</tr>
<tr>
<td><code>subspace_angles(A, B)</code></td>
<td>Compute the subspace angles between two matrices.</td>
</tr>
<tr>
<td><code>LinAlgError</code></td>
<td>Generic Python-exception-derived object raised by linalg functions.</td>
</tr>
<tr>
<td><code>LinAlgWarning</code></td>
<td>The warning emitted when a linear algebra related operation is close to fail conditions of the algorithm or loss of accuracy is expected.</td>
</tr>
</tbody>
</table>

#### scipy.linalg.inv

scipy.linalg.inv(a, overwrite_a=False, check_finite=True)

Compute the inverse of a matrix.

**Parameters**

- `a` [array_like] Square matrix to be inverted.
- `overwrite_a` [bool, optional] Discard data in \( a \) (may improve performance). Default is False.
check_finite
[bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns
ainv [ndarray] Inverse of the matrix a.

Raises
LinAlgError
If a is singular.
ValueError
If a is not square, or not 2-dimensional.

Examples
```python
>>> from scipy import linalg
>>> a = np.array([[1., 2.], [3., 4.]])
>>> linalg.inv(a)
array([[-2., 1. ],
       [ 1.5, -0.5]])
>>> np.dot(a, linalg.inv(a))
array([[ 1., 0. ],
       [ 0., 1. ]])
```

scipy.linalg.solve
scipy.linalg.solve(a, b, sym_pos=False, lower=False, overwrite_a=False, overwrite_b=False, debug=None, check_finite=True, assume_a='gen', transposed=False)
Solves the linear equation set \( a \times x = b \) for the unknown \( x \) for square \( a \) matrix.

If the data matrix is known to be a particular type then supplying the corresponding string to assume_a key chooses the dedicated solver. The available options are

<table>
<thead>
<tr>
<th>Assume Type</th>
<th>String</th>
</tr>
</thead>
<tbody>
<tr>
<td>Generic matrix</td>
<td>'gen'</td>
</tr>
<tr>
<td>Symmetric</td>
<td>'sym'</td>
</tr>
<tr>
<td>Hermitian</td>
<td>'her'</td>
</tr>
<tr>
<td>Positive definite</td>
<td>'pos'</td>
</tr>
</tbody>
</table>

If omitted, 'gen' is the default structure.

The datatype of the arrays define which solver is called regardless of the values. In other words, even when the complex array entries have precisely zero imaginary parts, the complex solver will be called based on the data type of the array.

Parameters
a [(N, N) array_like] Square input data
b [(N, NRHS) array_like] Input data for the right hand side.
sym_pos [bool, optional] Assume a is symmetric and positive definite. This key is deprecated and assume_a = 'pos' keyword is recommended instead. The functionality is the same. It will be removed in the future.
lower [bool, optional] If True, only the data contained in the lower triangle of a. Default is to use upper triangle. (ignored for 'gen')

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overwrite_a

[bool, optional] Allow overwriting data in a (may enhance performance). Default is False.

overwrite_b

[bool, optional] Allow overwriting data in b (may enhance performance). Default is False.

check_finite

[bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

assume_a

[str, optional] Valid entries are explained above.

transposed

bool, optional
If True, \(a^T x = b\) for real matrices, raises \(\text{NotImplementedError}\) for complex matrices (only for True).

Returns

x

[(N, NRHS) ndarray] The solution array.

Raises

ValueError
If size mismatches detected or input a is not square.

LinAlgError
If the matrix is singular.

LinAlgWarning
If an ill-conditioned input a is detected.

NotImplementedError
If transposed is True and input a is a complex matrix.

Notes
If the input b matrix is a 1D array with N elements, when supplied together with an NxN input a, it is assumed as a valid column vector despite the apparent size mismatch. This is compatible with the numpy.dot() behavior and the returned result is still 1D array.

The generic, symmetric, hermitian and positive definite solutions are obtained via calling ?GESV, ?SYSV, ?HESV, and ?POSV routines of LAPACK respectively.

Examples
Given a and b, solve for x:

```python
>>> a = np.array([[3, 2, 0], [1, -1, 0], [0, 5, 1]])
>>> b = np.array([2, 4, -1])
>>> from scipy import linalg
>>> x = linalg.solve(a, b)
>>> x
array([2., -2., 9.])
>>> np.dot(a, x) == b
array([True, True, True], dtype=bool)
```

scipy.linalg.solve_banded

scipy.linalg.solve_banded(l_and_u, ab, b, overwrite_ab=False, overwrite_b=False, debug=None, check_finite=True)
Solve the equation \(a x = b\) for \(x\), assuming \(a\) is banded matrix.

The matrix \(a\) is stored in \(ab\) using the matrix diagonal ordered form:
Example of ab (shape of a is (6,6), u =1, l =2):

<table>
<thead>
<tr>
<th></th>
<th>a01</th>
<th>a12</th>
<th>a23</th>
<th>a34</th>
<th>a45</th>
</tr>
</thead>
<tbody>
<tr>
<td>a00</td>
<td>a11</td>
<td>a22</td>
<td>a33</td>
<td>a44</td>
<td>a55</td>
</tr>
<tr>
<td>a10</td>
<td>a21</td>
<td>a32</td>
<td>a43</td>
<td>a54</td>
<td>*</td>
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<tr>
<td>a20</td>
<td>a31</td>
<td>a42</td>
<td>a53</td>
<td>*</td>
<td>*</td>
</tr>
</tbody>
</table>

Parameters

(l, u) (integer, integer) Number of non-zero lower and upper diagonals
ab (l + u + 1, M) array_like Banded matrix
b (M,) or (M, K) array_like Right-hand side
overwrite_ab [bool, optional] Discard data in ab (may enhance performance)
overwrite_b [bool, optional] Discard data in b (may enhance performance)
check_finite [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

x (M,) or (M, K) ndarray The solution to the system a x = b. Returned shape depends on the shape of b.

Examples

Solve the banded system a x = b, where:

```
[5 2 -1 0 0]    [0]
[1 4 2 -1 0]    [1]
a = [0 1 3 2 -1] b = [2]
[0 0 1 2 2]    [2]
[0 0 0 1 1]    [3]
```

There is one nonzero diagonal below the main diagonal (l = 1), and two above (u = 2). The diagonal banded form of the matrix is:

```
[5 4 3 2 1]
[1 1 1 1 *]
```

```python
>>> from scipy.linalg import solve_banded
>>> ab = np.array([[0, 0, -1, -1, -1],  # [0, 0, -1, -1, -1],
                  [0, 2, 2, 2, 2],
                  [5, 4, 3, 2, 1],
                  [1, 1, 1, 1, 0]])
>>> b = np.array([0, 1, 2, 2, 3])
>>> x = solve_banded((1, 2), ab, b)
>>> x
array([-2.37288136,  3.93220339, -4. ,  4.3559322 , -1.3559322 ])
```
scipy.linalg.solveh_banded

scipy.linalg.solveh_banded(ab, b, overwrite_ab=False, overwrite_b=False, lower=False, check_finite=True)

Solve equation \( a x = b \). \( a \) is Hermitian positive-definite banded matrix.

The matrix \( a \) is stored in \( ab \) either in lower diagonal or upper diagonal ordered form:
\[
ab[u + i - j, j] == a[i,j] \quad \text{(if upper form; i <= j)}
ab[i - j, j] == a[i,j] \quad \text{(if lower form; i >= j)}
\]

Example of \( ab \) (shape of \( a \) is (6, 6), \( u =2 \)):

<table>
<thead>
<tr>
<th></th>
<th></th>
<th>a02</th>
<th>a13</th>
<th>a24</th>
<th>a35</th>
</tr>
</thead>
<tbody>
<tr>
<td>**</td>
<td></td>
<td>a01</td>
<td>a12</td>
<td>a23</td>
<td>a34</td>
</tr>
<tr>
<td></td>
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<td>a00</td>
<td>a11</td>
<td>a22</td>
<td>a33</td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th></th>
<th>a10</th>
<th>a21</th>
<th>a32</th>
<th>a43</th>
<th>a54</th>
<th>*</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>a20</td>
<td>a31</td>
<td>a42</td>
<td>a53</td>
<td>*</td>
<td>*</td>
</tr>
</tbody>
</table>

Cells marked with * are not used.

**Parameters**

- **ab** [(\( u + 1, M \)) array_like] Banded matrix
- **b** [(\( M, \)) or (\( M, K \)) array_like] Right-hand side
- **overwrite_ab** [bool, optional] Discard data in \( ab \) (may enhance performance)
- **overwrite_b** [bool, optional] Discard data in \( b \) (may enhance performance)
- **lower** [bool, optional] Is the matrix in the lower form. (Default is upper form)
- **check_finite** [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

**Returns**

- **x** [(\( M, \)) or (\( M, K \)) ndarray] The solution to the system \( a x = b \). Shape of return matches shape of \( b \).

**Examples**

Solve the banded system \( A x = b \), where:

\[
A = \begin{bmatrix}
4 & 2 & -1 & 0 & 0 & 0 \\
2 & 5 & 2 & -1 & 0 & 0 \\
-1 & 2 & 6 & 2 & -1 & 0 \\
0 & -1 & 2 & 7 & 2 & -1 \\
0 & 0 & -1 & 2 & 8 & 2 \\
0 & 0 & 0 & -1 & 2 & 9 \\
\end{bmatrix} \quad b = \begin{bmatrix}
1 \\
2 \\
2 \\
3 \\
3 \\
3 \\
\end{bmatrix}
\]

```python
>>> from scipy.linalg import solveh_banded

ab contains the main diagonal and the nonzero diagonals below the main diagonal. That is, we use the lower form:
Solve the Hermitian banded system $H x = b$, where:

$$H = \begin{bmatrix}
8 & 2-1j & 0 & 0 \\
2+1j & 5 & 1j & 0 \\
0 & -1j & 9 & -2-1j \\
0 & 0 & -2+1j & 6
\end{bmatrix} \quad b = \begin{bmatrix} 1+1j \\ 1-2j \\ 1-1j \end{bmatrix}$$

In this example, we put the upper diagonals in the array $hb$:

```python
>>> hb = np.array([[0, 2-1j, 1j, -2-1j],
                 ... [8, 5, 9, 6]])
>>> b = np.array([1, 1+1j, 1-2j, 0])
>>> x = solveh_banded(hb, b)
>>> x
array([ 0.07318536-0.02939412j, 0.11877624+0.17696461j,
        0.10077984-0.23035393j, -0.00479904-0.09358128j])
```

`scipy.linalg.solve_circulant`

`solve_circulant(c, b, singular='raise', tol=None, caxis=-1, baxis=0, outaxis=0)`

Solve $C x = b$ for $x$, where $C$ is the circulant matrix.

$C$ is the circulant matrix associated with the vector $c$.

The system is solved by doing division in Fourier space. The calculation is:

$$x = \text{ifft}(\text{fft}(b) / \text{fft}(c))$$

where `fft` and `ifft` are the fast Fourier transform and its inverse, respectively. For a large vector $c$, this is much faster than solving the system with the full circulant matrix.

**Parameters**

- `c` [array_like] The coefficients of the circulant matrix.
- `b` [array_like] Right-hand side matrix in $a x = b$.
- `singular` [str, optional] This argument controls how a near singular circulant matrix is handled. If `singular` is “raise” and the circulant matrix is near singular, a `LinAlgError` is raised. If `singular` is “lstsq”, the least squares solution is returned. Default is “raise”.
- `tol` [float, optional] If any eigenvalue of the circulant matrix has an absolute value that is less than or equal to `tol`, the matrix is considered to be near singular. If not given, `tol` is set to:

  $$tol = \text{abs}_eigs\cdot\text{abs}_eigs\cdot\text{size} \times \text{np.finfo(np.float64)}.\text{eps}$$

where `abs_eigs` is the array of absolute values of the eigenvalues of the circulant matrix.
caxis [int] When c has dimension greater than 1, it is viewed as a collection of circulant vectors. In this case, caxis is the axis of c that holds the vectors of circulant coefficients.

baxis [int] When b has dimension greater than 1, it is viewed as a collection of vectors. In this case, baxis is the axis of b that holds the right-hand side vectors.

outaxis [int] When c or b are multidimensional, the value returned by solve_circulant is multidimensional. In this case, outaxis is the axis of the result that holds the solution vectors.

Returns

x [ndarray] Solution to the system C x = b.

Raises

LinAlgError
If the circulant matrix associated with c is near singular.

See also:
circulant
circulant matrix

Notes
For a one-dimensional vector c with length m, and an array b with shape (m, ...),
solve_circulant(c, b)
returns the same result as
solve(circulant(c), b)
where solve and circulant are from scipy.linalg.

New in version 0.16.0.

Examples

>>> from scipy.linalg import solve_circulant, solve, circulant, lstsq

>>> c = np.array([2, 2, 4])
>>> b = np.array([1, 2, 3])
>>> solve_circulant(c, b)
array([ 0.75, -0.25, 0.25])

Compare that result to solving the system with scipy.linalg.solve:

>>> solve(circulant(c), b)
array([ 0.75, -0.25, 0.25])

A singular example:

>>> c = np.array([1, 1, 0, 0])
>>> b = np.array([1, 2, 3, 4])

Calling solve_circulant(c, b) will raise a LinAlgError. For the least square solution, use the option singular='lstsq':

>>> solve_circulant(c, b, singular='lstsq')
array([ 0.25, 1.25, 2.25, 1.25])
Compare to `scipy.linalg.lstsq`:

```python
>>> x, resid, rnk, s = lstsq(circulant(c), b)
>>> x
array([[ 0.25,  1.25,  2.25,  1.25]])
```

A broadcasting example:

Suppose we have the vectors of two circulant matrices stored in an array with shape (2, 5), and three
$b$ vectors stored in an array with shape (3, 5). For example,

```python
>>> c = np.array([[1.5, 2, 3, 0, 0], [1, 1, 4, 3, 2]])
>>> b = np.arange(15).reshape(-1, 5)
```

We want to solve all combinations of circulant matrices and $b$ vectors, with the result stored in an
array with shape (2, 3, 5). When we disregard the axes of $c$ and $b$ that hold the vectors of coefficients,
the shapes of the collections are (2,) and (3,), respectively, which are not compatible for broadcasting.
To have a broadcast result with shape (2, 3), we add a trivial dimension to $c$: `c[:, np.newaxis, :]`
has shape (2, 1, 5). The last dimension holds the coefficients of the circulant matrices, so when we call
`solve_circulant`, we can use the default `caxis=-1`. The coefficients of the $b$ vectors are in the last
dimension of the array $b$, so we use `baxis=-1`. If we use the default `outaxis`, the result will have shape
(5, 2, 3), so we’ll use `outaxis=-1` to put the solution vectors in the last dimension.

```python
>>> x = solve_circulant(c[:, np.newaxis, :], b, baxis=-1, outaxis=-1)
>>> x.shape
(2, 3, 5)
>>> np.set_printoptions(precision=3)  # For compact output of numbers.
>>> x
array([[-0.118,  0.220,  1.277, -0.142,  0.302],
        [ 0.651,  0.989,  2.046,  0.627,  1.072],
        [ 1.420,  1.758,  2.816,  1.396,  1.841]],
       [[ 0.401,  0.304,  0.694, -0.867,  0.377],
        [ 0.856,  0.758,  1.149, -0.412,  0.831],
        [ 1.310,  1.213,  1.603,  0.042,  1.286]])
```

Check by solving one pair of $c$ and $b$ vectors (cf. $x[1, 1, :]$):

```python
>>> solve_circulant(c[1], b[1, :])
array([[ 0.856,  0.758,  1.149, -0.412,  0.831]])
```

`scipy.linalg.solve_triangular`

`scipy.linalg.solve_triangular(a, b, trans=0, lower=False, unit_diagonal=False, overwrite_b=False, debug=None, check_finite=True)`

Solve the equation $a x = b$ for $x$, assuming $a$ is a triangular matrix.

**Parameters**

- `a` ([M, M] array_like) A triangular matrix
- `b` ([M,) or (M, N] array_like) Right-hand side matrix in $a x = b$
- `lower` (bool, optional) Use only data contained in the lower triangle of $a$. Default is to use upper triangle.
- `trans` ([0, 1, 2, ‘N’, ‘T’, ‘C’], optional) Type of system to solve:
<table>
<thead>
<tr>
<th>trans</th>
<th>system</th>
</tr>
</thead>
<tbody>
<tr>
<td>0 or ‘N’</td>
<td>a x = b</td>
</tr>
<tr>
<td>1 or ‘T’</td>
<td>a^T x = b</td>
</tr>
<tr>
<td>2 or ‘C’</td>
<td>a^H x = b</td>
</tr>
</tbody>
</table>

**unit_diagonal**
[bool, optional] If True, diagonal elements of a are assumed to be 1 and will not be referenced.

**overwrite_b**
[bool, optional] Allow overwriting data in b (may enhance performance)

**check_finite**
[bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

**Returns**

x
[(M,) or (M, N) ndarray] Solution to the system a x = b. Shape of return matches b.

**Raises**

LinAlgError
If a is singular

**Notes**
New in version 0.9.0.

**Examples**
Solve the lower triangular system a x = b, where:

\[
\begin{bmatrix}
3 & 0 & 0 & 0 \\
2 & 1 & 0 & 0 \\
1 & 0 & 1 & 0 \\
1 & 1 & 1 & 1
\end{bmatrix}
\begin{bmatrix}
x_1 \\
x_2 \\
x_3 \\
x_4
\end{bmatrix}
= 
\begin{bmatrix}
4 \\
2 \\
4 \\
2
\end{bmatrix}
\]

```python
>>> from scipy.linalg import solve_triangular
>>> a = np.array([[3, 0, 0, 0], [2, 1, 0, 0], [1, 0, 1, 0], [1, 1, 1, 1]])
>>> b = np.array([4, 2, 4, 2])
>>> x = solve_triangular(a, b, lower=True)
>>> x
array([ 1.33333333, -0.66666667,  2.66666667, -1.33333333])
```

scipy.linalg.solve_toeplitz

scipy.linalg.solve_toeplitz(c_or_cr, b, check_finite=True)
Solve a Toeplitz system using Levinson Recursion

The Toeplitz matrix has constant diagonals, with c as its first column and r as its first row. If r is not given, r == conjugate(c) is assumed.

**Parameters**

**c_or_cr**
[array_like or tuple of (array_like, array_like)] The vector c, or a tuple of arrays (c, r). Whatever the actual shape of c, it will be converted to a 1-D array. If not supplied, r = conjugate(c) is assumed; in this case, if c[0] is real, the Toeplitz
matrix is Hermitian. \( r[0] \) is ignored; the first row of the Toeplitz matrix is \([c[0],\]
\([r[1:]]\). Whatever the actual shape of \( r \), it will be converted to a 1-D array.

- \( b \): \((M,)\) or \((M, K)\) array_like
  - Right-hand side in \( T x = b \).
- \( \text{check\_finite} \):
  - bool, optional
    - Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (result entirely NaNs) if the inputs do contain infinities or NaNs.

**Returns**

- \( x \):
  - \((M,)\) or \((M, K)\) ndarray
    - The solution to the system \( T x = b \). Shape of return matches shape of \( b \).

**See also:**

toeplitz

Toeplitz matrix

**Notes**

The solution is computed using Levinson-Durbin recursion, which is faster than generic least-squares methods, but can be less numerically stable.

**Examples**

Solve the Toeplitz system \( T x = b \), where:

\[
\begin{bmatrix}
1 & -1 & -2 & -3 \\
3 & 1 & -1 & -2 \\
6 & 3 & 1 & -1 \\
10 & 6 & 3 & 1
\end{bmatrix}
\begin{bmatrix}
1 \\
2 \\
2 \\
5
\end{bmatrix}
\]

To specify the Toeplitz matrix, only the first column and the first row are needed.

```python
>>> c = np.array([1, 3, 6, 10])  # First column of T
>>> r = np.array([1, -1, -2, -3])  # First row of T
>>> b = np.array([1, 2, 2, 5])

>>> from scipy.linalg import solve_toeplitz, toeplitz
>>> x = solve_toeplitz((c, r), b)
>>> x
array([ 1.66666667, -1. , -2.66666667, 2.33333333])
```

Check the result by creating the full Toeplitz matrix and multiplying it by \( x \). We should get \( b \).

```python
>>> T = toeplitz(c, r)
>>> T.dot(x)
array([ 1., 2., 2., 5.])
```

**scipy.linalg.det**

\[
\text{scipy.linalg.det}(a, \text{overwrite\_a}=False, \text{check\_finite}=True)
\]

Compute the determinant of a matrix

The determinant of a square matrix is a value derived arithmetically from the coefficients of the matrix.

The determinant for a 3x3 matrix, for example, is computed as follows:
\[ \text{det}(A) = a \cdot e \cdot i + b \cdot f \cdot g + c \cdot d \cdot h - c \cdot e \cdot g - b \cdot d \cdot i - a \cdot f \cdot h \]

**Parameters**

- **a** [(M, M) array_like] A square matrix.
- **overwrite_a** [bool, optional] Allow overwriting data in a (may enhance performance).
- **check__finite** [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

**Returns**

- **det** [float or complex] Determinant of \( a \).

**Notes**

The determinant is computed via LU factorization, LAPACK routine z/dgetrf.

**Examples**

```python
>>> from scipy import linalg
>>> a = np.array([[1, 2, 3], [4, 5, 6], [7, 8, 9]])
>>> linalg.det(a)
0.0
>>> a = np.array([[0, 2, 3], [4, 5, 6], [7, 8, 9]])
>>> linalg.det(a)
3.0
```

**scipy.linalg.norm**

`scipy.linalg.norm(a, ord=None, axis=None, keepdims=False)`

Matrix or vector norm.

This function is able to return one of seven different matrix norms, or one of an infinite number of vector norms (described below), depending on the value of the ord parameter.

**Parameters**

- **a** [(M,) or (M, N) array_like] Input array. If \( axis \) is None, \( a \) must be 1-D or 2-D.
- **ord** [{non-zero int, inf, -inf, ‘fro’}, optional] Order of the norm (see table under Notes). inf means numpy’s inf object
- **axis** [{int, 2-tuple of ints, None}, optional] If \( axis \) is an integer, it specifies the axis of \( a \) along which to compute the vector norms. If \( axis \) is a 2-tuple, it specifies the axes that hold 2-D matrices, and the matrix norms of these matrices are computed. If \( axis \) is None then either a vector norm (when \( a \) is 1-D) or a matrix norm (when \( a \) is 2-D) is returned.
- **keepdims** [bool, optional] If this is set to True, the axes which are normed over are left in the result as dimensions with size one. With this option the result will broadcast correctly against the original \( a \).

**Returns**
n
[float or ndarray] Norm of the matrix or vector(s).

Notes
For values of ord \( \leq 0 \), the result is, strictly speaking, not a mathematical ‘norm’, but it may still be useful for various numerical purposes.

The following norms can be calculated:

<table>
<thead>
<tr>
<th>ord</th>
<th>norm for matrices</th>
<th>norm for vectors</th>
</tr>
</thead>
<tbody>
<tr>
<td>None</td>
<td>Frobenius norm</td>
<td>2-norm</td>
</tr>
<tr>
<td>‘fro’</td>
<td>Frobenius norm</td>
<td>–</td>
</tr>
<tr>
<td>inf</td>
<td>max(sum(abs(x), axis=1))</td>
<td>max(abs(x))</td>
</tr>
<tr>
<td>-inf</td>
<td>min(sum(abs(x), axis=1))</td>
<td>min(abs(x))</td>
</tr>
<tr>
<td>0</td>
<td>–</td>
<td>sum(x != 0)</td>
</tr>
<tr>
<td>1</td>
<td>max(sum(abs(x), axis=0))</td>
<td>as below</td>
</tr>
<tr>
<td>-1</td>
<td>min(sum(abs(x), axis=0))</td>
<td>as below</td>
</tr>
<tr>
<td>2</td>
<td>2-norm (largest sing. value)</td>
<td>as below</td>
</tr>
<tr>
<td>-2</td>
<td>smallest singular value</td>
<td>as below</td>
</tr>
<tr>
<td>other</td>
<td>–</td>
<td>sum(abs(x)<strong>ord)</strong>(1./ord)</td>
</tr>
</tbody>
</table>

The Frobenius norm is given by \( /|A|_F = [\sum_{i,j} abs(a_{i,j})^2]^{1/2} /\):

The axis and keepdims arguments are passed directly to numpy.linalg.norm and are only usable if they are supported by the version of numpy in use.

References
[1]

Examples

```python
>>> from scipy.linalg import norm
>>> a = np.arange(9) - 4.0
>>> a
array([-4., -3., -2., -1., 0., 1., 2., 3., 4.])
>>> b = a.reshape((3, 3))
>>> b
array([[-4., -3., -2.],
       [-1.,  0.,  1.],
       [ 2.,  3.,  4.]])

>>> norm(a)
7.745966692414834
>>> norm(b)
7.745966692414834
>>> norm(b, 'fro')
7.745966692414834
>>> norm(a, np.inf)
4
>>> norm(b, np.inf)
9
>>> norm(a, -np.inf)
0
>>> norm(b, -np.inf)
2
```
scipy.linalg.lstsq

scipy.linalg.lstsq(a, b, cond=None, overwrite_a=False, overwrite_b=False, check_finite=True, lapack_driver=None)

Compute least-squares solution to equation $Ax = b$.

Compute a vector $x$ such that the 2-norm $|b - A x|$ is minimized.

**Parameters**

- **a** *(M, N) array_like*  
  Left hand side matrix (2-D array).

- **b** *(M,) or (M, K) array_like*  
  Right hand side matrix or vector (1-D or 2-D array).

- **cond** *float, optional*  
  Cutoff for ‘small’ singular values; used to determine effective rank of $a$. Singular values smaller than $rcond * largest_singular_value$ are considered zero.

- **overwrite_a** *bool, optional*  
  Discard data in $a$ (may enhance performance). Default is False.

- **overwrite_b** *bool, optional*  
  Discard data in $b$ (may enhance performance). Default is False.

- **check_finite** *bool, optional*  
  Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

- **lapack_driver** *str, optional*  
  Which LAPACK driver is used to solve the least-squares problem. Options are `'gelsd'`, `'gelsy'`, `'gelss'`. Default (`'gelsd'`) is a good choice. However, `'gelsy'` can be slightly faster on many problems. `'gelss'` was used historically. It is generally slow but uses less memory.

  New in version 0.17.0.

**Returns**

- **x** *[N,) or (N, K) ndarray*  
  Least-squares solution. Return shape matches shape of $b$. 

---

```python
>>> norm(a, 1)
20
>>> norm(b, 1)
7
>>> norm(a, -1)
-4.6566128774142013e-010
>>> norm(b, -1)
6
>>> norm(a, 2)
7.745966692414834
>>> norm(b, 2)
7.348492283495345

>>> norm(a, -2)
0
>>> norm(b, -2)
1.8570331885190563e-016
>>> norm(a, 3)
5.8480354764257312
>>> norm(a, -3)
0
```
SciPy Reference Guide, Release 1.2.0

residues: [(0,) or () or (K,) ndarray] Sums of residues, squared 2-norm for each column in `b - a @ x`. If the rank of matrix `a` is less than `M` or `N` or `M` or `gelsy` is used, this is a length zero array. If `b` was 1-D, this is a () shape array (numpy scalar), otherwise the shape is (K,).

rank: [int] Effective rank of matrix `a`.

s: [(min(M,N),) ndarray or None] Singular values of `a`. The condition number of `a` is `abs(s[0] / s[-1])`. None is returned when 'gelsy' is used.

Raises:

LinAlgError
If computation does not converge.

ValueError
When parameters are wrong.

See also:

optimize.nnls
linear least squares with non-negativity constraint

Examples:

```python
>>> from scipy.linalg import lstsq
>>> import matplotlib.pyplot as plt
```

Suppose we have the following data:

```python
>>> x = np.array([1, 2.5, 3.5, 4, 5, 7, 8.5])
>>> y = np.array([0.3, 1.1, 1.5, 2.0, 3.2, 6.6, 8.6])
```

We want to fit a quadratic polynomial of the form `y = a + b * x ** 2` to this data. We first form the “design matrix” `M`, with a constant column of 1s and a column containing `x ** 2`:

```python
>>> M = x[:, np.newaxis] ** [0, 2]
>>> M
array([[ 1. ,  1. ],
       [ 1. ,  6.25],
       [ 1. , 12.25],
       [ 1. , 16. ],
       [ 1. , 25. ],
       [ 1. , 49. ],
       [ 1. , 72.25]])
```

We want to find the least-squares solution to `M @ p = y`, where `p` is a vector with length 2 that holds the parameters `a` and `b`.

```python
>>> p, res, rnk, s = lstsq(M, y)
>>> p
array([ 0.20925829,  0.12013861])
```

Plot the data and the fitted curve.

```python
>>> plt.plot(x, y, 'o', label='data')
>>> xx = np.linspace(0, 9, 101)
>>> yy = p[0] + p[1] * xx ** 2
>>> plt.plot(xx, yy, label='least squares fit, $y = a + bx^2$')
```

(continues on next page)
```python
>>> plt.xlabel('x')
>>> plt.ylabel('y')
>>> plt.legend(framealpha=1, shadow=True)
>>> plt.grid(alpha=0.25)
>>> plt.show()
```

![Graph showing data and least squares fit, \(y = a + bx^2\)](image)

**scipy.linalg.pinv**

Calculate a generalized inverse of a matrix using a least-squares solver.

**Parameters**

- `a` ([M, N] array_like) Matrix to be pseudo-inverted.
- `cond`, `rcond` [float, optional] Cutoff for ‘small’ singular values in the least-squares solver. Singular values smaller than \(rcond \times \text{largest singular value}\) are considered zero.
- `return_rank` [bool, optional] if True, return the effective rank of the matrix
- `check_finite` [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

**Returns**

- `rank` [int] The effective rank of the matrix. Returned if `return_rank == True`

**Raises**

- LinAlgError
  If computation does not converge.
Examples

```python
from scipy import linalg
>>> a = np.random.randn(9, 6)
>>> B = linalg.pinv(a)
>>> np.allclose(a, np.dot(a, np.dot(B, a)))
True
>>> np.allclose(B, np.dot(B, np.dot(a, B)))
True
```

scipy.linalg.pinv2

`scipy.linalg.pinv2(a, cond=None, rcond=None, return_rank=False, check_finite=True)`

Compute the (Moore-Penrose) pseudo-inverse of a matrix.

Calculate a generalized inverse of a matrix using its singular-value decomposition and including all ‘large’ singular values.

**Parameters**

- `a` *(M, N) array_like* Matrix to be pseudo-inverted.
- `cond, rcond` *[float or None]* Cutoff for ‘small’ singular values. Singular values smaller than `rcond*largest_singular_value` are considered zero. If None or -1, suitable machine precision is used.
- `return_rank` *[bool, optional]* if True, return the effective rank of the matrix
- `check_finite` *[bool, optional]* Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

**Returns**

- `B` *[(N, M) ndarray]* The pseudo-inverse of matrix `a`.
- `rank` *[int]* The effective rank of the matrix. Returned if `return_rank == True`

**Raises**

- `LinAlgError` If SVD computation does not converge.

Examples

```python
from scipy import linalg
>>> a = np.random.randn(9, 6)
>>> B = linalg.pinv2(a)
>>> np.allclose(a, np.dot(a, np.dot(B, a)))
True
>>> np.allclose(B, np.dot(B, np.dot(a, B)))
True
```

scipy.linalg.pinvh

`scipy.linalg.pinvh(a, cond=None, rcond=None, lower=True, return_rank=False, check_finite=True)`

Compute the (Moore-Penrose) pseudo-inverse of a Hermitian matrix.

Calculate a generalized inverse of a Hermitian or real symmetric matrix using its eigenvalue decomposition and including all eigenvalues with ‘large’ absolute value.
Parameters

- **a** [(N, N) array_like] Real symmetric or complex hermitian matrix to be pseudo-inverted
- **cond, rcond** [float or None] Cutoff for ‘small’ eigenvalues. Singular values smaller than rcond * largest_eigenvalue are considered zero.
  - If None or -1, suitable machine precision is used.
- **lower** [bool, optional] Whether the pertinent array data is taken from the lower or upper triangle of a. (Default: lower)
- **return_rank** [bool, optional] if True, return the effective rank of the matrix
- **check_finite** [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

- **rank** [int] The effective rank of the matrix. Returned if return_rank == True

Raises

- **LinAlgError** If eigenvalue does not converge

Examples

```python
>>> from scipy.linalg import pinvh
>>> a = np.random.randn(9, 6)
>>> a = np.dot(a, a.T)
>>> B = pinvh(a)
>>> np.allclose(a, np.dot(a, np.dot(B, a)))
True
>>> np.allclose(B, np.dot(B, np.dot(a, B)))
True
```

**scipy.linalg.kron**

scipy.linalg.kron(a, b)

Kronecker product.

The result is the block matrix:

```
| a[0,0]*b | a[0,1]*b | ... | a[0,-1]*b |
| a[1,0]*b | a[1,1]*b | ... | a[1,-1]*b |
| ...      | ...      |     | ...       |
| a[-1,0]*b| a[-1,1]*b| ... | a[-1,-1]*b|
```

Parameters

- **a** [(M, N) ndarray] Input array
- **b** [(P, Q) ndarray] Input array

Returns

- **A** [(M*P, N*Q) ndarray] Kronecker product of a and b.
Examples

```python
>>> from numpy import array
>>> from scipy.linalg import kron
>>> kron(array([[1, 2], [3, 4]]), array([[1, 1], [1, 1]]))
array([[1, 1, 2, 2, 3, 3, 4, 4],
       [1, 1, 2, 2, 3, 3, 4, 4]])
```

scipy.linalg.tril

scipy.linalg.tril(m, k=0)
Make a copy of a matrix with elements above the k-th diagonal zeroed.

Parameters

- **m** [array_like] Matrix whose elements to return
- **k** [int, optional] Diagonal above which to zero elements. k == 0 is the main diagonal, k < 0 subdiagonal and k > 0 superdiagonal.

Returns

- **tril** [ndarray] Return is the same shape and type as m.

Examples

```python
>>> from scipy.linalg import tril
>>> tril([[1, 2, 3], [4, 5, 6], [7, 8, 9], [10, 11, 12]], -1)
array([[0, 0, 0],
       [4, 0, 0],
       [7, 8, 0],
       [10, 11, 12]])
```

scipy.linalg.triu

scipy.linalg.triu(m, k=0)
Make a copy of a matrix with elements below the k-th diagonal zeroed.

Parameters

- **m** [array_like] Matrix whose elements to return
- **k** [int, optional] Diagonal below which to zero elements. k == 0 is the main diagonal, k < 0 subdiagonal and k > 0 superdiagonal.

Returns

- **triu** [ndarray] Return matrix with zeroed elements below the k-th diagonal and has same shape and type as m.

Examples

```python
>>> from scipy.linalg import triu
>>> triu([[1, 2, 3], [4, 5, 6], [7, 8, 9], [10, 11, 12]], -1)
array([[1, 2, 3],
       [4, 5, 6],
       [0, 8, 9],
       [0, 0, 12]])
```

scipy.linalg.orthogonal_procrustes

scipy.linalg.orthogonal_procrustes(A, B, check_finite=True)
Compute the matrix solution of the orthogonal Procrustes problem.
Given matrices A and B of equal shape, find an orthogonal matrix R that most closely maps A to B using the algorithm given in [1].

**Parameters**

- **A**
  
  [(M, N) array_like] Matrix to be mapped.

- **B**
  
  [(M, N) array_like] Target matrix.

- **check_finite**
  
  [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

**Returns**

- **R**
  
  [(N, N) ndarray] The matrix solution of the orthogonal Procrustes problem. Minimizes the Frobenius norm of \((A @ R) - B\) subject to \(R.T @ R = I\).

- **scale**
  
  [float] Sum of the singular values of \(A.T @ B\).

**Raises**

**ValueError**

If the input array shapes don’t match or if check_finite is True and the arrays contain Inf or NaN.

**Notes**

Note that unlike higher level Procrustes analyses of spatial data, this function only uses orthogonal transformations like rotations and reflections, and it does not use scaling or translation.

New in version 0.15.0.

**References**

[1]

**Examples**

```python
>>> from scipy.linalg import orthogonal_procrustes
>>> A = np.array([[ 2,  0,  1], [-2,  0,  0]])
```

Flip the order of columns and check for the anti-diagonal mapping

```python
>>> R, sca = orthogonal_procrustes(A, np.fliplr(A))
>>> R
array([[5.34384992e-17, 0.00000000e+00, 1.00000000e+00],
       [0.00000000e+00, 1.00000000e+00, 0.00000000e+00],
       [1.00000000e+00, 0.00000000e+00, -7.85941422e-17]])
```

```python
>>> sca
9.0
```

**scipy.linalg.matrix_balance**

**scipy.linalg.matrix_balance**(A, permute=True, scale=True, separate=False, overwrite_a=False)

Compute a diagonal similarity transformation for row/column balancing.

The balancing tries to equalize the row and column 1-norms by applying a similarity transformation such that the magnitude variation of the matrix entries is reflected to the scaling matrices.

Moreover, if enabled, the matrix is first permuted to isolate the upper triangular parts of the matrix and, again if scaling is also enabled, only the remaining subblocks are subjected to scaling.

The balanced matrix satisfies the following equality

\[ B = T^{-1}AT \]
The scaling coefficients are approximated to the nearest power of 2 to avoid round-off errors.

**Parameters**

- **A**
  - [(n, n) array_like] Square data matrix for the balancing.
- **permute**
  - [bool, optional] The selector to define whether permutation of A is also performed prior to scaling.
- **scale**
  - [bool, optional] The selector to turn on and off the scaling. If False, the matrix will not be scaled.
- **separate**
  - [bool, optional] This switches from returning a full matrix of the transformation to a tuple of two separate 1D permutation and scaling arrays.
- **overwrite_a**
  - [bool, optional] This is passed to xGEBAL directly. Essentially, overwrites the result to the data. It might increase the space efficiency. See LAPACK manual for details. This is False by default.

**Returns**

- **B**
  - [(n, n) ndarray] Balanced matrix
- **T**
  - [(n, n) ndarray] A possibly permuted diagonal matrix whose nonzero entries are integer powers of 2 to avoid numerical truncation errors.
- **scale**, **perm**
  - [(n,) ndarray] If `separate` keyword is set to True then instead of the array T above, the scaling and the permutation vectors are given separately as a tuple without allocating the full array T.

**Notes**

This algorithm is particularly useful for eigenvalue and matrix decompositions and in many cases it is already called by various LAPACK routines.

The algorithm is based on the well-known technique of [1] and has been modified to account for special cases. See [2] for details which have been implemented since LAPACK v3.5.0. Before this version there are corner cases where balancing can actually worsen the conditioning. See [3] for such examples.

The code is a wrapper around LAPACK’s xGEBAL routine family for matrix balancing.

New in version 0.19.0.

**References**

[1], [2], [3]

**Examples**

```python
>>> from scipy import linalg
>>> x = np.array([[1,2,0], [9,1,0.01], [1,2,10*np.pi]])
```

```python
>>> y, permscale = linalg.matrix_balance(x)
>>> np.abs(x).sum(axis=0) / np.abs(x).sum(axis=1)
array([3.66666667, 0.4995005 , 0.91312162])
```

```python
>>> np.abs(y).sum(axis=0) / np.abs(y).sum(axis=1)
array([1.2 , 1.27041742, 0.92658316]) # may vary
```

```python
>>> permscale  # only powers of 2 (0.5 == 2^(-1))
array([[ 0.5, 0. , 0. ],  # may vary
        [ 0. , 1. , 0. ],
        [ 0. , 0. , 1. ]])
```

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scipy.linalg.subspace_angles

scipy.linalg.subspace_angles(A, B)

Compute the subspace angles between two matrices.

Parameters

A [(M, N) array_like] The first input array.
B [(M, K) array_like] The second input array.

Returns

angles [ndarray, shape (min(N, K),)] The subspace angles between the column spaces of
A and B in descending order.

See also:

orth, svd

Notes

This computes the subspace angles according to the formula provided in [1]. For equivalence with
MATLAB and Octave behavior, use angles[0].

New in version 1.0.

References

[1]

Examples

A Hadamard matrix, which has orthogonal columns, so we expect that the subspace angle to be \( \frac{\pi}{2} \):

```python
>>> from scipy.linalg import hadamard, subspace_angles
>>> H = hadamard(4)
>>> print(H)
[[ 1  1  1  1]
 [ 1 -1  1 -1]
 [ 1  1 -1 -1]
 [ 1 -1 -1  1]]
>>> np.rad2deg(subspace_angles(H[:, :2], H[:, 2:]))
array([ 90., 90.])
```

And the subspace angle of a matrix to itself should be zero:

```python
>>> subspace_angles(H[:, :2], H[:, :2]) <= 2 * np.finfo(float).eps
array([[ True,  True],
        [ True,  True]], dtype=bool)
```

The angles between non-orthogonal subspaces are in between these extremes:

```python
>>> x = np.random.RandomState(0).randn(4, 3)
>>> np.rad2deg(subspace_angles(x[:, :2], x[:, [2]]))
array([[ 55.832]])
```

scipy.linalg.LinAlgError

exception scipy.linalg.LinAlgError

Generic Python-exception-derived object raised by linalg functions.

General purpose exception class, derived from Python’s exception.Exception class, programmatically
raised in linalg functions when a Linear Algebra-related condition would prevent further correct exe-
cution of the function.
Parameters
None

Examples
>>> from numpy import linalg as LA
>>> LA.inv(np.zeros((2,2)))
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
  File "numpy/linalg.py", line 350,
in inv return wrap(solve(a, identity(a.shape[0], dtype=a.dtype)))
  File "numpy/linalg.py", line 249,
  in solve
    raise LinAlgError('Singular matrix')
numpy.linalg.LinAlgError: Singular matrix

scipy.linalg.LinAlgWarning

exception scipy.linalg.LinAlgWarning
The warning emitted when a linear algebra related operation is close to fail conditions of the algorithm or loss of accuracy is expected.

6.9.2 Eigenvalue Problems

<table>
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<th>Function</th>
<th>Description</th>
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<td><code>eig(a[, b, left, right, overwrite_a, ...])</code></td>
<td>Solve an ordinary or generalized eigenvalue problem of a square matrix.</td>
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<tr>
<td><code>eigvals(a[, b, overwrite_a, check_finite, ...])</code></td>
<td>Compute eigenvalues from an ordinary or generalized eigenvalue problem.</td>
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<tr>
<td><code>eigh(a[, b, lower, eigvals_only, ...])</code></td>
<td>Solve an ordinary or generalized eigenvalue problem for a complex Hermitian or real symmetric matrix.</td>
</tr>
<tr>
<td><code>eighsh(a[, b, lower, overwrite_a, ...])</code></td>
<td>Solve an ordinary or generalized eigenvalue problem for a complex Hermitian or real symmetric matrix.</td>
</tr>
<tr>
<td><code>eig_banded(a_band[, lower, eigvals_only, ...])</code></td>
<td>Solve real symmetric or complex hermitian band matrix eigenvalue problem.</td>
</tr>
<tr>
<td><code>eigvals_banded(a_band[, lower, ...])</code></td>
<td>Solve real symmetric or complex hermitian band matrix eigenvalue problem.</td>
</tr>
<tr>
<td><code>eigh_tridiagonal(d, e[, eigvals_only, ...])</code></td>
<td>Solve eigenvalue problem for a real symmetric tridiagonal matrix.</td>
</tr>
<tr>
<td><code>eigvalsh_tridiagonal(d, e[, select, ...])</code></td>
<td>Solve eigenvalue problem for a real symmetric tridiagonal matrix.</td>
</tr>
</tbody>
</table>

scipy.linalg.eig

scipy.linalg.eig(a, b=None, left=False, right=True, overwrite_a=False, overwrite_b=False, check_finite=True, homogeneous_eigvals=False)

Solve an ordinary or generalized eigenvalue problem of a square matrix.

Find eigenvalues w and right or left eigenvectors of a general matrix:

\[
\begin{align*}
    a \ v_r[:,i] &= w[i] \ b \ v_r[:,i] \\
    a.\text{H} \ v_l[:,i] &= w[i].\text{conj()} \ b.\text{H} \ v_l[:,i]
\end{align*}
\]

where .\text{H} is the Hermitian conjugation.

Parameters
a  [(M, M) array_like] A complex or real matrix whose eigenvalues and eigenvectors will be computed.

b  [(M, M) array_like, optional] Right-hand side matrix in a generalized eigenvalue problem. Default is None, identity matrix is assumed.

left  [bool, optional] Whether to calculate and return left eigenvectors. Default is False.

right  [bool, optional] Whether to calculate and return right eigenvectors. Default is True.

overwrite_a  [bool, optional] Whether to overwrite a; may improve performance. Default is False.

overwrite_b  [bool, optional] Whether to overwrite b; may improve performance. Default is False.

check_finite  [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

homogeneous_eigvals  [bool, optional] If True, return the eigenvalues in homogeneous coordinates. In this case w is a (2, M) array so that:

\[
w[1,i] \ a \ vr[:,i] = w[0,i] \ b \ vr[:,i]
\]

Default is False.

Returns

w  [(M,) or (2, M) double or complex ndarray] The eigenvalues, each repeated according to its multiplicity. The shape is (M,) unless homogeneous_eigvals=True.

vl  [(M, M) double or complex ndarray] The normalized left eigenvector corresponding to the eigenvalue w[i] is the column vl[:,i]. Only returned if left=True.

vr  [(M, M) double or complex ndarray] The normalized right eigenvector corresponding to the eigenvalue w[i] is the column vr[:,i]. Only returned if right=True.

Raises

LinAlgError

If eigenvalue computation does not converge.

See also:

eigvals

eigenvalues of general arrays

eigh

Eigenvalues and right eigenvectors for symmetric/Hermitian arrays.

eig_banded

eigenvalues and right eigenvectors for symmetric/Hermitian band matrices

eigh_tridiagonal

eigenvalues and right eigenvectors for symmetric/Hermitian tridiagonal matrices

Examples
```python
from scipy import linalg

a = np.array([[0., -1.], [1., 0.]])
linalg.eigvals(a)
array([0.+1.j, 0.-1.j])

b = np.array([[0., 1.], [1., 1.]])
linalg.eigvals(a, b)
array([ 1.+0.j, -1.+0.j])

da = np.array([[3., 0., 0.], [0., 8., 0.], [0., 0., 7.]])
linalg.eigvals(a, homogeneous_eigvals=True)
array([[3.+0.j, 8.+0.j, 7.+0.j],
       [1.+0.j, 1.+0.j, 1.+0.j]])

linalg.eig(a, left=True, right=False)[1] # normalized left eigenvector
array([[-0.70710678+0.j , -0.70710678-0.j ,
       [-0. , +0.70710678j, -0. , -0.70710678j]],
      [[0.70710678+0.j , 0.70710678-0.j ,
       [0. , -0.70710678j, 0. , +0.70710678j]])

linalg.eig(a, left=False, right=True)[1] # normalized right eigenvector
array([[-0.70710678+0.j , -0.70710678-0.j ,
       [-0.70710678j, 0. , 0.70710678-0.j]],
      [[0.70710678+0.j , 0.70710678-0.j ,
       [0.70710678j, 0. , -0.70710678j]])]
```

**scipy.linalg.eigvals**

`scipy.linalg.eigvals(a, b=None, overwrite_a=False, check_finite=True, homogeneous_eigvals=False)`

Compute eigenvalues from an ordinary or generalized eigenvalue problem.

Find eigenvalues of a general matrix:

```python
a vr[:,i] = w[i] b vr[:,i]
```

**Parameters**

- `a` [(M, M) array_like] A complex or real matrix whose eigenvalues and eigenvectors will be computed.
- `overwrite_a` [bool, optional] Whether to overwrite data in a (may improve performance)
- `check_finite` [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.
- `homogeneous_eigvals` [bool, optional] If True, return the eigenvalues in homogeneous coordinates. In this case `w` is a (2, M) array so that:

```python
w[1,i] a vr[:,i] = w[0,i] b vr[:,i]
```

Default is False.
Returns

\(w\) [(M,) or (2, M) double or complex ndarray] The eigenvalues, each repeated according to its multiplicity but not in any specific order. The shape is (M,) unless homogeneous_eigvals=True.

Raises

LinAlgError

If eigenvalue computation does not converge

See also:

eig
eigenvalues and right eigenvectors of general arrays.
eigvalsh
eigenvalues of symmetric or Hermitian arrays
eigvals_banded
eigenvalues for symmetric/Hermitian band matrices
eigvalsh_tridiagonal
eigenvalues of symmetric/Hermitian tridiagonal matrices

Examples

```python
>>> from scipy import linalg
>>> a = np.array([[0., 1.], [1., 0.]])
>>> linalg.eigvals(a)
array([0. + 1.0j, 0. - 1.0j])

>>> b = np.array([[0., 1.], [1., 1.]])
>>> linalg.eigvals(a, b)
array([ 1. + 0.0j, -1. + 0.0j])

>>> a = np.array([[3., 0., 0.], [0., 8., 0.], [0., 0., 7.]])
>>> linalg.eigvals(a, homogeneous_eigvals=True)
array([[3.+0.j, 8.+0.j, 7.+0.j],
       [1.+0.j, 1.+0.j, 1.+0.j]])
```

scipy.linalg.eigh

Solve an ordinary or generalized eigenvalue problem for a complex Hermitian or real symmetric matrix.

Find eigenvalues \(w\) and optionally eigenvectors \(v\) of matrix \(a\), where \(b\) is positive definite:

```python
a v[:,i] = w[i] b v[:,i]
v[:,i].conj() a v[:,i] = w[i]
v[:,i].conj() b v[:,i] = 1
```

Parameters
a  [(M, M) array_like] A complex Hermitian or real symmetric matrix whose eigenvalues and eigenvectors will be computed.
b  [(M, M) array_like, optional] A complex Hermitian or real symmetric definite positive matrix in. If omitted, identity matrix is assumed.
lower [bool, optional] Whether the pertinent array data is taken from the lower or upper triangle of a. (Default: lower)
eigvals_only [bool, optional] Whether to calculate only eigenvalues and no eigenvectors. (Default: both are calculated)
turbo [bool, optional] Use divide and conquer algorithm (faster but expensive in memory, only for generalized eigenvalue problem and if eigvals=None)
eigvals [tuple (lo, hi), optional] Indexes of the smallest and largest (in ascending order) eigenvalues and corresponding eigenvectors to be returned: 0 <= lo <= hi <= M-1. If omitted, all eigenvalues and eigenvectors are returned.
type [int, optional] Specifies the problem type to be solved:
  type = 1: a v[:,i] = w[i] b v[:,i]
  type = 2: a b v[:,i] = w[i] v[:,i]
  type = 3: b a v[:,i] = w[i] v[:,i]
overwrite_a [bool, optional] Whether to overwrite data in a (may improve performance)
overwrite_b [bool, optional] Whether to overwrite data in b (may improve performance)
check_finite [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns
  w  [(N,) float ndarray] The N (1<=N<=M) selected eigenvalues, in ascending order, each repeated according to its multiplicity.
  v  [(M, N) complex ndarray] (if eigvals_only == False) The normalized selected eigenvector corresponding to the eigenvalue w[i] is the column v[:,i].
    Normalization:
      type 1 and 3: v.conj() a v = w
      type 2: inv(v).conj() a inv(v) = w
      type 1 or 2: v.conj() b v = I
      type 3: v.conj() inv(b) v = I

Raises
  LinAlgError
If eigenvalue computation does not converge, an error occurred, or b matrix is not definite positive. Note that if input matrices are not symmetric or hermitian, no error is reported but results will be wrong.

See also:
  eigvalsh
eigenvalues of symmetric or Hermitian arrays
eig
eigenvalues and right eigenvectors for non-symmetric arrays

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eigh

eigenvalues and right eigenvectors for symmetric/Hermitian arrays

eigh_tridiagonal

eigenvalues and right eigenvectors for symmetric/Hermitian tridiagonal matrices

Notes
This function does not check the input array for being hermitian/symmetric in order to allow for representing arrays with only their upper/lower triangular parts.

Examples

```python
>>> from scipy.linalg import eigh
>>> A = np.array([[5, 3, 5], [3, 0, 5], [1, 5, 6]])
>>> w, v = eigh(A)
>>> np.allclose(A @ v - v @ np.diag(w), np.zeros((4, 4)))
True
```

scipy.linalg.eigvalsh

scipy.linalg.eigvalsh(a, b=None, lower=True, overwrite_a=False, overwrite_b=False, turbo=True, eigvals=None, type=1, check_finite=True)

Solve an ordinary or generalized eigenvalue problem for a complex Hermitian or real symmetric matrix.

Find eigenvalues w of matrix a, where b is positive definite:

```
a v[:,i] = w[i] b v[:,i]
v[i,:].conj() a v[:,i] = w[i] v[i,:].conj() b v[:,i] = 1
```

Parameters

- **a**
  
  [(M, M) array_like] A complex Hermitian or real symmetric matrix whose eigenvalues and eigenvectors will be computed.

- **b**
  
  [(M, M) array_like, optional] A complex Hermitian or real symmetric definite positive matrix in. If omitted, identity matrix is assumed.

- **lower**
  
  [bool, optional] Whether the pertinent array data is taken from the lower or upper triangle of a. (Default: lower)

- **turbo**
  
  [bool, optional] Use divide and conquer algorithm (faster but expensive in memory, only for generalized eigenvalue problem and if eigvals=None)

- **eigvals**
  
  [tuple (lo, hi), optional] Indexes of the smallest and largest (in ascending order) eigenvalues and corresponding eigenvectors to be returned: 0 <= lo <= hi <= M-1. If omitted, all eigenvalues and eigenvectors are returned.

- **type**
  
  [int, optional] Specifies the problem type to be solved:

  - type = 1: a v[:,i] = w[i] b v[:,i]
  - type = 2: a b v[:,i] = w[i] v[:,i]
  - type = 3: b a v[:,i] = w[i] v[:,i]

- **overwrite_a**
  
  [bool, optional] Whether to overwrite data in a (may improve performance)

- **overwrite_b**
  
  [bool, optional] Whether to overwrite data in b (may improve performance)

- **check_finite**
  
  [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.
Returns

w  [(N,) float ndarray] The N (1<=N<=M) selected eigenvalues, in ascending order, each repeated according to its multiplicity.

Raises

LinAlgError

If eigenvalue computation does not converge, an error occurred, or b matrix is not definite positive. Note that if input matrices are not symmetric or hermitian, no error is reported but results will be wrong.

See also:

eigh

eigenvalues and right eigenvectors for symmetric/Hermitian arrays

eigvals

eigenvalues of general arrays

eigvals_banded

eigenvalues for symmetric/Hermitian band matrices

eigvalsh_tridiagonal

eigenvalues of symmetric/Hermitian tridiagonal matrices

Notes

This function does not check the input array for being hermitian/symmetric in order to allow for representing arrays with only their upper/lower triangular parts.

Examples

```python
>>> from scipy.linalg import eigvalsh
>>> A = np.array([[6, 3, 1, 5], [3, 0, 5, 1], [1, 5, 6, 2], [5, 1, 2, 2]])
>>> w = eigvalsh(A)
>>> w
array([-3.74637491, -0.76263923, 6.08502336, 12.42399079])
```

scipy.linalg.eig_banded

Solve real symmetric or complex hermitian band matrix eigenvalue problem.

Find eigenvalues w and optionally right eigenvectors v of a:

```python
a v[:,i] = w[i] v[:,i]
v.H v = identity
```

The matrix a is stored in a_band either in lower diagonal or upper diagonal ordered form:

```
a_band[u + i - j, j] == a[i,j] (if upper form; i <= j) a_band[ i - j, j] == a[i,j] (if lower form; i >= j)
```

where u is the number of bands above the diagonal.

Example of a_band (shape of a is (6,6), u=2):
upper form:
*  *  a02 a13 a24 a35
*  a01 a12 a23 a34 a45
a00 a11 a22 a33 a44 a55

lower form:
a00 a11 a22 a33 a44 a55
a10 a21 a32 a43 a54 *
a20 a31 a42 a53 * *

Cells marked with * are not used.

Parameters

**a_band** *(u+1, M) array_like* The bands of the M by M matrix a.

**lower** *[bool, optional]* Is the matrix in the lower form. (Default is upper form)

**eigvals_only** *[bool, optional]* Compute only the eigenvalues and no eigenvectors. (Default: calculate also eigenvectors)

**overwrite_a_band** *[bool, optional]* Discard data in a_band (may enhance performance)

**select** *[{'a', 'v', 'i'}, optional]* Which eigenvalues to calculate

<table>
<thead>
<tr>
<th>select</th>
<th>calculated</th>
</tr>
</thead>
<tbody>
<tr>
<td>'a'</td>
<td>All eigenvalues</td>
</tr>
<tr>
<td>'v'</td>
<td>Eigenvalues in the interval (min, max)</td>
</tr>
<tr>
<td>'i'</td>
<td>Eigenvalues with indices min &lt;= i &lt;= max</td>
</tr>
</tbody>
</table>

**select_range** *[min, max), optional]* Range of selected eigenvalues

**max_ev** *[int, optional]* For select='v', maximum number of eigenvalues expected. For other values of select, has no meaning. In doubt, leave this parameter untouched.

**check_finite** *[bool, optional]* Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

**w** *[M,) ndarray]* The eigenvalues, in ascending order, each repeated according to its multiplicity.

**v** *[M, M) float or complex ndarray]* The normalized eigenvector corresponding to the eigenvalue w[i] is the column v[:,i].

Raises

**LinAlgError** If eigenvalue computation does not converge.

See also:

**eigvals_banded**

eigenvalues for symmetric/Hermitian band matrices

**eig**
eigenvalues and right eigenvectors of general arrays.
**eigh**

eigenvalues and right eigenvectors for symmetric/Hermitian arrays

**eigh_tridiagonal**

eigenvalues and right eigenvectors for symmetric/Hermitian tridiagonal matrices

**Examples**

```python
>>> from scipy.linalg import eig_banded
>>> A = np.array([[1, 5, 2, 0], [5, 2, 5, 2], [2, 5, 3, 5], [0, 2, 5, 4]])
>>> Ab = np.array([[1, 2, 3, 4], [5, 5, 5, 0], [2, 2, 0, 0]])
>>> w, v = eig_banded(Ab, lower=True)
>>> np.allclose(A @ v - v @ np.diag(w), np.zeros((4, 4)))
True
>>> w = eig_banded(Ab, lower=True, eigvals_only=True)
>>> w
array([-4.26200532, -2.22987175, 3.95222349, 12.53965359])
```

Request only the eigenvalues between [-3, 4]

```python
>>> w, v = eig_banded(Ab, lower=True, select='v', select_range=[-3, 4])
>>> w
array([-2.22987175, 3.95222349])
```

**scipy.linalg.eigvals_banded**

`scipy.linalg.eigvals_banded(a_band, lower=False, overwrite_a_band=False, select='a', select_range=None, check_finite=True)`

Solve real symmetric or complex hermitian band matrix eigenvalue problem.

Find eigenvalues w of a:

```python
a v[:,i] = w[i] v[:,i]
```

```python
v.H v = identity
```

The matrix a is stored in a_band either in lower diagonal or upper diagonal ordered form:

```
a_band[u + i - j, j] == a[i,j] (if upper form; i <= j)
a_band[i - j, j] == a[i,j] (if lower form; i >= j)
```

where u is the number of bands above the diagonal.

Example of a_band (shape of a is (6,6), u=2):

```text
upper form:
    * * a02 a13 a24 a35
    * a01 a12 a23 a34 a45
a00 a11 a22 a33 a44 a55

lower form:
a00 a11 a22 a33 a44 a55
a10 a21 a32 a43 a54 *
a20 a31 a42 a53 * *
```

Cells marked with * are not used.

**Parameters**
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**eigvals_banded**

- **a_band** [(u+1, M) array_like] The bands of the M by M matrix a.
- **lower** [bool, optional] Is the matrix in the lower form. (Default is upper form)
- **overwrite_a_band** [bool, optional] Discard data in a_band (may enhance performance)
- **select** [{‘a’, ‘v’, ‘i’}, optional] Which eigenvalues to calculate

<table>
<thead>
<tr>
<th>select</th>
<th>calculated</th>
</tr>
</thead>
<tbody>
<tr>
<td>‘a’</td>
<td>All eigenvalues</td>
</tr>
<tr>
<td>‘v’</td>
<td>Eigenvalues in the interval (min, max)</td>
</tr>
<tr>
<td>‘i’</td>
<td>Eigenvalues with indices min &lt;= i &lt;= max</td>
</tr>
</tbody>
</table>

- **select_range** [(min, max), optional] Range of selected eigenvalues
- **check_finite** [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

**Returns**

- **w** [(M,) ndarray] The eigenvalues, in ascending order, each repeated according to its multiplicity.

**Raises**

- **LinAlgError**
  If eigenvalue computation does not converge.

**See also:**

- **eig_banded**
  eigenvalues and right eigenvectors for symmetric/Hermitian band matrices
- **eigvalsh_tridiagonal**
  eigenvalues of symmetric/Hermitian tridiagonal matrices
- **eigvals**
  eigenvalues of general arrays
- **eigh**
  eigenvalues and right eigenvectors for symmetric/Hermitian arrays
- **eig**
  eigenvalues and right eigenvectors for non-symmetric arrays

**Examples**

```python
>>> from scipy.linalg import eigvals_banded
>>> A = np.array([[1, 5, 2, 0], [5, 2, 5, 2], [2, 5, 3, 5], [0, 2, 5, 4]])
>>> Ab = np.array([[1, 2, 3, 4], [5, 5, 5, 0], [2, 2, 0, 0]])
>>> w = eigvals_banded(Ab, lower=True)
>>> w
array([-4.26200532, -2.22987175, 3.95222349, 12.53965359])
```
scipy.linalg.eigh_tridiagonal

scipy.linalg.eigh_tridiagonal(d, e, eigvals_only=False, select='a', select_range=None, check_finite=True, tol=0.0, lapack_driver='auto')

Solve eigenvalue problem for a real symmetric tridiagonal matrix.

Find eigenvalues $w$ and optionally right eigenvectors $v$ of $a$:

\[
\begin{align*}
    a \cdot v[\cdot, i] &= w[i] \cdot v[\cdot, i] \\
    v \cdot H \cdot v &= \text{identity}
\end{align*}
\]

For a real symmetric matrix $a$ with diagonal elements $d$ and off-diagonal elements $e$.

**Parameters**

- **d**  
  [ndarray, shape (ndim,)] The diagonal elements of the array.
- **e**  
  [ndarray, shape (ndim-1,)] The off-diagonal elements of the array.
- **select**  
  ['a', 'v', 'i'], optional) Which eigenvalues to calculate

<table>
<thead>
<tr>
<th>select</th>
<th>calculated</th>
</tr>
</thead>
<tbody>
<tr>
<td>'a'</td>
<td>All eigenvalues</td>
</tr>
<tr>
<td>'v'</td>
<td>Eigenvalues in the interval $\text{min, max}$</td>
</tr>
<tr>
<td>'i'</td>
<td>Eigenvalues with indices $\text{min} \leq i \leq \text{max}$</td>
</tr>
</tbody>
</table>

- **select_range**  
  [(min, max), optional] Range of selected eigenvalues
- **check_finite**  
  [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.
- **tol**  
  [float] The absolute tolerance to which each eigenvalue is required (only used when 'stebz' is the lapack_driver). An eigenvalue (or cluster) is considered to have converged if it lies in an interval of this width. If $\leq 0$. (default), the value $\text{eps} \times |a|$ is used where $\text{eps}$ is the machine precision, and $|a|$ is the 1-norm of the matrix $a$.
- **lapack_driver**  
  [str] LAPACK function to use, can be 'auto', 'stemr', 'stebz', 'sterf', or 'stev'. When 'auto' (default), it will use 'stemr' if select='a' and 'stebz' otherwise. When 'stebz' is used to find the eigenvalues and eigvals_only=False, then a second LAPACK call (to ?STEIN) is used to find the corresponding eigenvectors. 'sterf' can only be used when eigvals_only=True and select='a'. 'stev' can only be used when select='a'.

**Returns**

- **w**  
  [(M,) ndarray] The eigenvalues, in ascending order, each repeated according to its multiplicity.
- **v**  
  [(M, M) ndarray] The normalized eigenvector corresponding to the eigenvalue $w[i]$ is the column $v[\cdot, i]$.

**Raises**

- **LinAlgError**  
  If eigenvalue computation does not converge.

See also:

eigvalsh_tridiagonal

eigenvalues of symmetric/Hermitian tridiagonal matrices
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**eig**
eigenvalues and right eigenvectors for non-symmetric arrays

**eigh**
eigenvalues and right eigenvectors for symmetric/Hermitian arrays

**eig_banded**
eigenvalues and right eigenvectors for symmetric/Hermitian band matrices

**Notes**
This function makes use of LAPACK S/DSTEMR routines.

**Examples**

```python
>>> from scipy.linalg import eigh_tridiagonal
>>> d = 3*np.ones(4)
>>> e = -1*np.ones(3)
>>> w, v = eigh_tridiagonal(d, e)
>>> A = np.diag(d) + np.diag(e, k=1) + np.diag(e, k=-1)
>>> np.allclose(A @ v - v @ np.diag(w), np.zeros((4, 4)))
True
```

scipy.linalg.eigvalsh_tridiagonal

Solve eigenvalue problem for a real symmetric tridiagonal matrix.

Find eigenvalues \( w \) of \( a \):

```python
a v[:,i] = w[i] v[:,i]
v.H v = identity
```

For a real symmetric matrix \( a \) with diagonal elements \( d \) and off-diagonal elements \( e \).

**Parameters**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>d</strong></td>
<td>[ndarray, shape (ndim,)] The diagonal elements of the array.</td>
</tr>
<tr>
<td><strong>e</strong></td>
<td>[ndarray, shape (ndim-1,)] The off-diagonal elements of the array.</td>
</tr>
<tr>
<td><strong>select</strong></td>
<td>['a', 'v', 'i'], optional Which eigenvalues to calculate</td>
</tr>
</tbody>
</table>

select

<table>
<thead>
<tr>
<th>select</th>
<th>calculated</th>
</tr>
</thead>
<tbody>
<tr>
<td>'a'</td>
<td>All eigenvalues</td>
</tr>
<tr>
<td>'v'</td>
<td>Eigenvalues in the interval ([\text{min}, \text{max}])</td>
</tr>
<tr>
<td>'i'</td>
<td>Eigenvalues with indices ( \text{min} \leq i \leq \text{max} )</td>
</tr>
</tbody>
</table>

select_range

| (min, max), optional | Range of selected eigenvalues |

check_finite

| bool, optional | Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. |

tol

| float | The absolute tolerance to which each eigenvalue is required (only used when `lapack_driver='stebz'`). An eigenvalue (or cluster) is considered to have converged if it lies in an interval of this width. If <= 0. (default), the value \( \text{eps} \times |a| \) is used where eps is the machine precision, and \( |a| \) is the 1-norm of the matrix \( a \). |
lapack_driver

[str] LAPACK function to use, can be ‘auto’, ‘stemr’, ‘stebz’, ‘sterf’, or ‘stev’. When ‘auto’ (default), it will use ‘stemr’ if select='a' and ‘stebz’ otherwise. ‘sterf’ and ‘stev’ can only be used when select='a'.

Returns

w [(M,) ndarray] The eigenvalues, in ascending order, each repeated according to its multiplicity.

Raises

LinAlgError If eigenvalue computation does not converge.

See also:

eigh_tridiagonal
eigenvalues and right eigenvectors for symmetric/Hermitian tridiagonal matrices

Examples

>>> from scipy.linalg import eigvalsh_tridiagonal, eigvalsh
>>> d = 3*np.ones(4)
>>> e = -1*np.ones(3)
>>> w = eigvalsh_tridiagonal(d, e)
>>> A = np.diag(d) + np.diag(e, k=1) + np.diag(e, k=-1)
>>> w2 = eigvalsh(A)  # Verify with other eigenvalue routines
>>> np.allclose(w - w2, np.zeros(4))
True

6.9.3 Decompositions

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>lu(a[, permute_l, overwrite_a, check_finite])</td>
<td>Compute pivoted LU decomposition of a matrix.</td>
</tr>
<tr>
<td>lu_factor(a[, overwrite_a, check_finite])</td>
<td>Compute pivoted LU decomposition of a matrix.</td>
</tr>
<tr>
<td>lu_solve(lu_and_piv, b[, trans, ...])</td>
<td>Solve an equation system, a x = b, given the LU factorization of a</td>
</tr>
<tr>
<td>svd(a[, full_matrices, compute_uv, ...])</td>
<td>Singular Value Decomposition.</td>
</tr>
<tr>
<td>svdvals(a[, overwrite_a, check_finite])</td>
<td>Compute singular values of a matrix.</td>
</tr>
<tr>
<td>diagsvd(s, M, N)</td>
<td>Construct the sigma matrix in SVD from singular values and size M, N.</td>
</tr>
<tr>
<td>orth(A[, rcond])</td>
<td>Construct an orthonormal basis for the range of A using SVD</td>
</tr>
<tr>
<td>null_space(A[, rcond])</td>
<td>Construct an orthonormal basis for the null space of A using SVD</td>
</tr>
<tr>
<td>ldl(A[, lower, hermitian, overwrite_a, ...])</td>
<td>Computes the LDLt or Bunch-Kaufman factorization of a symmetric/ hermitian matrix.</td>
</tr>
<tr>
<td>cholesky(a[, lower, overwrite_a, check_finite])</td>
<td>Compute the Cholesky decomposition of a matrix.</td>
</tr>
<tr>
<td>cholesky_banded(ab[, overwrite_ab, lower, ...])</td>
<td>Cholesky decompose a banded Hermitian positive-definite matrix</td>
</tr>
<tr>
<td>cho_factor(a[, lower, overwrite_a, check_finite])</td>
<td>Compute the Cholesky decomposition of a matrix, to use in cho_solve</td>
</tr>
<tr>
<td>cho_solve(c_and_lower, b[, overwrite_b, ...])</td>
<td>Solve the linear equations A x = b, given the Cholesky factorization of A.</td>
</tr>
</tbody>
</table>
Table 82 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>cho_solve_banded</code></td>
<td>Solve the linear equations $A x = b$, given the Cholesky factorization of the banded hermitian $A$.</td>
</tr>
<tr>
<td><code>polar</code></td>
<td>Compute the polar decomposition.</td>
</tr>
<tr>
<td><code>qr</code></td>
<td>Compute QR decomposition of a matrix.</td>
</tr>
<tr>
<td><code>qr_multiply</code></td>
<td>Calculate the QR decomposition and multiply Q with a matrix.</td>
</tr>
<tr>
<td><code>qr_update</code></td>
<td>Rank-k QR update</td>
</tr>
<tr>
<td><code>qr_delete</code></td>
<td>QR downdate on row or column deletions</td>
</tr>
<tr>
<td><code>qr_insert</code></td>
<td>QR update on row or column insertions</td>
</tr>
<tr>
<td><code>rq</code></td>
<td>Compute RQ decomposition of a matrix.</td>
</tr>
<tr>
<td><code>qz</code></td>
<td>QZ decomposition for generalized eigenvalues of a pair of matrices.</td>
</tr>
<tr>
<td><code>ordqz</code></td>
<td>QZ decomposition for a pair of matrices with reordering.</td>
</tr>
<tr>
<td><code>schur</code></td>
<td>Compute Schur decomposition of a matrix.</td>
</tr>
<tr>
<td><code>rsf2csf</code></td>
<td>Convert real Schur form to complex Schur form.</td>
</tr>
<tr>
<td><code>hessenberg</code></td>
<td>Compute Hessenberg form of a matrix.</td>
</tr>
<tr>
<td><code>cdf2rdf</code></td>
<td>Converts complex eigenvalues $w$ and eigenvectors $v$ to real eigenvalues in a block diagonal form $wr$ and the associated real eigenvectors $vr$, such that:</td>
</tr>
</tbody>
</table>

```python
scipy.linalg.lu
```

`scipy.linalg.lu(a, permute_l=False, overwrite_a=False, check_finite=True)`

Compute pivoted LU decomposition of a matrix.

The decomposition is:

$$A = P L U$$

where $P$ is a permutation matrix, $L$ lower triangular with unit diagonal elements, and $U$ upper triangular.

**Parameters**

- `a` : [(M, N) array_like] Array to decompose
- `permute_l` : [bool, optional] Perform the multiplication $P^T L$ (Default: do not permute)
- `overwrite_a` : [bool, optional] Whether to overwrite data in a (may improve performance)
- `check_finite` : [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

**Returns**

- `p` : [(M, M) ndarray] Permutation matrix
- `l` : [(M, K) ndarray] Lower triangular or trapezoidal matrix with unit diagonal. $K = \min(M, N)$
- `u` : [(K, N) ndarray] Upper triangular or trapezoidal matrix

***(If permute_l == False)***

- `pl` : [(M, K) ndarray] Permuted L matrix. $K = \min(M, N)$
- `u` : [(K, N) ndarray] Upper triangular or trapezoidal matrix
Notes
This is a LU factorization routine written for Scipy.

Examples

```python
>>> from scipy.linalg import lu
>>> A = np.array([[2, 5, 8, 7], [5, 2, 2, 8], [7, 5, 6, 6], [5, 4, 4, 8]])
>>> p, l, u = lu(A)
>>> np.allclose(A - p @ l @ u, np.zeros((4, 4)))
True
```

scipy.linalg.lu_factor

scipy.linalg.lu_factor(a, overwrite_a=False, check_finite=True)
Compute pivoted LU decomposition of a matrix.
The decomposition is:

$$A = P L U$$

where P is a permutation matrix, L lower triangular with unit diagonal elements, and U upper triangular.

Parameters

- **a**
  [(M, M) array_like] Matrix to decompose

- **overwrite_a**
  [bool, optional] Whether to overwrite data in A (may increase performance)

- **check_finite**
  [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

- **lu**
  [(N, N) ndarray] Matrix containing U in its upper triangle, and L in its lower triangle. The unit diagonal elements of L are not stored.

- **piv**
  [(N,) ndarray] Pivot indices representing the permutation matrix P: row i of matrix was interchanged with row piv[i].

See also:

lu_solve
solve an equation system using the LU factorization of a matrix

Notes
This is a wrapper to the *GETRF routines from LAPACK.

Examples

```python
>>> from scipy.linalg import lu_factor
>>> from numpy import tril, triu, allclose, zeros, eye

A = np.array([[2, 5, 8, 7], [5, 2, 2, 8], [7, 5, 6, 6], [5, 4, 4, 8]])
lu, piv = lu_factor(A)
piv
array([2, 2, 3, 3], dtype=int32)
```

Convert LAPACK’s piv array to NumPy index and test the permutation
>>> piv_py = [2, 0, 3, 1]
>>> L, U = np.tril(lu, k=-1) + np.eye(4), np.triu(lu)
>>> np.allclose(A[piv_py] - L @ U, np.zeros((4, 4)))
True

cipy.linalg.lu_solve

cipy.linalg.lu_solve(lu_and_piv, b, trans=0, overwrite_b=False, check_finite=True)
Solve an equation system, \( Ax = b \), given the LU factorization of \( A \)

**Parameters**

- *(lu, piv)*: Factorization of the coefficient matrix \( A \), as given by `lu_factor`
- *b*: Right-hand side
- *trans*: A system to solve:

<table>
<thead>
<tr>
<th>trans</th>
<th>system</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>( Ax = b )</td>
</tr>
<tr>
<td>1</td>
<td>( A^T x = b )</td>
</tr>
<tr>
<td>2</td>
<td>( A^H x = b )</td>
</tr>
</tbody>
</table>

- *overwrite_b*: Whether to overwrite data in \( b \) (may increase performance)
- *check_finite*: Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

**Returns**

- *x*: Solution to the system

**See also:**

- `lu_factor`
  LU factorize a matrix

**Examples**

```python
>>> from scipy.linalg import lu_factor, lu_solve
>>> A = np.array([[2, 5, 8], [5, 2, 8], [7, 5, 6], [5, 4, 8]])
>>> b = np.array([1, 1, 1, 1])
>>> lu, piv = lu_factor(A)
>>> x = lu_solve((lu, piv), b)
>>> np.allclose(A @ x - b, np.zeros((4,)))
True
```

scipy.linalg.svd

scipy.linalg.svd(a, full_matrices=True, compute_uv=True, overwrite_a=False,
check_finite=True, lapack_driver='gesvd')
Singular Value Decomposition.

Factorizes the matrix \( A \) into two unitary matrices \( U \) and \( V_h \), and a 1-D array \( s \) of singular values (real, non-negative) such that \( A = U S \ V_h \), where \( S \) is a suitably shaped matrix of zeros with main diagonal \( s \).
Parameters

- **a** ([(M, N) array_like]) Matrix to decompose.
- **full_matrices** (bool, optional) If True (default), U and Vh are of shape (M, M), (N, N). If False, the shapes are (M, K) and (K, N), where K = min(M, N).
- **compute_uv** (bool, optional) Whether to compute also U and Vh in addition to s. Default is True.
- **overwrite_a** (bool, optional) Whether to overwrite a; may improve performance. Default is False.
- **check_finite** (bool, optional) Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.
- **lapack_driver** (['gesdd', 'gesvd'], optional) Whether to use the more efficient divide-and-conquer approach (‘gesdd’) or general rectangular approach (‘gesvd’) to compute the SVD. MATLAB and Octave use the ‘gesvd’ approach. Default is ‘gesdd’.

New in version 0.18.

Returns

- **U** [ndarray] Unitary matrix having left singular vectors as columns. Of shape (M, M) or (M, K), depending on full_matrices.
- **s** [ndarray] The singular values, sorted in non-increasing order. Of shape (K,), with K = min(M, N).
- **Vh** [ndarray] Unitary matrix having right singular vectors as rows. Of shape (N, N) or (K, N) depending on full_matrices.

For “compute_uv=False”, only “s” is returned.

Raises

LinAlgError

If SVD computation does not converge.

See also:

- **svdvals**
  Compute singular values of a matrix.
- **diagsvd**
  Construct the Sigma matrix, given the vector s.

Examples

```python
>>> from scipy import linalg
>>> m, n = 9, 6
>>> a = np.random.randn(m, n) + 1.j*np.random.randn(m, n)
>>> U, s, Vh = linalg.svd(a)
>>> U.shape, s.shape, Vh.shape
((9, 9), (6,), (6, 6))
```

Reconstruct the original matrix from the decomposition:
```python
>>> sigma = np.zeros((m, n))
>>> for i in range(min(m, n)):
...     sigma[i, i] = s[i]
>>> a1 = np.dot(U, np.dot(sigma, Vh))
>>> np.allclose(a, a1)
True

Alternatively, use `full_matrices=False` (notice that the shape of U is then (m, n) instead of (m, m)):

```python
>>> U, s, Vh = linalg.svd(a, full_matrices=False)
>>> U.shape, s.shape, Vh.shape
((9, 6), (6,), (6, 6))
>>> S = np.diag(s)
>>> np.allclose(a, np.dot(U, np.dot(S, Vh)))
True
```

```python
>>> s2 = linalg.svd(a, compute_uv=False)
>>> np.allclose(s, s2)
True
```

**scipy.linalg.svdvals**

`scipy.linalg.svdvals(a, overwrite_a=False, check_finite=True)`  
Compute singular values of a matrix.

- **Parameters**
  - `overwrite_a` : [bool, optional] Whether to overwrite `a`; may improve performance. Default is False.
  - `check_finite` : [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

- **Returns**
  - `s` : [(min(M, N),) ndarray] The singular values, sorted in decreasing order.

- **Raises**
  - `LinAlgError`
    If SVD computation does not converge.

- **See also:**
  - `svd`
    Compute the full singular value decomposition of a matrix.
  - `diagsvd`
    Construct the Sigma matrix, given the vector `s`.  

728 Chapter 6. API Reference
Notes
svdvals(a) only differs from svd(a, compute_uv=False) by its handling of the edge case of empty a, where it returns an empty sequence:

```python
>>> a = np.empty((0, 2))
>>> from scipy.linalg import svdvals
>>> svdvals(a)
array([], dtype=float64)
```

Examples

```python
>>> m = np.array([[1.0, 0.0],
                ... [2.0, 3.0],
                ... [1.0, 1.0],
                ... [0.0, 2.0],
                ... [1.0, 0.0]])
>>> svdvals(m)
array([ 4.28091555, 1.63516424])
```

We can verify the maximum singular value of m by computing the maximum length of m.dot(u) over all the unit vectors u in the (x,y) plane. We approximate “all” the unit vectors with a large sample. Because of linearity, we only need the unit vectors with angles in [0, pi].

```python
>>> t = np.linspace(0, np.pi, 2000)
>>> u = np.array([np.cos(t), np.sin(t)])
>>> np.linalg.norm(m.dot(u), axis=0).max()
4.2809152422538475
```

p is a projection matrix with rank 1. With exact arithmetic, its singular values would be [1, 0, 0, 0].

```python
>>> v = np.array([0.1, 0.3, 0.9, 0.3])
>>> p = np.outer(v, v)
>>> svdvals(p)
array([ 1.00000000e+00, 2.02021698e-17, 1.56692500e-17,
       8.15115104e-34])
```

The singular values of an orthogonal matrix are all 1. Here we create a random orthogonal matrix by using the rvs() method of scipy.stats.ortho_group.

```python
>>> from scipy.stats import ortho_group
>>> np.random.seed(123)
>>> orth = ortho_group.rvs(4)
>>> svdvals(orth)
array([ 1.,  1.,  1.,  1.])
```

```python
scipy.linalg.diagsvd
```

scipy.linalg.diagsvd(s, M, N)
Construct the sigma matrix in SVD from singular values and size M, N.

```
Parameters
s     [(M,) or (N,) array_like] Singular values
M     [int] Size of the matrix whose singular values are s.
N     [int] Size of the matrix whose singular values are s.
```
Returns

S [(M, N) ndarray] The S-matrix in the singular value decomposition

See also:

svd

Singular value decomposition of a matrix

svdvals

Compute singular values of a matrix.

Examples

```python
>>> from scipy.linalg import diagsvd
>>> vals = np.array([1, 2, 3])  # The array representing the computed svd
>>> diagsvd(vals, 3, 4)
array([[1, 0, 0, 0],
       [0, 2, 0, 0],
       [0, 0, 3, 0]])
>>> diagsvd(vals, 4, 3)
array([[1, 0, 0],
       [0, 2, 0],
       [0, 0, 3],
       [0, 0, 0]])
```

scipy.linalg.orth

scipy.linalg.orth(A, rcond=None)

Construct an orthonormal basis for the range of A using SVD

Parameters

A [(M, N) array_like] Input array
rcond [float, optional] Relative condition number. Singular values s smaller than rcond * max(s) are considered zero. Default: floating point eps * max(M,N).

Returns

Q [(M, K) ndarray] Orthonormal basis for the range of A. K = effective rank of A, as determined by rcond

See also:

svd

Singular value decomposition of a matrix

null_space

Matrix null space

Examples

```python
>>> from scipy.linalg import orth
>>> A = np.array([[2, 0, 0], [0, 5, 0]])  # rank 2 array
>>> orth(A)
array([[0., 1.],
       [1., 0.]])
```
```python
>>> orth(A.T)
array([[0., 1.],
       [1., 0.],
       [0., 0.]])
```

**scipy.linalg.null_space**

`scipy.linalg.null_space(A, rcond=None)`

Construct an orthonormal basis for the null space of A using SVD

**Parameters**

- **A**
  
  [(M, N) array_like] Input array

- **rcond**
  
  [float, optional] Relative condition number. Singular values \( s \) smaller than \( rcond \times \max(s) \) are considered zero. Default: floating point eps * max(M,N).

**Returns**

- **Z**
  
  [(N, K) ndarray] Orthonormal basis for the null space of A. K = dimension of effective null space, as determined by rcond

**See also:**

- **svd**
  
  Singular value decomposition of a matrix

- **orth**
  
  Matrix range

**Examples**

One-dimensional null space:

```python
>>> from scipy.linalg import null_space
>>> A = np.array([[1, 1], [1, 1]])
>>> ns = null_space(A)
>>> ns * np.sign(ns[0,0])  # Remove the sign ambiguity of the vector
array([[ 0.70710678],
       [-0.70710678]])
```

Two-dimensional null space:

```python
>>> B = np.random.rand(3, 5)
>>> Z = null_space(B)
>>> Z.shape
(5, 2)
>>> np.allclose(B.dot(Z), 0)
True
```

The basis vectors are orthonormal (up to rounding error):

```python
>>> Z.T.dot(Z)
array([[ 1.00000000e+00,  6.92087741e-17],
       [ 6.92087741e-17,  1.00000000e+00]])
```
scipy.linalg.ldl

scipy.linalg.ldl(A, lower=True, hermitian=True, overwrite_a=False, check_finite=True)

Computes the LDLt or Bunch-Kaufman factorization of a symmetric/ hermitian matrix.

This function returns a block diagonal matrix D consisting blocks of size at most 2x2 and also a possibly permuted unit lower triangular matrix L such that the factorization \( A = L D L^\top \) or \( A = L D L^H \) holds. If lower is False then (again possibly permuted) upper triangular matrices are returned as outer factors.

The permutation array can be used to triangularize the outer factors simply by a row shuffle, i.e., \( lu[\text{perm}, :] \) is an upper/lower triangular matrix. This is also equivalent to multiplication with a permutation matrix \( P . \text{dot}(lu) \) where \( P \) is a column-permuted identity matrix \( I[:, \text{perm}] \).

Depending on the value of the boolean lower, only upper or lower triangular part of the input array is referenced. Hence a triangular matrix on entry would give the same result as if the full matrix is supplied.

**Parameters**

- **a** [array_like] Square input array
- **lower** [bool, optional] This switches between the lower and upper triangular outer factors of the factorization. Lower triangular (lower=True) is the default.
- **hermitian** [bool, optional] For complex-valued arrays, this defines whether \( a = a . \text{conj()}. \text{T} \) or \( a = a . \text{T} \) is assumed. For real-valued arrays, this switch has no effect.
- **overwrite_a** [bool, optional] Allow overwriting data in \( a \) (may enhance performance). The default is False.
- **check_finite** [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

**Returns**

- **lu** [ndarray] The (possibly) permuted upper/lower triangular outer factor of the factorization.
- **d** [ndarray] The block diagonal multiplier of the factorization.
- **perm** [ndarray] The row-permutation index array that brings \( lu \) into triangular form.

**Raises**

- **ValueError** If input array is not square.
- **ComplexWarning** If a complex-valued array with nonzero imaginary parts on the diagonal is given and hermitian is set to True.

**See also:**

cholesky, lu

**Notes**

This function uses ?SYTRF routines for symmetric matrices and ?HETRF routines for Hermitian matrices from LAPACK. See [1] for the algorithm details.

Depending on the lower keyword value, only lower or upper triangular part of the input array is referenced. Moreover, this keyword also defines the structure of the outer factors of the factorization. New in version 1.1.0.
References
[1]

Examples
Given an upper triangular array \( a \) that represents the full symmetric array with its entries, obtain \( l \), ‘d’ and the permutation vector \( perm \):

```python
>>> import numpy as np
>>> from scipy.linalg import ldl
>>> a = np.array([[2, -1, 3], [0, 2, 0], [0, 0, 1]])
>>> lu, d, perm = ldl(a, lower=0)  # Use the upper part
>>> lu
array([[ 0.,  0.,  1.],
        [ 0.,  1., -0.5],
        [ 1.,  1.,  1.5]])
>>> d
array([[-5.,  0.,  0.],
        [ 0.,  1.5,  0.],
        [ 0.,  0.,  2.]])
>>> perm
array([2, 1, 0])
>>> lu[perm, :]
array([[ 1.,  1.,  1.5],
        [ 0.,  1., -0.5],
        [ 0.,  0.,  1.]])
>>> lu.dot(d).dot(lu.T)
array([[ 2., -1.,  3.],
        [-1.,  2.,  0.],
        [ 3.,  0.,  1.]])
```

scipy.linalg.cholesky

`scipy.linalg.cholesky(a, lower=False, overwrite_a=False, check_finite=True)`

Compute the Cholesky decomposition of a matrix.

Returns the Cholesky decomposition, \( A = LL^* \) or \( A = U^*U \) of a Hermitian positive-definite matrix \( A \).

**Parameters**

- **a** ([M, M] array_like) Matrix to be decomposed
- **lower** [bool, optional] Whether to compute the upper or lower triangular Cholesky factorization. Default is upper-triangular.
- **overwrite_a** [bool, optional] Whether to overwrite data in \( a \) (may improve performance).
- **check_finite** [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

**Returns**

- **c** ([M, M] ndarray) Upper- or lower-triangular Cholesky factor of \( a \).

** Raises**

- **LinAlgError** [if decomposition fails.]
Examples

>>> from scipy.linalg import cholesky
>>> a = np.array([[1,-2j],[2j,5]])
>>> L = cholesky(a, lower=True)

```
>>> a
array([[ 1.+0.j, 0.+0.j],
       [ 0.+2.j, 1.+0.j]])
>>> L @ L.T.conj()  # L @ L.T.conj() = A
array([[ 1.+0.j, 0.-2.j],
       [ 0.+2.j, 5.+0.j]])
```

```
scipy.linalg.cholesky_banded
scipy.linalg.cholesky_banded(ab, overwrite_ab=False, lower=False, check_finite=True)
```

Cholesky decompose a banded Hermitian positive-definite matrix

The matrix a is stored in ab either in lower diagonal or upper diagonal ordered form:

```
[ a00 a11 a22 a33 a44 a55]
[ a10 a21 a32 a43 a54]
[ a20 a31 a42 a53]
```

Example of ab (shape of a is (6,6), u=2):

```
upper form:
*   *   a02 a13 a24 a35
* a01 a12 a23 a34 a45
a00 a11 a22 a33 a44 a55
```

```
lower form:
a00 a11 a22 a33 a44 a55
a10 a21 a32 a43 a54 *
a20 a31 a42 a53 *
```

Parameters

- **ab** : [(u + 1, M) array_like] Banded matrix
- **overwrite_ab** : [bool, optional] Discard data in ab (may enhance performance)
- **lower** : [bool, optional] Is the matrix in the lower form. (Default is upper form)
- **check_finite** : [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

- **c** : [(u + 1, M) ndarray] Cholesky factorization of a, in the same banded format as ab

See also:

- **cho_solve_banded**

Solve a linear set equations, given the Cholesky factorization of a banded hermitian.
sciPy.linalg.cho_factor

SciPy.linalg.cho_factor(a, lower=False, overwrite_a=False, check_finite=True)

Compute the Cholesky decomposition of a matrix, to use in cho_solve

Returns a matrix containing the Cholesky decomposition, \( A = L L^* \) or \( A = U^* U \) of a Hermitian positive-definite matrix \( a \). The return value can be directly used as the first parameter to cho_solve.

**Warning:** The returned matrix also contains random data in the entries not used by the Cholesky decomposition. If you need to zero these entries, use the function `cholesky` instead.

**Parameters**

- **a** [(M, M) array_like] Matrix to be decomposed
- **lower** [bool, optional] Whether to compute the upper or lower triangular Cholesky factorization (Default: upper-triangular)
- **overwrite_a** [bool, optional] Whether to overwrite data in a (may improve performance)
- **check_finite** [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

**Returns**

- **c** [(M, M) ndarray] Matrix whose upper or lower triangle contains the Cholesky factor of \( a \). Other parts of the matrix contain random data.
- **lower** [bool] Flag indicating whether the factor is in the lower or upper triangle

**Raises**

- LinAlgError
  
  Raised if decomposition fails.

**See also:**

- **cho_solve**
  
  Solve a linear set equations using the Cholesky factorization of a matrix.

**Examples**
scipy.linalg.cho_factor

scipy.linalg.cho_factor(c_and_lower, b, overwrite_b=False, check_finite=True)
Solve the linear equations \( A x = b \), given the Cholesky factorization of \( A \).

Parameters

- \( (c, \text{lower}) \) [tuple, (array, bool)] Cholesky factorization of \( A \), as given by \text{cho_factor}
- \( b \) [array] Right-hand side
- \( \text{overwrite}_b \) [bool, optional] Whether to overwrite data in \( b \) (may improve performance)
- \( \text{check}_\text{finite} \) [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

- \( x \) [array] The solution to the system \( A x = b \)

See also:

- \text{cho_factor}
  Cholesky factorization of a matrix

Examples

```python
>>> from scipy.linalg import cho_factor, cho_solve
>>> A = np.array([[9, 3, 1, 5], [3, 7, 5, 1], [1, 5, 9, 2], [5, 1, 2, 6]])
>>> c, low = cho_factor(A)
>>> c
array([[3. , 1. , 0.33333333, 1.66666667],
       [3. , 2.44948974, 1.90515869, -0.27216553],
       [1. , 5. , 2.9330749, 0.8559528 ],
       [5. , 1. , 2. , 1.55418563]])
>>> np.allclose(np.triu(c).T @ np.triu(c) - A, np.zeros((4, 4)))
True
```
b  [array_like] Right-hand side
overwrite_b  [bool, optional] If True, the function will overwrite the values in b.
check_finite  [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns
x  [array] The solution to the system A x = b

See also:
cholesky_banded
Cholesky factorization of a banded matrix

Notes
New in version 0.8.0.

Examples

```python
>>> from scipy.linalg import cholesky_banded, cho_solve_banded
>>> Ab = np.array([[0, 1j, 2, 3j], [0, -1, 2, 4], [9, 8, 7, 6], [9]])
>>> A = np.diag(Ab[0,2:], k=2) + np.diag(Ab[1,1:], k=1)
>>> A = A + A.conj().T + np.diag(Ab[2, :])
>>> c = cholesky_banded(A)
>>> x = cho_solve_banded((c, False), np.ones(5))
>>> np.allclose(A @ x - np.ones(5), np.zeros(5))
True
```

scipy.linalg.polar

scipy.linalg.polar(a, side='right')

Compute the polar decomposition.

Returns the factors of the polar decomposition [1] u and p such that a = up (if side is “right”) or a = pu (if side is “left”), where p is positive semidefinite. Depending on the shape of a, either the rows or columns of u are orthonormal. When a is a square array, u is a square unitary array. When a is not square, the “canonical polar decomposition” [2] is computed.

Parameters

a  [(m, n) array_like] The array to be factored.
side  [{‘left’, ‘right’}, optional] Determines whether a right or left polar decomposition is computed. If side is “right”, then a = up. If side is “left”, then a = pu. The default is “right”.

Returns

u  [(m, n) ndarray] If a is square, then u is unitary. If m > n, then the columns of a are orthonormal, and if m < n, then the rows of u are orthonormal.
p  [ndarray] p is Hermitian positive semidefinite. If a is nonsingular, p is positive definite. The shape of p is (n, n) or (m, m), depending on whether side is “right” or “left”, respectively.

References

[1], [2]
Examples

```python
>>> from scipy.linalg import polar
>>> a = np.array([[1, -1], [2, 4]])
>>> u, p = polar(a)
>>> u
array([[ 0.85749293, -0.51449576],
       [ 0.51449576,  0.85749293]])
>>> p
array([[ 1.88648444,  1.2004901 ],
       [ 1.2004901 ,  3.94446746]])

A non-square example, with m < n:

```python
>>> b = np.array([[0.5, 1, 2], [1.5, 3, 4]])
>>> u, p = polar(b)
>>> u
array([[-0.21196618,  0.39378971,  0.88054056],
       [-0.42393237,  0.78757942,  0.4739708 ]])
>>> p
array([[ 0.48470147,  0.96940295,  1.15122648],
       [ 0.96940295,  1.93880589,  2.30245295],
       [ 1.15122648,  2.30245295,  3.65696431]])
>>> u.dot(p)  # Verify the decomposition.
array([[ 0.5,  1. ,  2. ],
       [ 1.5,  3. ,  4. ]])
``` 

Another non-square example, with m > n:

```python
>>> c = b.T
>>> u, p = polar(c)
>>> u
array([[-0.21196618,  0.96940295,  1.15122648],
       [-0.42393237,  1.93880589,  2.30245295],
       [ 0.88054056,  2.30245295,  3.65696431]])
>>> p
array([[ 1.23116567,  1.93241587],
       [ 1.93241587,  4.84930602]])
>>> u.dot(p)  # Verify the decomposition.
array([[ 0.5,  1.5],
       [ 1. ,  3. ],
       [ 2. ,  4. ]])
>>> u.T.dot(u)  # The columns of u are orthonormal.
array([[ 1.00000000e+00, -1.26363763e-16],
       [ -1.26363763e-16,  1.00000000e+00]])
``` 

**scipy.linalg.qr**

`scipy.linalg.qr(a, overwrite_a=False, lwork=None, mode='full', pivoting=False, check_finite=True)`

Compute QR decomposition of a matrix.

Calculate the decomposition `A = Q R` where Q is unitary/orthogonal and R upper triangular.
Parameters

- **a**: [(M, N) array_like] Matrix to be decomposed
- **overwrite_a**: [bool, optional] Whether data in a is overwritten (may improve performance)
- **lwork**: [int, optional] Work array size, lwork >= a.shape[1]. If None or -1, an optimal size is computed.
- **mode**: ['full', 'r', 'economic', 'raw'], optional Determines what information is to be returned: either both Q and R ('full', default), only R ('r') or both Q and R but computed in economy-size ('economic', see Notes). The final option 'raw' (added in Scipy 0.11) makes the function return two matrices (Q, TAU) in the internal format used by LAPACK.
- **pivoting**: [bool, optional] Whether or not factorization should include pivoting for rank-revealing qr decomposition. If pivoting, compute the decomposition \( A \ P = Q \ R \) as above, but where P is chosen such that the diagonal of R is non-increasing.
- **check_finite**: [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

- **Q**: [float or complex ndarray] Of shape (M, M), or (M, K) for mode='economic'. Not returned if mode='r'.
- **R**: [float or complex ndarray] Of shape (M, N), or (K, N) for mode='economic'. \( K = \min(M, N) \).

Raises

- **LinAlgError** Raised if decomposition fails

Notes

This is an interface to the LAPACK routines dgeqrf, zgeqrf, dorgqr, zungqr, dgeqp3, and zgeqp3.

If mode='economic', the shapes of Q and R are (M, K) and (K, N) instead of (M,M) and (M,N), with K=\min(M,N).

Examples

```python
>>> from scipy import random, linalg, dot, diag, all, allclose
>>> a = random.randn(9, 6)

>>> q, r = linalg.qr(a)
>>> allclose(a, np.dot(q, r))
True
>>> q.shape, r.shape
((9, 9), (9, 6))

>>> r2 = linalg.qr(a, mode='r')
>>> allclose(r, r2)
True

>>> q3, r3 = linalg.qr(a, mode='economic')
>>> q3.shape, r3.shape
((9, 6), (6, 6))
```

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```python
>>> q4, r4, p4 = linalg.qr(a, pivoting=True)
>>> d = abs(diag(r4))
>>> all(d[1:] <= d[:-1])
True
>>> allclose(a[:, p4], dot(q4, r4))
True
>>> q4.shape, r4.shape, p4.shape
((9, 9), (9, 6), (6,))
```

```python
>>> q5, r5, p5 = linalg.qr(a, mode='economic', pivoting=True)
>>> q5.shape, r5.shape, p5.shape
((9, 6), (6, 6), (6,))
```

### scipy.linalg.qr_multiply

**scipy.linalg.qr_multiply**

```python
scipy.linalg.qr_multiply(a, c, mode='right', pivoting=False, conjugate=False, overwrite_a=False, overwrite_c=False)
```

Calculate the QR decomposition and multiply Q with a matrix.

Calculate the decomposition \( A = Q R \) where Q is unitary/orthogonal and R upper triangular. Multiply Q with a vector or a matrix c.

**Parameters**

- **a** : [(M, N), array_like] Input array
- **c** : [array_like] Input array to be multiplied by q.
- **mode** : [‘left’, ‘right’], optional] \( Q \odot c \) is returned if mode is ‘left’, \( c \odot Q \) is returned if mode is ‘right’. The shape of c must be appropriate for the matrix multiplications, if mode is ‘left’, \( \min(a.shape) == c.shape[0] \), if mode is ‘right’, \( a.shape[0] == c.shape[1] \).
- **pivoting** : [bool, optional] Whether or not factorization should include pivoting for rank-revealing qr decomposition, see the documentation of qr.
- **conjugate** : [bool, optional] Whether Q should be complex-conjugated. This might be faster than explicit conjugation.
- **overwrite_a** : [bool, optional] Whether data in a is overwritten (may improve performance)
- **overwrite_c** : [bool, optional] Whether data in c is overwritten (may improve performance). If this is used, c must be big enough to keep the result, i.e. \( c.shape[0] == a.shape[0] \) if mode is ‘left’.

**Returns**

- **CQ** : [ndarray] The product of Q and c.
- **R** : [(K, N), ndarray] R array of the resulting QR factorization where \( K = \min(M, N) \).
- **P** : [(N,), ndarray] Integer pivot array. Only returned when **pivoting**=True.

**Raises**

- **LinAlgError**

**Notes**

This is an interface to the LAPACK routines ?GEQRF, ?ORMQR, ?UNMQR, and ?GEQP3.

New in version 0.11.0.
Examples

```python
>>> from scipy.linalg import qr_multiply, qr
>>> A = np.array([[1, 3, 3], [2, 3, 2], [2, 3, 3], [1, 3, 2]])
>>> qc, r1, piv1 = qr_multiply(A, 2*np.eye(4), pivoting=1)
>>> qc
array([[-1.,  1., -1.],
        [-1., -1.,  1.],
        [-1., -1., -1.],
        [-1.,  1.,  1.]])
>>> r1
array([[-6., -3., -5.],
        [ 0., -1., -1.11022302e-16],
        [ 0.,  0., -1.],
        [ 0.,  0.,  0.]])
>>> piv1
array([1, 0, 2], dtype=int32)
>>> q2, r2, piv2 = qr(A, mode='economic', pivoting=1)
>>> np.allclose(2*q2 - qc, np.zeros((4, 3)))
True
```

**scipy.linalg.qr_update**

The `scipy.linalg.qr_update` function performs a rank-k QR update. If \( A = QR \) is the QR factorization of \( A \), return the QR factorization of \( A + uv^T \) for real \( A \) or \( A + uv^H \) for complex \( A \).

### Parameters

- **Q**
  - [(M, M) or (M, N) array_like] Unitary/orthogonal matrix from the qr decomposition of \( A \).
- **R**
  - [(M, N) or (N, N) array_like] Upper triangular matrix from the qr decomposition of \( A \).
- **u**
  - [(M,) or (M, k) array_like] Left update vector
- **v**
  - [(N,) or (N, k) array_like] Right update vector
- **overwrite_qruv**
  - [bool, optional] If True, consume Q, R, u, and v, if possible, while performing the update, otherwise make copies as necessary. Defaults to False.
- **check_finite**
  - [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default is True.

### Returns

- **Q1**
  - [ndarray] Updated unitary/orthogonal factor
- **R1**
  - [ndarray] Updated upper triangular factor

### Notes

This routine does not guarantee that the diagonal entries of \( R1 \) are real or positive.

New in version 0.16.0.

### References

[1], [2], [3]
Examples

```python
>>> from scipy import linalg
>>> a = np.array([[3., -2., -2.],
...    [6., -9., -3.],
...    [-3., 10., 1.],
...    [6., -7., 4.],
...    [7., 8., -6.]])
```

Given this q, r decomposition, perform a rank 1 update.

```python
>>> u = np.array([7., -2., 4., 3., 5.])
>>> v = np.array([1., 3., -5.])
>>> q_up, r_up = linalg.qr_update(q, r, u, v, False)
```

The update is equivalent, but faster than the following.

```python
>>> a_up = a + np.outer(u, v)
>>> q_direct, r_direct = linalg.qr(a_up)
```

Check that we have equivalent results:

```python
>>> np.allclose(np.dot(q_up, r_up), a_up)
True
```

And the updated Q is still unitary:

```python
>>> np.allclose(np.dot(q_up.T, q_up), np.eye(5))
True
```

Updating economic (reduced, thin) decompositions is also possible:

```python
>>> qe, re = linalg.qr(a, mode='economic')
>>> qe_up, re_up = linalg.qr_update(qe, re, u, v, False)
>>> qe_up
array([[0.54073807, 0.18645997, 0.81707661, -0.02136616, 0.06902409],
       [0.21629523, -0.63257324, 0.06567893, 0.34125904, -0.65749222],
       [0.05407381, 0.64757787, -0.12781284, -0.20031219, -0.72198188],
       [0.48666426, -0.30467178, -0.27487277, -0.77079214, 0.0256951],
       [0.64888568, 0.23001, -0.4859845, 0.49883891, 0.20253783]])
```

(continues on next page)
Similarly to the above, perform a rank 2 update.

```python
>>> u2 = np.array([[ 7., -1.],
    ... [-2.,  4.],
    ... [ 4.,  2.],
    ... [ 3., -6.],
    ... [ 5.,  3.]]
>>> v2 = np.array([[ 1.,  2.],
    ... [ 3.,  4.],
    ... [ 5.,  2.]]
>>> q_up2, r_up2 = linalg.qr_update(q, r, u2, v2, False)
>>> q_up2
array([[-0.33626508, -0.03477253, 0.61956287, -0.64352987, -0.29618884],
       [-0.50439762, 0.58319694, -0.43010077, -0.33395279, 0.33008064],
       [-0.21016568, -0.63123106, 0.0582249 , -0.13675572, 0.73163206],
       [ 0.12609941, 0.49694436, 0.64590024, 0.31191919, 0.47187344],
       [-0.75659643, -0.11517748, 0.10284903, 0.5986227 , -0.21299983]])
>>> r_up2
array([[ 23.79075451, -41.1084062 , 24.71548348],
       [ 0. , -33.83931057, 11.02226551],
       [ 0. , 0. , 48.91476811],
       [ 0. , 0. , 0. ],
       [ 0. , 0. , 0. ]])
This update is also a valid qr decomposition of \( A + U V^T \).

```
p [int, optional] Number of rows or columns to delete, defaults to 1.

which: {'row', 'col'}, optional
Determines if rows or columns will be deleted, defaults to 'row'

overwrite_qr [bool, optional] If True, consume Q and R, overwriting their contents with their
downdated versions, and returning appropriately sized views. Defaults to False.

check_finite [bool, optional] Whether to check that the input matrix contains only finite num-
bers. Disabling may give a performance gain, but may result in problems (crashes,
non-termination) if the inputs do contain infinities or NaNs. Default is True.

Returns

Q1 [ndarray] Updated unitary/orthogonal factor
R1 [ndarray] Updated upper triangular factor

See also:

qr, qr_multiply, qr_insert, qr_update

Notes
This routine does not guarantee that the diagonal entries of R1 are positive.

New in version 0.16.0.

References

[1], [2], [3]

Examples

```python
>>> from scipy import linalg
>>> a = np.array([[ 3., -2., -2.],
...                [ 6., -9., -3.],
...                [-3., 10.,  1.],
...                [ 6., -7.,  4.],
...                [ 7.,  8., -6.]])
>>> q, r = linalg.qr(a)
```

Given this QR decomposition, update q and r when 2 rows are removed.

```python
>>> q1, r1 = linalg.qr_delete(q, r, 2, 2, 'row', False)
>>> q1
array([[ 0.30942637, 0.15347579, 0.93845645],  # may vary (signs)
       [ 0.61885275, 0.71680171, -0.32127338],
       [ 0.72199487, -0.68017681, -0.12681844]])
>>> r1
array([[ 9.69535971, -0.4125685 , -6.80738023],  # may vary (signs)
        [ 0. , -12.19958144, 1.62370412],
        [ 0. , 0. , -0.15218213]])
```

The update is equivalent, but faster than the following.

```python
>>> a1 = np.delete(a, slice(2,4), 0)
>>> a1
array([[ 3., -2., -2.],
        [ 6., -9., -3.],
        [ 7.,  8., -6.]])
>>> q_direct, r_direct = linalg.qr(a1)
```
Check that we have equivalent results:

```python
>>> np.dot(q1, r1)
array([[ 3., -2., -2.],
       [ 6., -9., -3.],
       [ 7.,  8., -6.]])
>>> np.allclose(np.dot(q1, r1), a1)
True
```

And the updated Q is still unitary:

```python
>>> np.allclose(np.dot(q1.T, q1), np.eye(3))
True
```

**scipy.linalg.qr_insert**

If $A = QR$ is the QR factorization of $A$, return the QR factorization of $A$ where rows or columns have been inserted starting at row or column $k$.

**Parameters**

- **Q** [(M, M) array_like] Unitary/orthogonal matrix from the QR decomposition of $A$.
- **R** [(M, N) array_like] Upper triangular matrix from the QR decomposition of $A$.
- **u** [(N,), (p, N), (M,), or (M, p) array_like] Rows or columns to insert.
- **k** [int] Index before which $u$ is to be inserted.
- **which** {'row', 'col'}, optional
  - Determines if rows or columns will be inserted, defaults to 'row'
- **rcond** [float] Lower bound on the reciprocal condition number of $Q$ augmented with $u$/||$u||$. Only used when updating economic mode (thin, (M,N) (N,N)) decompositions. If None, machine precision is used. Defaults to None.
- **overwrite_qru** [bool, optional]
  - If True, consume $Q$, $R$, and $u$, if possible, while performing the update, otherwise make copies as necessary. Defaults to False.
- **check_finite** [bool, optional]
  - Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default is True.

**Returns**

- **Q1** [ndarray] Updated unitary/orthogonal factor
- **R1** [ndarray] Updated upper triangular factor

**Raises**

- **LinAlgError**
  - If updating a (M,N) (N,N) factorization and the reciprocal condition number of $Q$ augmented with $u$/||$u||$ is smaller than rcond.

**See also:**

- `qr`, `qr_multiply`, `qr_delete`, `qr_update`
Notes
This routine does not guarantee that the diagonal entries of $R_1$ are positive.

New in version 0.16.0.

References
[1], [2], [3]

Examples

```python
>>> from scipy import linalg
>>> a = np.array([[ 3.,  -2.,  -2.],
...                [ 6.,  -7.,   4.],
...                [ 7.,   8.,  -6.]]
>>> q, r = linalg.qr(a)
Given this QR decomposition, update $q$ and $r$ when 2 rows are inserted.

```python
>>> u = np.array([[ 6.,  -9.,  -3.],
...                [-3.,  10.,   1.]]
>>> q1, r1 = linalg.qr_insert(q, r, u, 2, 'row')
```python
>>> q1
array([[-0.25445668, 0.02246245, 0.18146236, -0.72798806, 0.60979671],  
       [-0.50891336, 0.23226178, -0.82836478, -0.02837033, -0.00828114],  
       [-0.50891336, 0.35715302, 0.38937158, 0.58110733, 0.35235345],  
       [ 0.25445668, -0.52202743, -0.32165498, 0.36263239, 0.65404509],  
       [-0.59373225, -0.73856549, 0.16065817, -0.0063658 , -0.27595554]])
```

```python
>>> r1
array([[ 11.78982612, 6.44623587, 3.81685018],   # may vary (signs)
       [ 0.        , -16.01393278, 3.72202865],
       [ 0.        ,  0.        , -6.13010256],
       [ 0.        ,  0.        ,  0.        ],
       [ 0.        ,  0.        ,  0.        ]])
```

The update is equivalent, but faster than the following.

```python
>>> a1 = np.insert(a, 2, u, 0)
>>> a1
array([[ 3.,  -2.,  -2.],
       [ 6.,  -7.,   4.],
       [ 6.,  -9.,  -3.],
       [-3.,  10.,   1.],
       [ 7.,   8.,  -6.]]
>>> q_direct, r_direct = linalg.qr(a1)
Check that we have equivalent results:

```python
>>> np.dot(q1, r1)
array([[ 3.,  -2.,  -2.],
       [ 6.,  -7.,   4.],
       [ 6.,  -9.,  -3.],
       [-3.,  10.,   1.],
       [ 7.,   8.,  -6.]]
```
```
And the updated Q is still unitary:

```python
>>> np.allclose(np.dot(q1.T, q1), np.eye(5))
True
```

### scipy.linalg.rq

`scipy.linalg.rq(a, overwrite_a=False, lwork=None, mode='full', check_finite=True)`

Compute RQ decomposition of a matrix.

Calculate the decomposition \( \mathbf{A} = \mathbf{R} \mathbf{Q} \) where \( \mathbf{Q} \) is unitary/orthogonal and \( \mathbf{R} \) upper triangular.

**Parameters**
- `a` : [(M, N) array_like] Matrix to be decomposed
- `overwrite_a` : [bool, optional] Whether data in \( \mathbf{a} \) is overwritten (may improve performance)
- `lwork` : [int, optional] Work array size, \( \text{lwork} >= \text{a.shape[1]} \). If None or -1, an optimal size is computed.
- `mode` : [{'full', 'r', 'economic'}, optional] Determines what information is to be returned: either both \( \mathbf{Q} \) and \( \mathbf{R} \) ('full', default), only \( \mathbf{R} \) ('r') or both \( \mathbf{Q} \) and \( \mathbf{R} \) but computed in economy-size ('economic', see Notes).
- `check_finite` : [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

**Returns**
- \( \mathbf{R} \) : [float or complex ndarray] Of shape (M, N) or (M, K) for mode='economic'. \( K = \min(M, N) \).
- \( \mathbf{Q} \) : [float or complex ndarray] Of shape (N, N) or (K, N) for mode='economic'. Not returned if mode='r'.

**Raises**
- `LinAlgError` : If decomposition fails.

**Notes**
This is an interface to the LAPACK routines sgerqf, dgerqf, cgerqf, zgerqf, sorgqr, dorgqr, cungrq and zungqr.

If mode=economic, the shapes of \( \mathbf{Q} \) and \( \mathbf{R} \) are \( (K, N) \) and \( (M, K) \) instead of \( (N,N) \) and \( (M,N) \), with \( K=\min(M,N) \).

**Examples**

```python
>>> from scipy import linalg
>>> a = np.random.randn(6, 9)
>>> r, q = linalg.rq(a)
>>> np.allclose(a, r @ q)
True
>>> r.shape, q.shape
((6, 9), (9, 9))
```
>>> r2 = linalg.rq(a, mode='r')
>>> np.allclose(r, r2)
True
>>> r3, q3 = linalg.rq(a, mode='economic')
>>> r3.shape, q3.shape
((6, 6), (6, 9))

scipy.linalg.qz

scipy.linalg.qz(A, B, output='real', lwork=None, sort=None, overwrite_a=False, overwrite_b=False, check_finite=True)
QZ decomposition for generalized eigenvalues of a pair of matrices.

The QZ, or generalized Schur, decomposition for a pair of N x N nonsymmetric matrices (A,B) is:

\[(A,B) = (Q*AA*Z', Q*BB*Z')\]

where AA, BB is in generalized Schur form if BB is upper-triangular with non-negative diagonal and AA is upper-triangular, or for real QZ decomposition (output='real') block upper triangular with 1x1 and 2x2 blocks. In this case, the 1x1 blocks correspond to real generalized eigenvalues and 2x2 blocks are 'standardized' by making the corresponding elements of BB have the form:

\[
\begin{bmatrix}
 a & 0 \\
 0 & b
\end{bmatrix}
\]

and the pair of corresponding 2x2 blocks in AA and BB will have a complex conjugate pair of generalized eigenvalues. If (output='complex') or A and B are complex matrices, Z' denotes the conjugate-transpose of Z. Q and Z are unitary matrices.

Parameters

- A : [(N, N) array_like] 2d array to decompose
- B : [(N, N) array_like] 2d array to decompose
- lwork : [int, optional] Work array size. If None or -1, it is automatically computed.
- sort : [{None, callable, ‘lhp’, ‘rhp’, ‘iuc’, ‘ouc’}, optional] NOTE: THIS INPUT IS DISABLED FOR NOW. Use ordqz instead. Specifies whether the upper eigenvalues should be sorted. A callable may be passed that, given a eigenvalue, returns a boolean denoting whether the eigenvalue should be sorted to the top-left (True). For real matrix pairs, the sort function takes three real arguments (alphar, alphai, beta). The eigenvalue x = (alphar + alphai*1j)/beta. For complex matrix pairs or output=’complex’, the sort function takes two complex arguments (alpha, beta). The eigenvalue x = (alpha/beta). Alternatively, string parameters may be used:
  - ‘lhp’ Left-hand plane (x.real < 0.0)
  - ‘rhp’ Right-hand plane (x.real > 0.0)
  - ‘iuc’ Inside the unit circle (x*x.conjugate() < 1.0)
  - ‘ouc’ Outside the unit circle (x*x.conjugate() > 1.0)
 Defaults to None (no sorting).
- overwrite_a : [bool, optional] Whether to overwrite data in a (may improve performance)
- overwrite_b : [bool, optional] Whether to overwrite data in b (may improve performance)
check_finite
[bool, optional] If true checks the elements of A and B are finite numbers. If false does no checking and passes matrix through to underlying algorithm.

Returns

AA [(N, N) ndarray] Generalized Schur form of A.
BB [(N, N) ndarray] Generalized Schur form of B.
Q [(N, N) ndarray] The left Schur vectors.
Z [(N, N) ndarray] The right Schur vectors.

See also:
ordqz

Notes
Q is transposed versus the equivalent function in Matlab.

New in version 0.11.0.

Examples

```python
>>> from scipy import linalg
>>> np.random.seed(1234)
>>> A = np.arange(9).reshape((3, 3))
>>> B = np.random.randn(3, 3)
```

```python
>>> AA, BB, Q, Z = linalg.qz(A, B)
>>> AA
array([[ -13.40928183,  -4.62471562,  1.09215523],
       [  0.        ,  0.        ,  1.22805978],
       [  0.        ,  0.        ,  0.31973817]])
>>> BB
array([[  0.33362547,  -1.37393632,  0.02179805],
       [  0.        ,  1.68144922,  0.74683866],
       [  0.        ,  0.        ,  0.9258294 ]])
>>> Q
array([[  0.14134727,  -0.97562773,  0.16784365],
       [  0.49835904,  -0.07636948, -0.86360059],
       [  0.85537081,  0.20571399,  0.47541828]])
>>> Z
array([[-0.24900855,  -0.51772687,  0.81850696],
       [-0.79813178,  0.58842606,  0.12938478],
       [-0.54861681,  -0.6210585 , -0.55973739]])
```

scipy.linalg.ordqz

scipy.linalg.ordqz(A, B, sort='lhp', output='real', overwrite_a=False, overwrite_b=False, check_finite=True)

QZ decomposition for a pair of matrices with reordering.

New in version 0.17.0.

Parameters

A  [(N, N) array_like] 2d array to decompose
B  [(N, N) array_like] 2d array to decompose
sort  [{callable, ‘lhp’, ‘rhp’, ‘iuc’, ‘ouc’}, optional] Specifies whether the upper eigenvalues should be sorted. A callable may be passed that, given an ordered pair (alpha, beta) representing the eigenvalue x = (alpha/beta), returns a boolean
denoting whether the eigenvalue should be sorted to the top-left (True). For the
real matrix pairs \( \beta \) is real while \( \alpha \) can be complex, and for complex matrix
pairs both \( \alpha \) and \( \beta \) can be complex. The callable must be able to accept a
nurary array. Alternatively, string parameters may be used:

- ‘lhp’ Left-hand plane (x.real < 0.0)
- ‘rhp’ Right-hand plane (x.real > 0.0)
- ‘iuc’ Inside the unit circle (x*x.conjugate() < 1.0)
- ‘ouc’ Outside the unit circle (x*x.conjugate() > 1.0)

With the predefined sorting functions, an infinite eigenvalue (i.e. \( \alpha \neq 0 \) and
\( \beta = 0 \)) is considered to lie in neither the left-hand nor the right-hand plane,
but it is considered to lie outside the unit circle. For the eigenvalue \( (\alpha, \beta) = (0, 0) \)
the predefined sorting functions all return \( False \).

**output**

[**str** \{‘real’,‘complex’\}, optional] Construct the real or complex QZ decomposition
for real matrices. Default is ‘real’.

**overwrite_a**

[**bool**, optional] If True, the contents of A are overwritten.

**overwrite_b**

[**bool**, optional] If True, the contents of B are overwritten.

**check_finite**

[**bool**, optional] If true checks the elements of \( A \) and \( B \) are finite numbers. If false
does no checking and passes matrix through to underlying algorithm.

**Returns**

- **AA**  
  [(\( N, N \) ndarray] Generalized Schur form of A.

- **BB**  
  [(\( N, N \) ndarray] Generalized Schur form of B.

- **alpha**  
  [(\( N, \) ndarray] \( \alpha = \) alphar + alphai * 1j]. See notes.

- **beta**  
  [(\( N, \) ndarray] See notes.

- **Q**  
  [(\( N, N \) ndarray] The left Schur vectors.

- **Z**  
  [(\( N, N \) ndarray] The right Schur vectors.

**See also:**

**qz**

**Notes**

On exit, \( \alpha(j) + \alpha(j) \ast \beta(j) / \beta(j) \), \( j=1,\ldots,N \), will be the generalized eigenvalues.
\( \alpha(j) + \alpha(j) \ast \beta(j) \ast 1 \) and \( \beta(j) \ast 1 \) are the diagonals of the complex Schur form
\( (S,T) \) that would result if the 2-by-2 diagonal blocks of the real generalized Schur form of \( (A,B) \) were
further reduced to triangular form using complex unitary transformations. If \( \alpha(j) \) is zero, then
the \( j \)-th eigenvalue is real; if positive, then the \( j \)-th and \( (j+1) \)-st eigenvalues are a complex conjugate
pair, with \( \alpha(j+1) \) negative.

**Examples**

```python
>>> from scipy.linalg import ordqz
>>> A = np.array([[2, 5, 8, 7], [5, 2, 2, 8], [7, 5, 6, 6], [5, 4, 4, 8]])
>>> B = np.array([[0, 6, 0, 01], [5, 0, 2, 1], [5, 2, 6, 6], [4, 7, 7, 7]])
>>> AA, BB, alpha, beta, Q, Z = ordqz(A, B, sort='lhp')
```

Since we have sorted for left half plane eigenvalues, negatives come first

```python
>>> (alpha/beta).real < 0
array([True, True, False, False], dtype=bool)
```
The Schur decomposition is:

\[ A = Z \mathbf{T} Z^H \]

where \( Z \) is unitary and \( \mathbf{T} \) is either upper-triangular, or for real Schur decomposition (output='real'), quasi-upper triangular. In the quasi-triangular form, 2x2 blocks describing complex-valued eigenvalue pairs may extrude from the diagonal.

**Parameters**

- **a** [(M, M) array_like] Matrix to decompose
- **output** [{'real', 'complex'}, optional] Construct the real or complex Schur decomposition (for real matrices).
- **lwork** [int, optional] Work array size. If None or -1, it is automatically computed.
- **overwrite_a** [bool, optional] Whether to overwrite data in a (may improve performance).
- **sort** [{None, callable, 'lhp', 'rhp', 'iuc', 'ouc'}, optional] Specifies whether the upper eigenvalues should be sorted. A callable may be passed that, given a eigenvalue, returns a boolean denoting whether the eigenvalue should be sorted to the top-left (True). Alternatively, string parameters may be used:

  - 'lhp'  | Left-hand plane (x.real < 0.0)
  - 'rhp'  | Right-hand plane (x.real > 0.0)
  - 'iuc'  | Inside the unit circle (x*x.conjugate() <= 1.0)
  - 'ouc'  | Outside the unit circle (x*x.conjugate() > 1.0)

  Defaults to None (no sorting).
- **check_finite** [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

**Returns**

- **T** [(M, M) ndarray] Schur form of A. It is real-valued for the real Schur decomposition.
- **Z** [(M, M) ndarray] An unitary Schur transformation matrix for A. It is real-valued for the real Schur decomposition.
- **sdim** [int] If and only if sorting was requested, a third return value will contain the number of eigenvalues satisfying the sort condition.

**Raises**

- **LinAlgError**
  
  Error raised under three conditions:
  1. The algorithm failed due to a failure of the QR algorithm to compute all eigenvalues
  2. If eigenvalue sorting was requested, the eigenvalues could not be reordered due to a failure to separate eigenvalues, usually because of poor conditioning
  3. If eigenvalue sorting was requested, roundoff errors caused the leading eigenvalues to no longer satisfy the sorting condition

See also:
rsf2csf

Convert real Schur form to complex Schur form

Examples

```python
>>> from scipy.linalg import schur, eigvals
>>> A = np.array([[0, 2, 2], [0, 1, 2], [1, 0, 1]])
>>> T, Z = schur(A)
>>> T
array([[ 2.65896708, 1.42440458, -1.92933439],
       [ 0.        , -0.32948354, -0.49063704],
       [ 0.        ,  1.31178921, -0.32948354]])
>>> Z
array([[0.72711591, -0.60156188, 0.33079564],
       [0.52839428, 0.79801892, 0.28976765],
       [0.43829436, 0.03590414, -0.89811411]])
```

An arbitrary custom eig-sorting condition, having positive imaginary part, which is satisfied by only one eigenvalue

```python
>>> T2, Z2 = schur(A, output='complex')
>>> T2
array([[ 2.65896708, -1.22839825+1.32378589j, 0.42590089+1.51937378j],
       [ 0.        , -0.32948354+0.80225456j, -0.59877807+0.56192146j],
       [ 0.        ,  0.        , -0.32948354-0.80225456j]])
>>> eigvals(T2)
array([2.65896708, -0.32948354+0.80225456j, -0.32948354-0.80225456j])
```

```python
>>> T3, Z3, sdim = schur(A, output='complex', sort=lambda x: x.imag > 0)
>>> sdim
1
```

scipy.linalg.rsf2csf

```
scipy.linalg.rsf2csf(T, Z, check_finite=True)
```

Convert real Schur form to complex Schur form.

Parameters

- **T** : [(M, M) array_like] Real Schur form of the original array
- **Z** : [(M, M) array_like] Schur transformation matrix
- **check_finite** : [bool, optional] Whether to check that the input arrays contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

- **T** : [(M, M) ndarray] Complex Schur form of the original array
- **Z** : [(M, M) ndarray] Schur transformation matrix corresponding to the complex form

See also:

schur

Schur decomposition of an array


**Examples**

```python
>>> from scipy.linalg import schur, rsf2csf
>>> A = np.array([[0, 2, 2], [0, 1, 2], [1, 0, 1]])
>>> T, Z = schur(A)
>>> T
array([[ 2.65896708,  1.42440458, -1.92933439],
       [ 0.      , -0.32948354,  0.49063704],
       [ 0.      ,  1.31178921, -0.32948354]])
>>> Z
array([[ 0.72711591,  0.60156188,  0.33079564],
       [ 0.52839428,  0.79801892,  0.28976765],
       [ 0.43829436,  0.03590414, -0.89811411]])
>>> T2, Z2 = rsf2csf(T, Z)
>>> T2
array([[ 2.65896708+0.j, -1.64592781+0.743164187j, -1.21516887+1.00660462j],
       [ 0.+0.j ,  0.52839428+0.79801892j,  0.28976765+0.28976765j],
       [ 0.+0.j ,  0.60156188+0.82981141j, -0.32948354-0.28976765j]])
>>> Z2
array([[ 0.72711591+0.j,  0.28220393-0.31385693j,  0.51319638-0.17258824j],
       [ 0.52839428+0.j,  0.24720268+0.41635578j, -0.68079517-0.15118243j],
       [ 0.43829436+0.j, -0.76618703+0.01873251j, -0.03063006+0.46857912j]])
```

**Examples**

```python
>>> from scipy.linalg import hessenberg
>>> A = np.array([[2, 5, 8, 7], [5, 2, 2, 8], [7, 5, 6, 6], [5, 4, 4, 8]])
>>> H, Q = hessenberg(A, calc_q=True)
>>> H
```

The Hessenberg decomposition is:

\[
A = Q H Q^H
\]

where \(Q\) is unitary/orthogonal and \(H\) has only zero elements below the first sub-diagonal.

**Parameters**

- **a** 
  [(M, M) array_like] Matrix to bring into Hessenberg form.
- **calc_q**
  [bool, optional] Whether to compute the transformation matrix. Default is False.
- **overwrite_a**
  [bool, optional] Whether to overwrite \(a\); may improve performance. Default is False.
- **check_finite**
  [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

**Returns**

- **H**
  [(M, M) ndarray] Hessenberg form of \(a\).
- **Q**
  [(M, M) ndarray] Unitary/orthogonal similarity transformation matrix \(A = Q H Q^H\). Only returned if \(\text{calc}_q\)=True.

**Examples**

```python
>>> from scipy.linalg import hessenberg
>>> A = np.array([[2, 5, 8, 7], [5, 2, 2, 8], [7, 5, 6, 6], [5, 4, 4, 8]])
>>> H, Q = hessenberg(A, calc_q=True)
>>> H
```

(continues on next page)
array([[ 2. , -11.65843866,  1.42005301,  0.25349066],
[ -9.94987437,  14.53535354, -5.31022304,  2.43081618],
[  0. , -1.83299243,  0.38969961, -0.51527034],
[  0. ,  0. , -3.83189513,  1.07494686]])

```python
>>> np.allclose(Q @ H @ Q.conj().T - A, np.zeros((4, 4)))
True
```

### scipy.linalg.cdf2rdf

#### scipy.linalg.cdf2rdf(w, v)

Converts complex eigenvalues `w` and eigenvectors `v` to real eigenvalues in a block diagonal form `wr` and the associated real eigenvectors `vr`, such that:

```
vr @ wr = X @ vr
```

continues to hold, where `X` is the original array for which `w` and `v` are the eigenvalues and eigenvectors.

New in version 1.1.0.

**Parameters**

- `w` [(…, M) array_like] Complex or real eigenvalues, an array or stack of arrays
  Conjugate pairs must not be interleaved, else the wrong result will be produced. So `[1+1j, 1, 1-1j]` will give a correct result, but `[1+1j, 2+1j, 1-1j, 2-1j]` will not.
- `v` [(…, M, M) array_like] Complex or real eigenvectors, a square array or stack of square arrays.

**Returns**

- `wr` [(…, M, M) ndarray] Real diagonal block form of eigenvalues
- `vr` [(…, M, M) ndarray] Real eigenvectors associated with `wr`

**See also:**

- `eig`
  Eigenvalues and right eigenvectors for non-symmetric arrays
- `rsf2csf`
  Convert real Schur form to complex Schur form

**Notes**

`w, v` must be the eigenstructure for some real matrix `X`. For example, obtained by `w, v = scipy.linalg.eig(X)` or `w, v = numpy.linalg.eig(X)` in which case `X` can also represent stacked arrays.

New in version 1.1.0.

**Examples**

```python
>>> X = np.array([[1, 2, 3], [0, 4, 5], [0, -5, 4]])
>>> X
array([[ 1,  2,  3],
[ 0,  4,  5],
[ 0, -5,  4]])
```
>>> from scipy import linalg
>>> w, v = linalg.eig(X)
>>> w
array([[ 1.+0.j, 4.+5.j, 4.-5.j]])
>>> v
array([[ 1.00000+0.j , -0.01906-0.40016j, -0.01906+0.40016j],
       [ 0.00000+0.j , 0.00000-0.64788j, 0.00000+0.64788j],
       [ 0.00000+0.j , 0.64788+0.j , 0.64788-0.j ]])

>>> wr, vr = linalg.cdf2rdf(w, v)
>>> wr
array([[ 1., 0., 0.],
       [ 0., 4., 5.],
       [ 0., -5., 4.]])
>>> vr
array([[ 1. , 0.40016, -0.01906],
       [ 0. , 0.64788, 0. ],
       [ 0. , 0. , 0.64788]])

See also:

scipy.linalg.interpolative – Interpolative matrix decompositions

6.9.4 Matrix Functions

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scipy.linalg.expm

scipy.linalg.expm(A)
   Compute the matrix exponential using Pade approximation.

   Parameters
   A    [(N, N) array_like or sparse matrix] Matrix to be exponentiated.

   Returns
   expm    [(N, N) ndarray] Matrix exponential of A.

scipy.linalg.logm

scipy.linalg.logm(A, disp=True)
   Compute matrix logarithm.

   The matrix logarithm is the inverse of expm: expm(logm(A)) == A

   Parameters
   A    [(N, N) array_like] Matrix whose logarithm to evaluate
   disp  [bool, optional] Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)

   Returns
   logm    [(N, N) ndarray] Matrix logarithm of A
   errest  [float] (if disp == False)
            1-norm of the estimated error, ||err||_1 / ||A||_1
```python
>>> from scipy.linalg import logm, expm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> b = logm(a)
>>> b
array([[-1.02571087,  2.05142174],
       [ 0.68380725,  1.02571087]])
```

```python
>>> expm(b)  # Verify expm(logm(a)) returns a
array([[ 1.,  3.],
        [ 1.,  4.]])
```

### scipy.linalg.cosm

#### scipy.linalg.cosm(A)

Compute the matrix cosine.

This routine uses expm to compute the matrix exponentials.

**Parameters**
- `A` : [(N, N) array_like] Input array

**Returns**
- `cosm` : [(N, N) ndarray] Matrix cosine of A

#### Examples

```python
>>> from scipy.linalg import expm, sinm, cosm
```

Euler’s identity \((\exp(i*\theta) = \cos(\theta) + i*\sin(\theta))\) applied to a matrix:

```python
>>> a = np.array([[1.0, 2.0], [-1.0, 3.0]])
>>> expm(1j*a)
array([[ 0.42645930+1.89217551j, -2.13721484-0.97811252j],
       [ 1.06860742+0.48905626j, -1.71075555+0.91406299j]])
```

### scipy.linalg.sinm

#### scipy.linalg.sinm(A)

Compute the matrix sine.

This routine uses expm to compute the matrix exponentials.

**Parameters**
- `A` : [(N, N) array_like] Input array.

**Returns**
- `sinm` : [(N, N) ndarray] Matrix sine of A

#### Examples

```python
>>> from scipy.linalg import expm, sinm, cosm
```

Euler’s identity \((\exp(i*\theta) = \cos(\theta) + i*\sin(\theta))\) applied to a matrix:

```python
>>> a = np.array([[1.0, 2.0], [-1.0, 3.0]])
>>> expm(1j*a)
array([[ 0.42645930+1.89217551j, -2.13721484-0.97811252j],
       [ 1.06860742+0.48905626j, -1.71075555+0.91406299j]])
```
>>> a = np.array([[1.0, 2.0], [-1.0, 3.0]])
>>> expm(1j*a)
array([[ 0.42645930+1.89217551j, -2.13721484-0.97811252j],
       [ 1.06860742+0.48905626j, -1.71075555+0.91406299j]])

scipy.linalg.tanm

scipy.linalg.tanm(A)
Compute the matrix tangent.

This routine uses expm to compute the matrix exponentials.

Parameters
A       [(N, N) array_like] Input array.

Returns
tanm    [(N, N) ndarray] Matrix tangent of A

Examples

>>> from scipy.linalg import tanm, sinm, cosm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> t = tanm(a)
array([[-2.00876993, -8.41880636],
       [-2.80626879, -10.42757629]])

Verify tanm(a) = sinm(a).dot(inv(cosm(a)))

>>> s = sinm(a)
>>> c = cosm(a)
>>> s.dot(np.linalg.inv(c))
array([[-2.00876993, -8.41880636],
       [-2.80626879, -10.42757629]])

scipy.linalg.coshm

scipy.linalg.coshm(A)
Compute the hyperbolic matrix cosine.

This routine uses expm to compute the matrix exponentials.

Parameters
A       [(N, N) array_like] Input array.

Returns
coshm   [(N, N) ndarray] Hyperbolic matrix cosine of A

Examples

>>> from scipy.linalg import tanhm, sinhm, coshm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> c = coshm(a)
>>> c
array([[ 11.24592233, 38.76236492],
       [ 12.92078831, 50.00828725]])

Verify tanhm(a) = sinh(a).dot(inv(coshm(a)))

```python
>>> t = tanhm(a)
>>> s = sinh(a)
>>> t - s.dot(np.linalg.inv(c))
array([[ 2.72004641e-15, 4.55191440e-15],
       [ 0.00000000e+00, -5.55111512e-16]])
```

scipy.linalg.sinhm

scipy.linalg.sinhm(A)
Compute the hyperbolic matrix sine.

This routine uses expm to compute the matrix exponentials.

**Parameters**
- A  
  
  [[(N, N) array_like] Input array.

**Returns**
- sinh  
  
  [(N, N) ndarray] Hyperbolic matrix sine of A

**Examples**

```python
>>> from scipy.linalg import tanhm, sinh, coshm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> s = sinh(a)
>>> s
array([[ 10.57300653, 39.28826594],
       [ 13.09608865, 49.86127247]])

Verify tanhm(a) = sinh(a).dot(inv(coshm(a)))

```python
>>> t = tanhm(a)
>>> c = coshm(a)
>>> t - s.dot(np.linalg.inv(c))
array([[ 2.72004641e-15, 4.55191440e-15],
       [ 0.00000000e+00, -5.55111512e-16]])
```

scipy.linalg.tanhm

scipy.linalg.tanhm(A)
Compute the hyperbolic matrix tangent.

This routine uses expm to compute the matrix exponentials.

**Parameters**
- A  
  
  [[(N, N) array_like] Input array

**Returns**
- tanhm  
  
  [(N, N) ndarray] Hyperbolic matrix tangent of A
Examples

```python
>>> from scipy.linalg import tanhm, sinh, coshm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> t = tanhm(a)
>>> t
array([[ 0.3428582,  0.51987926],
       [ 0.17329309,  0.86273746]])

Verify tanhm(a) = sinh(a).dot(inv(coshm(a)))

```
sqrtm

[(N, N) ndarray] Value of the sqrt function at A

errest

[float] (if disp == False)

Frobenius norm of the estimated error, ||err||_F / ||A||_F

References

[1]

Examples

```python
>>> from scipy.linalg import sqrtm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> r = sqrtm(a)
>>> r
array([[ 0.75592895, 1.13389342],
       [ 0.37796447, 1.88982237]])
>>> r.dot(r)
array([[ 1., 3.],
       [ 1., 4.]])
```

scipy.linalg.funm

scipy.linalg.funm(A, func, disp=True)

Evaluate a matrix function specified by a callable.

Returns the value of matrix-valued function f at A. The function f is an extension of the scalar-valued function func to matrices.

Parameters

- **A** : [(N, N) array_like] Matrix at which to evaluate the function
- **func** : [callable] Callable object that evaluates a scalar function f. Must be vectorized (e.g. using vectorize).
- **disp** : [bool, optional] Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)

Returns

- **funm** : [(N, N) ndarray] Value of the matrix function specified by func evaluated at A
- **errest** : [float] (if disp == False)

1-norm of the estimated error, ||err||_1 / ||A||_1

Notes

This function implements the general algorithm based on Schur decomposition (Algorithm 9.1.1. in [1]).

If the input matrix is known to be diagonalizable, then relying on the eigendecomposition is likely to be faster. For example, if your matrix is Hermitian, you can do

```python
>>> from scipy.linalg import eigh
>>> def funm_herm(a, func, check_finite=False):
...     w, v = eigh(a, check_finite=check_finite)
...     ## if you further know that your matrix is positive semidefinite,
...     ## you can optionally guard against precision errors by doing
...     ## w = np.maximum(w, 0)
...     w = func(w)
...     return (v * w).dot(v.conj().T)
```

References

[1]
Examples

```python
>>> from scipy.linalg import funm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> funm(a, lambda x: x*x)
array([[ 4., 15.],
       [ 5., 19.]])
>>> a.dot(a)
array([[ 4., 15.],
       [ 5., 19.]])
```

scipy.linalg.expm_frechet

`scipy.linalg.expm_frechet(A, E, method=None, compute_expm=True, check_finite=True)`

Frechet derivative of the matrix exponential of A in the direction E.

Parameters

- **A**  
  [(N, N) array_like] Matrix of which to take the matrix exponential.
- **E**  
  [(N, N) array_like] Matrix direction in which to take the Frechet derivative.
- **method**  
  [str, optional] Choice of algorithm. Should be one of
  - `SPS` (default)
  - `blockEnlarge`
- **compute_expm**  
  [bool, optional] Whether to compute also `expm_A` in addition to `expm_frechet_AE`. Default is True.
- **check_finite**  
  [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

- **expm_A**  
  [ndarray] Matrix exponential of A.
- **expm_frechet_AE**  
  [ndarray] Frechet derivative of the matrix exponential of A in the direction E.

For "compute_expm = False", only ‘expm_frechet_AE’ is returned.

See also:

- `expm`
  
  Compute the exponential of a matrix.

Notes

This section describes the available implementations that can be selected by the `method` parameter. The default method is `SPS`.

Method `blockEnlarge` is a naive algorithm.

Method `SPS` is Scaling-Pade-Squaring [1]. It is a sophisticated implementation which should take only about 3/8 as much time as the naive implementation. The asymptotics are the same.

New in version 0.13.0.

References

[1]
Examples

```python
>>> import scipy.linalg
>>> A = np.random.randn(3, 3)
>>> E = np.random.randn(3, 3)
>>> expm_A, expm_frechet_AE = scipy.linalg.expm_frechet(A, E)
>>> expm_A.shape, expm_frechet_AE.shape
((3, 3), (3, 3))
```

```python
>>> import scipy.linalg
>>> A = np.random.randn(3, 3)
>>> E = np.random.randn(3, 3)
>>> expm_A, expm_frechet_AE = scipy.linalg.expm_frechet(A, E)
>>> M = np.zeros((6, 6))
>>> M[3:, 3:] = A; M[:, :3] = E; M[3:, 3:] = A
>>> expm_M = scipy.linalg.expm(M)
>>> np.allclose(expm_A, expm_M[3:, :])
True
```

```python
>>> np.allclose(expm_frechet_AE, expm_M[3:, 3:])
True
```

**scipy.linalg.expm_cond**

scipy.linalg.expm_cond(A, check_finite=True)

Relative condition number of the matrix exponential in the Frobenius norm.

**Parameters**

- `check_finite` [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

**Returns**

- `kappa` [float] The relative condition number of the matrix exponential in the Frobenius norm

**See also:**

- expm
  - Compute the exponential of a matrix.
- expm_frechet
  - Compute the Frechet derivative of the matrix exponential.

**Notes**

A faster estimate for the condition number in the 1-norm has been published but is not yet implemented in scipy.

New in version 0.14.0.

**Examples**

```python
>>> from scipy.linalg import expm_cond
>>> A = np.array([[-0.3, 0.2, 0.6], [0.6, 0.3, -0.1], [-0.7, 1.2, 0.9]])
```

(continues on next page)
```python
>>> k = expm_cond(A)
>>> k
1.7787805864469866
```

### scipy.linalg.fractional_matrix_power

**scipy.linalg.fractional_matrix_power(A, t)**

Compute the fractional power of a matrix.

Proceeds according to the discussion in section (6) of [1].

**Parameters**

- **A** [(N, N) array_like] Matrix whose fractional power to evaluate.
- **t** [float] Fractional power.

**Returns**

- **X** [(N, N) array_like] The fractional power of the matrix.

**References**

[1]

**Examples**

```python
>>> from scipy.linalg import fractional_matrix_power
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> b = fractional_matrix_power(a, 0.5)
>>> b
array([[ 0.75592895, 1.13389342],
       [ 0.37796447, 1.88982237]])
>>> np.dot(b, b) # Verify square root
array([[ 1., 3.],
       [ 1., 4.]])
```

### 6.9.5 Matrix Equation Solvers

- **solve_sylvester(a, b, q)**
  Computes a solution (X) to the Sylvester equation $AX + XB = Q$.

- **solve_continuous_are(a, b, q[, e, s, ...])**
  Solves the continuous-time algebraic Riccati equation (CARE).

- **solve_discrete_are(a, b, q[, e, s, balanced])**
  Solves the discrete-time algebraic Riccati equation (DARE).

- **solve_continuous_lyapunov(a, q)**
  Solves the continuous Lyapunov equation $AX + XA^H = Q$.

- **solve_discrete_lyapunov(a, q[, method])**
  Solves the discrete Lyapunov equation $AXA^H - X + Q = 0$.

### scipy.linalg.solve_sylvester

**scipy.linalg.solve_sylvester(a, b, q)**
Computes a solution (X) to the Sylvester equation $AX + XB = Q$.

**Parameters**

- **a** [(M, M) array_like] Leading matrix of the Sylvester equation
- **b** [(N, N) array_like] Trailing matrix of the Sylvester equation
q  [(M, N) array_like] Right-hand side

Returns  

x  [(M, N) ndarray] The solution to the Sylvester equation.

Raises  

LinAlgError  
If solution was not found

Notes  
Computes a solution to the Sylvester matrix equation via the Bartels- Stewart algorithm. The A and B matrices first undergo Schur decompositions. The resulting matrices are used to construct an alternative Sylvester equation \((RY + YS^T = F)\) where the R and S matrices are in quasi-triangular form (or, when R, S or F are complex, triangular form). The simplified equation is then solved using *TRSYL from LAPACK directly.

New in version 0.11.0.

Examples  
Given \(a\), \(b\), and \(q\) solve for \(x\):

```python
>>> from scipy import linalg
>>> a = np.array([[-3, -2, 0], [-1, -1, 3], [3, -5, -1]])
>>> b = np.array([[1]])
>>> q = np.array([[1,2],[2,3]])
>>> x = linalg.solve_sylvester(a, b, q)
>>> x
array([[ 0.0625],
       [-0.5625],
       [ 0.6875]])
>>> np.allclose(a.dot(x) + x.dot(b), q)
True
```

scipy.linalg.solve_continuous_are  
scipy.linalg.solve_continuous_are(a, b, q, e=None, s=None, balanced=True)  
Solves the continuous-time algebraic Riccati equation (CARE).

The CARE is defined as

\[XA + A^HX - XBR^{-1}B^HX + Q = 0\]

The limitations for a solution to exist are :

- All eigenvalues of \(A\) on the right half plane, should be controllable.
- The associated hamiltonian pencil (See Notes), should have eigenvalues sufficiently away from the imaginary axis.

Moreover, if \(e\) or \(s\) is not precisely None, then the generalized version of CARE

\[E^HXA + A^HXE - (E^HXB + S)R^{-1}(B^HXE + SH) + Q = 0\]

is solved. When omitted, \(e\) is assumed to be the identity and \(s\) is assumed to be the zero matrix with sizes compatible with \(a\) and \(b\) respectively.

Parameters  
a  [(M, M) array_like] Square matrix
SciPy Reference Guide, Release 1.2.0

b [(M, N) array_like] Input
q [(M, M) array_like] Input
r [(N, N) array_like] Nonsingular square matrix
e [(M, M) array_like, optional] Nonsingular square matrix
s [(M, N) array_like, optional] Input
balanced [bool, optional] The boolean that indicates whether a balancing step is performed on the data. The default is set to True.

Returns
x [(M, M) ndarray] Solution to the continuous-time algebraic Riccati equation.

Raises
LinAlgError
For cases where the stable subspace of the pencil could not be isolated. See Notes section and the references for details.

See also:
solve_discrete_are
Solves the discrete-time algebraic Riccati equation

Notes
The equation is solved by forming the extended hamiltonian matrix pencil, as described in [1], \( H - \lambda J \) given by the block matrices

\[
\begin{bmatrix}
A & 0 & B \\
-Q & -A^T & S \\
S^T & B^T & R
\end{bmatrix} - \lambda \begin{bmatrix}
E & 0 & 0 \\
0 & E^T & 0 \\
0 & 0 & 0
\end{bmatrix}
\]

and using a QZ decomposition method.

In this algorithm, the fail conditions are linked to the symmetry of the product \( U_2 U_1^{-1} \) and condition number of \( U_1 \). Here, \( U \) is the 2m-by-m matrix that holds the eigenvectors spanning the stable subspace with 2m rows and partitioned into two m-row matrices. See [1] and [2] for more details.

In order to improve the QZ decomposition accuracy, the pencil goes through a balancing step where the sum of absolute values of \( H \) and \( J \) entries (after removing the diagonal entries of the sum) is balanced following the recipe given in [3].

New in version 0.11.0.

References
[1], [2], [3]

Examples
Given \( a \), \( b \), \( q \), and \( r \) solve for \( x \):

```python
>>> from scipy import linalg
>>> a = np.array([[4, 3], [-4.5, -3.5]])
>>> b = np.array([[1], [-i]])
>>> q = np.array([[9, 6], [6, 4.]])
>>> r = 1
>>> x = linalg.solve_continuous_are(a, b, q, r)
>>> x
array([[ 21.72792206,  14.48528137],
        [ 14.48528137,   9.65685425]])
```

(continues on next page)
```python
>>> np.allclose(a.T.dot(x) + x.dot(a) - x.dot(b).dot(b.T).dot(x), -q)
True
```

**scipy.linalg.solve_discrete_are**

**scipy.linalg.solve_discrete_are**(a, b, q, r, e=None, s=None, balanced=True)

Solves the discrete-time algebraic Riccati equation (DARE).

The DARE is defined as

\[
A^H X A - X - (A^H X B) (R + B^H X B)^{-1} (B^H X A) + Q = 0
\]

The limitations for a solution to exist are:

- All eigenvalues of \( A \) outside the unit disc, should be controllable.
- The associated symplectic pencil (See Notes), should have eigenvalues sufficiently away from the unit circle.

Moreover, if \( e \) and \( s \) are not both precisely None, then the generalized version of DARE

\[
A^H X A - E^H X E - (A^H X B + S) (R + B^H X B)^{-1} (B^H X A + S^H) + Q = 0
\]

is solved. When omitted, \( e \) is assumed to be the identity and \( s \) is assumed to be the zero matrix.

**Parameters**

- **a** : (M, M) array_like, Square matrix
- **b** : (M, N) array_like, Input
- **q** : (M, M) array_like, Input
- **r** : (N, N) array_like, Square matrix
- **e** : (M, M) array_like, optional, Nonsingular square matrix
- **s** : (M, N) array_like, optional, Input
- **balanced** : bool, The boolean that indicates whether a balancing step is performed on the data. The default is set to True.

**Returns**

- **x** : (M, M) ndarray, Solution to the discrete algebraic Riccati equation.

**Raises**

- LinAlgError

For cases where the stable subspace of the pencil could not be isolated. See Notes section and the references for details.

**See also:**

- solve_continuous_are

Solves the continuous algebraic Riccati equation

**Notes**

The equation is solved by forming the extended symplectic matrix pencil, as described in [1], \( H - \lambda J \) given by the block matrices

\[
\begin{bmatrix}
A & 0 & B \\
-Q & E^H & -S \\
S^H & 0 & R
\end{bmatrix} - \lambda \begin{bmatrix}
E & 0 & B \\
0 & A^H & 0 \\
0 & -B^H & 0
\end{bmatrix}
\]
and using a QZ decomposition method.

In this algorithm, the fail conditions are linked to the symmetry of the product $U_2 U_1^{-1}$ and condition number of $U_1$. Here, $U$ is the 2m-by-m matrix that holds the eigenvectors spanning the stable subspace with 2m rows and partitioned into two m-row matrices. See [1] and [2] for more details.

In order to improve the QZ decomposition accuracy, the pencil goes through a balancing step where the sum of absolute values of $H$ and $J$ rows/cols (after removing the diagonal entries) is balanced following the recipe given in [3]. If the data has small numerical noise, balancing may amplify their effects and some clean up is required.

New in version 0.11.0.

References
[1], [2], [3]

Examples
Given $a$, $b$, $q$, and $r$ solve for $x$:

```python
>>> from scipy import linalg as la
>>> a = np.array([[0, 1], [0, -1]])
>>> b = np.array([[1, 0], [2, 1]])
>>> q = np.array([[-4, -4], [-4, 7]])
>>> r = np.array([[9, 3], [3, 1]])
>>> x = la.solve_discrete_are(a, b, q, r)
>>> x
array([[-4., -4.],
       [-4.,  7.]])
>>> R = la.solve(r + b.T.dot(x).dot(b), b.T.dot(x).dot(a))
>>> np.allclose(a.T.dot(x).dot(a) - x - a.T.dot(x).dot(b).dot(R), -q)
True
```

`sparse.linalg.solve_continuous_lyapunov`

`sparse.linalg.solve_continuous_lyapunov(a, q)`
Solves the continuous Lyapunov equation $AX + XA^H = Q$.

Uses the Bartels-Stewart algorithm to find $X$.

Parameters

a  [array_like] A square matrix
q  [array_like] Right-hand side square matrix

Returns

x  [ndarray] Solution to the continuous Lyapunov equation

See also:

`sparse.linalg.solve_discrete_lyapunov`
computes the solution to the discrete-time Lyapunov equation

`sparse.linalg.solve_sylvester`
computes the solution to the Sylvester equation
Notes
The continuous Lyapunov equation is a special form of the Sylvester equation, hence this solver relies on LAPACK routine ?TRSYL.

New in version 0.11.0.

Examples
Given $a$ and $q$ solve for $x$:

```python
>>> from scipy import linalg
>>> a = np.array([[-3, -2, 0], [-1, -1, 0], [0, -5, -1]])
>>> b = np.array([2, 4, -1])
>>> q = np.eye(3)
>>> x = linalg.solve_continuous_lyapunov(a, q)
>>> x
array([[ 0.75  ,  0.875 , -3.75  ],
        [ 0.875 , -1.375 ,  5.3125],
        [-3.75  ,  5.3125, -27.0625]])
>>> np.allclose(a.dot(x) + x.dot(a.T), q)
True
```

scipy.linalg.solve_discrete_lyapunov

Solves the discrete Lyapunov equation $AXA^H - X + Q = 0$.

Parameters
- **a**, **q** : [[M, M] array_like] Square matrices corresponding to $A$ and $Q$ in the equation above respectively. Must have the same shape.
- **method** : [{'direct', 'bilinear'}, optional] Type of solver. If not given, chosen to be `direct` if $M$ is less than 10 and `bilinear` otherwise.

Returns
- **x** : [ndarray] Solution to the discrete Lyapunov equation

See also:
- `solve_continuous_lyapunov`
  computes the solution to the continuous-time Lyapunov equation

Notes
This section describes the available solvers that can be selected by the `method` parameter. The default method is `direct` if $M$ is less than 10 and `bilinear` otherwise.

Method `direct` uses a direct analytical solution to the discrete Lyapunov equation. The algorithm is given in, for example, [1]. However it requires the linear solution of a system with dimension $M^2$ so that performance degrades rapidly for even moderately sized matrices.

Method `bilinear` uses a bilinear transformation to convert the discrete Lyapunov equation to a continuous Lyapunov equation ($BX+XB'= -C$) where $B = (A-I)(A+I)^{-1}$ and $C = 2(A'+I)^{-1}Q(A+I)^{-1}$. The continuous equation can be efficiently solved since it is a special case of a Sylvester equation. The transformation algorithm is from Popov (1964) as described in [2].

New in version 0.11.0.

References
[1], [2]
Examples

Given $a$ and $q$ solve for $x$:

```python
>>> from scipy import linalg
>>> a = np.array([[0.2, 0.5], [0.7, -0.9]])
>>> q = np.eye(2)
>>> x = linalg.solve_discrete_lyapunov(a, q)
>>> x
array([[ 0.70872893, 1.43518822],
        [ 1.43518822, -2.4266315 ]])
>>> np.allclose(a.dot(x).dot(a.T)-x, -q)
True
```

6.9.6 Sketches and Random Projections

```python
clarkson_woodruff_transform(input_matrix, ...)  " Find low-rank matrix approximation via the Clarkson-Woodruff Transform.

scipy.linalg.clarkson_woodruff_transform

scipy.linalg.clarkson_woodruff_transform(input_matrix, sketch_size, seed=None)

" Find low-rank matrix approximation via the Clarkson-Woodruff Transform.

Given an input_matrix $A$ of size ($n$, $d$), compute a matrix $A'$ of size (sketch_size, $d$) which holds:

$$||Ax|| = (1 \pm \epsilon)||A'x||$$

with high probability.

The error is related to the number of rows of the sketch and it is bounded

$$poly(r(\epsilon^{-1}))$$

Parameters

- **input_matrix**: array_like
  Input matrix, of shape ($n$, $d$).
- **sketch_size**: int
  Number of rows for the sketch.
- **seed**
  [None or int or numpy.random.RandomState instance, optional] This parameter defines the RandomState object to use for drawing random variates. If None (or np.random), the global np.random state is used. If integer, it is used to seed the local RandomState instance. Default is None.

Returns

- **A'**
  [array_like] Sketch of the input matrix $A$, of size (sketch_size, $d$).

Notes

This is an implementation of the Clarkson-Woodruff Transform (CountSketch). $A'$ can be computed in principle in $O(nnz(A))$ (with $nnz$ meaning the number of nonzero entries), however we don’t take advantage of sparse matrices in this implementation.

References

[1]
Examples
Given a big dense matrix \( A \):

```python
>>> from scipy import linalg
>>> n_rows, n_columns, sketch_n_rows = (2000, 100, 100)
>>> threshold = 0.1
>>> tmp = np.random.normal(0, 0.1, n_rows*n_columns)
>>> A = np.reshape(tmp, (n_rows, n_columns))
>>> sketch = linalg.clarkson_woodruff_transform(A, sketch_n_rows)
>>> sketch.shape
(100, 100)
>>> normA = linalg.norm(A)
>>> norm_sketch = linalg.norm(sketch)
```

Now with high probability, the condition \( \text{abs}(\text{normA-normSketch}) < \text{threshold} \) holds.

### 6.9.7 Special Matrices

- **block_diag(*arrs)**: Create a block diagonal matrix from provided arrays.
- **circulant(c)**: Construct a circulant matrix.
- **companion(a)**: Create a companion matrix.
- **dft(n[, scale])**: Discrete Fourier transform matrix.
- **hadamard(n[, dtype])**: Construct a Hadamard matrix.
- **hankel(c[, r])**: Construct a Hankel matrix.
- **helmert(n[, full])**: Create a Helmert matrix of order \( n \).
- **hilbert(n)**: Create a Hilbert matrix of order \( n \).
- **invhilbert(n[, exact])**: Compute the inverse of the Hilbert matrix of order \( n \).
- **leslie(f, s)**: Create a Leslie matrix.
- **pascal(n[, kind, exact])**: Returns the \( n \times n \) Pascal matrix.
- **invpascal(n[, kind, exact])**: Returns the inverse of the \( n \times n \) Pascal matrix.
- **toeplitz(c[, r])**: Construct a Toeplitz matrix.
- **tri(N[, M, k, dtype])**: Construct \( (N, M) \) matrix filled with ones at and below the \( k \)-th diagonal.

**scipy.linalg.block_diag**

`scipy.linalg.block_diag(*arrs)`

Create a block diagonal matrix from provided arrays.

Given the inputs \( A, B \) and \( C \), the output will have these arrays arranged on the diagonal:

\[
\begin{bmatrix}
[A, 0, 0],
[0, B, 0],
[0, 0, C]
\end{bmatrix}
\]

**Parameters**

- **A, B, C, ...**
  
  [array_like, up to 2-D] Input arrays. A 1-D array or array_like sequence of length \( n \) is treated as a 2-D array with shape \((1, n)\).

**Returns**

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D  [ndarray] Array with A, B, C, ... on the diagonal. D has the same dtype as A.

Notes
If all the input arrays are square, the output is known as a block diagonal matrix.

Empty sequences (i.e., array-likes of zero size) will not be ignored. Noteworthy, both [] and [[]] are treated as matrices with shape (1,0).

Examples

```python
>>> from scipy.linalg import block_diag
>>> A = [[1, 0],
      ... [0, 1]]
>>> B = [[3, 4, 5],
      ... [6, 7, 8]]
>>> C = [[7]]
>>> P = np.zeros((2, 0), dtype='int32')
>>> block_diag(A, B, C)
array([[1, 0, 0, 0, 0, 0],
       [0, 1, 0, 0, 0, 0],
       [0, 0, 3, 4, 5, 0],
       [0, 0, 6, 7, 8, 0],
       [0, 0, 0, 0, 0, 7]])
>>> block_diag(A, P, B, C)
array([[1, 0, 0, 0, 0, 0],
       [0, 1, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 3, 4, 5, 0],
       [0, 0, 6, 7, 8, 0],
       [0, 0, 0, 0, 0, 7]])
>>> block_diag(1.0, [2, 3], [[4, 5], [6, 7]])
array([[ 1.,  0.,  0.,  0.],
       [ 0.,  2.,  3.,  0.],
       [ 0.,  0.,  4.,  5.],
       [ 0.,  0.,  0.,  6.]])
```

`scipy.linalg.circulant`

`scipy.linalg.circulant(c)`

Construct a circulant matrix.

**Parameters**

- `c`  [(N,) array_like] 1-D array, the first column of the matrix.

**Returns**

- `A`  [(N, N) ndarray] A circulant matrix whose first column is `c`.

**See also:**

`toeplitz`

Toeplitz matrix

`hankel`

Hankel matrix
**solve_circulant**

Solve a circulant system.

**Notes**
New in version 0.8.0.

**Examples**

```python
>>> from scipy.linalg import circulant
>>> circulant([1, 2, 3])
array([[1, 3, 2],
      [2, 1, 3],
      [3, 2, 1]])
```

**scipy.linalg.companion**

**scipy.linalg.companion(a)**

Create a companion matrix.

Create the companion matrix [1] associated with the polynomial whose coefficients are given in a.

**Parameters**

- **a**: [(N,) array_like] 1-D array of polynomial coefficients. The length of a must be at least two, and a[0] must not be zero.

**Returns**

- **c**: [(N-1, N-1) ndarray] The first row of c is \(-a[1:] / a[0]\), and the first sub-diagonal is all ones. The data-type of the array is the same as the data-type of \(1.0 * a[0]\).

**Raises**

ValueError

If any of the following are true: a) a.ndim != 1; b) a.size < 2; c) a[0] == 0.

**Notes**
New in version 0.8.0.

**References**

[1]

**Examples**

```python
>>> from scipy.linalg import companion
>>> companion([1, -10, 31, -30])
array([[ 10., -31.,  30.],
      [  1.,  0.,  0.],
      [  0.,  1.,  0.]])
```

**scipy.linalg.dft**

**scipy.linalg.dft(n, scale=None)**

Discrete Fourier transform matrix.

Create the matrix that computes the discrete Fourier transform of a sequence [1]. The n-th primitive root of unity used to generate the matrix is \(\exp(-2\pi i / n)\), where \(i = \sqrt{-1}\).

**Parameters**

- **n**: [int] Size the matrix to create.
scale  [str, optional] Must be None, ‘sqrtn’, or ‘n’. If scale is ‘sqrtn’, the matrix is divided by sqrt(n). If scale is ‘n’, the matrix is divided by n. If scale is None (the default), the matrix is not normalized, and the return value is simply the Vandermonde matrix of the roots of unity.

Returns

m  [(n, n) ndarray] The DFT matrix.

Notes

When scale is None, multiplying a vector by the matrix returned by dft is mathematically equivalent to (but much less efficient than) the calculation performed by scipy.fftpack.fft.

New in version 0.14.0.

References

[1]

Examples

```python
>>> from scipy.linalg import dft
>>> np.set_printoptions(precision=5, suppress=True)
>>> x = np.array([1, 2, 3, 0, 3, 2, 1, 0])
>>> m = dft(8)
>>> m.dot(x)  # Compute the DFT of x
array([ 12.+0.j, -2.-2.j,  0.-4.j, -2.+2.j,  4.+0.j, -2.-2.j,
       -0.+4.j, -2.+2.j])
```

Verify that m.dot(x) is the same as fft(x).

```python
>>> from scipy.fftpack import fft
>>> fft(x)  # Same result as m.dot(x)
array([ 12.+0.j, -2.-2.j,  0.-4.j, -2.+2.j,  4.+0.j, -2.-2.j,
       -0.+4.j, -2.+2.j])
```

scipy.linalg.hadamard

scipy.linalg.hadamard(n, dtype=class 'int'>)

Construct a Hadamard matrix.

Constructs an n-by-n Hadamard matrix, using Sylvester’s construction. n must be a power of 2.

Parameters

n  [int] The order of the matrix. n must be a power of 2.

dtype [dtype, optional] The data type of the array to be constructed.

Returns

H  [(n, n) ndarray] The Hadamard matrix.

Notes

New in version 0.8.0.

Examples

```python
>>> from scipy.linalg import hadamard
>>> hadamard(2, dtype=complex)
array([[ 1.+0.j,  1.+0.j],
       [ 1.+0.j, -1.-0.j]])
>>> hadamard(4)
array([[ 1,  1,  1,  1],
       [ 1, -1,  1, -1],
       [ 1,  1, -1, -1],
       [ 1, -1, -1,  1]])
```

(continues on next page)
scipy.linalg.hankel

scipy.linalg.hankel(c, r=None)

Construct a Hankel matrix.

The Hankel matrix has constant anti-diagonals, with c as its first column and r as its last row. If r is not given, then r = zeros_like(c) is assumed.

**Parameters**

- **c**: [array_like] First column of the matrix. Whatever the actual shape of c, it will be converted to a 1-D array.
- **r**: [array_like, optional] Last row of the matrix. If None, r = zeros_like(c) is assumed. r[0] is ignored; the last row of the returned matrix is [c[-1], r[1:]]. Whatever the actual shape of r, it will be converted to a 1-D array.

**Returns**

- **A**: [(len(c), len(r)) ndarray] The Hankel matrix. Dtype is the same as (c[0] + r[0]). dtype.

See also:

- toeplitz
- Toeplitz matrix
- circulant
- circulant matrix

**Examples**

```python
>>> from scipy.linalg import hankel

>>> hankel([1, 17, 99])
array([[ 1, 17, 99],
      [17, 99,  0],
      [99,  0,  0]])

>>> hankel([1,2,3,4], [4,7,7,8,9])
array([[ 1,  2,  3,  4,  7],
      [ 2,  3,  4,  7,  7],
      [ 3,  4,  7,  7,  8],
      [ 4,  7,  7,  8,  9]])
```

scipy.linalg.helmert

scipy.linalg.helmert(n, full=False)

Create a Helmert matrix of order n.

This has applications in statistics, compositional or simplicial analysis, and in Aitchison geometry.

**Parameters**

- **n**: [int] The size of the array to create.
**full**  [bool, optional] If True the (n, n) ndarray will be returned. Otherwise the submatrix that does not include the first row will be returned. Default: False.

**Returns**

M  [ndarray] The Helmert matrix. The shape is (n, n) or (n-1, n) depending on the `full` argument.

**Examples**

```python
>>> from scipy.linalg import helmert
>>> helmert(5, full=True)
array([[ 0.4472136 , 0.4472136 , 0.4472136 , 0.4472136 , 0.4472136 ],
       [ 0.70710678, -0.70710678, 0. , 0. , 0. ],
       [ 0.40824829, 0.40824829, -0.81649658, 0. , 0. ],
       [ 0.28867513, 0.28867513, 0.28867513, -0.8660254 , 0. ],
       [ 0.2236068 , 0.2236068 , 0.2236068 , 0.2236068 , -0.89442719]])
```

**scipy.linalg.hilbert**

**scipy.linalg.hilbert(n)**

Create a Hilbert matrix of order $n$.

Returns the $n$ by $n$ array with entries $h[i,j] = 1 / (i + j + 1)$.

**Parameters**

n  [int] The size of the array to create.

**Returns**

h  [(n, n) ndarray] The Hilbert matrix.

**See also:**

invhilbert

Compute the inverse of a Hilbert matrix.

**Notes**

New in version 0.10.0.

**Examples**

```python
>>> from scipy.linalg import hilbert
>>> hilbert(3)
array([[ 1. , 0.5 , 0.33333333],
       [ 0.5 , 0.33333333, 0.25 ],
       [ 0.33333333, 0.25 , 0.2 ]])
```

**scipy.linalg.invhilbert**

**scipy.linalg.invhilbert(n, exact=False)**

Compute the inverse of the Hilbert matrix of order $n$.

The entries in the inverse of a Hilbert matrix are integers. When $n$ is greater than 14, some entries in the inverse exceed the upper limit of 64 bit integers. The `exact` argument provides two options for dealing with these large integers.

**Parameters**

n  [int] The order of the Hilbert matrix.
exact  [bool, optional] If False, the data type of the array that is returned is np.float64, and the array is an approximation of the inverse. If True, the array is the exact integer inverse array. To represent the exact inverse when n > 14, the returned array is an object array of long integers. For n <= 14, the exact inverse is returned as an array with data type np.int64.

Returns

invh  [(n, n) ndarray] The data type of the array is np.float64 if exact is False. If exact is True, the data type is either np.int64 (for n <= 14) or object (for n > 14). In the latter case, the objects in the array will be long integers.

See also:

hilbert

Create a Hilbert matrix.

Notes

New in version 0.10.0.

Examples

```python
>>> from scipy.linalg import invhilbert
>>> invhilbert(4)
array([[ 16., -120.,  240., -140.],
      [-120.,  1200., -2700.,  1680.],
      [ 240., -2700.,  6480., -4200.],
      [-140.,  1680., -4200.,  2800.]])
>>> invhilbert(4, exact=True)
array([[ 16, -120,  240, -140],
      [-120,  1200, -2700,  1680],
      [ 240, -2700,  6480, -4200],
      [-140,  1680, -4200,  2800]], dtype=int64)
>>> invhilbert(16)[7,7]
4.2475099528537378560L
>>> invhilbert(16, exact=True)[7,7]
42475099528537378560L
```

scipy.linalg.leslie

scipy.linalg.leslie(f, s)

Create a Leslie matrix.

Given the length n array of fecundity coefficients \( f \) and the length n-1 array of survival coefficients \( s \), return the associated Leslie matrix.

Parameters

- \( f \)  
  
  [(N,) array_like] The “fecundity” coefficients.

- \( s \)  
  
  [(N-1,) array_like] The “survival” coefficients, has to be 1-D. The length of \( s \) must be one less than the length of \( f \), and it must be at least 1.

Returns

- \( L \)  
  
  [(N, N) ndarray] The array is zero except for the first row, which is \( f \), and the first sub-diagonal, which is \( s \). The data-type of the array will be the data-type of \( f[0]+s[0] \).
Notes
New in version 0.8.0.

The Leslie matrix is used to model discrete-time, age-structured population growth [1] [2]. In a population with \( n \) age classes, two sets of parameters define a Leslie matrix: the \( n \) “fecundity coefficients”, which give the number of offspring per-capita produced by each age class, and the \( n - 1 \) “survival coefficients”, which give the per-capita survival rate of each age class.

References
[1], [2]

Examples
```python
>>> from scipy.linalg import leslie
>>> leslie([[0.1, 2.0, 1.0, 0.1], [0.2, 0.8, 0.7]])
array([[ 0.1, 2. , 1. , 0.1],
       [ 0.2, 0. , 0. , 0. ],
       [ 0. , 0.8, 0. , 0. ],
       [ 0. , 0. , 0.7, 0. ]])
```

scipy.linalg.pascal

scipy.linalg.pascal\((n, \text{kind}='\text{symmetric}', \text{exact}=\text{True})\)

Returns the \( n \times n \) Pascal matrix.

The Pascal matrix is a matrix containing the binomial coefficients as its elements.

Parameters

- \( n \) [int] The size of the matrix to create; that is, the result is an \( n \times n \) matrix.
- \( \text{kind} \) [str, optional] Must be one of ‘symmetric’, ‘lower’, or ‘upper’. Default is ‘symmetric’.
- \( \text{exact} \) [bool, optional] If \( \text{exact} \) is True, the result is either an array of type numpy.uint64 (if \( n < 35 \)) or an object array of Python long integers. If \( \text{exact} \) is False, the coefficients in the matrix are computed using scipy.special.comb with \( \text{exact}=\text{False} \). The result will be a floating point array, and the values in the array will not be the exact coefficients, but this version is much faster than \( \text{exact}=\text{True} \).

Returns

- \( p \) [\((n, n)\) ndarray] The Pascal matrix.

See also:

invpascal

Notes

See https://en.wikipedia.org/wiki/Pascal_matrix for more information about Pascal matrices.

New in version 0.11.0.

Examples
```python
>>> from scipy.linalg import pascal
>>> pascal(4)
array([[1, 1, 1, 1],
       [1, 2, 3, 4],
       [1, 3, 6, 10],
       [1, 4, 10, 20]], dtype=uint64)
>>> pascal(4, \text{kind}='\text{lower}')
array([[1, 0, 0, 0],
       [0, 1, 0, 0],
       [0, 0, 1, 0],
       [0, 0, 0, 1]])
```
.. _invpascal:

.. currentsection:: 6.9. Linear algebra (scipy.linalg)

.. _invpascal:

pascal(50)[1-1] 2547761225898085902730428600L

scipy.linalg.invpascal

scipy.linalg.invpascal(n, kind='symmetric', exact=True)

Returns the inverse of the n x n Pascal matrix.

The Pascal matrix is a matrix containing the binomial coefficients as its elements.

**Parameters**

- **n** [int] The size of the matrix to create; that is, the result is an n x n matrix.
- **kind** [str, optional] Must be one of 'symmetric', 'lower', or 'upper'. Default is 'symmetric'.
- **exact** [bool, optional] If `exact` is True, the result is either an array of type `numpy.int64` (if n <= 35) or an object array of Python integers. If `exact` is False, the coefficients in the matrix are computed using `scipy.special.comb` with `exact=False`. The result will be a floating point array, and for large n, the values in the array will not be the exact coefficients.

**Returns**

- **invp** [(n, n) ndarray] The inverse of the Pascal matrix.

See also:

pascal

Notes

New in version 0.16.0.

References

[1], [2]

Examples

```python
>>> from scipy.linalg import invpascal, pascal
>>> invp = invpascal(5)
>>> invp
array([[  5., -10.,  10., -5.,  1.],
        [-10.,  30., -35., 19., -4.],
        [ 10., -35.,  46., -27.,  6.],
        [ -5.,  19., -27., 17., -4.],
        [  1.,  -4.,   6., -4.,  1.]])
```

```python
>>> p = pascal(5)
>>> p.dot(invp)
array([[ 1.0,  0.0,  0.0,  0.0,  0.0],
        [ 0.0,  1.0,  0.0,  0.0,  0.0],
        [ 0.0,  0.0,  1.0,  0.0,  0.0],
        [ 0.0,  0.0,  0.0,  1.0,  0.0],
        [ 0.0,  0.0,  0.0,  0.0,  1.0]])
```

(continues on next page)
An example of the use of `kind` and `exact`:

```python
>>> invpascal(5, kind='lower', exact=False)
array([[ 1., -0., 0., -0., 0.],
       [-1., 1., -0., 0., -0.],
       [ 1., -2., 1., -0., 0.],
       [-1., 3., -3., 1., -0.],
       [ 1., -4., 6., -4., 1.]])
```

```
scipy.linalg.toeplitz
scipy.linalg.toeplitz(c, r=None)
```

Construct a Toeplitz matrix.

The Toeplitz matrix has constant diagonals, with c as its first column and r as its first row. If r is not given, r == `conjugate(c)` is assumed.

**Parameters**

- **c** [array_like] First column of the matrix. Whatever the actual shape of c, it will be converted to a 1-D array.
- **r** [array_like, optional] First row of the matrix. If None, r = `conjugate(c)` is assumed; in this case, if c[0] is real, the result is a Hermitian matrix. r[0] is ignored; the first row of the returned matrix is [c[0], r[1:]]. Whatever the actual shape of r, it will be converted to a 1-D array.

**Returns**

- **A** [(len(c), len(r)) ndarray] The Toeplitz matrix. Dtype is the same as (c[0] + r[0]).dtype.

See also:

- **circulant**
  - circulant matrix
- **hankel**
  - Hankel matrix
- **solve_toeplitz**
  - Solve a Toeplitz system.

**Notes**

The behavior when c or r is a scalar, or when c is complex and r is None, was changed in version 0.8.0. The behavior in previous versions was undocumented and is no longer supported.

**Examples**

```python
>>> from scipy.linalg import toeplitz
>>> toeplitz([1,2,3], [1,4,5,6])
array([[1, 2, 3, 0, 0],
       [2, 1, 4, 5, 0],
       [3, 2, 1, 4, 0],
       [0, 3, 2, 1, 4],
       [0, 0, 0, 3, 2]])
```
scipy.linalg.toeplitz

scipy.linalg.toeplitz([1.0, 2+3j, 4-1j])
array([[ 1.+0.j,  2.-3.j,  4.+1.j],
       [ 2.+3.j,  1.+0.j,  2.-3.j],
       [ 4.-1.j,  2.+3.j,  1.+0.j]])

scipy.linalg.tri

scipy.linalg.tri(N, M=None, k=0, dtype=None)
Construct (N, M) matrix filled with ones at and below the k-th diagonal.

The matrix has A[i,j] == 1 for i <= j + k

Parameters
N [int] The size of the first dimension of the matrix.
M [int or None, optional] The size of the second dimension of the matrix. If M is None, M = N is assumed.
k [int, optional] Number of subdiagonal below which matrix is filled with ones. k = 0 is the main diagonal, k < 0 subdiagonal and k > 0 superdiagonal.
dtype [dtype, optional] Data type of the matrix.

Returns
tri [(N, M) ndarray] Tri matrix.

Examples
>>> from scipy.linalg import tri
>>> tri(3, 5, 2, dtype=int)
array([[1, 1, 1, 0, 0],
       [1, 1, 1, 1, 0],
       [1, 1, 1, 1, 1]])
>>> tri(3, 5, -1, dtype=int)
array([[0, 0, 0, 0, 0],
       [1, 0, 0, 0, 0],
       [1, 1, 0, 0, 0]])

6.9.8 Low-level routines

get_blas_funcs(names[, arrays, dtype]) Return available BLAS function objects from names.
get_lapack_funcs(names[, arrays, dtype]) Return available LAPACK function objects from names.
find_best_blas_type([arrays, dtype]) Find best-matching BLAS/LAPACK type.

scipy.linalg.get_blas_funcs

scipy.linalg.get_blas_funcs(names, arrays=(), dtype=None)
Return available BLAS function objects from names.

Arrays are used to determine the optimal prefix of BLAS routines.

Parameters
names [str or sequence of str] Name(s) of BLAS functions without type prefix.
arrays [sequence of ndarrays, optional] Arrays can be given to determine optimal prefix of BLAS routines. If not given, double-precision routines will be used, otherwise
the most generic type in arrays will be used.

**dtype**  [str or dtype, optional] Data-type specifier. Not used if `arrays` is non-empty.

**Returns**

- **funcs**  [list] List containing the found function(s).

**Notes**

This routine automatically chooses between Fortran/C interfaces. Fortran code is used whenever possible for arrays with column major order. In all other cases, C code is preferred.

In BLAS, the naming convention is that all functions start with a type prefix, which depends on the type of the principal matrix. These can be one of {'s', 'd', 'c', 'z'} for the numpy types {float32, float64, complex64, complex128} respectively. The code and the dtype are stored in attributes `typecode` and `dtype` of the returned functions.

**Examples**

```python
>>> import scipy.linalg as LA
>>> a = np.random.rand(3,2)
>>> x_gemv = LA.get_blas_funcs('gemv', (a,))
>>> x_gemv.typecode
'd'
>>> x_gemv = LA.get_blas_funcs('gemv', (a*1j,))
>>> x_gemv.typecode
'z'
```

### scipy.linalg.get_lapack_funcs

**scipy.linalg.get_lapack_funcs(names, arrays=(), dtype=None)**

Return available LAPACK function objects from names.

Arrays are used to determine the optimal prefix of LAPACK routines.

**Parameters**

- **names**  [str or sequence of str] Name(s) of LAPACK functions without type prefix.
- **arrays**  [sequence of ndarrays, optional] Arrays can be given to determine optimal prefix of LAPACK routines. If not given, double-precision routines will be used, otherwise the most generic type in arrays will be used.
- **dtype**  [str or dtype, optional] Data-type specifier. Not used if `arrays` is non-empty.

**Returns**

- **funcs**  [list] List containing the found function(s).

**Notes**

This routine automatically chooses between Fortran/C interfaces. Fortran code is used whenever possible for arrays with column major order. In all other cases, C code is preferred.

In LAPACK, the naming convention is that all functions start with a type prefix, which depends on the type of the principal matrix. These can be one of {'s', 'd', 'c', 'z'} for the numpy types {float32, float64, complex64, complex128} respectively, and are stored in attribute `typecode` of the returned functions.

**Examples**

Suppose we would like to use ‘?lange’ routine which computes the selected norm of an array. We pass our array in order to get the correct ‘lange’ flavor.
Several LAPACK routines work best when its internal WORK array has the optimal size (big enough for fast computation and small enough to avoid waste of memory). This size is determined also by a dedicated query to the function which is often wrapped as a standalone function and commonly denoted as ###_lwork. Below is an example for ?sysv.

```python
>>> import scipy.linalg as LA
>>> a = np.random.rand(1000,1000)
>>> b = np.random.rand(1000,1)*1j
>>> # We pick up zsysv and zsysv_lwork due to b array
... xsysv, xlwork = LA.get_lapack_funcs(("sysv", 'sysv_lwork'), (a, b))
>>> opt_lwork, _ = xlwork(a.shape[0])  # returns a complex for 'z' prefix
>>> udut, ipiv, x, info = xsysv(a, b, lwork=int(opt_lwork.real))
```

`sparse.linalg.find_best_blas_type`

`sparse.linalg.find_best_blas_type(arrays=(), dtype=None)`

Find best-matching BLAS/LAPACK type.

Arrays are used to determine the optimal prefix of BLAS routines.

**Parameters**

- **arrays** [sequence of ndarrays, optional] Arrays can be given to determine optimal prefix of BLAS routines. If not given, double-precision routines will be used, otherwise the most generic type in arrays will be used.
- **dtype** [str or dtype, optional] Data-type specifier. Not used if arrays is non-empty.

**Returns**

- **prefix** [str] BLAS/LAPACK prefix character.
- **dtype** [dtype] Inferred Numpy data type.
- **prefer_fortran** [bool] Whether to prefer Fortran order routines over C order.

**Examples**

```python
>>> import scipy.linalg.blas as bla
>>> a = np.random.rand(10,15)
>>> b = np.asfortranarray(a)  # Change the memory layout order
>>> bla.find_best_blas_type((a,))
('d', dtype('float64'), False)
>>> bla.find_best_blas_type((a*1j,))
('z', dtype('complex128'), False)
>>> bla.find_best_blas_type((b,))
('d', dtype('float64'), True)
```

See also:

`sparse.linalg.blas` — Low-level BLAS functions
scipy.linalg.lapack – Low-level LAPACK functions
scipy.linalg.cython_blas – Low-level BLAS functions for Cython
scipy.linalg.cython_lapack – Low-level LAPACK functions for Cython

6.10 Low-level BLAS functions (scipy.linalg.blas)

This module contains low-level functions from the BLAS library.
New in version 0.12.0.

Note: The common overwrite_<> option in many routines, allows the input arrays to be overwritten to avoid extra memory allocation. However this requires the array to satisfy two conditions which are memory order and the data type to match exactly the order and the type expected by the routine.

As an example, if you pass a double precision float array to any S... routine which expects single precision arguments, f2py will create an intermediate array to match the argument types and overwriting will be performed on that intermediate array.

Similarly, if a C-contiguous array is passed, f2py will pass a FORTRAN-contiguous array internally. Please make sure that these details are satisfied. More information can be found in the f2py documentation.

Warning: These functions do little to no error checking. It is possible to cause crashes by mis-using them, so prefer using the higher-level routines in scipy.linalg.

6.10.1 Finding functions

get_blas_funcs(names[, arrays, dtype]) Return available BLAS function objects from names.
find_best_blas_type([arrays, dtype]) Find best-matching BLAS/LAPACK type.

scipy.linalg.blas.get_blas_funcs

scipy.linalg.blas.get_blas_funcs(names, arrays=(), dtype=None)
Return available BLAS function objects from names.

Arrays are used to determine the optimal prefix of BLAS routines.

Parameters

names [str or sequence of str] Name(s) of BLAS functions without type prefix.
arrays [sequence of ndarrays, optional] Arrays can be given to determine optimal prefix of BLAS routines. If not given, double-precision routines will be used, otherwise the most generic type in arrays will be used.
dtype [str or dtype, optional] Data-type specifier. Not used if arrays is non-empty.

Returns

funcs [list] List containing the found function(s).

Notes
This routine automatically chooses between Fortran/C interfaces. Fortran code is used whenever possible for arrays with column major order. In all other cases, C code is preferred.
In BLAS, the naming convention is that all functions start with a type prefix, which depends on the type of the principal matrix. These can be one of \{'s', 'd', 'c', 'z'\} for the numpy types {float32, float64, complex64, complex128} respectively. The code and the dtype are stored in attributes `typecode` and `dtype` of the returned functions.

**Examples**

```python
>>> import scipy.linalg as LA
>>> a = np.random.rand(3,2)
>>> x_gemv = LA.get_blas_funcs('gemv', (a,))
>>> x_gemv.typecode 'd'
>>> x_gemv = LA.get_blas_funcs('gemv', (a*1j,))
>>> x_gemv.typecode 'z'
```

```python
scipy.linalg.blas.find_best_blas_type
```

`scipy.linalg.blas.find_best_blas_type(arrays=(), dtype=None)`  
Find best-matching BLAS/LAPACK type.

Arrays are used to determine the optimal prefix of BLAS routines.

**Parameters**

arrays [sequence of ndarrays, optional] Arrays can be given to determine optimal prefix of BLAS routines. If not given, double-precision routines will be used, otherwise the most generic type in arrays will be used.

dtype [str or dtype, optional] Data-type specifier. Not used if arrays is non-empty.

**Returns**

prefix [str] BLAS/LAPACK prefix character.
dtype [dtype] Inferred Numpy data type.
prefer_fortran [bool] Whether to prefer Fortran order routines over C order.

**Examples**

```python
>>> import scipy.linalg.blas as bla
>>> a = np.random.rand(10,15)
>>> b = np.asfortranarray(a)  # Change the memory layout order
>>> bla.find_best_blas_type((a,))
('d', dtype('float64'), False)
>>> bla.find_best_blas_type((a*1j,))
('z', dtype('complex128'), False)
>>> bla.find_best_blas_type((b,))
('d', dtype('float64'), True)
```

### 6.10.2 BLAS Level 1 functions

- `caxpy(x,y,[n,a,offx,incx,offy,incy])`  
  Wrapper for `caxpy`.
- `ccopy(x,y,[n,offx,incx,offy,incy])`  
  Wrapper for `ccopy`.
- `cdotc(x,y,[n,offx,incx,offy,incy])`  
  Wrapper for `cdotc`.
- `cdotu(x,y,[n,offx,incx,offy,incy])`  
  Wrapper for `cdotu`.
- `crotg(a,b)`  
  Wrapper for `crotg`.
- `cscal(a,x,[n,offx,incx])`  
  Wrapper for `cscal`.

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<td>zswap(x,y,[n,a,offx,incx,offy,incy])</td>
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**scipy.linalg.blas.caxpy**

`scipy.linalg.blas.caxpy(x, y[, n, a, offx, incx, offy, incy]) = <fortran object>`

Wrapper for caxpy.

**Parameters**

- **x** [input rank-1 array(‘F’) with bounds (*)]
- **y** [input rank-1 array(‘F’) with bounds (*)]
Returns

\[ z \quad \text{[rank-1 array('F') with bounds (*) and y storage]} \]

Other Parameters

- \( n \quad \text{[input int, optional] Default: (len(x)-offx)/abs(incx)} \)
- \( a \quad \text{[input complex, optional] Default: (1.0, 0.0)} \)
- \( \text{offx} \quad \text{[input int, optional] Default: 0} \)
- \( \text{incx} \quad \text{[input int, optional] Default: 1} \)
- \( \text{offy} \quad \text{[input int, optional] Default: 0} \)
- \( \text{incy} \quad \text{[input int, optional] Default: 1} \)

**scipy.linalg.blas.ccopy**

\[
\text{scipy.linalg.blas.ccopy}(x, y[, n, offx, incx, offy, incy]) = \text{<fortran object>}
\]

Wrapper for \texttt{ccopy}.

Parameters

- \( x \quad \text{[input rank-1 array('F') with bounds (*)]} \)
- \( y \quad \text{[input rank-1 array('F') with bounds (*)]} \)

Returns

- \( y \quad \text{[rank-1 array('F') with bounds (*)]} \)

Other Parameters

- \( n \quad \text{[input int, optional] Default: (len(x)-offx)/abs(incx)} \)
- \( \text{offx} \quad \text{[input int, optional] Default: 0} \)
- \( \text{incx} \quad \text{[input int, optional] Default: 1} \)
- \( \text{offy} \quad \text{[input int, optional] Default: 0} \)
- \( \text{incy} \quad \text{[input int, optional] Default: 1} \)

**scipy.linalg.blas.ctdotc**

\[
\text{scipy.linalg.blas.ctdotc}(x, y[, n, offx, incx, offy, incy]) = \text{<fortran cdotc>}
\]

Wrapper for \texttt{cdotc}.

Parameters

- \( x \quad \text{[input rank-1 array('F') with bounds (*)]} \)
- \( y \quad \text{[input rank-1 array('F') with bounds (*)]} \)

Returns

- \( xy \quad \text{[complex]} \)

Other Parameters

- \( n \quad \text{[input int, optional] Default: (len(x)-offx)/abs(incx)} \)
- \( \text{offx} \quad \text{[input int, optional] Default: 0} \)
- \( \text{incx} \quad \text{[input int, optional] Default: 1} \)
- \( \text{offy} \quad \text{[input int, optional] Default: 0} \)
- \( \text{incy} \quad \text{[input int, optional] Default: 1} \)
SciPy Reference Guide, Release 1.2.0

scipy.linalg.blas.cdotu

scipy.linalg.blas.cdotu(x, y[, n, offx, incx, offy, incy]) = <fortran cdotu>
Wrapper for cdotu.

Parameters

x        [input rank-1 array('F') with bounds (*)]
y        [input rank-1 array('F') with bounds (*)]

Returns

xy        [complex]

Other Parameters

n        [input int, optional] Default: (len(x)-offx)/abs(incx)
offx        [input int, optional] Default: 0
incx        [input int, optional] Default: 1
offy        [input int, optional] Default: 0
incy        [input int, optional] Default: 1

scipy.linalg.blas.crotg

scipy.linalg.blas.crotg(a, b) = <fortran object>
Wrapper for crotg.

Parameters

a        [input complex]
b        [input complex]

Returns

c        [complex]
s        [complex]

scipy.linalg.blas.cscal

scipy.linalg.blas.cscal(a, x[, n, offx, incx]) = <fortran object>
Wrapper for cscal.

Parameters

a        [input complex]
x        [input rank-1 array('F') with bounds (*)]

Returns

x        [rank-1 array('F') with bounds (*)]

Other Parameters

n        [input int, optional] Default: (len(x)-offx)/abs(incx)
offx        [input int, optional] Default: 0
incx        [input int, optional] Default: 1
scipy.linalg.blas.csrot

scipy.linalg.blas.csrot(x, y, c, s, n, offx, incx, offy, incy, overwrite_x, overwrite_y) = <fortran object>

Wrapper for csrot.

Parameters

- x [input rank-1 array('F') with bounds (*)]
- y [input rank-1 array('F') with bounds (*)]
- c [input float]
- s [input float]

Returns

- x [rank-1 array('F') with bounds (*)]
- y [rank-1 array('F') with bounds (*)]

Other Parameters

- n [input int, optional] Default: (len(x)-1-offx)/abs(incx)+1
- overwrite_x [input int, optional] Default: 0
- offx [input int, optional] Default: 0
- incx [input int, optional] Default: 1
- overwrite_y [input int, optional] Default: 0
- offy [input int, optional] Default: 0
- incy [input int, optional] Default: 1

scipy.linalg.blas.csscal

scipy.linalg.blas.csscal(a, x, n, offx, incx) = <fortran object>

Wrapper for csscal.

Parameters

- a [input float]
- x [input rank-1 array('F') with bounds (*)]

Returns

- x [rank-1 array('F') with bounds (*)]

Other Parameters

- n [input int, optional] Default: (len(x)-offx)/abs(incx)
- overwrite_x [input int, optional] Default: 0
- offx [input int, optional] Default: 0
- incx [input int, optional] Default: 1

scipy.linalg.blas.cswap

scipy.linalg.blas.cswap(x, y, n, offx, incx, offy, incy) = <fortran object>

Wrapper for cswap.

Parameters

- x [input rank-1 array('F') with bounds (*)]
- y [input rank-1 array('F') with bounds (*)]
Returns

\[ x \text{ [rank-1 array('F') with bounds (*)]} \]
\[ y \text{ [rank-1 array('F') with bounds (*)]} \]

Other Parameters

- \( n \) [input int, optional] Default: \( (\text{len}(x)-\text{offx})/\text{abs}(\text{incx}) \)
- \( \text{offx} \) [input int, optional] Default: 0
- \( \text{incx} \) [input int, optional] Default: 1
- \( \text{offy} \) [input int, optional] Default: 0
- \( \text{incy} \) [input int, optional] Default: 1

scipy.linalg.blas.dasum

scipy.linalg.blas.dasum(\( x, n, \text{offx}, \text{incx} \)) = <fortran dasum>
Wrapper for dasum.

Parameters

\( x \) [input rank-1 array('d') with bounds (*)]

Returns

\( s \) [float]

Other Parameters

- \( n \) [input int, optional] Default: \( (\text{len}(x)-\text{offx})/\text{abs}(\text{incx}) \)
- \( \text{offx} \) [input int, optional] Default: 0
- \( \text{incx} \) [input int, optional] Default: 1

scipy.linalg.blas.daxpy

scipy.linalg.blas.daxpy(\( x, y, n, a, \text{offx}, \text{incx}, \text{offy}, \text{incy} \)) = <fortran object>
Wrapper for daxpy.

Parameters

\( x \) [input rank-1 array('d') with bounds (*)]
\( y \) [input rank-1 array('d') with bounds (*)]

Returns

\( z \) [rank-1 array('d') with bounds (*) and y storage]

Other Parameters

- \( n \) [input int, optional] Default: \( (\text{len}(x)-\text{offx})/\text{abs}(\text{incx}) \)
- \( a \) [input float, optional] Default: 1.0
- \( \text{offx} \) [input int, optional] Default: 0
- \( \text{incx} \) [input int, optional] Default: 1
- \( \text{offy} \) [input int, optional] Default: 0
- \( \text{incy} \) [input int, optional] Default: 1
scipy.linalg.blas.dcopy

scipy.linalg.blas.dcopy(x, y[, n, offx, incx, offy, incy]) = <fortran object>
Wrapper for dcopy.

**Parameters**

- **x** [input rank-1 array('d') with bounds (*)]
- **y** [input rank-1 array('d') with bounds (*)]

**Returns**

- **y** [rank-1 array('d') with bounds (*)]

**Other Parameters**

- **n** [input int, optional] Default: (len(x)-offx)/abs(incx)
- **offx** [input int, optional] Default: 0
- **incx** [input int, optional] Default: 1
- **offy** [input int, optional] Default: 0
- **incy** [input int, optional] Default: 1

scipy.linalg.blas.ddot

scipy.linalg.blas.ddot(x, y[, n, offx, incx, offy, incy]) = <fortran ddot>
Wrapper for ddot.

**Parameters**

- **x** [input rank-1 array('d') with bounds (*)]
- **y** [input rank-1 array('d') with bounds (*)]

**Returns**

- **xy** [float]

**Other Parameters**

- **n** [input int, optional] Default: (len(x)-offx)/abs(incx)
- **offx** [input int, optional] Default: 0
- **incx** [input int, optional] Default: 1
- **offy** [input int, optional] Default: 0
- **incy** [input int, optional] Default: 1

scipy.linalg.blas.dnrm2

scipy.linalg.blas.dnrm2(x[, n, offx, incx]) = <fortran dnrm2>
Wrapper for dnrm2.

**Parameters**

- **x** [input rank-1 array('d') with bounds (*)]

**Returns**

- **n2** [float]

**Other Parameters**

- **n** [input int, optional] Default: (len(x)-offx)/abs(incx)
- **offx** [input int, optional] Default: 0
- **incx** [input int, optional] Default: 1
scipy.linalg.blas.drot

```
scipy.linalg.blas.drot(x, y, c, s, n, offx, incx, offy, incy, overwrite_x, overwrite_y) = <fortran object>
```

Wrapper for drot.

**Parameters**

- **x** [input rank-1 array('d') with bounds (*)]
- **y** [input rank-1 array('d') with bounds (*)]
- **c** [input float]
- **s** [input float]

**Returns**

- **x** [rank-1 array('d') with bounds (*)]
- **y** [rank-1 array('d') with bounds (*)]

**Other Parameters**

- **n** [input int, optional] Default: (len(x)-1-offx)/abs(incx)+1
- **overwrite_x** [input int, optional] Default: 0
- **offx** [input int, optional] Default: 0
- **incx** [input int, optional] Default: 1
- **overwrite_y** [input int, optional] Default: 0
- **offy** [input int, optional] Default: 0
- **incy** [input int, optional] Default: 1

scipy.linalg.blas.drotg

```
scipy.linalg.blas.drotg(a, b) = <fortran object>
```

Wrapper for drotg.

**Parameters**

- **a** [input float]
- **b** [input float]

**Returns**

- **c** [float]
- **s** [float]

scipy.linalg.blas.drotm

```
scipy.linalg.blas.drotm(x, y, param, n, offx, incx, offy, incy, overwrite_x, overwrite_y) = <fortran object>
```

Wrapper for drotm.

**Parameters**

- **x** [input rank-1 array('d') with bounds (*)]
- **y** [input rank-1 array('d') with bounds (*)]
- **param** [input rank-1 array('d') with bounds (5)]

**Returns**

- **x** [rank-1 array('d') with bounds (*)]
- **y** [rank-1 array('d') with bounds (*)]
Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
overwrite_x [input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
overwrite_y [input int, optional] Default: 0
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.drotmg

scipy.linalg.blas.drotmg(d1, d2, x1, y1) = <fortran object>
Wrapper for drotmg.

Parameters

d1 [input float]
d2 [input float]
x1 [input float]
y1 [input float]

Returns

param [rank-1 array('d') with bounds (5)]

scipy.linalg.blas.dscal

scipy.linalg.blas.dscal(a, x[, n, offx, incx]) = <fortran object>
Wrapper for dscal.

Parameters

a [input float]
x [input rank-1 array('d') with bounds (*)]

Returns

x [rank-1 array('d') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.dswap

scipy.linalg.blas.dswap(x, y[, n, offx, incx, offy, incy]) = <fortran object>
Wrapper for dswap.

Parameters

x [input rank-1 array('d') with bounds (*)]
y [input rank-1 array('d') with bounds (*)]

Returns

x [rank-1 array('d') with bounds (*)]
y [rank-1 array('d') with bounds (*)]
**Other Parameters**

- **n** [input int, optional] Default: (len(x)-offx)/abs(incx)
- **offx** [input int, optional] Default: 0
- **incx** [input int, optional] Default: 1
- **offy** [input int, optional] Default: 0
- **incy** [input int, optional] Default: 1

```python
c scipy.linalg.blas.dzasum

scipy.linalg.blas.dzasum(x[, n, offx, incx]) = <fortran dzasum>
Wrapper for dzasum.

Parameters
- **x** [input rank-1 array('D') with bounds (*)]

Returns
- **s** [float]

Other Parameters
- **n** [input int, optional] Default: (len(x)-offx)/abs(incx)
- **offx** [input int, optional] Default: 0
- **incx** [input int, optional] Default: 1

```python
c scipy.linalg.blas.dznrm2

scipy.linalg.blas.dznrm2(x[, n, offx, incx]) = <fortran dznrm2>
Wrapper for dznrm2.

Parameters
- **x** [input rank-1 array('D') with bounds (*)]

Returns
- **n2** [float]

Other Parameters
- **n** [input int, optional] Default: (len(x)-offx)/abs(incx)
- **offx** [input int, optional] Default: 0
- **incx** [input int, optional] Default: 1

```python
c scipy.linalg.blas.icamax

scipy.linalg.blas.icamax(x[, n, offx, incx]) = <fortran object>
Wrapper for icamax.

Parameters
- **x** [input rank-1 array('F') with bounds (*)]

Returns
- **k** [int]

Other Parameters
- **n** [input int, optional] Default: (len(x)-offx)/abs(incx)
- **offx** [input int, optional] Default: 0
incx  [input int, optional] Default: 1

scipy.linalg.blas.idamax

scipy.linalg.blas.idamax(x, n, offx, incx) = <fortran object>
Wrapper for idamax.

Parameters
x  [input rank-1 array('d') with bounds (*)]

Returns
k  [int]

Other Parameters
n  [input int, optional] Default: (len(x)-offx)/abs(incx)
offx  [input int, optional] Default: 0
incx  [input int, optional] Default: 1

scipy.linalg.blas.isamax

scipy.linalg.blas.isamax(x, n, offx, incx) = <fortran object>
Wrapper for isamax.

Parameters
x  [input rank-1 array('f') with bounds (*)]

Returns
k  [int]

Other Parameters
n  [input int, optional] Default: (len(x)-offx)/abs(incx)
offx  [input int, optional] Default: 0
incx  [input int, optional] Default: 1

scipy.linalg.blas.izamax

scipy.linalg.blas.izamax(x, n, offx, incx) = <fortran object>
Wrapper for izamax.

Parameters
x  [input rank-1 array('D') with bounds (*)]

Returns
k  [int]

Other Parameters
n  [input int, optional] Default: (len(x)-offx)/abs(incx)
offx  [input int, optional] Default: 0
incx  [input int, optional] Default: 1

6.10. Low-level BLAS functions (scipy.linalg.blas)
scipy.linalg.blas.sasum

scipy.linalg.blas.sasum(x, n, offx, incx) = <fortran sasum>
Wrapper for sasum.

Parameters
x [input rank-1 array('f') with bounds (*)]

Returns
s [float]

Other Parameters
n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.saxpy

scipy.linalg.blas.saxpy(x, y, n, a, offx, incx, offy, incy) = <fortran object>
Wrapper for saxpy.

Parameters
x [input rank-1 array('f') with bounds (*)]
y [input rank-1 array('f') with bounds (*)]

Returns
z [rank-1 array('f') with bounds (*) and y storage]

Other Parameters
n [input int, optional] Default: (len(x)-offx)/abs(incx)
a [input float, optional] Default: 1.0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.scasum

scipy.linalg.blas.scasum(x, n, offx, incx) = <fortran scasum>
Wrapper for scasum.

Parameters
x [input rank-1 array('F') with bounds (*)]

Returns
s [float]

Other Parameters
n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
scipy.linalg.blas.scnrm2

scipy.linalg.blas.scnrm2(x[, n, offx, incx]) = <fortran scnrm2>
Wrapper for scnrm2.

Parameters
x [input rank-1 array('F') with bounds (*)]

Returns
n2 [float]

Other Parameters
n [input int, optional] Default: (len(x)-offx)/abs(incx)
onnx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.scopy

scipy.linalg.blas.scopy(x, y[, n, offx, incx, offy, incy]) = <fortran object>
Wrapper for scopy.

Parameters
x [input rank-1 array('f') with bounds (*)]
y [input rank-1 array('f') with bounds (*)]

Returns
y [rank-1 array('f') with bounds (*)]

Other Parameters
n [input int, optional] Default: (len(x)-offx)/abs(incx)
onnx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.sdot

scipy.linalg.blas.sdot(x, y[, n, offx, incx, offy, incy]) = <fortran sdot>
Wrapper for sdot.

Parameters
x [input rank-1 array('f') with bounds (*)]
y [input rank-1 array('f') with bounds (*)]

Returns
xy [float]

Other Parameters
n [input int, optional] Default: (len(x)-offx)/abs(incx)
onnx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

6.10. Low-level BLAS functions (scipy.linalg.blas)
scipy.linalg.blas.snrm2

scipy.linalg.blas.snrm2(x[, n, offx, incx]) = <fortran snrm2>
Wrapper for snrm2.

Parameters

x [input rank-1 array('f') with bounds (*)]

Returns

n2 [float]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.srot

scipy.linalg.blas.srot(x, y, c[, n, offx, incx, offy, incy, overwrite_x, overwrite_y]) = <fortran object>
Wrapper for srot.

Parameters

x [input rank-1 array('f') with bounds (*)]
y [input rank-1 array('f') with bounds (*)]
c [input float]
s [input float]

Returns

x [rank-1 array('f') with bounds (*)]
y [rank-1 array('f') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-1-offx)/abs(incx)+1
overwrite_x [input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
overwrite_y [input int, optional] Default: 0
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.srotg

scipy.linalg.blas.srotg(a, b) = <fortran object>
Wrapper for srotg.

Parameters

a [input float]
b [input float]

Returns

c [float]
s [float]
scipy.linalg.blas.srotm

```python
scipy.linalg.blas.srotm(x, y, param[, n, offx, incx, offy, incy, overwrite_x, overwrite_y]) = <fortran object>
```

Wrapper for srotm.

**Parameters**

- `x` [input rank-1 array('f') with bounds (*)]
- `y` [input rank-1 array('f') with bounds (*)]
- `param` [input rank-1 array('f') with bounds (5)]

**Returns**

- `x` [rank-1 array('f') with bounds (*)]
- `y` [rank-1 array('f') with bounds (*)]

**Other Parameters**

- `n` [input int, optional] Default: (len(x)-offx)/abs(incx)
- `overwrite_x` [input int, optional] Default: 0
- `offx` [input int, optional] Default: 0
- `incx` [input int, optional] Default: 1
- `overwrite_y` [input int, optional] Default: 0
- `offy` [input int, optional] Default: 0
- `incy` [input int, optional] Default: 1

scipy.linalg.blas.srotmg

```python
scipy.linalg.blas.srotmg(d1, d2, x1, y1) = <fortran object>
```

Wrapper for srotmg.

**Parameters**

- `d1` [input float]
- `d2` [input float]
- `x1` [input float]
- `y1` [input float]

**Returns**

- `param` [rank-1 array('f') with bounds (5)]

scipy.linalg.blas.sscal

```python
scipy.linalg.blas.sscal(a[, x[, n, offx, incx]]) = <fortran object>
```

Wrapper for sscal.

**Parameters**

- `a` [input float]
- `x` [input rank-1 array('f') with bounds (*)]

**Returns**

- `x` [rank-1 array('f') with bounds (*)]

**Other Parameters**

- `n` [input int, optional] Default: (len(x)-offx)/abs(incx)
- `offx` [input int, optional] Default: 0
incx  [input int, optional] Default: 1

scipy.linalg.blas.sswap

scipy.linalg.blas.sswap(x, y[, n, offx, incx, offy, incy]) = <fortran object>
Wrapper for sswap.

Parameters

x   [input rank-1 array('f') with bounds (*)]
y   [input rank-1 array('f') with bounds (*)]

Returns

x   [rank-1 array('f') with bounds (*)]
y   [rank-1 array('f') with bounds (*)]

Other Parameters

n   [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.zaxpy

scipy.linalg.blas.zaxpy(x, y[, n, a, offx, incx, offy, incy]) = <fortran object>
Wrapper for zaxpy.

Parameters

x   [input rank-1 array('D') with bounds (*)]
y   [input rank-1 array('D') with bounds (*)]

Returns

z   [rank-1 array('D') with bounds (*) and y storage]

Other Parameters

n   [input int, optional] Default: (len(x)-offx)/abs(incx)
a   [input complex, optional] Default: (1.0, 0.0)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.zcopy

scipy.linalg.blas.zcopy(x, y[, n, offx, incx, offy, incy]) = <fortran object>
Wrapper for zcopy.

Parameters

x   [input rank-1 array('D') with bounds (*)]
y   [input rank-1 array('D') with bounds (*)]

Returns

y   [rank-1 array('D') with bounds (*)]
**Other Parameters**

- `n` [input int, optional] Default: `(len(x)-offx)/abs(incx)`
- `offx` [input int, optional] Default: 0
- `incx` [input int, optional] Default: 1
- `offy` [input int, optional] Default: 0
- `incy` [input int, optional] Default: 1

```python
scipy.linalg.blas.zdotc
```

```python
scipy.linalg.blas.zdotc(x, y, n, offx, incx, offy, incy) = <fortran zdotc>
```

Wrapper for `zdotc`.

**Parameters**

- `x` [input rank-1 array('D') with bounds (*)]
- `y` [input rank-1 array('D') with bounds (*)]

**Returns**

- `xy` [complex]

**Other Parameters**

- `n` [input int, optional] Default: `(len(x)-offx)/abs(incx)`
- `offx` [input int, optional] Default: 0
- `incx` [input int, optional] Default: 1
- `offy` [input int, optional] Default: 0
- `incy` [input int, optional] Default: 1

```python
scipy.linalg.blas.zdotu
```

```python
scipy.linalg.blas.zdotu(x, y, n, offx, incx, offy, incy) = <fortran zdotu>
```

Wrapper for `zdotu`.

**Parameters**

- `x` [input rank-1 array('D') with bounds (*)]
- `y` [input rank-1 array('D') with bounds (*)]

**Returns**

- `xy` [complex]

**Other Parameters**

- `n` [input int, optional] Default: `(len(x)-offx)/abs(incx)`
- `offx` [input int, optional] Default: 0
- `incx` [input int, optional] Default: 1
- `offy` [input int, optional] Default: 0
- `incy` [input int, optional] Default: 1

```python
scipy.linalg.blas.zdrot
```

```python
scipy.linalg.blas.zdrot(x, y, c, s, n, offx, incx, offy, incy, overwrite_x, overwrite_y) = <fortran object>
```

Wrapper for `zdrot`.

**Parameters**

- `x` [input rank-1 array('D') with bounds (*)]
- `y` [input rank-1 array('D') with bounds (*)]
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\[c, s\] [input float]

Returns

\[x\] [rank-1 array('D') with bounds (*)]
\[y\] [rank-1 array('D') with bounds (*)]

Other Parameters

\[n\] [input int, optional] Default: (len(x)-offx)/abs(incx)+1
\[overwrite_x\] [input int, optional] Default: 0
\[offx\] [input int, optional] Default: 0
\[incx\] [input int, optional] Default: 1
\[overwrite_y\] [input int, optional] Default: 0
\[offy\] [input int, optional] Default: 0
\[incy\] [input int, optional] Default: 1

\texttt{scipy.linalg.blas.zdscal}

\texttt{scipy.linalg.blas.zdscal}(a, x[, n, offx, incx, overwrite_x]) = <fortran object>

Wrapper for \texttt{zdscal}.

Parameters

\[a\] [input float]
\[x\] [input rank-1 array('D') with bounds (*)]

Returns

\[x\] [rank-1 array('D') with bounds (*)]

Other Parameters

\[n\] [input int, optional] Default: (len(x)-offx)/abs(incx)
\[overwrite_x\] [input int, optional] Default: 0
\[offx\] [input int, optional] Default: 0
\[incx\] [input int, optional] Default: 1

\texttt{scipy.linalg.blas.zrotg}

\texttt{scipy.linalg.blas.zrotg}(a, b) = <fortran object>

Wrapper for \texttt{zrotg}.

Parameters

\[a\] [input complex]
\[b\] [input complex]

Returns

\[c\] [complex]
\[s\] [complex]
scipy.linalg.blas.zscal

scipy.linalg.blas.zscal(a, x[, n, offx, incx]) = <fortran object>
Wrapper for zscal.

Parameters

a [input complex]
x [input rank-1 array('D') with bounds (*)]

Returns

x [rank-1 array('D') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.zswap

scipy.linalg.blas.zswap(x, y[, n, offx, incx, offy, incy]) = <fortran object>
Wrapper for zswap.

Parameters

x [input rank-1 array('D') with bounds (*)]
y [input rank-1 array('D') with bounds (*)]

Returns

x [rank-1 array('D') with bounds (*)]
y [rank-1 array('D') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

6.10.3 BLAS Level 2 functions

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<td>Wrapper for zsysyr.</td>
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scipy.linalg.blas.sgbmv

scipy.linalg.blas.sgbmv(m, n, kl, ku, alpha, a, x[, incx, offx, beta, y, incy, offy, trans, overwrite_y]) = <fortran object>

Wrapper for sgbmv.

Parameters
- m [input int]
- n [input int]
- kl [input int]
- ku [input int]
- alpha [input float]
- a [input rank-2 array('f') with bounds (lda,n)]
- x [input rank-1 array('f') with bounds (*)]

Returns
- yout [rank-1 array('f') with bounds (ly) and y storage]

Other Parameters
- incx [input int, optional] Default: 1
- offx [input int, optional] Default: 0
- beta [input float, optional] Default: 0.0
- y [input rank-1 array('f') with bounds (ly)]
- overwrite_y [input int, optional] Default: 0
- incy [input int, optional] Default: 1
- offy [input int, optional] Default: 0
- trans [input int, optional] Default: 0

scipy.linalg.blas.sgemv

scipy.linalg.blas.sgemv(alpha, a, x[, beta, y, offx, incx, offy, incy, trans, overwrite_y]) = <fortran object>

Wrapper for sgemv.

Parameters
- alpha [input float]
- a [input rank-2 array('f') with bounds (m,n)]
- x [input rank-1 array('f') with bounds (*)]

Returns
- y [rank-1 array('f') with bounds (ly)]

Other Parameters
- beta [input float, optional] Default: 0.0
- y [input rank-1 array('f') with bounds (ly)]
- overwrite_y [input int, optional] Default: 0
- offx [input int, optional] Default: 0
- incx [input int, optional] Default: 1
- offy [input int, optional] Default: 0
- incy [input int, optional] Default: 1
- trans [input int, optional] Default: 0
scipy.linalg.blas.sger

scipy.linalg.blas.sger(\(alpha, x, y, incx, incy, a, overwrite_x, overwrite_y, overwrite_a\)) = <fortran object>

Wrapper for \texttt{sger}.

\textbf{Parameters}

\begin{itemize}
  \item \texttt{alpha} \hspace{1em} \text{[input float]}
  \item \texttt{x} \hspace{1em} \text{[input rank-1 array('f') with bounds (m)]}
  \item \texttt{y} \hspace{1em} \text{[input rank-1 array('f') with bounds (n)]}
\end{itemize}

\textbf{Returns}

\texttt{a} \hspace{1em} \text{[rank-2 array('f') with bounds (m,n)]}

\textbf{Other Parameters}

\begin{itemize}
  \item \texttt{overwrite_x} \hspace{1em} \text{[input int, optional] Default: 1}
  \item \texttt{incx} \hspace{1em} \text{[input int, optional] Default: 1}
  \item \texttt{overwrite_y} \hspace{1em} \text{[input int, optional] Default: 1}
  \item \texttt{incy} \hspace{1em} \text{[input int, optional] Default: 1}
  \item \texttt{a} \hspace{1em} \text{[input rank-2 array('f') with bounds (m,n), optional] Default: 0.0}
  \item \texttt{overwrite_a} \hspace{1em} \text{[input int, optional] Default: 0}
\end{itemize}

scipy.linalg.blas.ssbmv

scipy.linalg.blas.ssbmv(\(k, alpha, a, x, incx, offx, beta, y, incy, offy, lower, overwrite_y\)) = <fortran object>

Wrapper for \texttt{ssbmv}.

\textbf{Parameters}

\begin{itemize}
  \item \texttt{k} \hspace{1em} \text{[input int]}
  \item \texttt{alpha} \hspace{1em} \text{[input float]}
  \item \texttt{a} \hspace{1em} \text{[input rank-2 array('f') with bounds (lda,n)]}
  \item \texttt{x} \hspace{1em} \text{[input rank-1 array('f') with bounds (*)]}
\end{itemize}

\textbf{Returns}

\texttt{yout} \hspace{1em} \text{[rank-1 array('f') with bounds (ly) and y storage]}

\textbf{Other Parameters}

\begin{itemize}
  \item \texttt{incx} \hspace{1em} \text{[input int, optional] Default: 1}
  \item \texttt{offx} \hspace{1em} \text{[input int, optional] Default: 0}
  \item \texttt{beta} \hspace{1em} \text{[input float, optional] Default: 0.0}
  \item \texttt{y} \hspace{1em} \text{[input rank-1 array('f') with bounds (ly)]}
  \item \texttt{overwrite_y} \hspace{1em} \text{[input int, optional] Default: 0}
  \item \texttt{incy} \hspace{1em} \text{[input int, optional] Default: 1}
  \item \texttt{offy} \hspace{1em} \text{[input int, optional] Default: 0}
  \item \texttt{lower} \hspace{1em} \text{[input int, optional] Default: 0}
\end{itemize}
scipy.linalg.blas.sspr

scipy.linalg.blas.sspr(n, alpha, x[, incx, offx, lower, overwrite_ap]) = <fortran object>

Wrapper for sspr.

**Parameters**

- **n** [input int]
- **alpha** [input float]
- **x** [input rank-1 array('f') with bounds (*)]
- **ap** [input rank-1 array('f') with bounds (*)]

**Returns**

- **apu** [rank-1 array('f') with bounds (*) and ap storage]

**Other Parameters**

- **incx** [input int, optional] Default: 1
- **offx** [input int, optional] Default: 0
- **overwrite_ap** [input int, optional] Default: 0
- **lower** [input int, optional] Default: 0

scipy.linalg.blas.sspr2

scipy.linalg.blas.sspr2(n, alpha, x, y[, incx, offx, incy, offy, lower, overwrite_ap]) = <fortran object>

Wrapper for sspr2.

**Parameters**

- **n** [input int]
- **alpha** [input float]
- **x** [input rank-1 array('f') with bounds (*)]
- **y** [input rank-1 array('f') with bounds (*)]
- **ap** [input rank-1 array('f') with bounds (*)]

**Returns**

- **apu** [rank-1 array('f') with bounds (*) and ap storage]

**Other Parameters**

- **incx** [input int, optional] Default: 1
- **offx** [input int, optional] Default: 0
- **incy** [input int, optional] Default: 1
- **offy** [input int, optional] Default: 0
- **overwrite_ap** [input int, optional] Default: 0
- **lower** [input int, optional] Default: 0

scipy.linalg.blas.ssymv

scipy.linalg.blas.ssymv(alpha, a[, x], beta, y[, incx, offx, incy, offy, lower, overwrite_y]) = <fortran object>

Wrapper for ssymv.

**Parameters**

- **alpha** [input float]
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a  [input rank-2 array('f') with bounds (n,n)]
x  [input rank-1 array('f') with bounds (*)]

Returns

y  [rank-1 array('f') with bounds (ly)]

Other Parameters

beta  [input float, optional] Default: 0.0
y  [input rank-1 array('f') with bounds (ly)]
overwrite_y  [input int, optional] Default: 0
offx  [input int, optional] Default: 0
incy  [input int, optional] Default: 1
offy  [input int, optional] Default: 0
lower  [input int, optional] Default: 0

scipy.linalg.blas.ssyr

scipy.linalg.blas.ssyr(alpha, x[, lower, incx, offx, n, a, overwrite_a]) = <fortran object>
Wrapper for ssyr.

Parameters

alpha  [input float]
x  [input rank-1 array('f') with bounds (*)]

Returns

a  [rank-2 array('f') with bounds (n,n)]

Other Parameters

lower  [input int, optional] Default: 0
incy  [input int, optional] Default: 1
offx  [input int, optional] Default: 1
n  [input int, optional] Default: (len(x)-1-offx)/abs(incx)+1
a  [input rank-2 array('f') with bounds (n,n)]
overwrite_a  [input int, optional] Default: 0

scipy.linalg.blas.ssyr2

scipy.linalg.blas.ssyr2(alpha, x, y[, lower, incx, offx, incy, offy, n, a, overwrite_a]) = <fortran object>
Wrapper for ssyr2.

Parameters

alpha  [input float]
x  [input rank-1 array('f') with bounds (*)]
y  [input rank-1 array('f') with bounds (*)]

Returns

a  [rank-2 array('f') with bounds (n,n)]

Other Parameters

lower  [input int, optional] Default: 0
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incx  [input int, optional] Default: 1
offx  [input int, optional] Default: 0
incy  [input int, optional] Default: 1
offy  [input int, optional] Default: 0
n    [input int, optional] Default: \[\frac{(\text{len}(x)-1-offx)}{\text{abs}(incx)}+1 \leq \frac{(\text{len}(y)-1-offy)}{\text{abs}(incy)}+1 ?\frac{(\text{len}(x)-1-offx)}{\text{abs}(incx)}+1 :\frac{(\text{len}(y)-1-offy)}{\text{abs}(incy)}+1\]
a    [input rank-2 array('f') with bounds (n,n)]
overwrite_a  [input int, optional] Default: 0

scipy.linalg.blas.stbmv

scipy.linalg.blas.stbmv(k, a, x[incx, offx, lower, trans, diag, overwrite_x]) = <fortran object>

Wrapper for stbmv.

Parameters

k    [input int]
a    [input rank-2 array('f') with bounds (lda,n)]
x    [input rank-1 array('f') with bounds (*)]

Returns

xout  [rank-1 array('f') with bounds (*) and x storage]

Other Parameters

overwrite_x  [input int, optional] Default: 0
incx  [input int, optional] Default: 0
offx  [input int, optional] Default: 1
lower  [input int, optional] Default: 0
trans  [input int, optional] Default: 0
diag  [input int, optional] Default: 0

scipy.linalg.blas.stpsv

scipy.linalg.blas.stpsv(n, ap, x[incx, offx, lower, trans, diag, overwrite_x]) = <fortran object>

Wrapper for stpsv.

Parameters

n    [input int]
ap    [input rank-1 array('f') with bounds (*)]
x    [input rank-1 array('f') with bounds (*)]

Returns

xout  [rank-1 array('f') with bounds (*) and x storage]

Other Parameters

overwrite_x  [input int, optional] Default: 0
incx  [input int, optional] Default: 0
offx  [input int, optional] Default: 1
lower  [input int, optional] Default: 0
trans  [input int, optional] Default: 0

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```python
diag    [input int, optional] Default: 0

scipy.linalg.blas.strmv
scipy.linalg.blas.strmv(a, x[, offx, incx, lower, trans, diag, overwrite_x]) = <fortran object>
Wrapper for strmv.

Parameters
a      [input rank-2 array('f') with bounds (n,n)]
x      [input rank-1 array('f') with bounds (*)]

Returns
x      [rank-1 array('f') with bounds (*)]

Other Parameters
overwrite_x
    [input int, optional] Default: 0
offx   [input int, optional] Default: 0
incx   [input int, optional] Default: 1
lower  [input int, optional] Default: 0
trans  [input int, optional] Default: 0
diag   [input int, optional] Default: 0

scipy.linalg.blas.strsv
scipy.linalg.blas.strsv(a, x[, incx, offx, lower, trans, diag, overwrite_x]) = <fortran object>
Wrapper for strsv.

Parameters
a      [input rank-2 array('f') with bounds (n,n)]
x      [input rank-1 array('f') with bounds (*)]

Returns
xout   [rank-1 array('f') with bounds (*) and x storage]

Other Parameters
overwrite_x
    [input int, optional] Default: 0
incx   [input int, optional] Default: 1
offx   [input int, optional] Default: 0
lower  [input int, optional] Default: 0
trans  [input int, optional] Default: 0
diag   [input int, optional] Default: 0

scipy.linalg.blas.dgbmv
scipy.linalg.blas.dgbmv(m, n, kl, ku, alpha, a, x[, incx, offx, beta, y, incy, offy, trans, overwrite_y]) = <fortran object>
Wrapper for dgbmv.

Parameters
m      [input int]
n      [input int]
kl     [input int]
```

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ku [input int]
alpha [input float]
a [input rank-2 array('d') with bounds (lda,n)]
x [input rank-1 array('d') with bounds (*)]

Returns
yout [rank-1 array('d') with bounds (ly) and y storage]

Other Parameters
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
beta [input float, optional] Default: 0.0
y [input rank-1 array('d') with bounds (ly)]
overwrite_y [input int, optional] Default: 0
incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
trans [input int, optional] Default: 0

scipy.linalg.blas.dgemv

scipy.linalg.blas.dgemv(alpha, a, x[, beta, y, offx, incx, offy, incy, trans, overwrite_y]) =
<fortran object>

Wrapper for dgemv.

Parameters
alpha [input float]
a [input rank-2 array('d') with bounds (m,n)]
x [input rank-1 array('d') with bounds (*)]

Returns
y [rank-1 array('d') with bounds (ly)]

Other Parameters
beta [input float, optional] Default: 0.0
y [input rank-1 array('d') with bounds (ly)]
overwrite_y [input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1
trans [input int, optional] Default: 0

scipy.linalg.blas.dger

scipy.linalg.blas.dger(alpha, x, y[, incx, incy, a, overwrite_x, overwrite_y, overwrite_a]) =
<fortran object>

Wrapper for dger.

Parameters
alpha [input float]
x [input rank-1 array('d') with bounds (m)]
y [input rank-1 array('d') with bounds (n)]
`scipy.linalg.blas.dsbmv`  

Wrapper for `dsbmv`.  

**Parameters**  
- `k` [input int]  
- `alpha` [input float]  
- `a` [input rank-2 array('d') with bounds (lda,n)]  
- `x` [input rank-1 array('d') with bounds (*)]  

**Returns**  
- `yout` [rank-1 array('d') with bounds (ly) and y storage]  

**Other Parameters**  
- `incx` [input int, optional] Default: 1  
- `offx` [input int, optional] Default: 0  
- `beta` [input float, optional] Default: 0.0  
- `y` [input rank-1 array('d') with bounds (ly)]  
- `overwrite_y` [input int, optional] Default: 0  
- `incy` [input int, optional] Default: 1  
- `offy` [input int, optional] Default: 0  
- `lower` [input int, optional] Default: 0  

`scipy.linalg.blas.dspr`  

Wrapper for `dspr`.  

**Parameters**  
- `n` [input int]  
- `alpha` [input float]  
- `x` [input rank-1 array('d') with bounds (*)]  
- `ap` [input rank-1 array('d') with bounds (*)]  

**Returns**  
- `apu` [rank-1 array('d') with bounds (*) and ap storage]  

**Other Parameters**  
- `incx` [input int, optional] Default: 1  
- `offx` [input int, optional] Default: 0  
- `beta` [input float, optional] Default: 0.0  
- `y` [input rank-1 array('d') with bounds (ly)]  
- `overwrite_y` [input int, optional] Default: 0  
- `incy` [input int, optional] Default: 1  
- `offy` [input int, optional] Default: 0  
- `lower` [input int, optional] Default: 0  

**Returns**  
- `a` [rank-2 array('d') with bounds (m,n)]
Other Parameters

- incx [input int, optional] Default: 1
- offx [input int, optional] Default: 0
- overwrite_ap [input int, optional] Default: 0
- lower [input int, optional] Default: 0

scipy.linalg.blas.dspr2

scipy.linalg.blas.dspr2(n, alpha, x, y, ap[, incx, offx, incy, offy, lower, overwrite_ap]) =
<fortran object>

Wrapper for dspr2.

Parameters

- n [input int]
- alpha [input float]
- x [input rank-1 array('d') with bounds (*)]
- y [input rank-1 array('d') with bounds (*)]
- ap [input rank-1 array('d') with bounds (*)]

Returns

- apu [rank-1 array('d') with bounds (*) and ap storage]

Other Parameters

- incx [input int, optional] Default: 1
- offx [input int, optional] Default: 0
- incy [input int, optional] Default: 1
- offy [input int, optional] Default: 0
- overwrite_ap [input int, optional] Default: 0
- lower [input int, optional] Default: 0

scipy.linalg.blas.dsymv

scipy.linalg.blas.dsymv(alpha, a, x[, beta, y, offx, incx, offy, incy, lower, overwrite_y]) =
<fortran object>

Wrapper for dsymv.

Parameters

- alpha [input float]
- a [input rank-2 array('d') with bounds (n,n)]
- x [input rank-1 array('d') with bounds (*)]

Returns

- y [rank-1 array('d') with bounds (ly)]

Other Parameters

- beta [input float, optional] Default: 0.0
- y [input rank-1 array('d') with bounds (ly)]
- overwrite_y [input int, optional] Default: 0
- offx [input int, optional] Default: 0
- incx [input int, optional] Default: 1
- offy [input int, optional] Default: 0
incy  [input int, optional] Default: 1
lower  [input int, optional] Default: 0

scipy.linalg.blas.dsy

scipy.linalg.blas.dsy(alpha, x[, lower, incx, offx, n, a, overwrite_a]) = <fortran object>
Wrapper for dsyr.

Parameters

- alpha  [input float]
- x  [input rank-1 array('d') with bounds (*)]

Returns

- a  [rank-2 array('d') with bounds (n,n)]

Other Parameters

- lower  [input int, optional] Default: 0
- incx  [input int, optional] Default: 1
- offx  [input int, optional] Default: 0
- n  [input int, optional] Default: (len(x)-1-offx)/abs(incx)+1
- a  [input rank-2 array('d') with bounds (n,n)]
- overwrite_a  [input int, optional] Default: 0

scipy.linalg.blas.dsy2

scipy.linalg.blas.dsy2(alpha, x, y[, lower, incx, offx, incy, offy, n, a, overwrite_a]) = <fortran object>
Wrapper for dsyr2.

Parameters

- alpha  [input float]
- x  [input rank-1 array('d') with bounds (*)]
- y  [input rank-1 array('d') with bounds (*)]

Returns

- a  [rank-2 array('d') with bounds (n,n)]

Other Parameters

- lower  [input int, optional] Default: 0
- incx  [input int, optional] Default: 1
- offx  [input int, optional] Default: 0
- incy  [input int, optional] Default: 1
- offy  [input int, optional] Default: 0
- n  [input int, optional] Default: ((len(x)-1-offx)/abs(incx)+1 <=(len(y)-1-offy)/abs(incy)+1 ?(len(x)-1-offx)/abs(incx)+1 :(len(y)-1-offy)/abs(incy)+1)
- a  [input rank-2 array('d') with bounds (n,n)]
- overwrite_a  [input int, optional] Default: 0
scipy.linalg.blas.dtbmv

scipy.linalg.blas.dtbmv(k, a, x[, incx, offx, lower, trans, diag, overwrite_x]) = <fortran object>

Wrapper for dtbmv.

Parameters

k [input int]
a [input rank-2 array('d') with bounds (lda,n)]
x [input rank-1 array('d') with bounds (*)]

Returns

xout [rank-1 array('d') with bounds (*) and x storage]

Other Parameters

overwrite_x [input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.dtpsv

scipy.linalg.blas.dtpsv(n, ap, x[, incx, offx, lower, trans, diag, overwrite_x]) = <fortran object>

Wrapper for dtpsv.

Parameters

n [input int]
ap [input rank-1 array('d') with bounds (*)]
x [input rank-1 array('d') with bounds (*)]

Returns

xout [rank-1 array('d') with bounds (*) and x storage]

Other Parameters

overwrite_x [input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.dtrmv

scipy.linalg.blas.dtrmv(a, x[, offx, incx, lower, trans, diag, overwrite_x]) = <fortran object>

Wrapper for dtrmv.

Parameters

a [input rank-2 array('d') with bounds (n,n)]
x [input rank-1 array('d') with bounds (*)]


**Returns**

x  
(rank-1 array('d') with bounds (*))

**Other Parameters**

overwrite_x  
(input int, optional) Default: 0

offx  
(input int, optional) Default: 0

incx  
(input int, optional) Default: 1

lower  
(input int, optional) Default: 0

trans  
(input int, optional) Default: 0

diag  
(input int, optional) Default: 0

scipy.linalg.blas.dtrsv

scipy.linalg.blas.dtrsv(a, x[, incx, offx, lower, trans, diag, overwrite_x]) = <fortran object>

Wrapper for dtrsv.

**Parameters**

a  
(input rank-2 array('d') with bounds (n,n))

x  
(input rank-1 array('d') with bounds (*))

**Returns**

xout  
(rank-1 array('d') with bounds (*) and x storage)

**Other Parameters**

overwrite_x  
(input int, optional) Default: 0

incx  
(input int, optional) Default: 1

offx  
(input int, optional) Default: 0

lower  
(input int, optional) Default: 0

trans  
(input int, optional) Default: 0

diag  
(input int, optional) Default: 0

scipy.linalg.blas.cgbmv

scipy.linalg.blas.cgbmv(m, n, kl, ku, alpha, a, x[, incx, offx, beta, y, incy, offy, trans, overwrite_y]) = <fortran object>

Wrapper for cgbmv.

**Parameters**

m  
(input int)

n  
(input int)

kl  
(input int)

ku  
(input int)

alpha  
(input complex)

a  
(input rank-2 array('F') with bounds (lda,n))

x  
(input rank-1 array('F') with bounds (*))

**Returns**

yout  
(rank-1 array('F') with bounds (ly) and y storage)

**Other Parameters**

incx  
(input int, optional) Default: 1
offx  [input int, optional] Default: 0
beta  [input complex, optional] Default: (0.0, 0.0)
y  [input rank-1 array(‘F’) with bounds (ly)]
overwrite_y  [input int, optional] Default: 0
incy  [input int, optional] Default: 1
offy  [input int, optional] Default: 0
trans  [input int, optional] Default: 0

scipy.linalg.blas.cgemv

scipy.linalg.blas.cgemv(alpha, a, x[, beta, y, offx, incx, offy, incy, trans, overwrite_y]) =
<fortran object>
Wrapper for cgemv.

Parameters

alpha  [input complex]
a  [input rank-2 array(‘F’) with bounds (m,n)]
x  [input rank-1 array(‘F’) with bounds (*)]

Returns

y  [rank-1 array(‘F’) with bounds (ly)]

Other Parameters

beta  [input complex, optional] Default: (0.0, 0.0)
y  [input rank-1 array(‘F’) with bounds (ly)]
overwrite_y  [input int, optional] Default: 0
offx  [input int, optional] Default: 0
incx  [input int, optional] Default: 1
offy  [input int, optional] Default: 0
incy  [input int, optional] Default: 1
trans  [input int, optional] Default: 0

scipy.linalg.blas.cgerc

scipy.linalg.blas.cgerc(alpha, x, y[, incx, incy, a, overwrite_x, overwrite_y, overwrite_a]) =
<fortran object>
Wrapper for cgerc.

Parameters

alpha  [input complex]
x  [input rank-1 array(‘F’) with bounds (m)]
y  [input rank-1 array(‘F’) with bounds (n)]

Returns

a  [rank-2 array(‘F’) with bounds (m,n)]

Other Parameters

overwrite_x  [input int, optional] Default: 1
incx  [input int, optional] Default: 1
overwrite_y  [input int, optional] Default: 1
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```python
cipy.linalg.blas.cgeru
scipy.linalg.blas.cgeru(alpha, x, y, incx, incy, a, overwrite_x, overwrite_y, overwrite_a)

Wrapper for cgeru.

Parameters
- alpha [input complex]
- x [input rank-1 array('F') with bounds (m)]
- y [input rank-1 array('F') with bounds (n)]

Returns
- a [rank-2 array('F') with bounds (m,n)]

Other Parameters
- overwrite_x [input int, optional] Default: 1
- incx [input int, optional] Default: 1
- overwrite_y [input int, optional] Default: 1
- incy [input int, optional] Default: 1
- a [input rank-2 array('F') with bounds (m,n), optional] Default: (0.0,0.0)
- overwrite_a [input int, optional] Default: 0
```

```python
cipy.linalg.blas.chbmv
scipy.linalg.blas.chbmv(k, alpha, a, x, incx, offx, beta, y, incy, offy, lower, overwrite_y)

Wrapper for chbmv.

Parameters
- k [input int]
- alpha [input complex]
- a [input rank-2 array('F') with bounds (lda,n)]
- x [input rank-1 array('F') with bounds (*)]

Returns
- yout [rank-1 array('F') with bounds (ly) and y storage]

Other Parameters
- incx [input int, optional] Default: 1
- offx [input int, optional] Default: 0
- beta [input complex, optional] Default: (0.0, 0.0)
- y [input rank-1 array('F') with bounds (ly)]
- overwrite_y [input int, optional] Default: 0
- incy [input int, optional] Default: 1
- offy [input int, optional] Default: 0
```
lower [input int, optional] Default: 0

_scipy.linalg.blas._chemv_

scipy.linalg.blas._chemv_(alpha, a, x[, beta, y, offx, incx, offy, incy, lower, overwrite_y]) = <fortran object>

Wrapper for _chemv_.

**Parameters**

- **alpha** [input complex]
- **a** [input rank-2 array(‘F’) with bounds (n,n)]
- **x** [input rank-1 array(‘F’) with bounds (*)]

**Returns**

- **y** [rank-1 array(‘F’) with bounds (ly)]

**Other Parameters**

- **beta** [input complex, optional] Default: (0.0, 0.0)
- **y** [input rank-1 array(‘F’) with bounds (ly)]
- **overwrite_y** [input int, optional] Default: 0
- **offx** [input int, optional] Default: 0
- **incx** [input int, optional] Default: 1
- **offy** [input int, optional] Default: 0
- **incy** [input int, optional] Default: 1
- **lower** [input int, optional] Default: 0

_scipy.linalg.blas._cher_

scipy.linalg.blas._cher_(alpha, x[, lower, incx, offx, n, a, overwrite_a]) = <fortran object>

Wrapper for _cher_.

**Parameters**

- **alpha** [input complex]
- **x** [input rank-1 array(‘F’) with bounds (*)]

**Returns**

- **a** [rank-2 array(‘F’) with bounds (n,n)]

**Other Parameters**

- **lower** [input int, optional] Default: 0
- **incx** [input int, optional] Default: 1
- **offx** [input int, optional] Default: 0
- **n** [input int, optional] Default: (len(x)-1-offx)/abs(incx)+1
- **a** [input rank-2 array(‘F’) with bounds (n,n)]
- **overwrite_a** [input int, optional] Default: 0

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scipy.linalg.blas.cher2

scipy.linalg.blas.cher2(alpha, x, y[, lower, incx, offx, incy, offy, n, a, overwrite_a]) = <fortran object>

Wrapper for cher2.

**Parameters**

- **alpha** [input complex]
- **x** [input rank-1 array(‘F’) with bounds (*)]
- **y** [input rank-1 array(‘F’) with bounds (*)]

**Returns**

- **a** [rank-2 array(‘F’) with bounds (n,n)]

**Other Parameters**

- **lower** [input int, optional] Default: 0
- **incx** [input int, optional] Default: 1
- **offx** [input int, optional] Default: 0
- **incy** [input int, optional] Default: 1
- **offy** [input int, optional] Default: 0
- **n** [input int, optional] Default: ((len(x)-1-offx)/abs(incx)+1 <=(len(y)-1-offy)/abs(incy)+1 ?(len(x)-1-offx)/abs(incx)+1 :(len(y)-1-offy)/abs(incy)+1)
- **a** [input rank-2 array(‘F’) with bounds (n,n)]
- **overwrite_a** [input int, optional] Default: 0

scipy.linalg.blas.chpmv

scipy.linalg.blas.chpmv(n, alpha, ap, x[, incx, offx, beta, y, incy, offy, lower, overwrite_y]) = <fortran object>

Wrapper for chpmv.

**Parameters**

- **n** [input int]
- **alpha** [input complex]
- **ap** [input rank-1 array(‘F’) with bounds (*)]
- **x** [input rank-1 array(‘F’) with bounds (*)]

**Returns**

- **yout** [rank-1 array(‘F’) with bounds (ly) and y storage]

**Other Parameters**

- **incx** [input int, optional] Default: 1
- **offx** [input int, optional] Default: 0
- **beta** [input complex, optional] Default: (0.0, 0.0)
- **y** [input rank-1 array(‘F’) with bounds (ly)]
- **overwrite_y** [input int, optional] Default: 0
- **incy** [input int, optional] Default: 1
- **offy** [input int, optional] Default: 0
- **lower** [input int, optional] Default: 0
scipy.linalg.blas.chpr

```python
scipy.linalg.blas.chpr(n, alpha, x[, incx, offx, lower, overwrite_ap]) = <fortran object>
```

Wrapper for chpr.

**Parameters**

- `n` [input int]
- `alpha` [input float]
- `x` [input rank-1 array('F') with bounds (*)]
- `ap` [input rank-1 array('F') with bounds (*)]

**Returns**

- `apu` [rank-1 array('F') with bounds (*) and ap storage]

**Other Parameters**

- `incx` [input int, optional] Default: 1
- `offx` [input int, optional] Default: 0
- `overwrite_ap` [input int, optional] Default: 0
- `lower` [input int, optional] Default: 0

scipy.linalg.blas.chpr2

```python
scipy.linalg.blas.chpr2(n, alpha, x, y, ap[, incx, offx, incy, offy, lower, overwrite_ap]) = <fortran object>
```

Wrapper for chpr2.

**Parameters**

- `n` [input int]
- `alpha` [input complex]
- `x` [input rank-1 array('F') with bounds (*)]
- `y` [input rank-1 array('F') with bounds (*)]
- `ap` [input rank-1 array('F') with bounds (*)]

**Returns**

- `apu` [rank-1 array('F') with bounds (*) and ap storage]

**Other Parameters**

- `incx` [input int, optional] Default: 1
- `offx` [input int, optional] Default: 0
- `incy` [input int, optional] Default: 1
- `offy` [input int, optional] Default: 0
- `overwrite_ap` [input int, optional] Default: 0
- `lower` [input int, optional] Default: 0

scipy.linalg.blas.ctbmv

```python
scipy.linalg.blas.ctbmv(k, a, x[, incx, offx, lower, trans, diag, overwrite_x]) = <fortran object>
```

Wrapper for ctbmv.

**Parameters**

- `k` [input int]
SciPy Reference Guide, Release 1.2.0

\[ \text{input rank-2 array('F') with bounds (lda,n)} \]
\[ \text{input rank-1 array('F') with bounds (*)} \]

Returns
\[ \text{xout} \]
\[ \text{rank-1 array('F') with bounds (*) and x storage} \]

Other Parameters
- overwrite_x
  \[ \text{input int, optional} \] Default: 0
- incx
  \[ \text{input int, optional} \] Default: 1
- offx
  \[ \text{input int, optional} \] Default: 0
- lower
  \[ \text{input int, optional} \] Default: 0
- trans
  \[ \text{input int, optional} \] Default: 0
- diag
  \[ \text{input int, optional} \] Default: 0

scipy.linalg.blas.ctbsv

scipy.linalg.blas.ctbsv(k, a, x[incx, offx, lower, trans, diag, overwrite_x]) = <fortran object>

Wrapper for ctbsv.

Parameters
- k \[ \text{input int} \]
- a \[ \text{input rank-2 array('F') with bounds (lda,n)} \]
- x \[ \text{input rank-1 array('F') with bounds (*)} \]

Returns
\[ \text{xout} \]
\[ \text{rank-1 array('F') with bounds (*) and x storage} \]

Other Parameters
- overwrite_x
  \[ \text{input int, optional} \] Default: 0
- incx
  \[ \text{input int, optional} \] Default: 1
- offx
  \[ \text{input int, optional} \] Default: 0
- lower
  \[ \text{input int, optional} \] Default: 0
- trans
  \[ \text{input int, optional} \] Default: 0
- diag
  \[ \text{input int, optional} \] Default: 0

scipy.linalg.blas.ctpmv

scipy.linalg.blas.ctpmv(n, ap, x[incx, offx, lower, trans, diag, overwrite_x]) = <fortran object>

Wrapper for ctpmv.

Parameters
- n \[ \text{input int} \]
- ap \[ \text{input rank-1 array('F') with bounds (*)} \]
- x \[ \text{input rank-1 array('F') with bounds (*)} \]

Returns
\[ \text{xout} \]
\[ \text{rank-1 array('F') with bounds (*) and x storage} \]

Other Parameters
overwrite_x
  [input int, optional] Default: 0
incx  [input int, optional] Default: 1
offx  [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
diag  [input int, optional] Default: 0

scipy.linalg.blas.ctpsv

scipy.linalg.blas.ctpsv(n, ap, x[, incx, offx, lower, trans, diag, overwrite_x]) = <fortran object>

Wrapper for ctpsv.

Parameters
  n  [input int]
  ap [input rank-1 array('F') with bounds (*)]
  x  [input rank-1 array('F') with bounds (*)]

Returns
  xout [rank-1 array('F') with bounds (*) and x storage]

Other Parameters
  overwrite_x  [input int, optional] Default: 0
  incx  [input int, optional] Default: 1
  offx  [input int, optional] Default: 0
  lower [input int, optional] Default: 0
  trans [input int, optional] Default: 0
  diag  [input int, optional] Default: 0

scipy.linalg.blas.ctrmv

scipy.linalg.blas.ctrmv(a, x[, offx, incx, lower, trans, diag, overwrite_x]) = <fortran object>

Wrapper for ctrmv.

Parameters
  a  [input rank-2 array('F') with bounds (n,n)]
  x  [input rank-1 array('F') with bounds (*)]

Returns
  x  [rank-1 array('F') with bounds (*)]

Other Parameters
  overwrite_x  [input int, optional] Default: 0
  offx  [input int, optional] Default: 0
  incx  [input int, optional] Default: 1
  lower [input int, optional] Default: 0
  trans [input int, optional] Default: 0
  diag  [input int, optional] Default: 0
scipy.linalg.blas.ctrsv

scipy.linalg.blas.ctrsv(a, x[, inx, offx, lower, trans, diag, overwrite_x]) = <fortran object>

Wrapper for ctrsv.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
x [input rank-1 array('F') with bounds (*)]

Returns

xout [rank-1 array('F') with bounds (*) and x storage]

Other Parameters

overwrite_x [input int, optional] Default: 0
inx [input int, optional] Default: 1
offx [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.csyr

scipy.linalg.blas.csyr(alpha, x[, lower, inx, offx, n, a, overwrite_a]) = <fortran object>

Wrapper for csyr.

Parameters

alpha [input complex]
x [input rank-1 array('F') with bounds (*)]

Returns

a [rank-2 array('F') with bounds (n,n)]

Other Parameters

lower [input int, optional] Default: 0
inx [input int, optional] Default: 1
offx [input int, optional] Default: 0
n [input int, optional] Default: (len(x)-1-offx)/abs(inx)+1
a [input rank-2 array('F') with bounds (n,n)]
overwrite_a [input int, optional] Default: 0

scipy.linalg.blas.zgbmv

scipy.linalg.blas.zgbmv(m, n, kl, ku, alpha, a, x[, inx, offx, beta, y, incy, offy, trans, overwrite_y]) = <fortran object>

Wrapper for zgbmv.

Parameters

m [input int]
n [input int]
kl [input int]
ku [input int]
alpha [input complex]
a  [input rank-2 array('D') with bounds (lda,n)]
x  [input rank-1 array('D') with bounds (*)]

Returns
yout  [rank-1 array('D') with bounds (ly) and y storage]

Other Parameters
incx  [input int, optional] Default: 1
offx [input int, optional] Default: 0
beta [input complex, optional] Default: (0.0, 0.0)
y  [input rank-1 array('D') with bounds (ly)]
overwrite_y [input int, optional] Default: 0
incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
trans [input int, optional] Default: 0

scipy.linalg.blas.zgemv

scipy.linalg.blas.zgemv(alpha, a, x, beta, y, offx, incx, offy, incy, trans, overwrite_y)
<fortran object>
Wrapper for zgemv.

Parameters
alpha [input complex]
a  [input rank-2 array('D') with bounds (m,n)]
x  [input rank-1 array('D') with bounds (*)]

Returns
y  [rank-1 array('D') with bounds (ly)]

Other Parameters
beta [input complex, optional] Default: (0.0, 0.0)
y  [input rank-1 array('D') with bounds (ly)]
overwrite_y [input int, optional] Default: 0
offx [input int, optional] Default: 0
incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
trans [input int, optional] Default: 0

scipy.linalg.blas.zgerc

scipy.linalg.blas.zgerc(alpha, x, y, incx, incy, a, overwrite_x, overwrite_y, overwrite_a)
<fortran object>
Wrapper for zgerc.

Parameters
alpha [input complex]
x  [input rank-1 array('D') with bounds (m)]
y  [input rank-1 array('D') with bounds (n)]

Returns
a  [rank-2 array('D') with bounds (m,n)]

Other Parameters

overwrite_x
  [input int, optional] Default: 1
inx
  [input int, optional] Default: 1
overwrite_y
  [input int, optional] Default: 1
incy
  [input int, optional] Default: 1
a  [input rank-2 array('D') with bounds (m,n), optional] Default: (0.0,0.0)
overwrite_a
  [input int, optional] Default: 0

scipy.linalg.blas.zgeru

scipy.linalg.blas.zgeru(alpha, x, y, [inx, incy, a, overwrite_x, overwrite_y, overwrite_a]) =
<fortran object>

Wrapper for zgeru.

Parameters

alpha  [input complex]
x  [input rank-1 array('D') with bounds (m)]
y  [input rank-1 array('D') with bounds (n)]

Returns

a  [rank-2 array('D') with bounds (m,n)]

Other Parameters

overwrite_x
  [input int, optional] Default: 1
inx
  [input int, optional] Default: 1
overwrite_y
  [input int, optional] Default: 1
incy
  [input int, optional] Default: 1
a  [input rank-2 array('D') with bounds (m,n), optional] Default: (0.0,0.0)
overwrite_a
  [input int, optional] Default: 0

scipy.linalg.blas.zhbmv

scipy.linalg.blas.zhbmv(k, alpha, a, x, [inx, offx, beta, y, incy, offy, lower, overwrite_y]) =
<fortran object>

Wrapper for zhbmv.

Parameters

k  [input int]
alpha  [input complex]
a  [input rank-2 array('D') with bounds (lda,n)]
x  [input rank-1 array('D') with bounds (*)]

Returns

yout  [rank-1 array('D') with bounds (ly) and y storage]

Other Parameters
SciPy Reference Guide, Release 1.2.0

6.10. Low-level BLAS functions (scipy.linalg.blas)

```
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
beta [input complex, optional] Default: (0.0, 0.0)
y [input rank-1 array('D') with bounds (ly)]
overwrite_y [input int, optional] Default: 0
incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.zhemv

scipy.linalg.blas.zhemv(alpha, x[, beta, y, offx, incx, offy, incy, lower, overwrite_y]) = <fortran object>
Wrapper for zhemv.

Parameters
alpha [input complex]
a [input rank-2 array('D') with bounds (n,n)]
x [input rank-1 array('D') with bounds (*)]

Returns
y [rank-1 array('D') with bounds (ly)]

Other Parameters
beta [input complex, optional] Default: (0.0, 0.0)
y [input rank-1 array('D') with bounds (ly)]
overwrite_y [input int, optional] Default: 0
offx [input int, optional] Default: 0
incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.zher

scipy.linalg.blas.zher(alpha, x[, lower, incx, offx, n, a, overwrite_a]) = <fortran object>
Wrapper for zher.

Parameters
alpha [input complex]
x [input rank-1 array('D') with bounds (*)]

Returns
a [rank-2 array('D') with bounds (n,n)]

Other Parameters
lower [input int, optional] Default: 0
incy [input int, optional] Default: 1
offx [input int, optional] Default: 0
n [input int, optional] Default: (len(x)-1-offx)/abs(incx)+1
a [input rank-2 array('D') with bounds (n,n)]
```
overwrite_a
[input int, optional] Default: 0

scipy.linalg.blas.zher2

scipy.linalg.blas.zher2(alpha, x, y[, lower, incx, offx,incy, offy, n, a, overwrite_a]) = <fortran object>
Wrapper for zher2.

Parameters
alpha [input complex]
x [input rank-1 array(‘D’) with bounds (*)]
y [input rank-1 array(‘D’) with bounds (*)]

Returns
a [rank-2 array(‘D’) with bounds (n,n)]

Other Parameters
lower [input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
n [input int, optional] Default: ((len(x)-1-offx)/abs(incx)+1 <=(len(y)-1-offy)/abs(incy)+1 ?(len(x)-1-offx)/abs(incx)+1 (:len(y)-1-offy)/abs(incy)+1)
a [input rank-2 array(‘D’) with bounds (n,n)]
overwrite_a [input int, optional] Default: 0

scipy.linalg.blas.zhpmv

scipy.linalg.blas.zhpmv(n, alpha, ap, x[, incx, offx, beta, incy, offy, lower, overwrite_y]) = <fortran object>
Wrapper for zhpmv.

Parameters
n [input int]
alpha [input complex]
ap [input rank-1 array(‘D’) with bounds (*)]
x [input rank-1 array(‘D’) with bounds (*)]

Returns
yout [rank-1 array(‘D’) with bounds (ly) and y storage]

Other Parameters
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
beta [input complex, optional] Default: (0.0, 0.0)
y [input rank-1 array(‘D’) with bounds (ly)]
overwrite_y [input int, optional] Default: 0
incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
lower [input int, optional] Default: 0
scipy.linalg.blas.zhpr

scipy.linalg.blas.zhpr\( (n, \alpha, x, ap[, \text{incx}, \text{offx}, \text{overwrite}_\text{ap}]) \) = \textit{<fortran object>}

Wrapper for zhpr.

\textbf{Parameters}

- \(n\) [input int]
- \(\alpha\) [input float]
- \(x\) [input rank-1 array('D') with bounds (*)]
- \(ap\) [input rank-1 array('D') with bounds (*)]

\textbf{Returns}

- \(apu\) [rank-1 array('D') with bounds (*) and \(ap\) storage]

\textbf{Other Parameters}

- \(\text{incx}\) [input int, optional] Default: 1
- \(\text{offx}\) [input int, optional] Default: 0
- \(\text{overwrite}_\text{ap}\) [input int, optional] Default: 0
- \(\text{lower}\) [input int, optional] Default: 0

\textbf{scipy.linalg.blas.zhpr2}

scipy.linalg.blas.zhpr2\( (n, \alpha, x, y, ap[, \text{incx}, \text{offx}, \text{incy}, \text{offy}, \text{overwrite}_\text{ap}]) \) = \textit{<fortran object>}

Wrapper for zhpr2.

\textbf{Parameters}

- \(n\) [input int]
- \(\alpha\) [input complex]
- \(x\) [input rank-1 array('D') with bounds (*)]
- \(y\) [input rank-1 array('D') with bounds (*)]
- \(ap\) [input rank-1 array('D') with bounds (*)]

\textbf{Returns}

- \(apu\) [rank-1 array('D') with bounds (*) and \(ap\) storage]

\textbf{Other Parameters}

- \(\text{incx}\) [input int, optional] Default: 1
- \(\text{offx}\) [input int, optional] Default: 0
- \(\text{incy}\) [input int, optional] Default: 1
- \(\text{offy}\) [input int, optional] Default: 0
- \(\text{overwrite}_\text{ap}\) [input int, optional] Default: 0
- \(\text{lower}\) [input int, optional] Default: 0

\textbf{scipy.linalg.blas.ztbmv}

scipy.linalg.blas.ztbmv\( (k, \ a, x[, \text{incx}, \text{offx}, \text{lower}, \text{trans}, \text{diag}, \text{overwrite}_x]) \) = \textit{<fortran object>}

Wrapper for ztbmv.

\textbf{Parameters}

- \(k\) [input int]
a [input rank-2 array('D') with bounds (lda,n)]
x [input rank-1 array('D') with bounds (*)]

Returns
xout [rank-1 array('D') with bounds (*) and x storage]

Other Parameters
overwrite_x [input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.ztbsv

scipy.linalg.blas.ztbsv(k, a, x[, incx, offx, lower, trans, diag, overwrite_x]) = <fortran object>
Wrapper for ztbsv.

Parameters
k [input int]
a [input rank-2 array('D') with bounds (lda,n)]
x [input rank-1 array('D') with bounds (*)]

Returns
xout [rank-1 array('D') with bounds (*) and x storage]

Other Parameters
overwrite_x [input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.ztpmv

scipy.linalg.blas.ztpmv(n, ap, x[, incx, offx, lower, trans, diag, overwrite_x]) = <fortran object>
Wrapper for ztpmv.

Parameters
n [input int]
ap [input rank-1 array('D') with bounds (*)]
x [input rank-1 array('D') with bounds (*)]

Returns
xout [rank-1 array('D') with bounds (*) and x storage]

Other Parameters
overwrite_x
[ input int, optional] Default: 0

incx
[ input int, optional] Default: 1

offx
[ input int, optional] Default: 0

lower
[ input int, optional] Default: 0

trans
[ input int, optional] Default: 0

diag
[ input int, optional] Default: 0

scipy.linalg.blas.ztrmv

scipy.linalg.blas.ztrmv(a, x[, offx, incx, lower, trans, diag, overwrite_x]) = <fortran object>
Wrapper for ztrmv.

Parameters

a
[ input rank-2 array('D') with bounds (n,n)]

x
[ input rank-1 array('D') with bounds (*)]

Returns

x
[ rank-1 array('D') with bounds (*)]

Other Parameters

overwrite_x
[ input int, optional] Default: 0

offx
[ input int, optional] Default: 0

incx
[ input int, optional] Default: 1

lower
[ input int, optional] Default: 0

trans
[ input int, optional] Default: 0

diag
[ input int, optional] Default: 0

scipy.linalg.blas.ztrsv

scipy.linalg.blas.ztrsv(a, x[, incx, offx, lower, trans, diag, overwrite_x]) = <fortran object>
Wrapper for ztrsv.

Parameters

a
[ input rank-2 array('D') with bounds (n,n)]

x
[ input rank-1 array('D') with bounds (*)]

Returns

xout
[ rank-1 array('D') with bounds (*) and x storage]

Other Parameters

overwrite_x
[ input int, optional] Default: 0

incx
[ input int, optional] Default: 1

offx
[ input int, optional] Default: 0

lower
[ input int, optional] Default: 0

trans
[ input int, optional] Default: 0

diag
[ input int, optional] Default: 0
scipy.linalg.blas.zsyr

Wrapper for zsyr.

Parameters

- **alpha** [input complex]
- **x** [input rank-1 array('D') with bounds (*)]

Returns

- **a** [rank-2 array('D') with bounds (n,n)]

Other Parameters

- **lower** [input int, optional] Default: 0
- **incx** [input int, optional] Default: 1
- **offx** [input int, optional] Default: 0
- **n** [input int, optional] Default: (len(x)-1-offx)/abs(incx)+1
- **a** [input rank-2 array('D') with bounds (n,n)]
- **overwrite_a** [input int, optional] Default: 0

6.10.4 BLAS Level 3 functions

- **sgemm(...)** Wrapper for sgemm.
- **ssyr2k(...)** Wrapper for ssyr2k.
- **ssyrk(...)** Wrapper for ssyrk.
- **strmm(...)** Wrapper for strmm.
- **dsymv(...)** Wrapper for dsymv.
- **dsyrk(...)** Wrapper for dsyrk.
- **dsyr2k(...)** Wrapper for dsyr2k.
- **dtrmm(...)** Wrapper for dtrmm.
- **ctemm(...)** Wrapper for ctemm.
- **cherk(...)** Wrapper for cherk.
- **cher2k(...)** Wrapper for cher2k.
- **csyrk(...)** Wrapper for csyrk.
- **ctrmm(...)** Wrapper for ctrmm.
- **zgemm(...)** Wrapper for zgemm.
- **zher2k(...)** Wrapper for zher2k.
- **zhemm(...)** Wrapper for zhemm.
### Table 91 – continued from previous page

```
ztrmm(...)  Wrapper for ztrmm.
ztrsm(...)  Wrapper for ztrsm.
```

---

**scipy.linalg.blas.sgemm**

```python
scipy.linalg.blas.sgemm(alpha, a, b[, beta, c, trans_a, trans_b, overwrite_c]) = <fortran object>
```

Wrapper for `sgemm`.

**Parameters**

- **alpha**
  - [input float]
- **a**
  - [input rank-2 array('f') with bounds (lda,ka)]
- **b**
  - [input rank-2 array('f') with bounds (ldb,kb)]

**Returns**

- **c**
  - [rank-2 array('f') with bounds (m,n)]

**Other Parameters**

- **beta**
  - [input float, optional] Default: 0.0
- **c**
  - [input rank-2 array('f') with bounds (m,n)]
- **overwrite_c**
  - [input int, optional] Default: 0
- **trans_a**
  - [input int, optional] Default: 0
- **trans_b**
  - [input int, optional] Default: 0

---

**scipy.linalg.blas.ssymm**

```python
scipy.linalg.blas.ssymm(alpha, a, b[, beta, c, side, lower, overwrite_c]) = <fortran object>
```

Wrapper for `ssymm`.

**Parameters**

- **alpha**
  - [input float]
- **a**
  - [input rank-2 array('f') with bounds (lda,ka)]
- **b**
  - [input rank-2 array('f') with bounds (ldb,kb)]

**Returns**

- **c**
  - [rank-2 array('f') with bounds (m,n)]

**Other Parameters**

- **beta**
  - [input float, optional] Default: 0.0
- **c**
  - [input rank-2 array('f') with bounds (m,n)]
- **overwrite_c**
  - [input int, optional] Default: 0
- **side**
  - [input int, optional] Default: 0
- **lower**
  - [input int, optional] Default: 0

---

**scipy.linalg.blas.ssyr2k**

```python
scipy.linalg.blas.ssyr2k(alpha, a, b[, beta, c, trans, lower, overwrite_c]) = <fortran object>
```

Wrapper for `ssyr2k`.

**Parameters**

- **alpha**
  - [input float]

a [input rank-2 array('f') with bounds (lda,ka)]
b [input rank-2 array('f') with bounds (ldb,kb)]

Returns
c [rank-2 array('f') with bounds (n,n)]

Other Parameters
beta [input float, optional] Default: 0.0
c [input rank-2 array('f') with bounds (n,n)]
overwrite_c [input int, optional] Default: 0
trans [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.ssyrk

scipy.linalg.blas.ssyrk(alpha, a[, beta, c, trans, lower, overwrite_c]) = <fortran object>
Wrapper for ssyrk.

Parameters
alpha [input float]
a [input rank-2 array('f') with bounds (lda,ka)]

Returns
c [rank-2 array('f') with bounds (n,n)]

Other Parameters
beta [input float, optional] Default: 0.0
c [input rank-2 array('f') with bounds (n,n)]
overwrite_c [input int, optional] Default: 0
trans [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.strmm

scipy.linalg.blas.strmm(alpha, a, b[, side, lower, trans_a, diag, overwrite_b]) = <fortran object>
Wrapper for strmm.

Parameters
alpha [input float]
a [input rank-2 array('f') with bounds (lda,k)]
b [input rank-2 array('f') with bounds (ldb,n)]

Returns
b [rank-2 array('f') with bounds (ldb,n)]

Other Parameters
overwrite_b [input int, optional] Default: 0
side [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans_a [input int, optional] Default: 0
diag  [input int, optional] Default: 0

**scipy.linalg.blas.strsm**

```python
scipy.linalg.blas.strsm(alpha, a, b[, side, lower, trans_a, diag, overwrite_b]) = <fortran object>
```

Wrapper for strsm.

**Parameters**

- **alpha**  [input float]
- **a**  [input rank-2 array('f') with bounds (lda,*)]
- **b**  [input rank-2 array('f') with bounds (ldb,n)]

**Returns**

- **x**  [rank-2 array('f') with bounds (ldb,n) and b storage]

**Other Parameters**

- **overwrite_b**  [input int, optional] Default: 0
- **side**  [input int, optional] Default: 0
- **lower**  [input int, optional] Default: 0
- **trans_a**  [input int, optional] Default: 0
- **diag**  [input int, optional] Default: 0

**scipy.linalg.blas.dgemm**

```python
scipy.linalg.blas.dgemm(alpha, a, b[, beta, c, trans_a, trans_b, overwrite_c]) = <fortran object>
```

Wrapper for dgemm.

**Parameters**

- **alpha**  [input float]
- **a**  [input rank-2 array('d') with bounds (lda,ka)]
- **b**  [input rank-2 array('d') with bounds (ldb,kb)]

**Returns**

- **c**  [rank-2 array('d') with bounds (m,n)]

**Other Parameters**

- **beta**  [input float, optional] Default: 0.0
- **c**  [input rank-2 array('d') with bounds (m,n)]
- **overwrite_c**  [input int, optional] Default: 0
- **trans_a**  [input int, optional] Default: 0
- **trans_b**  [input int, optional] Default: 0

**scipy.linalg.blas.dsymm**

```python
scipy.linalg.blas.dsymm(alpha, a, b[, beta, c, side, lower, overwrite_c]) = <fortran object>
```

Wrapper for dsymm.

**Parameters**

- **alpha**  [input float]
- **a**  [input rank-2 array('d') with bounds (lda,ka)]

6.10. Low-level BLAS functions (scipy.linalg.blas)
b  [input rank-2 array('d') with bounds (ldb,kb)]

Returns

c  [rank-2 array('d') with bounds (m,n)]

Other Parameters

beta  [input float, optional] Default: 0.0

c  [input rank-2 array('d') with bounds (m,n)]

overwrite_c  [input int, optional] Default: 0

side  [input int, optional] Default: 0

lower  [input int, optional] Default: 0

scipy.linalg.blas.dsyr2k

scipy.linalg.blas.dsyr2k(alpha, a, b, beta, c, trans, lower, overwrite_c) = <fortran object>
Wrapper for dsyr2k.

Parameters

alpha  [input float]
a  [input rank-2 array('d') with bounds (lda,ka)]
b  [input rank-2 array('d') with bounds (ldb,kb)]

Returns

c  [rank-2 array('d') with bounds (n,n)]

Other Parameters

beta  [input float, optional] Default: 0.0

c  [input rank-2 array('d') with bounds (n,n)]

overwrite_c  [input int, optional] Default: 0

trans  [input int, optional] Default: 0

lower  [input int, optional] Default: 0

scipy.linalg.blas.dsyrk

scipy.linalg.blas.dsyrk(alpha, a, beta, c, trans, lower, overwrite_c) = <fortran object>
Wrapper for dsyrk.

Parameters

alpha  [input float]
a  [input rank-2 array('d') with bounds (lda,ka)]

Returns

c  [rank-2 array('d') with bounds (n,n)]

Other Parameters

beta  [input float, optional] Default: 0.0

c  [input rank-2 array('d') with bounds (n,n)]

overwrite_c  [input int, optional] Default: 0

trans  [input int, optional] Default: 0

lower  [input int, optional] Default: 0
SciPy Reference Guide, Release 1.2.0

scipy.linalg.blas.dtrmm

scipy.linalg.blas.dtrmm(alpha, a[, side, lower, trans_a, diag, overwrite_b]) = <fortran object>

Wrapper for dtrmm.

Parameters

- alpha [input float]
- a [input rank-2 array('d') with bounds (lda,k)]
- b [input rank-2 array('d') with bounds (ldb,n)]

Returns

- b [rank-2 array('d') with bounds (ldb,n)]

Other Parameters

- overwrite_b [input int, optional] Default: 0
- side [input int, optional] Default: 0
- lower [input int, optional] Default: 0
- trans_a [input int, optional] Default: 0
- diag [input int, optional] Default: 0

scipy.linalg.blas.dtrsm

scipy.linalg.blas.dtrsm(alpha, a[, side, lower, trans_a, diag, overwrite_b]) = <fortran object>

Wrapper for dtrsm.

Parameters

- alpha [input float]
- a [input rank-2 array('d') with bounds (lda,*)]
- b [input rank-2 array('d') with bounds (ldb,n)]

Returns

- x [rank-2 array('d') with bounds (ldb,n) and b storage]

Other Parameters

- overwrite_b [input int, optional] Default: 0
- side [input int, optional] Default: 0
- lower [input int, optional] Default: 0
- trans_a [input int, optional] Default: 0
- diag [input int, optional] Default: 0

scipy.linalg.blas.cgemm

scipy.linalg.blas.cgemm(alpha, a[, beta, c, trans_a, trans_b, overwrite_c]) = <fortran object>

Wrapper for cgemm.

Parameters

- alpha [input complex]
- a [input rank-2 array('F') with bounds (lda,ka)]
- b [input rank-2 array('F') with bounds (ldb,kb)]
Returns

\[ c \ \text{[rank-2 array('F') with bounds (m,n)]} \]

Other Parameters

\[ \text{beta} \ \text{[input complex, optional] Default: (0.0, 0.0)} \]
\[ \text{c} \ \text{[input rank-2 array('F') with bounds (m,n)]} \]
\[ \text{overwrite}_\text{c} \ \text{[input int, optional] Default: 0} \]
\[ \text{trans}_\text{a} \ \text{[input int, optional] Default: 0} \]
\[ \text{trans}_\text{b} \ \text{[input int, optional] Default: 0} \]

scipy.linalg.blas.chemm

\[
\text{scipy.linalg.blas.chemm}(\alpha, a, b[, \beta, c, \text{side}, \text{lower}, \text{overwrite}_\text{c}]) = <\text{fortran object}>
\]
Wrapper for \text{chemm}.

Parameters

\[ \alpha \ \text{[input complex]} \]
\[ a \ \text{[input rank-2 array('F') with bounds (lda,ka)]} \]
\[ b \ \text{[input rank-2 array('F') with bounds (ldb,kb)]} \]

Returns

\[ c \ \text{[rank-2 array('F') with bounds (m,n)]} \]

Other Parameters

\[ \beta \ \text{[input complex, optional] Default: (0.0, 0.0)} \]
\[ c \ \text{[input rank-2 array('F') with bounds (m,n)]} \]
\[ \text{overwrite}_\text{c} \ \text{[input int, optional] Default: 0} \]
\[ \text{side} \ \text{[input int, optional] Default: 0} \]
\[ \text{lower} \ \text{[input int, optional] Default: 0} \]

scipy.linalg.blas.cher2k

\[
\text{scipy.linalg.blas.cher2k}(\alpha, a, b[, \beta, c, \text{trans}, \text{lower}, \text{overwrite}_\text{c}]) = <\text{fortran object}>
\]
Wrapper for \text{cher2k}.

Parameters

\[ \alpha \ \text{[input complex]} \]
\[ a \ \text{[input rank-2 array('F') with bounds (lda,ka)]} \]
\[ b \ \text{[input rank-2 array('F') with bounds (ldb,kb)]} \]

Returns

\[ c \ \text{[rank-2 array('F') with bounds (n,n)]} \]

Other Parameters

\[ \beta \ \text{[input complex, optional] Default: (0.0, 0.0)} \]
\[ c \ \text{[input rank-2 array('F') with bounds (n,n)]} \]
\[ \text{overwrite}_\text{c} \ \text{[input int, optional] Default: 0} \]
\[ \text{trans} \ \text{[input int, optional] Default: 0} \]
\[ \text{lower} \ \text{[input int, optional] Default: 0} \]
scipy.linalg.blas.cherk

scipy.linalg.blas.cherk(alpha, a, beta, c, trans, lower, overwrite_c) = <fortran object>
Wrapper for cherk.

Parameters

alpha [input complex]
a [input rank-2 array('F') with bounds (lda,ka)]

Returns
c [rank-2 array('F') with bounds (n,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('F') with bounds (n,n)]
overwrite_c [input int, optional] Default: 0
trans [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.csymmm

scipy.linalg.blas.csymmm(alpha, a, b, beta, c, side, lower, overwrite_c) = <fortran object>
Wrapper for csymmm.

Parameters

alpha [input complex]
a [input rank-2 array('F') with bounds (lda,ka)]
b [input rank-2 array('F') with bounds (ldb,kb)]

Returns
c [rank-2 array('F') with bounds (m,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('F') with bounds (m,n)]
overwrite_c [input int, optional] Default: 0
side [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.csyr2k

scipy.linalg.blas.csyr2k(alpha, a, b, beta, c, trans, lower, overwrite_c) = <fortran object>
Wrapper for csyr2k.

Parameters

alpha [input complex]
a [input rank-2 array('F') with bounds (lda,ka)]
b [input rank-2 array('F') with bounds (ldb,kb)]

Returns
c [rank-2 array('F') with bounds (n,n)]

Other Parameters
SciPy Reference Guide, Release 1.2.0

```
scipy.linalg.blas.csyrk

scipy.linalg.blas.csyrk(alpha, a[, beta, c, trans, lower, overwrite_c]) = <fortran object>
Wrapper for csyrk.

Parameters

alpha [input complex]
a [input rank-2 array('F') with bounds (lda,ka)]

Returns
c [rank-2 array('F') with bounds (n,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('F') with bounds (n,n)]
overwrite_c [input int, optional] Default: 0
trans [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.ctrm

scipy.linalg.blas.ctrm(alpha, a, b[, side, lower, trans_a, diag, overwrite_b]) = <fortran object>
Wrapper for ctrmm.

Parameters

alpha [input complex]
a [input rank-2 array('F') with bounds (lda,k)]
b [input rank-2 array('F') with bounds (ldb,n)]

Returns
b [rank-2 array('F') with bounds (ldb,n)]

Other Parameters

overwrite_b [input int, optional] Default: 0
side [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans_a [input int, optional] Default: 0
diag [input int, optional] Default: 0
```
**scipy.linalg.blas.ctrsm**

```python
scipy.linalg.blas.ctrsm(alpha, a, b[, side, lower, trans_a, diag, overwrite_b]) = <fortran object>
```

Wrapper for ctrsm.

**Parameters**

- **alpha**  [input complex]
- **a**  [input rank-2 array('F') with bounds (lda,*)]
- **b**  [input rank-2 array('F') with bounds (ldb,n)]

**Returns**

- **x**  [rank-2 array('F') with bounds (ldb,n) and b storage]

**Other Parameters**

- **overwrite_b**  [input int, optional] Default: 0
- **side**  [input int, optional] Default: 0
- **lower**  [input int, optional] Default: 0
- **trans_a**  [input int, optional] Default: 0
- **diag**  [input int, optional] Default: 0

---

**scipy.linalg.blas.zgemm**

```python
scipy.linalg.blas.zgemm(alpha, a, b[, beta, c, trans_a, trans_b, overwrite_c]) = <fortran object>
```

Wrapper for zgemm.

**Parameters**

- **alpha**  [input complex]
- **a**  [input rank-2 array('D') with bounds (lda,ka)]
- **b**  [input rank-2 array('D') with bounds (ldb,kb)]

**Returns**

- **c**  [rank-2 array('D') with bounds (m,n)]

**Other Parameters**

- **beta**  [input complex, optional] Default: (0.0, 0.0)
- **c**  [input rank-2 array('D') with bounds (m,n)]
- **overwrite_c**  [input int, optional] Default: 0
- **trans_a**  [input int, optional] Default: 0
- **trans_b**  [input int, optional] Default: 0

---

**scipy.linalg.blas.zhemm**

```python
scipy.linalg.blas.zhemm(alpha, a, b[, beta, c, side, lower, overwrite_c]) = <fortran object>
```

Wrapper for zhemm.

**Parameters**

- **alpha**  [input complex]
- **a**  [input rank-2 array('D') with bounds (lda,ka)]
- **b**  [input rank-2 array('D') with bounds (ldb,kb)]

**Returns**
\[ \text{c} \quad \text{[rank-2 array('D') with bounds (m,n)]} \]

Other Parameters

- **beta** [input complex, optional] Default: (0.0, 0.0)
- **c** [input rank-2 array('D') with bounds (m,n)]
- **overwrite_c** [input int, optional] Default: 0
- **side** [input int, optional] Default: 0
- **lower** [input int, optional] Default: 0

`scipy.linalg.blas.zher2k`

`scipy.linalg.blas.zher2k(alpha, a, b[, beta, c, trans, lower, overwrite_c]) = <fortran object>`

Wrapper for `zher2k`.

Parameters

- **alpha** [input complex]
- **a** [input rank-2 array('D') with bounds (lda,ka)]
- **b** [input rank-2 array('D') with bounds (ldb,kb)]

Returns

- **c** [rank-2 array('D') with bounds (n,n)]

Other Parameters

- **beta** [input complex, optional] Default: (0.0, 0.0)
- **c** [input rank-2 array('D') with bounds (n,n)]
- **overwrite_c** [input int, optional] Default: 0
- **trans** [input int, optional] Default: 0
- **lower** [input int, optional] Default: 0

`scipy.linalg.blas.zherk`

`scipy.linalg.blas.zherk(alpha, a[, beta, c, trans, lower, overwrite_c]) = <fortran object>`

Wrapper for `zherk`.

Parameters

- **alpha** [input complex]
- **a** [input rank-2 array('D') with bounds (lda,ka)]

Returns

- **c** [rank-2 array('D') with bounds (n,n)]

Other Parameters

- **beta** [input complex, optional] Default: (0.0, 0.0)
- **c** [input rank-2 array('D') with bounds (n,n)]
- **overwrite_c** [input int, optional] Default: 0
- **trans** [input int, optional] Default: 0
- **lower** [input int, optional] Default: 0
scipy.linalg.blas.zsymm

Wrapper for zsymm.

Parameters

alpha [input complex]
a [input rank-2 array('D') with bounds (lda,ka)]
b [input rank-2 array('D') with bounds (ldb,kb)]

Returns

c [rank-2 array('D') with bounds (m,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('D') with bounds (m,n)]
overwrite_c [input int, optional] Default: 0
side [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.zsyr2k

Wrapper for zsyr2k.

Parameters

alpha [input complex]
a [input rank-2 array('D') with bounds (lda,ka)]
b [input rank-2 array('D') with bounds (ldb,kb)]

Returns

c [rank-2 array('D') with bounds (n,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('D') with bounds (n,n)]
overwrite_c [input int, optional] Default: 0
trans [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.zsyrk

Wrapper for zsyrk.

Parameters

alpha [input complex]
a [input rank-2 array('D') with bounds (lda,ka)]

Returns

c [rank-2 array('D') with bounds (n,n)]

Other Parameters
SciPy Reference Guide, Release 1.2.0

beta  [input complex, optional] Default: (0.0, 0.0)
c  [input rank-2 array('D') with bounds (n,n)]
overwrite_c  [input int, optional] Default: 0
trans  [input int, optional] Default: 0
lower  [input int, optional] Default: 0

scipy.linalg.blas.ztrmm

scipy.linalg.blas.ztrmm(alpha, a, b[, side, lower, trans_a, diag, overwrite_b]) = <fortran object>

Wrapper for ztrmm.

Parameters
alpha  [input complex]
a  [input rank-2 array('D') with bounds (lda,k)]
b  [input rank-2 array('D') with bounds (ldb,n)]

Returns
b  [rank-2 array('D') with bounds (ldb,n)]

Other Parameters
overwrite_b  [input int, optional] Default: 0
side  [input int, optional] Default: 0
lower  [input int, optional] Default: 0
trans_a  [input int, optional] Default: 0
diag  [input int, optional] Default: 0

scipy.linalg.blas.ztrsm

scipy.linalg.blas.ztrsm(alpha, a, b[, side, lower, trans_a, diag, overwrite_b]) = <fortran object>

Wrapper for ztrsm.

Parameters
alpha  [input complex]
a  [input rank-2 array('D') with bounds (lda,*)]
b  [input rank-2 array('D') with bounds (ldb,n)]

Returns
x  [rank-2 array('D') with bounds (ldb,n) and b storage]

Other Parameters
overwrite_b  [input int, optional] Default: 0
side  [input int, optional] Default: 0
lower  [input int, optional] Default: 0
trans_a  [input int, optional] Default: 0
diag  [input int, optional] Default: 0
6.11 Low-level LAPACK functions (scipy.linalg.lapack)

This module contains low-level functions from the LAPACK library.

The *gegv family of routines have been removed from LAPACK 3.6.0 and have been deprecated in SciPy 0.17.0. They will be removed in a future release.

New in version 0.12.0.

**Note:** The common overwrite_<> option in many routines, allows the input arrays to be overwritten to avoid extra memory allocation. However this requires the array to satisfy two conditions which are memory order and the data type to match exactly the order and the type expected by the routine.

As an example, if you pass a double precision float array to any S... routine which expects single precision arguments, f2py will create an intermediate array to match the argument types and overwriting will be performed on that intermediate array.

Similarly, if a C-contiguous array is passed, f2py will pass a FORTRAN-contiguous array internally. Please make sure that these details are satisfied. More information can be found in the f2py documentation.

---

**Warning:** These functions do little to no error checking. It is possible to cause crashes by mis-using them, so prefer using the higher-level routines in scipy.linalg.

### 6.11.1 Finding functions

`get_lapack_funcs(names[, arrays, dtype])` Return available LAPACK function objects from names.

### 6.11.2 All functions

- `sgbsv(kl,ku,ab,b[,overwrite_ab,overwrite_b])` Wrapper for **sgbsv**.
- `dgbsv(kl,ku,ab,b[,overwrite_ab,overwrite_b])` Wrapper for **dgbsv**.
- `cgbsv(kl,ku,ab,b[,overwrite_ab,overwrite_b])` Wrapper for **cgbsv**.
- `zgbsv(kl,ku,ab,b[,overwrite_ab,overwrite_b])` Wrapper for **zgbsv**.
- `sgbtrf(ab,kl,ku[,m,n,ldab,overwrite_ab])` Wrapper for **sgbtrf**.
- `dgbtrf(ab,kl,ku[,m,n,ldab,overwrite_ab])` Wrapper for **dgbtrf**.
- `cgbtrf(ab,kl,ku[,m,n,ldab,overwrite_ab])` Wrapper for **cgbtrf**.
- `zgbtrf(ab,kl,ku[,m,n,ldab,overwrite_ab])` Wrapper for **zgbtrf**.
- `sgbtrs(…)` Wrapper for **sgbtrs**.
- `dgbtrs(…)` Wrapper for **dgbtrs**.
- `cgbtrs(…)` Wrapper for **cgbtrs**.
- `zgbtrs(…)` Wrapper for **zgbtrs**.
- `sgebal(a[,scale,permute,overwrite_a])` Wrapper for **sgebal**.
- `dgebal(a[,scale,permute,overwrite_a])` Wrapper for **dgebal**.
- `cgebal(a[,scale,permute,overwrite_a])` Wrapper for **cgebal**.
- `zgebal(a[,scale,permute,overwrite_a])` Wrapper for **zgebal**.
- `sgees(…)` Wrapper for **sgees**.
- `dgees(…)` Wrapper for **dgees**.
- `cgees(…)` Wrapper for **cgees**.
- `zgees(…)` Wrapper for **zgees**.

---

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- `sgeev(...)`: Wrapper for `sgeev`.
- `dgeev(...)`: Wrapper for `dgeev`.
- `cgeev(...)`: Wrapper for `cgeev`.
- `zgeev(...)`: Wrapper for `zgeev`.
- `sgeev_lwork(n,[compute_vl,compute_vr])`: Wrapper for `sgeev_lwork`.
- `dgeev_lwork(n,[compute_vl,compute_vr])`: Wrapper for `dgeev_lwork`.
- `cgeev_lwork(n,[compute_vl,compute_vr])`: Wrapper for `cgeev_lwork`.
- `zgeev_lwork(n,[compute_vl,compute_vr])`: Wrapper for `zgeev_lwork`.
- `sgev(*args,**kwds)`: `sgev` is deprecated! The `*gev` family of routines has been deprecated in LAPACK 3.6.0 in favor of the `*ggev` family of routines.
- `dgev(*args,**kwds)`: `dgev` is deprecated! The `*gev` family of routines has been deprecated in LAPACK 3.6.0 in favor of the `*ggev` family of routines.
- `cgev(*args,**kwds)`: `cgev` is deprecated! The `*gev` family of routines has been deprecated in LAPACK 3.6.0 in favor of the `*ggev` family of routines.
- `zgev(*args,**kwds)`: `zgev` is deprecated! The `*gev` family of routines has been deprecated in LAPACK 3.6.0 in favor of the `*ggev` family of routines.
- `sgehrd(a,[lo,hi,lwork,overwrite_a])`: Wrapper for `sgehrd`.
- `dgehrd(a,[lo,hi,lwork,overwrite_a])`: Wrapper for `dgehrd`.
- `cgehrd(a,[lo,hi,lwork,overwrite_a])`: Wrapper for `cgehrd`.
- `zgehrd(a,[lo,hi,lwork,overwrite_a])`: Wrapper for `zgehrd`.
- `sgehrd_lwork(n,[lo,hi])`: Wrapper for `sgehrd_lwork`.
- `dgehrd_lwork(n,[lo,hi])`: Wrapper for `dgehrd_lwork`.
- `cgehrd_lwork(n,[lo,hi])`: Wrapper for `cgehrd_lwork`.
- `zgehrd_lwork(n,[lo,hi])`: Wrapper for `zgehrd_lwork`.
- `sgelss(a,b,[cond,lwork,overwrite_a,overwrite_b])`: Wrapper for `sgelss`.
- `dgelss(a,b,[cond,lwork,overwrite_a,overwrite_b])`: Wrapper for `dgelss`.
- `cgelss(a,b,[cond,lwork,overwrite_a,overwrite_b])`: Wrapper for `cgelss`.
- `zgelss(a,b,[cond,lwork,overwrite_a,overwrite_b])`: Wrapper for `zgelss`.
- `sgelss_lwork(m,n,nrhs,[cond,lwork])`: Wrapper for `sgelss_lwork`.
- `dgelss_lwork(m,n,nrhs,[cond,lwork])`: Wrapper for `dgelss_lwork`.
- `cgelss_lwork(m,n,nrhs,[cond,lwork])`: Wrapper for `cgelss_lwork`.
- `zgelss_lwork(m,n,nrhs,[cond,lwork])`: Wrapper for `zgelss_lwork`.
- `sgelsd(...):`: Wrapper for `sgelsd`.
- `dgelss(...):`: Wrapper for `dgelss`.
- `cgelss(...):`: Wrapper for `cgelss`.
- `zgelss(...):`: Wrapper for `zgelss`.
- `sgelsd_lwork(m,n,nrhs,[cond,lwork])`: Wrapper for `sgelsd_lwork`.
- `dgelss_lwork(m,n,nrhs,[cond,lwork])`: Wrapper for `dgelss_lwork`.
- `cgelss_lwork(m,n,nrhs,[cond,lwork])`: Wrapper for `cgelss_lwork`.
- `zgelss_lwork(m,n,nrhs,[cond,lwork])`: Wrapper for `zgelss_lwork`.
- `sgelsy(...):`: Wrapper for `sgelsy`.
- `dgelss(...):`: Wrapper for `dgelss`.
- `cgelss(...):`: Wrapper for `cgelss`.
- `zgelss(...):`: Wrapper for `zgelss`.

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<td>Wrapper for <code>zgelsy_lwork</code>.</td>
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<tr>
<td><code>sgemv</code></td>
<td>Wrapper for <code>sgemv</code>.</td>
</tr>
<tr>
<td><code>dgemv</code></td>
<td>Wrapper for <code>dgemv</code>.</td>
</tr>
<tr>
<td><code>cgemv</code></td>
<td>Wrapper for <code>cgemv</code>.</td>
</tr>
<tr>
<td><code>zgemv</code></td>
<td>Wrapper for <code>zgemv</code>.</td>
</tr>
<tr>
<td><code>sgemv_lwork</code></td>
<td>Wrapper for <code>sgemv_lwork</code>.</td>
</tr>
<tr>
<td><code>dgemv_lwork</code></td>
<td>Wrapper for <code>dgemv_lwork</code>.</td>
</tr>
<tr>
<td><code>cgemv_lwork</code></td>
<td>Wrapper for <code>cgemv_lwork</code>.</td>
</tr>
<tr>
<td><code>zgemv_lwork</code></td>
<td>Wrapper for <code>zgemv_lwork</code>.</td>
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<tr>
<td><code>sgecon</code></td>
<td>Wrapper for <code>sgecon</code>.</td>
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<td><strong>dpftrs</strong>*(n,a,b,[transr,uplo,overwrite_b])**</td>
<td>Wrapper for <strong>dpftrs</strong>.</td>
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<tr>
<td><strong>cpftrs</strong>*(n,a,b,[transr,uplo,overwrite_b])**</td>
<td>Wrapper for <strong>cpftrs</strong>.</td>
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<td>ctzrzf(a, lwork, overwrite_a)</td>
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<td>stzrzf(a, lwork, overwrite_a)</td>
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<td>Wrapper for ilaver.</td>
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scipy.linalg.lapack.sgbsv

scipy.linalg.lapack.sgbsv(kl, ku, ab[, overwrite_ab, overwrite_b]) = <fortran object>
Wrapper for sgbsv.

Parameters

- **kl** [input int]
- **ku** [input int]
- **ab** [input rank-2 array('f') with bounds (2*kl+ku+1,n)]
- **b** [input rank-2 array('f') with bounds (n,nrhs)]

Returns

- **lub** [rank-2 array('f') with bounds (2*kl+ku+1,n) and ab storage]
- **piv** [rank-1 array('i') with bounds (n)]
- **x** [rank-2 array('f') with bounds (n,nrhs) and b storage]
- **info** [int]

Other Parameters

- **overwrite_ab** [input int, optional] Default: 0
- **overwrite_b** [input int, optional] Default: 0

scipy.linalg.lapack.dgbsv

scipy.linalg.lapack.dgbsv(kl, ku, ab[, overwrite_ab, overwrite_b]) = <fortran object>
Wrapper for dgbsv.

Parameters

- **kl** [input int]
- **ku** [input int]
- **ab** [input rank-2 array('d') with bounds (2*kl+ku+1,n)]
- **b** [input rank-2 array('d') with bounds (n,nrhs)]

Returns

- **lub** [rank-2 array('d') with bounds (2*kl+ku+1,n) and ab storage]
- **piv** [rank-1 array('i') with bounds (n)]
- **x** [rank-2 array('d') with bounds (n,nrhs) and b storage]
- **info** [int]
**Other Parameters**

overwrite_ab
[input int, optional] Default: 0

overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.cgbsv

scipy.linalg.lapack.cgbsv(\(kl, ku, ab, b[, \text{overwrite}_\text{ab}, \text{overwrite}_\text{b}]\)) = <fortran object>
Wrapper for cgbsv.

**Parameters**

\(kl\) [input int]
\(ku\) [input int]
\(ab\) [input rank-2 array(‘F’) with bounds (2*kl+ku+1,n)]
\(b\) [input rank-2 array(‘F’) with bounds (n,nrhs)]

**Returns**

\(lub\) [rank-2 array(‘F’) with bounds (2*kl+ku+1,n) and ab storage]
\(piv\) [rank-1 array(‘i’) with bounds (n)]
\(x\) [rank-2 array(‘F’) with bounds (n,nrhs) and b storage]
\(info\) [int]

**Other Parameters**

overwrite_ab
[input int, optional] Default: 0

overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.zgbsv

scipy.linalg.lapack.zgbsv(\(kl, ku, ab, b[, \text{overwrite}_\text{ab}, \text{overwrite}_\text{b}]\)) = <fortran object>
Wrapper for zgbsv.

**Parameters**

\(kl\) [input int]
\(ku\) [input int]
\(ab\) [input rank-2 array(‘D’) with bounds (2*kl+ku+1,n)]
\(b\) [input rank-2 array(‘D’) with bounds (n,nrhs)]

**Returns**

\(lub\) [rank-2 array(‘D’) with bounds (2*kl+ku+1,n) and ab storage]
\(piv\) [rank-1 array(‘i’) with bounds (n)]
\(x\) [rank-2 array(‘D’) with bounds (n,nrhs) and b storage]
\(info\) [int]

**Other Parameters**

overwrite_ab
[input int, optional] Default: 0

overwrite_b
[input int, optional] Default: 0
scipy.linalg.lapack.sgbtrf

```python
scipy.linalg.lapack.sgbtrf(ab, kl, ku[, m, n, ldab, overwrite_ab]) = <fortran object>
```

Wrapper for `sgbtrf`.

**Parameters**
- `ab` [input rank-2 array('f') with bounds (ldab,n)]
- `kl` [input int]
- `ku` [input int]

**Returns**
- `lu` [rank-2 array('f') with bounds (ldab,n) and ab storage]
- `ipiv` [rank-1 array('i') with bounds (MIN(m,n))]
- `info` [int]

**Other Parameters**
- `m` [input int, optional] Default: shape(ab,1)
- `n` [input int, optional] Default: shape(ab,1)
- `overwrite_ab` [input int, optional] Default: 0
- `ldab` [input int, optional] Default: max(shape(ab,0),1)

scipy.linalg.lapack.dgbtrf

```python
scipy.linalg.lapack.dgbtrf(ab, kl, ku[, m, n, ldab, overwrite_ab]) = <fortran object>
```

Wrapper for `dgbtrf`.

**Parameters**
- `ab` [input rank-2 array('d') with bounds (ldab,n)]
- `kl` [input int]
- `ku` [input int]

**Returns**
- `lu` [rank-2 array('d') with bounds (ldab,n) and ab storage]
- `ipiv` [rank-1 array('i') with bounds (MIN(m,n))]
- `info` [int]

**Other Parameters**
- `m` [input int, optional] Default: shape(ab,1)
- `n` [input int, optional] Default: shape(ab,1)
- `overwrite_ab` [input int, optional] Default: 0
- `ldab` [input int, optional] Default: max(shape(ab,0),1)

scipy.linalg.lapack.cgbtrf

```python
scipy.linalg.lapack.cgbtrf(ab, kl, ku[, m, n, ldab, overwrite_ab]) = <fortran object>
```

Wrapper for `cgbtrf`.

**Parameters**
- `ab` [input rank-2 array('F') with bounds (ldab,n)]
- `kl` [input int]
- `ku` [input int]

**Returns**
- `lu` [rank-2 array('f') with bounds (ldab,n) and ab storage]
- `ipiv` [rank-1 array('i') with bounds (MIN(m,n))]
- `info` [int]

**Other Parameters**
- `m` [input int, optional] Default: shape(ab,1)
- `n` [input int, optional] Default: shape(ab,1)
- `overwrite_ab` [input int, optional] Default: 0
- `ldab` [input int, optional] Default: max(shape(ab,0),1)

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```python
lu   [rank-2 array('F') with bounds (ldab,n) and ab storage]
ipiv [rank-1 array('i') with bounds (MIN(m,n))]
info  [int]

Other Parameters
m    [input int, optional] Default: shape(ab,1)
n    [input int, optional] Default: shape(ab,1)
overwrite_ab
    [input int, optional] Default: 0
ldab  [input int, optional] Default: max(shape(ab,0),1)

scipy.linalg.lapack.zgbtrf

scipy.linalg.lapack.zgbtrf(ab, kl, ku[, m, n, ldab, overwrite_ab]) = <fortran object>
Wrapper for zgbtrf.

Parameters
ab         [input rank-2 array('D') with bounds (ldab,n)]
kl         [input int]
ku         [input int]

Returns
lu         [rank-2 array('D') with bounds (ldab,n) and ab storage]
ipiv       [rank-1 array('i') with bounds (MIN(m,n))]
info        [int]

Other Parameters
m         [input int, optional] Default: shape(ab,1)
n         [input int, optional] Default: shape(ab,1)
overwrite_ab
            [input int, optional] Default: 0
ldab        [input int, optional] Default: max(shape(ab,0),1)

scipy.linalg.lapack.sgbtrs

scipy.linalg.lapack.sgbtrs(ab, kl, ku, b, ipiv[, trans, n, ldab, ldb, overwrite_b]) = <fortran object>
Wrapper for sgbtrs.

Parameters
ab         [input rank-2 array('f') with bounds (ldab,n)]
kl         [input int]
ku         [input int]
b         [input rank-2 array('f') with bounds (ldb,nrhs)]
ipiv       [input rank-1 array('i') with bounds (n)]

Returns
x            [rank-2 array('f') with bounds (ldb,nrhs) and b storage]
info         [int]

Other Parameters
overwrite_b
            [input int, optional] Default: 0
trans        [input int, optional] Default: 0
```
6.11. Low-level LAPACK functions (scipy.linalg.lapack)

```python
n: [input int, optional] Default: shape(ab,1)
ldab: [input int, optional] Default: shape(ab,0)
ldb: [input int, optional] Default: shape(b,0)
```

**scipy.linalg.lapack.dgbtrs**

```python
scipy.linalg.lapack.dgbtrs(ab, kl, ku, b, ipiv[, trans, n, ldab, ldb, overwrite_b]) = <fortran object>
```

Wrapper for dgbtrs.

**Parameters**

- `ab` [input rank-2 array('d') with bounds (ldab,n)]
- `kl` [input int]
- `ku` [input int]
- `b` [input rank-2 array('d') with bounds (ldb,nrhs)]
- `ipiv` [input rank-1 array('i') with bounds (n)]

**Returns**

- `x` [rank-2 array('d') with bounds (ldb,nrhs) and b storage]
- `info` [int]

**Other Parameters**

- `overwrite_b` [input int, optional] Default: 0
- `trans` [input int, optional] Default: 0
- `n` [input int, optional] Default: shape(ab,1)
- `ldab` [input int, optional] Default: shape(ab,0)
- `ldb` [input int, optional] Default: shape(b,0)

**scipy.linalg.lapack.cgbtrs**

```python
scipy.linalg.lapack.cgbtrs(ab, kl, ku, b, ipiv[, trans, n, ldab, ldb, overwrite_b]) = <fortran object>
```

Wrapper for cgbtrs.

**Parameters**

- `ab` [input rank-2 array('F') with bounds (ldab,n)]
- `kl` [input int]
- `ku` [input int]
- `b` [input rank-2 array('F') with bounds (ldb,nrhs)]
- `ipiv` [input rank-1 array('i') with bounds (n)]

**Returns**

- `x` [rank-2 array('F') with bounds (ldb,nrhs) and b storage]
- `info` [int]

**Other Parameters**

- `overwrite_b` [input int, optional] Default: 0
- `trans` [input int, optional] Default: 0
- `n` [input int, optional] Default: shape(ab,1)
- `ldab` [input int, optional] Default: shape(ab,0)
- `ldb` [input int, optional] Default: shape(b,0)
scipy.linalg.lapack.zgbtrs

\[ \text{scipy.linalg.lapack.zgbtrs}(ab, kl, ku, b, ipiv[, trans, n, ldab, ldb, overwrite_b]) = \text{<fortran object>} \]

Wrapper for zgbtrs.

**Parameters**

- **ab** [input rank-2 array('D') with bounds (ldab,n)]
- **kl** [input int]
- **ku** [input int]
- **b** [input rank-2 array('D') with bounds (ldb,nrhs)]
- **ipiv** [input rank-1 array('i') with bounds (n)]

**Returns**

- **x** [rank-2 array('D') with bounds (ldb,nrhs) and b storage]
- **info** [int]

**Other Parameters**

- **overwrite_b** [input int, optional] Default: 0
- **trans** [input int, optional] Default: 0
- **n** [input int, optional] Default: shape(ab,1)
- **ldab** [input int, optional] Default: shape(ab,0)
- **ldb** [input int, optional] Default: shape(b,0)

scipy.linalg.lapack.sgebal

\[ \text{scipy.linalg.lapack.sgebal}(a[, scale, permute, overwrite_a]) = \text{<fortran object>} \]

Wrapper for sgebal.

**Parameters**

- **a** [input rank-2 array('f') with bounds (m,n)]

**Returns**

- **ba** [rank-2 array('f') with bounds (m,n) and a storage]
- **lo** [int]
- **hi** [int]
- **pivscale** [rank-1 array('f') with bounds (n)]
- **info** [int]

**Other Parameters**

- **scale** [input int, optional] Default: 0
- **permute** [input int, optional] Default: 0
- **overwrite_a** [input int, optional] Default: 0

scipy.linalg.lapack.dgebal

\[ \text{scipy.linalg.lapack.dgebal}(a[, scale, permute, overwrite_a]) = \text{<fortran object>} \]

Wrapper for dgebal.

**Parameters**

- **a** [input rank-2 array('d') with bounds (m,n)]

**Returns**
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6.11. Low-level LAPACK functions (scipy.linalg.lapack)

```
ba [rank-2 array('d') with bounds (m,n) and a storage]
lo [int]
hi [int]
pivscale [rank-1 array('d') with bounds (n)]
info [int]

Other Parameters

scale [input int, optional] Default: 0
permute [input int, optional] Default: 0
overwrite_a [input int, optional] Default: 0

scipy.linalg.lapack.cgebal

scipy.linalg.lapack.cgebal(a[, scale, permute, overwrite_a]) = <fortran object>

Wrapper for cgebal.

Parameters

a [input rank-2 array('F') with bounds (m,n)]

Returns

ba [rank-2 array('F') with bounds (m,n) and a storage]
lo [int]
hi [int]
pivscale [rank-1 array('f') with bounds (n)]
info [int]

Other Parameters

scale [input int, optional] Default: 0
permute [input int, optional] Default: 0
overwrite_a [input int, optional] Default: 0

scipy.linalg.lapack.zgebal

scipy.linalg.lapack.zgebal(a[, scale, permute, overwrite_a]) = <fortran object>

Wrapper for zgebal.

Parameters

a [input rank-2 array('D') with bounds (m,n)]

Returns

ba [rank-2 array('D') with bounds (m,n) and a storage]
lo [int]
hi [int]
pivscale [rank-1 array('d') with bounds (n)]
info [int]

Other Parameters

scale [input int, optional] Default: 0
permute [input int, optional] Default: 0
overwrite_a [input int, optional] Default: 0
```
scipy.linalg.lapack.sgees

scipy.linalg.lapack.sgees(sselect, a[, compute_v, sort_t, lwork, sselect_extra_args, overwrite_a]) = <fortran object>

Wrapper for sgees.

Parameters

sselect [call-back function]
a [input rank-2 array('f') with bounds (n,n)]

Returns

t [rank-2 array('f') with bounds (n,n) and a storage]
sdim [int]
wr [rank-1 array('f') with bounds (n)]
wi [rank-1 array('f') with bounds (n)]
vs [rank-2 array('f') with bounds (ldvs,n)]
work [rank-1 array('f') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

compute_v [input int, optional] Default: 1
sort_t [input int, optional] Default: 0
sselect_extra_args [input tuple, optional] Default: ()
overwrite_a [input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

Notes

Call-back functions:

```python
def sselect(arg1, arg2): return sselect
```

Required arguments:
arg1 : input float
arg2 : input float

Return objects:
sselect : int

scipy.linalg.lapack.dgees

scipy.linalg.lapack.dgees(dselect, a[, compute_v, sort_t, lwork, dselect_extra_args, overwrite_a]) = <fortran object>

Wrapper for dgees.

Parameters

dselect [call-back function]
a [input rank-2 array('d') with bounds (n,n)]

Returns

t [rank-2 array('d') with bounds (n,n) and a storage]
sdim [int]
wr [rank-1 array('d') with bounds (n)]
wi [rank-1 array('d') with bounds (n)]
vs: [rank-2 array('d') with bounds (ldvs,n)]
work: [rank-1 array('d') with bounds (MAX(lwork,1))]
info: [int]

Other Parameters

compute_v: [input int, optional] Default: 1
sort_t: [input int, optional] Default: 0
dselect_extra_args: [input tuple, optional] Default: ()
overwrite_a: [input int, optional] Default: 0
lwork: [input int, optional] Default: max(3*n,1)

Notes

Call-back functions:

```
def dselect(arg1,arg2): return dselect
```

Required arguments:
arg1: input float
arg2: input float

Return objects:
dselect: int

scipy.linalg.lapack.cgees

scipy.linalg.lapack.cgees(cselect, a, compute_v, sort_t, lwork, cselect_extra_args, overwrite_a)

Wrapper for cgees.

Parameters

- cselect: [call-back function]
- a: [input rank-2 array('F') with bounds (n,n)]

Returns

- t: [rank-2 array('F') with bounds (n,n) and a storage]
- sdim: [int]
- w: [rank-1 array('F') with bounds (n)]
- vs: [rank-2 array('F') with bounds (ldvs,n)]
- work: [rank-1 array('F') with bounds (MAX(lwork,1))]
- info: [int]

Other Parameters

- compute_v: [input int, optional] Default: 1
- sort_t: [input int, optional] Default: 0
- cselect_extra_args: [input tuple, optional] Default: ()
- overwrite_a: [input int, optional] Default: 0
- lwork: [input int, optional] Default: max(3*n,1)
Notes
Call-back functions:

```python
def cselect(arg):
    return cselect
Required arguments:
    arg : input complex
Return objects:
    cselect : int
```

scipy.linalg.lapack.zgees

```python
scipy.linalg.lapack.zgees(zselect, a[, compute_v, sort_t, lwork, zselect_extra_args, overwrite_a]) = <fortran object>
```

Wrapper for zgees.

**Parameters**

- **zselect** [call-back function]
- **a** [input rank-2 array('D') with bounds (n,n)]

**Returns**

- **t** [rank-2 array('D') with bounds (n,n) and a storage]
- **sdim** [int]
- **w** [rank-1 array('D') with bounds (n)]
- **vs** [rank-2 array('D') with bounds (ldvs,n)]
- **work** [rank-1 array('D') with bounds (MAX(lwork,1))]
- **info** [int]

**Other Parameters**

- **compute_v** [input int, optional] Default: 1
- **sort_t** [input int, optional] Default: 0
- **zselect_extra_args** [input tuple, optional] Default: ()
- **overwrite_a** [input int, optional] Default: 0
- **lwork** [input int, optional] Default: max(3*n,1)

Notes
Call-back functions:

```python
def zselect(arg):
    return zselect
Required arguments:
    arg : input complex
Return objects:
    zselect : int
```

scipy.linalg.lapack.sgeev

```python
scipy.linalg.lapack.sgeev(a[, compute_vl, compute_vr, lwork, overwrite_a]) = <fortran object>
```

Wrapper for sgeev.

**Parameters**

- **a** [input rank-2 array('f') with bounds (n,n)]
Returns

\- \texttt{wr} [rank-1 array('f') with bounds (n)]
\- \texttt{wi} [rank-1 array('f') with bounds (n)]
\- \texttt{vl} [rank-2 array('f') with bounds (ldvl,n)]
\- \texttt{vr} [rank-2 array('f') with bounds (ldvr,n)]
\- \texttt{info} [int]

Other Parameters

\- \texttt{compute\_vl} [input int, optional] Default: 1
\- \texttt{compute\_vr} [input int, optional] Default: 1
\- \texttt{overwrite\_a} [input int, optional] Default: 0
\- \texttt{lwork} [input int, optional] Default: max(4*n,1)

\texttt{scipy.linalg.lapack.dgeev}

\texttt{scipy.linalg.lapack.dgeev(a[, compute\_vl, compute\_vr, lwork, overwrite\_a])} = \texttt{<fortran object>}

Wrapper for \texttt{dgeev}.

Parameters

\- \texttt{a} [input rank-2 array('d') with bounds (n,n)]

Returns

\- \texttt{wr} [rank-1 array('d') with bounds (n)]
\- \texttt{wi} [rank-1 array('d') with bounds (n)]
\- \texttt{vl} [rank-2 array('d') with bounds (ldvl,n)]
\- \texttt{vr} [rank-2 array('d') with bounds (ldvr,n)]
\- \texttt{info} [int]

Other Parameters

\- \texttt{compute\_vl} [input int, optional] Default: 1
\- \texttt{compute\_vr} [input int, optional] Default: 1
\- \texttt{overwrite\_a} [input int, optional] Default: 0
\- \texttt{lwork} [input int, optional] Default: max(4*n,1)

\texttt{scipy.linalg.lapack.cgeev}

\texttt{scipy.linalg.lapack.cgeev(a[, compute\_vl, compute\_vr, lwork, overwrite\_a])} = \texttt{<fortran object>}

Wrapper for \texttt{cgeev}.

Parameters

\- \texttt{a} [input rank-2 array('F') with bounds (n,n)]

Returns

\- \texttt{w} [rank-1 array('F') with bounds (n)]
\- \texttt{vl} [rank-2 array('F') with bounds (ldvl,n)]
\- \texttt{vr} [rank-2 array('F') with bounds (ldvr,n)]


Other Parameters

- `compute_vl` [input int, optional] Default: 1
- `compute_vr` [input int, optional] Default: 1
- `overwrite_a` [input int, optional] Default: 0
- `lwork` [input int, optional] Default: \(\max(2n, 1)\)

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scipy.linalg.lapack.dgeev_lwork

scipy.linalg.lapack.dgeev_lwork(n[, compute_vl, compute_vr]) = <fortran object>
Wrapper for dgeev_lwork.

Parameters

n    [input int]

Returns

work    [float]
info    [int]

Other Parameters

compute_vl
    [input int, optional] Default: 1
compute_vr
    [input int, optional] Default: 1

scipy.linalg.lapack.cgeev_lwork

scipy.linalg.lapack.cgeev_lwork(n[, compute_vl, compute_vr]) = <fortran object>
Wrapper for cgeev_lwork.

Parameters

n    [input int]

Returns

work    [complex]
info    [int]

Other Parameters

compute_vl
    [input int, optional] Default: 1
compute_vr
    [input int, optional] Default: 1

scipy.linalg.lapack.zgeev_lwork

scipy.linalg.lapack.zgeev_lwork(n[, compute_vl, compute_vr]) = <fortran object>
Wrapper for zgeev_lwork.

Parameters

n    [input int]

Returns

work    [complex]
info    [int]

Other Parameters

compute_vl
    [input int, optional] Default: 1
compute_vr
    [input int, optional] Default: 1
scipy.linalg.lapack.sgegv

scipy.linalg.lapack.sgegv(*args, **kwds)

*sgegv* is deprecated! The *gegv* family of routines has been deprecated in LAPACK 3.6.0 in favor of the *ggev* family of routines. The corresponding wrappers will be removed from SciPy in a future release.

alphar,alphai,beta,vl,vr,info = sgegv(a,b,[compute_vl,compute_vr,lwork,overwrite_a,overwrite_b])

Wrapper for *sgegv*.

**Parameters**

- **a**: [input rank-2 array(‘f’) with bounds (n,n)]
- **b**: [input rank-2 array(‘f’) with bounds (n,n)]

**Returns**

- **alphar**: [rank-1 array(‘f’) with bounds (n)]
- **alphai**: [rank-1 array(‘f’) with bounds (n)]
- **beta**: [rank-1 array(‘f’) with bounds (n)]
- **vl**: [rank-2 array(‘f’) with bounds (ldvl,n)]
- **vr**: [rank-2 array(‘f’) with bounds (ldvr,n)]
- **info**: [int]

**Other Parameters**

- **compute_vl**: [input int, optional] Default: 1
- **compute_vr**: [input int, optional] Default: 1
- **overwrite_a**: [input int, optional] Default: 0
- **overwrite_b**: [input int, optional] Default: 0
- **lwork**: [input int, optional] Default: max(8*n,1)

scipy.linalg.lapack.dgegv

scipy.linalg.lapack.dgegv(*args, **kwds)

dgegv is deprecated! The *gegv* family of routines has been deprecated in LAPACK 3.6.0 in favor of the *ggev* family of routines. The corresponding wrappers will be removed from SciPy in a future release.

alphar,alphai,beta,vl,vr,info = dgegv(a,b,[compute_vl,compute_vr,lwork,overwrite_a,overwrite_b])

Wrapper for *dgegv*.

**Parameters**

- **a**: [input rank-2 array(‘d’) with bounds (n,n)]
- **b**: [input rank-2 array(‘d’) with bounds (n,n)]

**Returns**

- **alphar**: [rank-1 array(‘d’) with bounds (n)]
- **alphai**: [rank-1 array(‘d’) with bounds (n)]
- **beta**: [rank-1 array(‘d’) with bounds (n)]
- **vl**: [rank-2 array(‘d’) with bounds (ldvl,n)]
- **vr**: [rank-2 array(‘d’) with bounds (ldvr,n)]
- **info**: [int]
### Other Parameters

- **compute_vl**
  
  [input int, optional] Default: 1

- **compute_vr**
  
  [input int, optional] Default: 1

- **overwrite_a**
  
  [input int, optional] Default: 0

- **overwrite_b**
  
  [input int, optional] Default: 0

- **lwork**
  
  [input int, optional] Default: max(8*n,1)

---

#### scipy.linalg.lapack.cgegv

scipy.linalg.lapack.cgegv(*args, **kwds)

cgegv is deprecated! The *ggev family of routines has been deprecated in LAPACK 3.6.0 in favor of the *ggev family of routines. The corresponding wrappers will be removed from SciPy in a future release.

alpha, beta, vl, vr, info = cgegv(a, b, [compute_vl, compute_vr, lwork, overwrite_a, overwrite_b])

Wrapper for cgegv.

**Parameters**

- **a**
  
  [input rank-2 array('F') with bounds (n,n)]

- **b**
  
  [input rank-2 array('F') with bounds (n,n)]

**Returns**

- **alpha**
  
  [rank-1 array('F') with bounds (n)]

- **beta**
  
  [rank-1 array('F') with bounds (n)]

- **vl**
  
  [rank-2 array('F') with bounds (ldvl,n)]

- **vr**
  
  [rank-2 array('F') with bounds (ldvr,n)]

- **info**
  
  [int]

### Other Parameters

- **compute_vl**
  
  [input int, optional] Default: 1

- **compute_vr**
  
  [input int, optional] Default: 1

- **overwrite_a**
  
  [input int, optional] Default: 0

- **overwrite_b**
  
  [input int, optional] Default: 0

- **lwork**
  
  [input int, optional] Default: max(2*n,1)

---

#### scipy.linalg.lapack.zgegv

scipy.linalg.lapack.zgegv(*args, **kwds)

zgegv is deprecated! The *ggev family of routines has been deprecated in LAPACK 3.6.0 in favor of the *ggev family of routines. The corresponding wrappers will be removed from SciPy in a future release.

alpha, beta, vl, vr, info = zgegv(a, b, [compute_vl, compute_vr, lwork, overwrite_a, overwrite_b])

Wrapper for zgegv.

**Parameters**
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a [input rank-2 array(‘D’) with bounds (n,n)]
b [input rank-2 array(‘D’) with bounds (n,n)]

Returns
alpha [rank-1 array(‘D’) with bounds (n)]
beta [rank-1 array(‘D’) with bounds (n)]
vl [rank-2 array(‘D’) with bounds (ldvl,n)]
vr [rank-2 array(‘D’) with bounds (ldvr,n)]
info [int]

Other Parameters
compute_vl [input int, optional] Default: 1
compute_vr [input int, optional] Default: 1
overwrite_a [input int, optional] Default: 0
overwrite_b [input int, optional] Default: 0
lwork [input int, optional] Default: max(2*n,1)

scipy.linalg.lapack.sgehrd

scipy.linalg.lapack.sgehrd(a,[lo,hi,lwork,overwrite_a]) = <fortran object>
Wrapper for sgehrd.

Parameters
a [input rank-2 array(‘f’) with bounds (n,n)]

Returns
ht [rank-2 array(‘f’) with bounds (n,n) and a storage]
tau [rank-1 array(‘f’) with bounds (n - 1)]
info [int]

Other Parameters
lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1
overwrite_a [input int, optional] Default: 0
lwork [input int, optional] Default: MAX(n,1)

scipy.linalg.lapack.dgehrd

scipy.linalg.lapack.dgehrd(a,[lo,hi,lwork,overwrite_a]) = <fortran object>
Wrapper for dgehrd.

Parameters
a [input rank-2 array(‘d’) with bounds (n,n)]

Returns
ht [rank-2 array(‘d’) with bounds (n,n) and a storage]
tau [rank-1 array(‘d’) with bounds (n - 1)]
info [int]

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**Other Parameters**

lo  [input int, optional] Default: 0
hi  [input int, optional] Default: n-1
overwrite_a  [input int, optional] Default: 0
lwork  [input int, optional] Default: MAX(n,1)

**scipy.linalg.lapack.cgehrd**

\[ \text{scipy.linalg.lapack.cgehrd}(a, \text{lo}, \text{hi}, \text{lwork}, \text{overwrite_a}) = \text{<fortran object>} \]

Wrapper for cgehrd.

**Parameters**

- a  [input rank-2 array(`F`) with bounds (n,n)]

**Returns**

- ht  [rank-2 array(`F`) with bounds (n,n) and a storage]
- tau  [rank-1 array(`F`) with bounds (n - 1)]
- info  [int]

**Other Parameters**

lo  [input int, optional] Default: 0
hi  [input int, optional] Default: n-1
overwrite_a  [input int, optional] Default: 0
lwork  [input int, optional] Default: MAX(n,1)

**scipy.linalg.lapack.zgehrd**

\[ \text{scipy.linalg.lapack.zgehrd}(a, \text{lo}, \text{hi}, \text{lwork}, \text{overwrite_a}) = \text{<fortran object>} \]

Wrapper for zgehrd.

**Parameters**

- a  [input rank-2 array(`D`) with bounds (n,n)]

**Returns**

- ht  [rank-2 array(`D`) with bounds (n,n) and a storage]
- tau  [rank-1 array(`D`) with bounds (n - 1)]
- info  [int]

**Other Parameters**

lo  [input int, optional] Default: 0
hi  [input int, optional] Default: n-1
overwrite_a  [input int, optional] Default: 0
lwork  [input int, optional] Default: MAX(n,1)
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scipy.linalg.lapack.sgehrd_lwork

scipy.linalg.lapack.sgehrd_lwork\(n, lo, hi\) = <fortran object>
Wrapper for sgehrd_lwork.

**Parameters**

\(n\) [input int]

**Returns**

work [float]
info [int]

**Other Parameters**

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1

scipy.linalg.lapack.dgehrd_lwork

scipy.linalg.lapack.dgehrd_lwork\(n, lo, hi\) = <fortran object>
Wrapper for dgehrd_lwork.

**Parameters**

\(n\) [input int]

**Returns**

work [float]
info [int]

**Other Parameters**

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1

scipy.linalg.lapack.cgehrd_lwork

scipy.linalg.lapack.cgehrd_lwork\(n, lo, hi\) = <fortran object>
Wrapper for cgehrd_lwork.

**Parameters**

\(n\) [input int]

**Returns**

work [complex]
info [int]

**Other Parameters**

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1
scipy.linalg.lapack.zgehrd_lwork

scipy.linalg.lapack.zgehrd_lwork(n[, lo, hi]) = <fortran object>
Wrapper for zgehrd_lwork.

Parameters
n [input int]

Returns
work [complex]
info [int]

Other Parameters
lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1

scipy.linalg.lapack.sgelss

scipy.linalg.lapack.sgelss(a, b[, cond, lwork, overwrite_a, overwrite_b]) = <fortran object>
Wrapper for sgelss.

Parameters
a [input rank-2 array('f') with bounds (m,n)]
b [input rank-2 array('f') with bounds (maxmn,nrhs)]

Returns
v [rank-2 array('f') with bounds (m,n) and a storage]
x [rank-2 array('f') with bounds (maxmn,nrhs) and b storage]
s [rank-1 array('f') with bounds (minmn)]
rank [int]
work [rank-1 array('f') with bounds (MAX(lwork,1))] info [int]

Other Parameters
overwrite_a [input int, optional] Default: 0
overwrite_b [input int, optional] Default: 0
cond [input float, optional] Default: -1.0
lwork [input int, optional] Default: max(3*minmn+MAX(2*minmn,MAX(maxmn,nrhs)),1)

scipy.linalg.lapack.dgelss

scipy.linalg.lapack.dgelss(a, b[, cond, lwork, overwrite_a, overwrite_b]) = <fortran object>
Wrapper for dgelss.

Parameters
a [input rank-2 array('d') with bounds (m,n)]
b [input rank-2 array('d') with bounds (maxmn,nrhs)]

Returns
v [rank-2 array('d') with bounds (m,n) and a storage]
x [rank-2 array('d') with bounds (maxmn,nrhs) and b storage]
s [rank-1 array('d') with bounds (minmn)]

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rank  [int]
work  [rank-1 array('d') with bounds (MAX(lwork,1))]
info  [int]

**Other Parameters**

 overwrite_a  
[input int, optional] Default: 0
 overwrite_b  
[input int, optional] Default: 0
 cond  
[input float, optional] Default: -1.0
 lwork  
[input int, optional] Default: max(3*minmn+MAX(2*minmn,MAX(maxmn,nrhs)),1)

**scipy.linalg.lapack.cgelss**

```python
scipy.linalg.lapack.cgelss(a, b, cond, lwork, overwrite_a, overwrite_b) = <fortran object>
```

Wrapper for cgelss.

**Parameters**

a  [input rank-2 array('F') with bounds (m,n)]
b  [input rank-2 array('F') with bounds (maxmn,nrhs)]

**Returns**

v  [rank-2 array('F') with bounds (m,n) and a storage]
x  [rank-2 array('F') with bounds (maxmn,nrhs) and b storage]
s  [rank-1 array('F') with bounds (minmn)]
rank  [int]
work  [rank-1 array('F') with bounds (MAX(lwork,1))]
info  [int]

**Other Parameters**

 overwrite_a  
[input int, optional] Default: 0
 overwrite_b  
[input int, optional] Default: 0
 cond  
[input float, optional] Default: -1.0
 lwork  
[input int, optional] Default: max(2*minmn+MAX(maxmn,nrhs),1)

**scipy.linalg.lapack.zgelss**

```python
scipy.linalg.lapack.zgelss(a, b, cond, lwork, overwrite_a, overwrite_b) = <fortran object>
```

Wrapper for zgelss.

**Parameters**

a  [input rank-2 array('D') with bounds (m,n)]
b  [input rank-2 array('D') with bounds (maxmn,nrhs)]

**Returns**

v  [rank-2 array('D') with bounds (m,n) and a storage]
x  [rank-2 array('D') with bounds (maxmn,nrhs) and b storage]
s  [rank-1 array('d') with bounds (minmn)]
rank  [int]
work  [rank-1 array('D') with bounds (MAX(lwork,1))]
info  [int]
Other Parameters

overwrite_a  [input int, optional] Default: 0
overwrite_b  [input int, optional] Default: 0
cond  [input float, optional] Default: -1.0
lwork  [input int, optional] Default: max(2*minmn+MAX(maxmn,nrhs),1)

scipy.linalg.lapack.sgelss_lwork

scipy.linalg.lapack.sgelss_lwork(m, n, nrhs[, cond, lwork]) = <fortran object>
Wrapper for sgelss_lwork.

Parameters

- m  [input int]
- n  [input int]
- nrhs  [input int]

Returns

- work  [float]
- info  [int]

Other Parameters

- cond  [input float, optional] Default: -1.0
- lwork  [input int, optional] Default: -1

scipy.linalg.lapack.dgelss_lwork

scipy.linalg.lapack.dgelss_lwork(m, n, nrhs[, cond, lwork]) = <fortran object>
Wrapper for dgelss_lwork.

Parameters

- m  [input int]
- n  [input int]
- nrhs  [input int]

Returns

- work  [float]
- info  [int]

Other Parameters

- cond  [input float, optional] Default: -1.0
- lwork  [input int, optional] Default: -1

scipy.linalg.lapack.cgelss_lwork

scipy.linalg.lapack.cgelss_lwork(m, n, nrhs[, cond, lwork]) = <fortran object>
Wrapper for cgelss_lwork.

Parameters

- m  [input int]
- n  [input int]
- nrhs  [input int]
Returns
work [complex]
info [int]

Other Parameters
cond [input float, optional] Default: -1.0
lwork [input int, optional] Default: -1

scipy.linalg.lapack.zgelss_lwork

scipy.linalg.lapack.zgelss_lwork(m, n, nrhs[, cond, lwork]) = <fortran object>
Wrapper for zgelss_lwork.

Parameters
m [input int]
n [input int]
nrhs [input int]

Returns
work [complex]
info [int]

Other Parameters
cond [input float, optional] Default: -1.0
lwork [input int, optional] Default: -1

scipy.linalg.lapack.sgelsd

scipy.linalg.lapack.sgelsd(a, b, lwork, size_iwork[, cond, overwrite_a, overwrite_b]) = <fortran object>
Wrapper for sgelsd.

Parameters
a [input rank-2 array(‘f’) with bounds (m,n)]
b [input rank-2 array(‘f’) with bounds (maxmn,nrhs)]
lwork [input int]
size_iwork [input int]

Returns
x [rank-2 array(‘f’) with bounds (maxmn,nrhs) and b storage]
s [rank-1 array(‘f’) with bounds (minmn)]
rank [int]
info [int]

Other Parameters
overwrite_a [input int, optional] Default: 0
overwrite_b [input int, optional] Default: 0
cond [input float, optional] Default: -1.0
scipy.linalg.lapack.dgelsd

\[
\text{scipy.linalg.lapack.dgelsd}(a, \ b, \ lwork, \ size\_iwork[, \ cond, \ overwrite\_a, \ overwrite\_b]) = \\
\quad <\text{fortran object}>
\]

Wrapper for dgelsd.

**Parameters**

- **a** [input rank-2 array('d') with bounds (m,n)]
- **b** [input rank-2 array('d') with bounds (maxmn,nrhs)]
- **lwork** [input int]
- **size\_iwork** [input int]

**Returns**

- **x** [rank-2 array('d') with bounds (maxmn,nrhs) and b storage]
- **s** [rank-1 array('d') with bounds (minmn)]
- **rank** [int]
- **info** [int]

**Other Parameters**

- **overwrite\_a** [input int, optional] Default: 0
- **overwrite\_b** [input int, optional] Default: 0
- **cond** [input float, optional] Default: -1.0

scipy.linalg.lapack.cgelsd

\[
\text{scipy.linalg.lapack.cgelsd}(a, \ b, \ lwork, \ size\_rwork, \ size\_iwork[, \ cond, \ overwrite\_a, \ overwrite\_b]) = <\text{fortran object}>
\]

Wrapper for cgelsd.

**Parameters**

- **a** [input rank-2 array('F') with bounds (m,n)]
- **b** [input rank-2 array('F') with bounds (maxmn,nrhs)]
- **lwork** [input int]
- **size\_rwork** [input int]
- **size\_iwork** [input int]

**Returns**

- **x** [rank-2 array('F') with bounds (maxmn,nrhs) and b storage]
- **s** [rank-1 array('F') with bounds (minmn)]
- **rank** [int]
- **info** [int]

**Other Parameters**

- **overwrite\_a** [input int, optional] Default: 0
- **overwrite\_b** [input int, optional] Default: 0
- **cond** [input float, optional] Default: -1.0
scipy.linalg.lapack.zgelsd

scipy.linalg.lapack.zgelsd(a, b, lwork, size_rwork, size_iwork[, cond, overwrite_a, overwrite_b]) = <fortran object>

Wrapper for zgelsd.

Parameters

a [input rank-2 array('D') with bounds (m,n)]
b [input rank-2 array('D') with bounds (maxmn,nrhs)]
lwork [input int]
size_rwork [input int]
size_iwork [input int]

Returns

x [rank-2 array('D') with bounds (maxmn,nrhs) and b storage]
s [rank-1 array('d') with bounds (minmn)]
rk [int]
info [int]

Other Parameters

overwrite_a [input int, optional] Default: 0
overwrite_b [input int, optional] Default: 0
cond [input float, optional] Default: -1.0

scipy.linalg.lapack.sgelsd_lwork

scipy.linalg.lapack.sgelsd_lwork(m, n, nrhs[, cond, lwork]) = <fortran object>

Wrapper for sgelsd_lwork.

Parameters

m [input int]
n [input int]
nrhs [input int]

Returns

work [float]
iwork [int]
info [int]

Other Parameters

cond [input float, optional] Default: -1.0
lwork [input int, optional] Default: -1

scipy.linalg.lapack.dgelsd_lwork

scipy.linalg.lapack.dgelsd_lwork(m, n, nrhs[, cond, lwork]) = <fortran object>

Wrapper for dgelsd_lwork.

Parameters

m [input int]
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```

n    [input int]
nrhs [input int]

Returns

work    [float]
iwork   [int]
info    [int]

Other Parameters

cond    [input float, optional] Default: -1.0
lwork   [input int, optional] Default: -1

scipy.linalg.lapack.cgelsd_lwork

scipy.linalg.lapack.cgelsd_lwork(m, n, nrhs[, cond, lwork]) = <fortran object>

Wrapper for cgelsd_lwork.

Parameters

m    [input int]
n    [input int]
nrhs [input int]

Returns

work    [complex]
rwork   [float]
iwork   [int]
info    [int]

Other Parameters

cond    [input float, optional] Default: -1.0
lwork   [input int, optional] Default: -1

scipy.linalg.lapack.zgelsd_lwork

scipy.linalg.lapack.zgelsd_lwork(m, n, nrhs[, cond, lwork]) = <fortran object>

Wrapper for zgelsd_lwork.

Parameters

m    [input int]
n    [input int]
nrhs [input int]

Returns

work    [complex]
rwork   [float]
iwork   [int]
info    [int]

Other Parameters

cond    [input float, optional] Default: -1.0
lwork   [input int, optional] Default: -1
```
scipy.linalg.lapack.sgelsy

scipy.linalg.lapack.sgelsy(a, b, jptv, cond, lwork[, overwrite_a, overwrite_b]) = <fortran object>

Wrapper for sgelsy.

**Parameters**

- **a**: [input rank-2 array('f') with bounds (m,n)]
- **b**: [input rank-2 array('f') with bounds (maxmn,nrhs)]
- **jptv**: [input rank-1 array('i') with bounds (n)]
- **cond**: [input float]
- **lwork**: [input int]

**Returns**

- **v**: [rank-2 array('f') with bounds (m,n) and a storage]
- **x**: [rank-2 array('f') with bounds (maxmn,nrhs) and b storage]
- **j**: [rank-1 array('i') with bounds (n) and jptv storage]
- **rank**: [int]
- **info**: [int]

**Other Parameters**

- **overwrite_a**: [input int, optional] Default: 0
- **overwrite_b**: [input int, optional] Default: 0

scipy.linalg.lapack.dgelsy

scipy.linalg.lapack.dgelsy(a, b, jptv, cond, lwork[, overwrite_a, overwrite_b]) = <fortran object>

Wrapper for dgelsy.

**Parameters**

- **a**: [input rank-2 array('d') with bounds (m,n)]
- **b**: [input rank-2 array('d') with bounds (maxmn,nrhs)]
- **jptv**: [input rank-1 array('i') with bounds (n)]
- **cond**: [input float]
- **lwork**: [input int]

**Returns**

- **v**: [rank-2 array('d') with bounds (m,n) and a storage]
- **x**: [rank-2 array('d') with bounds (maxmn,nrhs) and b storage]
- **j**: [rank-1 array('i') with bounds (n) and jptv storage]
- **rank**: [int]
- **info**: [int]

**Other Parameters**

- **overwrite_a**: [input int, optional] Default: 0
- **overwrite_b**: [input int, optional] Default: 0
scipy.linalg.lapack.cgelsy

\[ \begin{align*} 
\text{scipy.linalg.lapack.cgelsy}(a, b, jptv, \text{cond}, \text{lwork}[, \text{overwrite}_a, \text{overwrite}_b]) &= \text{<fortran object>} \\
\text{Wrapper for cgelsy.} \\
\text{Parameters} \\
\text{a} & \text{[input rank-2 array(‘F’) with bounds (m,n)]} \\
\text{b} & \text{[input rank-2 array(‘F’) with bounds (maxmn,nrhs)]} \\
\text{jptv} & \text{[input rank-1 array(‘i’) with bounds (n)]} \\
\text{cond} & \text{[input float]} \\
\text{lwork} & \text{[input int]} \\
\text{Returns} \\
\text{v} & \text{[rank-2 array(‘F’) with bounds (m,n) and a storage]} \\
\text{x} & \text{[rank-2 array(‘F’) with bounds (maxmn,nrhs) and b storage]} \\
\text{j} & \text{[rank-1 array(‘i’) with bounds (n) and jptv storage]} \\
\text{rank} & \text{[int]} \\
\text{info} & \text{[int]} \\
\text{Other Parameters} \\
\text{overwrite}_a & \text{[input int, optional] Default: 0} \\
\text{overwrite}_b & \text{[input int, optional] Default: 0} \\
\end{align*} \]

scipy.linalg.lapack.zgelsy

\[ \begin{align*} 
\text{scipy.linalg.lapack.zgelsy}(a, b, jptv, \text{cond}, \text{lwork}[, \text{overwrite}_a, \text{overwrite}_b]) &= \text{<fortran object>} \\
\text{Wrapper for zgelsy.} \\
\text{Parameters} \\
\text{a} & \text{[input rank-2 array(‘D’) with bounds (m,n)]} \\
\text{b} & \text{[input rank-2 array(‘D’) with bounds (maxmn,nrhs)]} \\
\text{jptv} & \text{[input rank-1 array(‘i’) with bounds (n)]} \\
\text{cond} & \text{[input float]} \\
\text{lwork} & \text{[input int]} \\
\text{Returns} \\
\text{v} & \text{[rank-2 array(‘D’) with bounds (m,n) and a storage]} \\
\text{x} & \text{[rank-2 array(‘D’) with bounds (maxmn,nrhs) and b storage]} \\
\text{j} & \text{[rank-1 array(‘i’) with bounds (n) and jptv storage]} \\
\text{rank} & \text{[int]} \\
\text{info} & \text{[int]} \\
\text{Other Parameters} \\
\text{overwrite}_a & \text{[input int, optional] Default: 0} \\
\text{overwrite}_b & \text{[input int, optional] Default: 0} \\
\end{align*} \]
scipy.linalg.lapack.sgelsy_lwork

scipy.linalg.lapack.sgelsy_lwork\( (m, n, nrhs, cond[, lwork]) \) = <fortran object>
Wrapper for sgelsy_lwork.

**Parameters**
- \( m \) [input int]
- \( n \) [input int]
- \( nrhs \) [input int]
- \( cond \) [input float]

**Returns**
- \( \text{work} \) [float]
- \( \text{info} \) [int]

**Other Parameters**
- \( lwork \) [input int, optional] Default: -1

scipy.linalg.lapack.dgelsy_lwork

scipy.linalg.lapack.dgelsy_lwork\( (m, n, nrhs, cond[, lwork]) \) = <fortran object>
Wrapper for dgelsy_lwork.

**Parameters**
- \( m \) [input int]
- \( n \) [input int]
- \( nrhs \) [input int]
- \( cond \) [input float]

**Returns**
- \( \text{work} \) [float]
- \( \text{info} \) [int]

**Other Parameters**
- \( lwork \) [input int, optional] Default: -1

scipy.linalg.lapack.cgelsy_lwork

scipy.linalg.lapack.cgelsy_lwork\( (m, n, nrhs, cond[, lwork]) \) = <fortran object>
Wrapper for cgelsy_lwork.

**Parameters**
- \( m \) [input int]
- \( n \) [input int]
- \( nrhs \) [input int]
- \( cond \) [input float]

**Returns**
- \( \text{work} \) [complex]
- \( \text{info} \) [int]

**Other Parameters**
- \( lwork \) [input int, optional] Default: -1
scipy.linalg.lapack.zgelsy_lwork

Wrapper for zgelsy_lwork.

Parameters
m [input int]
n [input int]
rhs [input int]
cond [input float]

Returns
work [complex]
info [int]

Other Parameters
lwork [input int, optional] Default: -1

scipy.linalg.lapack.sgeqp3

Wrapper for sgeqp3.

Parameters
a [input rank-2 array('f') with bounds (m,n)]

Returns
qr [rank-2 array('f') with bounds (m,n) and a storage]
jpvt [rank-1 array('i') with bounds (n)]
tau [rank-1 array('f') with bounds (MIN(m,n))]
work [rank-1 array('f') with bounds (MAX(lwork,1))]
info [int]

Other Parameters
overwrite_a [input int, optional] Default: 0
lwork [input int, optional] Default: max(3*(n+1),1)

scipy.linalg.lapack.dgeqp3

Wrapper for dgeqp3.

Parameters
a [input rank-2 array('d') with bounds (m,n)]

Returns
qr [rank-2 array('d') with bounds (m,n) and a storage]
jpvt [rank-1 array('i') with bounds (n)]
tau [rank-1 array('d') with bounds (MIN(m,n))]
work [rank-1 array('d') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
   [input int, optional] Default: 0
lwork   [input int, optional] Default: max(3*(n+1),1)

\texttt{scipy.linalg.lapack.cgeqp3}

\texttt{scipy.linalg.lapack.cgeqp3}(a[, lwork, overwrite_a]) = \texttt{<fortran object>}
Wrapper for cgeqp3.

\textbf{Parameters}

\begin{itemize}
  \item \texttt{a} [input rank-2 array('F') with bounds (m,n)]
\end{itemize}

\textbf{Returns}

\begin{itemize}
  \item \texttt{qr} [rank-2 array('F') with bounds (m,n) and a storage]
  \item \texttt{jpvt} [rank-1 array('i') with bounds (n)]
  \item \texttt{tau} [rank-1 array('F') with bounds (MIN(m,n))]
  \item \texttt{work} [rank-1 array('F') with bounds (MAX(lwork,1))]
  \item \texttt{info} [int]
\end{itemize}

\textbf{Other Parameters}

\begin{itemize}
  \item overwrite_a
        [input int, optional] Default: 0
  \item lwork
        [input int, optional] Default: max(3*(n+1),1)
\end{itemize}

\texttt{scipy.linalg.lapack.zgeqp3}

\texttt{scipy.linalg.lapack.zgeqp3}(a[, lwork, overwrite_a]) = \texttt{<fortran object>}
Wrapper for zgeqp3.

\textbf{Parameters}

\begin{itemize}
  \item \texttt{a} [input rank-2 array('D') with bounds (m,n)]
\end{itemize}

\textbf{Returns}

\begin{itemize}
  \item \texttt{qr} [rank-2 array('D') with bounds (m,n) and a storage]
  \item \texttt{jpvt} [rank-1 array('i') with bounds (n)]
  \item \texttt{tau} [rank-1 array('D') with bounds (MIN(m,n))]
  \item \texttt{work} [rank-1 array('D') with bounds (MAX(lwork,1))]
  \item \texttt{info} [int]
\end{itemize}

\textbf{Other Parameters}

\begin{itemize}
  \item overwrite_a
        [input int, optional] Default: 0
  \item lwork
        [input int, optional] Default: max(3*(n+1),1)
\end{itemize}

\texttt{scipy.linalg.lapack.sgeqrf}

\texttt{scipy.linalg.lapack.sgeqrf}(a[, lwork, overwrite_a]) = \texttt{<fortran object>}
Wrapper for sgeqrf.

\textbf{Parameters}

\begin{itemize}
  \item \texttt{a} [input rank-2 array('f') with bounds (m,n)]
\end{itemize}

\textbf{Returns}

\begin{itemize}
  \item \texttt{qr} [rank-2 array('f') with bounds (m,n) and a storage]
\end{itemize}
tau [rank-1 array('f') with bounds (MIN(m,n))]
work [rank-1 array('f') with bounds (MAX(lwork,1))]
info [int]

Other Parameters
overwrite_a [input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.dgeqrf
scipy.linalg.lapack.dgeqrf(a[:, lwork, overwrite_a]) = <fortran object>
Wrapper for dgeqrf.

Parameters
a [input rank-2 array('d') with bounds (m,n)]

Returns
qr [rank-2 array('d') with bounds (m,n) and a storage]
tau [rank-1 array('d') with bounds (MIN(m,n))]
work [rank-1 array('d') with bounds (MAX(lwork,1))]
info [int]

Other Parameters
overwrite_a [input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.cgeqrf
scipy.linalg.lapack.cgeqrf(a[*, lwork, overwrite_a]) = <fortran object>
Wrapper for cgeqrf.

Parameters
a [input rank-2 array('F') with bounds (m,n)]

Returns
qr [rank-2 array('F') with bounds (m,n) and a storage]
tau [rank-1 array('F') with bounds (MIN(m,n))]
work [rank-1 array('F') with bounds (MAX(lwork,1))]
info [int]

Other Parameters
overwrite_a [input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)
scipy.linalg.lapack.zgeqrf

scipy.linalg.lapack.zgeqrf(a[, lwork, overwrite_a]) = <fortran object>

Wrapper for zgeqrf.

Parameters

a
[input rank-2 array('D') with bounds (m,n)]

Returns

qr [rank-2 array('D') with bounds (m,n) and a storage]
tau [rank-1 array('D') with bounds (MIN(m,n))]
work [rank-1 array('D') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a [input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.sgerqf

scipy.linalg.lapack.sgerqf(a[, lwork, overwrite_a]) = <fortran object>

Wrapper for sgerqf.

Parameters

a
[input rank-2 array('f') with bounds (m,n)]

Returns

qr [rank-2 array('f') with bounds (m,n) and a storage]
tau [rank-1 array('f') with bounds (MIN(m,n))]
work [rank-1 array('f') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a [input int, optional] Default: 0
lwork [input int, optional] Default: max(3*m,1)

scipy.linalg.lapack.dgerqf

scipy.linalg.lapack.dgerqf(a[, lwork, overwrite_a]) = <fortran object>

Wrapper for dgerqf.

Parameters

a
[input rank-2 array('d') with bounds (m,n)]

Returns

qr [rank-2 array('d') with bounds (m,n) and a storage]
tau [rank-1 array('d') with bounds (MIN(m,n))]
work [rank-1 array('d') with bounds (MAX(lwork,1))]
info [int]

Other Parameters
overwrite_a
[input int, optional] Default: 0
lwork  [input int, optional] Default: max(3*m,1)

scipy.linalg.lapack.cgerqf

scipy.linalg.lapack.cgerqf(a, lwork, overwrite_a) = <fortran object>
Wrapper for cgerqf.

Parameters
a [input rank-2 array('F') with bounds (m,n)]

Returns
qr [rank-2 array('F') with bounds (m,n) and a storage]
tau [rank-1 array('F') with bounds (MIN(m,n))]
work [rank-1 array('F') with bounds (MAX(lwork,1))]
info [int]

Other Parameters
overwrite_a
[input int, optional] Default: 0
lwork  [input int, optional] Default: max(3*m,1)

scipy.linalg.lapack.zgerqf

scipy.linalg.lapack.zgerqf(a, lwork, overwrite_a) = <fortran object>
Wrapper for zgerqf.

Parameters
a [input rank-2 array('D') with bounds (m,n)]

Returns
qr [rank-2 array('D') with bounds (m,n) and a storage]
tau [rank-1 array('D') with bounds (MIN(m,n))]
work [rank-1 array('D') with bounds (MAX(lwork,1))]
info [int]

Other Parameters
overwrite_a
[input int, optional] Default: 0
lwork  [input int, optional] Default: max(3*m,1)

scipy.linalg.lapack.sgesdd

scipy.linalg.lapack.sgesdd(a, compute_uv, full_matrices, lwork, overwrite_a) = <fortran object>
Wrapper for sgesdd.

Parameters
a [input rank-2 array('f') with bounds (m,n)]

Returns
u [rank-2 array('f') with bounds (u0,u1)]
s [rank-1 array('f') with bounds (minmn)]
vt  [rank-2 array('f') with bounds (vt0,vt1)]
info  [int]

Other Parameters

overwrite_a  [input int, optional] Default: 0
compute_uv  [input int, optional] Default: 1
full_matrices  [input int, optional] Default: 1
lwork  [input int, optional] Default: max((compute_uv?4*minmn*minmn+MAX(m,n)+9*minmn+MAX(m,n)),1)

scipy.linalg.lapack.dgesdd
scipy.linalg.lapack.dgesdd(a[, compute_uv, full_matrices, lwork, overwrite_a]) = <fortran object>

Wrapper for dgesdd.

Parameters

a  [input rank-2 array('d') with bounds (m,n)]

Returns

u  [rank-2 array('d') with bounds (u0,u1)]
s  [rank-1 array('d') with bounds (minmn)]
vt  [rank-2 array('d') with bounds (vt0,vt1)]
info  [int]

Other Parameters

overwrite_a  [input int, optional] Default: 0
compute_uv  [input int, optional] Default: 1
full_matrices  [input int, optional] Default: 1
lwork  [input int, optional] Default: max((compute_uv?4*minmn*minmn+MAX(m,n)+9*minmn+MAX(m,n)),1)

scipy.linalg.lapack.cgesdd
scipy.linalg.lapack.cgesdd(a[, compute_uv, full_matrices, lwork, overwrite_a]) = <fortran object>

Wrapper for cgesdd.

Parameters

a  [input rank-2 array('F') with bounds (m,n)]

Returns

u  [rank-2 array('F') with bounds (u0,u1)]
s  [rank-1 array('f') with bounds (minmn)]
vt  [rank-2 array('F') with bounds (vt0,vt1)]
info  [int]

Other Parameters

overwrite_a  [input int, optional] Default: 0
compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1
lwork
[input int, optional] Default: max((compute_uv?2*minmn*minmn+MAX(m,n)+2*minmn:2*minmn+MAX(m,n)),1)

scipy.linalg.lapack.zgesdd

scipy.linalg.lapack.zgesdd(a[, compute_uv, full_matrices, lwork, overwrite_a]) = <fortran object>
Wrapper for zgesdd.

Parameters
a
[input rank-2 array('D') with bounds (m,n)]

Returns
u
[rank-2 array('D') with bounds (u0,u1)]
s
[rank-1 array('d') with bounds (minmn)]
vt
[rank-2 array('D') with bounds (vt0,vt1)]
info
[int]

Other Parameters
overwrite_a
[input int, optional] Default: 0
compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1
lwork
[input int, optional] Default: max((compute_uv?2*minmn*minmn+MAX(m,n)+2*minmn:2*minmn+MAX(m,n)),1)

scipy.linalg.lapack.sgesdd_lwork

scipy.linalg.lapack.sgesdd_lwork(m, n[, compute_uv, full_matrices]) = <fortran object>
Wrapper for sgesdd_lwork.

Parameters
m
[input int]
n
[input int]

Returns
work
[float]
info
[int]

Other Parameters
compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1
scipy.linalg.lapack.dgesdd_lwork

scipy.linalg.lapack.dgesdd_lwork(m, n[, compute_uv, full_matrices]) = <fortran object>
Wrapper for dgesdd_lwork.

Parameters
- m [input int]
- n [input int]

Returns
- work [float]
- info [int]

Other Parameters
- compute_uv [input int, optional] Default: 1
- full_matrices [input int, optional] Default: 1

scipy.linalg.lapack.cgesdd_lwork

scipy.linalg.lapack.cgesdd_lwork(m, n[, compute_uv, full_matrices]) = <fortran object>
Wrapper for cgesdd_lwork.

Parameters
- m [input int]
- n [input int]

Returns
- work [complex]
- info [int]

Other Parameters
- compute_uv [input int, optional] Default: 1
- full_matrices [input int, optional] Default: 1

scipy.linalg.lapack.zgesdd_lwork

scipy.linalg.lapack.zgesdd_lwork(m, n[, compute_uv, full_matrices]) = <fortran object>
Wrapper for zgesdd_lwork.

Parameters
- m [input int]
- n [input int]

Returns
- work [complex]
- info [int]

Other Parameters
- compute_uv [input int, optional] Default: 1
**full_matrices**
[input int, optional] Default: 1

**scipy.linalg.lapack.sgesvd**

```python
scipy.linalg.lapack.sgesvd(a[, compute_uv, full_matrices, lwork, overwrite_a]) = <fortran object>
```
Wrapper for sgesvd.

**Parameters**

- `a` [input rank-2 array('f') with bounds (m,n)]

**Returns**

- `u` [rank-2 array('f') with bounds (u0,u1)]
- `s` [rank-1 array('f') with bounds (minmn)]
- `vt` [rank-2 array('f') with bounds (vt0,vt1)]
- `info` [int]

**Other Parameters**

- `overwrite_a` [input int, optional] Default: 0
- `compute_uv` [input int, optional] Default: 1
- `full_matrices` [input int, optional] Default: 1
- `lwork` [input int, optional] Default: max(MAX(3*minmn+MAX(m,n),5*minmn),1)

**scipy.linalg.lapack.dgesvd**

```python
scipy.linalg.lapack.dgesvd(a[, compute_uv, full_matrices, lwork, overwrite_a]) = <fortran object>
```
Wrapper for dgesvd.

**Parameters**

- `a` [input rank-2 array('d') with bounds (m,n)]

**Returns**

- `u` [rank-2 array('d') with bounds (u0,u1)]
- `s` [rank-1 array('d') with bounds (minmn)]
- `vt` [rank-2 array('d') with bounds (vt0,vt1)]
- `info` [int]

**Other Parameters**

- `overwrite_a` [input int, optional] Default: 0
- `compute_uv` [input int, optional] Default: 1
- `full_matrices` [input int, optional] Default: 1
- `lwork` [input int, optional] Default: max(MAX(3*minmn+MAX(m,n),5*minmn),1)
scipy.linalg.lapack.cgesvd

scipy.linalg.lapack.cgesvd(a, compute_uv, full_matrices, lwork, overwrite_a) = <fortran object>

Wrapper for cgesvd.

Parameters

a [input rank-2 array('F') with bounds (m,n)]

Returns

u [rank-2 array('F') with bounds (u0,u1)]

s [rank-1 array('f') with bounds (minmn)]

vt [rank-2 array('F') with bounds (vt0,vt1)]

info [int]

Other Parameters

overwrite_a [input int, optional] Default: 0

compute_uv [input int, optional] Default: 1

full_matrices [input int, optional] Default: 1

lwork [input int, optional] Default: MAX(2*minmn+MAX(m,n),1)

scipy.linalg.lapack.zgesvd

scipy.linalg.lapack.zgesvd(a, compute_uv, full_matrices, lwork, overwrite_a) = <fortran object>

Wrapper for zgesvd.

Parameters

a [input rank-2 array('D') with bounds (m,n)]

Returns

u [rank-2 array('D') with bounds (u0,u1)]

s [rank-1 array('d') with bounds (minmn)]

vt [rank-2 array('D') with bounds (vt0,vt1)]

info [int]

Other Parameters

overwrite_a [input int, optional] Default: 0

compute_uv [input int, optional] Default: 1

full_matrices [input int, optional] Default: 1

lwork [input int, optional] Default: MAX(2*minmn+MAX(m,n),1)
scipy.linalg.lapack.sgesvd_lwork

scipy.linalg.lapack.sgesvd_lwork(m, n[, compute_uv, full_matrices]) = <fortran object>
Wrapper for sgesvd_lwork.

Parameters
- m [input int]
- n [input int]

Returns
- work [float]
- info [int]

Other Parameters
- compute_uv [input int, optional] Default: 1
- full_matrices [input int, optional] Default: 1

scipy.linalg.lapack.dgesvd_lwork

scipy.linalg.lapack.dgesvd_lwork(m, n[, compute_uv, full_matrices]) = <fortran object>
Wrapper for dgesvd_lwork.

Parameters
- m [input int]
- n [input int]

Returns
- work [float]
- info [int]

Other Parameters
- compute_uv [input int, optional] Default: 1
- full_matrices [input int, optional] Default: 1

scipy.linalg.lapack.cgesvd_lwork

scipy.linalg.lapack.cgesvd_lwork(m, n[, compute_uv, full_matrices]) = <fortran object>
Wrapper for cgesvd_lwork.

Parameters
- m [input int]
- n [input int]

Returns
- work [complex]
- info [int]

Other Parameters
- compute_uv [input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1

scipy.linalg.lapack.zgesvd_lwork

scipy.linalg.lapack.zgesvd_lwork(m, n[, compute_uv, full_matrices]) = <fortran object>
Wrapper for zgesvd_lwork.

Parameters
m [input int]
n [input int]

Returns
work [complex]
info [int]

Other Parameters
compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1

scipy.linalg.lapack.sgesv

scipy.linalg.lapack.sgesv(a, b[, overwrite_a, overwrite_b]) = <fortran object>
Wrapper for sgesv.

Parameters
a [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (n,nrhs)]

Returns
lu [rank-2 array('f') with bounds (n,n) and a storage]
piv [rank-1 array('i') with bounds (n)]
x [rank-2 array('f') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.dgesv

scipy.linalg.lapack.dgesv(a, b[, overwrite_a, overwrite_b]) = <fortran object>
Wrapper for dgesv.

Parameters
a [input rank-2 array('d') with bounds (n,n)]
b [input rank-2 array('d') with bounds (n,nrhs)]

Returns
lu [rank-2 array('d') with bounds (n,n) and a storage]
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piv  [rank-1 array('i') with bounds (n)]
x  [rank-2 array('d') with bounds (n,nrhs) and b storage]
info  [int]

Other Parameters
overwrite_a  [input int, optional] Default: 0
overwrite_b  [input int, optional] Default: 0

scipy.linalg.lapack.cgesv

scipy.linalg.lapack.cgesv(a, b[, overwrite_a, overwrite_b]) = <fortran object>
Wrapper for cgesv.

Parameters
a  [input rank-2 array('F') with bounds (n,n)]
b  [input rank-2 array('F') with bounds (n,nrhs)]

Returns
lu  [rank-2 array('F') with bounds (n,n) and a storage]
piv  [rank-1 array('i') with bounds (n)]
x  [rank-2 array('F') with bounds (n,nrhs) and b storage]
info  [int]

Other Parameters
overwrite_a  [input int, optional] Default: 0
overwrite_b  [input int, optional] Default: 0

scipy.linalg.lapack.zgesv

scipy.linalg.lapack.zgesv(a, b[, overwrite_a, overwrite_b]) = <fortran object>
Wrapper for zgesv.

Parameters
a  [input rank-2 array('D') with bounds (n,n)]
b  [input rank-2 array('D') with bounds (n,nrhs)]

Returns
lu  [rank-2 array('D') with bounds (n,n) and a storage]
piv  [rank-1 array('i') with bounds (n)]
x  [rank-2 array('D') with bounds (n,nrhs) and b storage]
info  [int]

Other Parameters
overwrite_a  [input int, optional] Default: 0
overwrite_b  [input int, optional] Default: 0

6.11. Low-level LAPACK functions (scipy.linalg.lapack)
scipy.linalg.lapack.sgesvx

scipy.linalg.lapack.sgesvx(a, b, fact, trans, af, ipiv, equed, r, c, overwrite_a, overwrite_b) =
<fortran object>

Wrapper for sgesvx.

Parameters
a [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (n, nrhs)]

Returns
as [rank-2 array('f') with bounds (n,n) and a storage]
lu [rank-2 array('f') with bounds (n,n) and af storage]
ipiv [rank-1 array('i') with bounds (n)]
equed [string(len=1)]
rs [rank-1 array('f') with bounds (n) and r storage]
cs [rank-1 array('f') with bounds (n) and c storage]
bs [rank-2 array('f') with bounds (n, nrhs) and b storage]
x [rank-2 array('f') with bounds (n, nrhs)]

Other Parameters
fact [input string(len=1), optional] Default: ‘E’
trans [input string(len=1), optional] Default: ‘N’
overwrite_a [input int, optional] Default: 0
af [input rank-2 array('f') with bounds (n,n)]
ipiv [input rank-1 array('i') with bounds (n)]
equed [input string(len=1), optional] Default: ‘B’
r [input rank-1 array('f') with bounds (n)]
c [input rank-1 array('f') with bounds (n)]
overwrite_b [input int, optional] Default: 0

scipy.linalg.lapack.dgesvx

scipy.linalg.lapack.dgesvx(a, b, fact, trans, af, ipiv, equed, r, c, overwrite_a, overwrite_b) =
<fortran object>

Wrapper for dgesvx.

Parameters
a [input rank-2 array('d') with bounds (n,n)]
b [input rank-2 array('d') with bounds (n, nrhs)]

Returns
as [rank-2 array('d') with bounds (n,n) and a storage]
lu [rank-2 array('d') with bounds (n,n) and af storage]
ipiv [rank-1 array('i') with bounds (n)]
equed [string(len=1)]
rs [rank-1 array('d') with bounds (n) and r storage]
cs [rank-1 array('d') with bounds (n) and c storage]
bs      [rank-2 array('d') with bounds (n,nrhs) and b storage]
         [rank-2 array('d') with bounds (n,nrhs)]
x rcond  [float]
ferr    [rank-1 array('d') with bounds (nrhs)]
berr    [rank-1 array('d') with bounds (nrhs)]
info    [int]

Other Parameters

fact    [input string(len=1), optional] Default: ‘E’
trans   [input string(len=1), optional] Default: ‘N’
overwrite_a [input int, optional] Default: 0
af      [input rank-2 array('d') with bounds (n,n)]
ipiv    [input rank-1 array('i') with bounds (n)]
equed   [input string(len=1), optional] Default: ‘B’
r       [input rank-1 array('d') with bounds (n)]
c       [input rank-1 array('d') with bounds (n)]
overwrite_b [input int, optional] Default: 0

scipy.linalg.lapack.cgesvx

scipy.linalg.lapack.cgesvx(a, b[, fact, trans, af, ipiv, equed, r, c, overwrite_a, overwrite_b]) =
<fortran object>

Wrapper for cgesvx.

Parameters

a      [input rank-2 array('F') with bounds (n,n)]
b      [input rank-2 array('F') with bounds (n,nrhs)]

Returns

as [rank-2 array('F') with bounds (n,n) and a storage]
lu [rank-2 array('F') with bounds (n,n) and af storage]
ipiv [rank-1 array('i') with bounds (n)]
equed [string(len=1)]
rs [rank-1 array('f') with bounds (n) and r storage]
cs [rank-1 array('f') with bounds (n) and c storage]
bs [rank-2 array('F') with bounds (n,nrhs) and b storage]
x [rank-2 array('F') with bounds (n,nrhs)]
rcond [float]
ferr [rank-1 array('f') with bounds (nrhs)]
berr [rank-1 array('f') with bounds (nrhs)]
info [int]

Other Parameters

fact    [input string(len=1), optional] Default: ‘E’
trans   [input string(len=1), optional] Default: ‘N’
overwrite_a [input int, optional] Default: 0
af      [input rank-2 array('F') with bounds (n,n)]
ipiv    [input rank-1 array('i') with bounds (n)]
equed   [input string(len=1), optional] Default: ‘B’
r       [input rank-1 array('f') with bounds (n)]
c       [input rank-1 array('f') with bounds (n)]

6.11. Low-level LAPACK functions (scipy.linalg.lapack)
scipy.linalg.lapack.zgesvx

scipy.linalg.lapack.zgesvx(a, b[, fact, trans, af, ipiv, equed, r, c, overwrite_a, overwrite_b]) = <fortran object>

Wrapper for zgesvx.

Parameters

- a [input rank-2 array('D') with bounds (n,n)]
- b [input rank-2 array('D') with bounds (n,nrhs)]

Returns

- as [rank-2 array('D') with bounds (n,n) and a storage]
- lu [rank-2 array('D') with bounds (n,n) and af storage]
- ipiv [rank-1 array('i') with bounds (n)]
- equed [string(len=1)]
- rs [rank-1 array('d') with bounds (n) and r storage]
- cs [rank-1 array('d') with bounds (n) and c storage]
- bs [rank-2 array('D') with bounds (n,nrhs) and b storage]
- x [rank-2 array('D') with bounds (n,nrhs)]
- rcond [float]
- ferr [rank-1 array('d') with bounds (nrhs)]
- berr [rank-1 array('d') with bounds (nrhs)]
- info [int]

Other Parameters

- fact [input string(len=1), optional] Default: ‘E’
- trans [input string(len=1), optional] Default: ‘N’
- overwrite_a [input int, optional] Default: 0
- af [input rank-2 array('D') with bounds (n,n)]
- ipiv [input rank-1 array('i') with bounds (n)]
- equed [input string(len=1), optional] Default: ‘B’
- r [input rank-1 array('d') with bounds (n)]
- c [input rank-1 array('d') with bounds (n)]
- overwrite_b [input int, optional] Default: 0

scipy.linalg.lapack.sgecon

scipy.linalg.lapack.sgecon(a, anorm[, norm]) = <fortran object>

Wrapper for sgecon.

Parameters

- a [input rank-2 array('F') with bounds (n,n)]
- anorm [input float]

Returns

- rcond [float]
- info [int]

Other Parameters

- norm [input string(len=1)]
norm \[ input \ string(len=1), \ optional \] Default: ‘1’

**scipy.linalg.lapack.dgecon**

`scipy.linalg.lapack.dgecon(a, anorm[, norm]) = <fortran object>`

Wrapper for dgecon.

**Parameters**

- `a` [input rank-2 array('d') with bounds (n,n)]
- `anorm` [input float]

**Returns**

- `rcond` [float]
- `info` [int]

**Other Parameters**

- `norm` [input string(len=1), optional] Default: ‘1’

**scipy.linalg.lapack.cgecon**

`scipy.linalg.lapack.cgecon(a, anorm[, norm]) = <fortran object>`

Wrapper for cgecon.

**Parameters**

- `a` [input rank-2 array('F') with bounds (n,n)]
- `anorm` [input float]

**Returns**

- `rcond` [float]
- `info` [int]

**Other Parameters**

- `norm` [input string(len=1), optional] Default: ‘1’

**scipy.linalg.lapack.zgecon**

`scipy.linalg.lapack.zgecon(a, anorm[, norm]) = <fortran object>`

Wrapper for zgecon.

**Parameters**

- `a` [input rank-2 array('D') with bounds (n,n)]
- `anorm` [input float]

**Returns**

- `rcond` [float]
- `info` [int]

**Other Parameters**

- `norm` [input string(len=1), optional] Default: ‘1’
scipy.linalg.lapack.ssysv

scipy.linalg.lapack.ssysv(a, b, lwork, lower, overwrite_a, overwrite_b) = <fortran object>
Wrapper for ssysv.

Parameters

a [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (n,nrhs)]

Returns

udut [rank-2 array('F') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
x [rank-2 array('f') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_a [input int, optional] Default: 0
overwrite_b [input int, optional] Default: 0
lwork [input int, optional] Default: max(n,1)
lower [input int, optional] Default: 0

scipy.linalg.lapack.dsysv

scipy.linalg.lapack.dsysv(a, b, lwork, lower, overwrite_a, overwrite_b) = <fortran object>
Wrapper for dsysv.

Parameters

a [input rank-2 array('d') with bounds (n,n)]
b [input rank-2 array('d') with bounds (n,nrhs)]

Returns

udut [rank-2 array('d') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
x [rank-2 array('d') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_a [input int, optional] Default: 0
overwrite_b [input int, optional] Default: 0
lwork [input int, optional] Default: max(n,1)
lower [input int, optional] Default: 0

scipy.linalg.lapack.csysv

scipy.linalg.lapack.csysv(a, b, lwork, lower, overwrite_a, overwrite_b) = <fortran object>
Wrapper for csysv.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
b [input rank-2 array('F') with bounds (n,nrhs)]
Returns

udut [rank-2 array('F') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
x [rank-2 array('F') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_a [input int, optional] Default: 0
overwrite_b [input int, optional] Default: 0
lwork [input int, optional] Default: max(n,1)
lower [input int, optional] Default: 0

scipy.linalg.lapack.zsysv

scipy.linalg.lapack.zsysv(a, b[, lwork, lower, overwrite_a, overwrite_b]) = <fortran object>

Wrapper for zsysv.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (n,nrhs)]

Returns

udut [rank-2 array('D') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
x [rank-2 array('D') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_a [input int, optional] Default: 0
overwrite_b [input int, optional] Default: 0
lwork [input int, optional] Default: max(n,1)
lower [input int, optional] Default: 0

scipy.linalg.lapack.ssysv_lwork

scipy.linalg.lapack.ssysv_lwork(n[, lower]) = <fortran object>

Wrapper for ssysv_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0
scipy.linalg.lapack.dsysv_lwork

scipy.linalg.lapack.dsysv_lwork(n[, lower]) = <fortran object>
   Wrapper for dsysv_lwork.

Parameters
   n       [input int]

Returns
   work    [float]
   info    [int]

Other Parameters
   lower   [input int, optional] Default: 0

scipy.linalg.lapack.csysv_lwork

scipy.linalg.lapack.csysv_lwork(n[, lower]) = <fortran object>
   Wrapper for csysv_lwork.

Parameters
   n       [input int]

Returns
   work    [complex]
   info    [int]

Other Parameters
   lower   [input int, optional] Default: 0

scipy.linalg.lapack.zsysv_lwork

scipy.linalg.lapack.zsysv_lwork(n[, lower]) = <fortran object>
   Wrapper for zsysv_lwork.

Parameters
   n       [input int]

Returns
   work    [complex]
   info    [int]

Other Parameters
   lower   [input int, optional] Default: 0

scipy.linalg.lapack.ssysvx

scipy.linalg.lapack.ssysvx(a, b[, af, ipiv, lwork, factored, lower, overwrite_a, overwrite_b]) =
   <fortran object>
   Wrapper for ssyevx.

Parameters
   a       [input rank-2 array('f') with bounds (n,n)]
   b       [input rank-2 array('f') with bounds (n,nrhs)]
Returns

- `a_s` [rank-2 array('f') with bounds (n,n) and a storage]
- `udut` [rank-2 array('f') with bounds (n,n) and af storage]
- `ipiv` [rank-1 array('i') with bounds (n)]
- `b_s` [rank-2 array('f') with bounds (n,nrhs) and b storage]
- `x` [rank-2 array('f') with bounds (n,nrhs)]
- `rcond` [float]
- `ferr` [rank-1 array('f') with bounds (nrhs)]
- `berr` [rank-1 array('f') with bounds (nrhs)]
- `info` [int]

Other Parameters

- `overwrite_a` [input int, optional] Default: 0
- `af` [input rank-2 array('f') with bounds (n,n)]
- `ipiv` [input rank-1 array('i') with bounds (n)]
- `overwrite_b` [input int, optional] Default: 0
- `lwork` [input int, optional] Default: max(3*n,1)
- `factored` [input int, optional] Default: 0
- `lower` [input int, optional] Default: 0

`scipy.linalg.lapack.dsysvx`

 Wrapper for dsyevx.

Parameters

- `a` [input rank-2 array('d') with bounds (n,n)]
- `b` [input rank-2 array('d') with bounds (n,nrhs)]

Returns

- `a_s` [rank-2 array('d') with bounds (n,n) and a storage]
- `udut` [rank-2 array('d') with bounds (n,n) and af storage]
- `ipiv` [rank-1 array('i') with bounds (n)]
- `b_s` [rank-2 array('d') with bounds (n,nrhs) and b storage]
- `x` [rank-2 array('d') with bounds (n,nrhs)]
- `rcond` [float]
- `ferr` [rank-1 array('d') with bounds (nrhs)]
- `berr` [rank-1 array('d') with bounds (nrhs)]
- `info` [int]

Other Parameters

- `overwrite_a` [input int, optional] Default: 0
- `af` [input rank-2 array('d') with bounds (n,n)]
- `ipiv` [input rank-1 array('i') with bounds (n)]
- `overwrite_b` [input int, optional] Default: 0
- `lwork` [input int, optional] Default: max(3*n,1)
- `factored` [input int, optional] Default: 0
- `lower` [input int, optional] Default: 0
scipy.linalg.lapack.csyevx

scipy.linalg.lapack.csyevx(a, b[, af, ipiv, lwork, factored, lower, overwrite_a, overwrite_b]) =
<fortran object>

Wrapper for csyevx.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
b [input rank-2 array('F') with bounds (n,nrhs)]

Returns

a_s [rank-2 array('F') with bounds (n,n) and a storage]
udut [rank-2 array('F') with bounds (n,n) and af storage]
ipiv [rank-1 array('i') with bounds (n)]
b_s [rank-2 array('F') with bounds (n,nrhs) and b storage]
x [rank-2 array('F') with bounds (n,nrhs)]
rcond [float]
ferr [rank-1 array('f') with bounds (nrhs)]
berr [rank-1 array('f') with bounds (nrhs)]
info [int]

Other Parameters

overwrite_a [input int, optional] Default: 0
af [input rank-2 array('F') with bounds (n,n)]
overwrite_b [input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)
factored [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.zsyevx

scipy.linalg.lapack.zsyevx(a, b[, af, ipiv, lwork, factored, lower, overwrite_a, overwrite_b]) =
<fortran object>

Wrapper for zsyevx.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (n,nrhs)]

Returns

a_s [rank-2 array('D') with bounds (n,n) and a storage]
udut [rank-2 array('D') with bounds (n,n) and af storage]
ipiv [rank-1 array('i') with bounds (n)]
b_s [rank-2 array('D') with bounds (n,nrhs) and b storage]
x [rank-2 array('D') with bounds (n,nrhs)]
rcond [float]
ferr [rank-1 array('d') with bounds (nrhs)]
berr [rank-1 array('d') with bounds (nrhs)]
info [int]

Other Parameters

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overwrite_a  
[input int, optional] Default: 0
af  
[input rank-2 array('D') with bounds (n,n)]
ipiv  
[input rank-1 array('i') with bounds (n)]
overwrite_b  
[input int, optional] Default: 0
lwork  
[input int, optional] Default: max(3*n,1)
factored  
[input int, optional] Default: 0
lower  
[input int, optional] Default: 0

**scipy.linalg.lapack.ssysvx_lwork**

```
scipy.linalg.lapack.ssysvx_lwork(n[, lower]) = <fortran object>
```
Wrapper for ssysvx_lwork.

**Parameters**

- `n` [input int]

**Returns**

- `work` [float]
- `info` [int]

**Other Parameters**

- `lower` [input int, optional] Default: 0

**scipy.linalg.lapack.dsysvx_lwork**

```
scipy.linalg.lapack.dsysvx_lwork(n[, lower]) = <fortran object>
```
Wrapper for dsysvx_lwork.

**Parameters**

- `n` [input int]

**Returns**

- `work` [float]
- `info` [int]

**Other Parameters**

- `lower` [input int, optional] Default: 0

**scipy.linalg.lapack.csysvx_lwork**

```
scipy.linalg.lapack.csysvx_lwork(n[, lower]) = <fortran object>
```
Wrapper for csysvx_lwork.

**Parameters**

- `n` [input int]

**Returns**

- `work` [complex]
- `info` [int]

**Other Parameters**

- `lower` [input int, optional] Default: 0
scipy.linalg.lapack.zsysvx_lwork

scipy.linalg.lapack.zsysvx_lwork(n[lower]) = <fortran object>
Wrapper for zsysvx_lwork.

Parameters
n [input int]

Returns
work [complex]
info [int]

Other Parameters
lower [input int, optional] Default: 0

scipy.linalg.lapack.ssygst

scipy.linalg.lapack.ssygst(a, b[itype, lower, overwrite_a]) = <fortran object>
Wrapper for ssygst.

Parameters
a [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (n,n)]

Returns
c [rank-2 array('f') with bounds (n,n) and a storage]
info [int]

Other Parameters
overwrite_a [input int, optional] Default: 0
itype [input int, optional] Default: 1
lower [input int, optional] Default: 0

scipy.linalg.lapack.dsygst

scipy.linalg.lapack.dsygst(a, b[itype, lower, overwrite_a]) = <fortran object>
Wrapper for dsygst.

Parameters
a [input rank-2 array('d') with bounds (n,n)]
b [input rank-2 array('d') with bounds (n,n)]

Returns
c [rank-2 array('d') with bounds (n,n) and a storage]
info [int]

Other Parameters
overwrite_a [input int, optional] Default: 0
itype [input int, optional] Default: 1
lower [input int, optional] Default: 0
scipy.linalg.lapack.ssytrd

scipy.linalg.lapack.ssytrd(a[, lower, lwork, overwrite_a]) = <fortran object>

Wrapper for ssytrd.

Parameters

a [input rank-2 array('f') with bounds (lda,n)]

Returns

c [rank-2 array('f') with bounds (lda,n) and a storage]
d [rank-1 array('f') with bounds (n)]
e [rank-1 array('f') with bounds (n - 1)]
tau [rank-1 array('f') with bounds (n - 1)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_a [input int, optional] Default: 0
lwork [input int, optional] Default: MAX(n,1)

scipy.linalg.lapack.dsytrd

scipy.linalg.lapack.dsytrd(a[, lower, lwork, overwrite_a]) = <fortran object>

Wrapper for dsytrd.

Parameters

a [input rank-2 array('d') with bounds (lda,n)]

Returns

c [rank-2 array('d') with bounds (lda,n) and a storage]
d [rank-1 array('d') with bounds (n)]
e [rank-1 array('d') with bounds (n - 1)]
tau [rank-1 array('d') with bounds (n - 1)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_a [input int, optional] Default: 0
lwork [input int, optional] Default: MAX(n,1)

scipy.linalg.lapack.ssytrd_lwork

scipy.linalg.lapack.ssytrd_lwork(n[, lower]) = <fortran object>

Wrapper for ssytrd_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters
lower [input int, optional] Default: 0

**scipy.linalg.lapack.dsytrd_lwork**

\[
\text{scipy.linalg.lapack.dsytrd_lwork}(n[, \text{lower}]) = \text{<fortran object>}
\]

Wrapper for `dsytrd_lwork`.

**Parameters**

- \( n \) [input int]

**Returns**

- \( \text{work} \) [float]
- \( \text{info} \) [int]

**Other Parameters**

- \( \text{lower} \) [input int, optional] Default: 0

**scipy.linalg.lapack.chetrd**

\[
\text{scipy.linalg.lapack.chetrd}(a[, \text{lower}, \text{lwork}, \text{overwrite}_a]) = \text{<fortran object>}
\]

Wrapper for `chetrd`.

**Parameters**

- \( a \) [input rank-2 array('F') with bounds (lda,n)]

**Returns**

- \( \text{c} \) [rank-2 array('F') with bounds (lda,n) and a storage]
- \( \text{d} \) [rank-1 array('f') with bounds (n)]
- \( \text{e} \) [rank-1 array('f') with bounds (n - 1)]
- \( \text{tau} \) [rank-1 array('F') with bounds (n - 1)]
- \( \text{info} \) [int]

**Other Parameters**

- \( \text{lower} \) [input int, optional] Default: 0
- \( \text{overwrite}_a \) [input int, optional] Default: 0
- \( \text{lwork} \) [input int, optional] Default: MAX(n,1)

**scipy.linalg.lapack.zhetrd**

\[
\text{scipy.linalg.lapack.zhetrd}(a[, \text{lower}, \text{lwork}, \text{overwrite}_a]) = \text{<fortran object>}
\]

Wrapper for `zhetrd`.

**Parameters**

- \( a \) [input rank-2 array('D') with bounds (lda,n)]

**Returns**

- \( \text{c} \) [rank-2 array('D') with bounds (lda,n) and a storage]
- \( \text{d} \) [rank-1 array('d') with bounds (n)]
- \( \text{e} \) [rank-1 array('d') with bounds (n - 1)]
- \( \text{tau} \) [rank-1 array('D') with bounds (n - 1)]
- \( \text{info} \) [int]

**Other Parameters**

- \( \text{lower} \) [input int, optional] Default: 0
- \( \text{overwrite}_a \) [input int, optional] Default: 0
- \( \text{lwork} \) [input int, optional] Default: MAX(n,1)
lower [input int, optional] Default: 0
overwrite_a [input int, optional] Default: 0
lwork [input int, optional] Default: MAX(n,1)

scipy.linalg.lapack.chetrd_lwork
scipy.linalg.lapack.chetrd_lwork(n[, lower]) = <fortran object>
Wrapper for chetrd_lwork.

Parameters
n [input int]

Returns
work [complex]
info [int]

Other Parameters
lower [input int, optional] Default: 0

scipy.linalg.lapack.zhetrd_lwork
scipy.linalg.lapack.zhetrd_lwork(n[, lower]) = <fortran object>
Wrapper for zhetrd_lwork.

Parameters
n [input int]

Returns
work [complex]
info [int]

Other Parameters
lower [input int, optional] Default: 0

scipy.linalg.lapack.chesv
scipy.linalg.lapack.chesv(a, b[, lwork, lower, overwrite_a, overwrite_b]) = <fortran object>
Wrapper for chesv.

Parameters
a [input rank-2 array('F') with bounds (n,n)]
b [input rank-2 array('F') with bounds (n,nrhs)]

Returns
uduh [rank-2 array('F') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
x [rank-2 array('F') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters
overwrite_a [input int, optional] Default: 0
overwrite_b

[input int, optional] Default: 0

lwork
[Input int, optional] Default: max(n,1)

lower
[Input int, optional] Default: 0

scipy.linalg.lapack.zhesv

scipy.linalg.lapack.zhesv(a, b[, lwork, lower, overwrite_a, overwrite_b]) = <fortran object>

Wrapper for zhesv.

Parameters
a
[Input rank-2 array('D') with bounds (n,n)]
b
[Input rank-2 array('D') with bounds (n,nrhs)]

Returns
uduh
[Rank-2 array('D') with bounds (n,n) and a storage]
ipiv
[Rank-1 array('i') with bounds (n)]
x
[Rank-2 array('D') with bounds (n,nrhs) and b storage]
info
[int]

Other Parameters
overwrite_a
[Input int, optional] Default: 0
overwrite_b
[Input int, optional] Default: 0
lwork
[Input int, optional] Default: max(n,1)
lower
[Input int, optional] Default: 0

scipy.linalg.lapack.chesv_lwork

scipy.linalg.lapack.chesv_lwork(n[, lower]) = <fortran object>

Wrapper for chesv_lwork.

Parameters
n
[Input int]

Returns
work
[Complex]
info
[int]

Other Parameters
lower
[Input int, optional] Default: 0

scipy.linalg.lapack.zhesv_lwork

scipy.linalg.lapack.zhesv_lwork(n[, lower]) = <fortran object>

Wrapper for zhesv_lwork.

Parameters
n
[Input int]

Returns
work
[Complex]
info
[int]
Other Parameters

lower  [input int, optional] Default: 0

scipy.linalg.lapack.chesvx

scipy.linalg.lapack.chesvx(a, b[, af, ipiv, lwork, factored, lower, overwrite_a, overwrite_b]) =
<fortran object>

Wrapper for chesvx.

Parameters

a  [input rank-2 array(‘F’) with bounds (n,n)]
b  [input rank-2 array(‘F’) with bounds (n,nrhs)]

Returns

uduh  [rank-2 array(‘F’) with bounds (n,n) and af storage]
ipiv  [rank-1 array(‘i’) with bounds (n)]
x  [rank-2 array(‘F’) with bounds (n,nrhs)]
rcond  [float]
ferr  [rank-1 array(‘f’) with bounds (nrhs)]
berr  [rank-1 array(‘f’) with bounds (nrhs)]
info  [int]

Other Parameters

overwrite_a  [input int, optional] Default: 0
af  [input rank-2 array(‘F’) with bounds (n,n)]
_ipiv  [input rank-1 array(‘i’) with bounds (n)]
overwrite_b  [input int, optional] Default: 0
lwork  [input int, optional] Default: max(2*n,1)
factored  [input int, optional] Default: 0
lower  [input int, optional] Default: 0

scipy.linalg.lapack.zhesvx

scipy.linalg.lapack.zhesvx(a, b[, af, ipiv, lwork, factored, lower, overwrite_a, overwrite_b]) =
<fortran object>

Wrapper for zhesvx.

Parameters

a  [input rank-2 array(‘D’) with bounds (n,n)]
b  [input rank-2 array(‘D’) with bounds (n,nrhs)]

Returns

uduh  [rank-2 array(‘D’) with bounds (n,n) and af storage]
ipiv  [rank-1 array(‘i’) with bounds (n)]
x  [rank-2 array(‘D’) with bounds (n,nrhs)]
rcond  [float]
ferr  [rank-1 array(‘d’) with bounds (nrhs)]
berr  [rank-1 array(‘d’) with bounds (nrhs)]
info  [int]

Other Parameters

6.11. Low-level LAPACK functions (scipy.linalg.lapack)
overwrite_a
    [input int, optional] Default: 0
af
    [input rank-2 array('D') with bounds (n,n)]
ipiv
    [input rank-1 array('i') with bounds (n)]
overwrite_b
    [input int, optional] Default: 0
lwork
    [input int, optional] Default: max(2*n,1)
factored
    [input int, optional] Default: 0
lower
    [input int, optional] Default: 0

scipy.linalg.lapack.chesvx_lwork

scipy.linalg.lapack.chesvx_lwork(n[, lower]) = <fortran object>
Wrapper for chesvx_lwork.

Parameters
n
    [input int]

Returns
work
    [complex]
info
    [int]

Other Parameters
lower
    [input int, optional] Default: 0

scipy.linalg.lapack.zhesvx_lwork

scipy.linalg.lapack.zhesvx_lwork(n[, lower]) = <fortran object>
Wrapper for zhesvx_lwork.

Parameters
n
    [input int]

Returns
work
    [complex]
info
    [int]

Other Parameters
lower
    [input int, optional] Default: 0

scipy.linalg.lapack.chegst

scipy.linalg.lapack.chegst(a, b[, itype, lower, overwrite_a]) = <fortran object>
Wrapper for chegst.

Parameters
a
    [input rank-2 array('F') with bounds (n,n)]
b
    [input rank-2 array('F') with bounds (n,n)]

Returns
c
    [rank-2 array('F') with bounds (n,n) and a storage]
info
    [int]

Other Parameters
**scipy.linalg.lapack.zhegst**

`scipy.linalg.lapack.zhegst(a, b[, itype, lower, overwrite_a]) = <fortran object>`

Wrapper for zhegst.

**Parameters**
- `a` [input rank-2 array(‘D’) with bounds (n,n)]
- `b` [input rank-2 array(‘D’) with bounds (n,n)]

**Returns**
- `c` [rank-2 array(‘D’) with bounds (n,n) and a storage]
- `info` [int]

**Other Parameters**
- `overwrite_a` [input int, optional] Default: 0
- `itype` [input int, optional] Default: 1
- `lower` [input int, optional] Default: 0

**scipy.linalg.lapack.sgetrf**

`scipy.linalg.lapack.sgetrf(a[, overwrite_a]) = <fortran object>`

Wrapper for sgetrf.

**Parameters**
- `a` [input rank-2 array(‘f’) with bounds (m,n)]

**Returns**
- `lu` [rank-2 array(‘f’) with bounds (m,n) and a storage]
- `piv` [rank-1 array(‘i’) with bounds (MIN(m,n))]`
- `info` [int]

**Other Parameters**
- `overwrite_a` [input int, optional] Default: 0

**scipy.linalg.lapack.dgetrf**

`scipy.linalg.lapack.dgetrf(a[, overwrite_a]) = <fortran object>`

Wrapper for dgetrf.

**Parameters**
- `a` [input rank-2 array(‘d’) with bounds (m,n)]

**Returns**
- `lu` [rank-2 array(‘d’) with bounds (m,n) and a storage]
- `piv` [rank-1 array(‘i’) with bounds (MIN(m,n))]`
- `info` [int]

6.11. Low-level LAPACK functions (`scipy.linalg.lapack`)
Other Parameters

overwrite_a

[input int, optional] Default: 0

scipy.linalg.lapack.cgetrf

scipy.linalg.lapack.cgetrf(a[, overwrite_a]) = <fortran object>
Wrapper for cgetrf.

Parameters

a

[input rank-2 array('F') with bounds (m,n)]

Returns

lu

[rank-2 array('F') with bounds (m,n) and a storage]
piv

[rank-1 array('i') with bounds (MIN(m,n))]
info

[int]

Other Parameters

overwrite_a

[input int, optional] Default: 0

scipy.linalg.lapack.zgetrf

scipy.linalg.lapack.zgetrf(a[, overwrite_a]) = <fortran object>
Wrapper for zgetrf.

Parameters

a

[input rank-2 array('D') with bounds (m,n)]

Returns

lu

[rank-2 array('D') with bounds (m,n) and a storage]
piv

[rank-1 array('i') with bounds (MIN(m,n))]
info

[int]

Other Parameters

overwrite_a

[input int, optional] Default: 0

scipy.linalg.lapack.sgetri

scipy.linalg.lapack.sgetri(lu, piv[, lwork, overwrite_lu]) = <fortran object>
Wrapper for sgetri.

Parameters

lu

[input rank-2 array('f') with bounds (n,n)]
piv

[input rank-1 array('i') with bounds (n)]

Returns

inv_a

[rank-2 array('f') with bounds (n,n) and lu storage]
info

[int]

Other Parameters
overwrite_lu  
[input int, optional] Default: 0
lwork  [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.dgetri

scipy.linalg.lapack.dgetri(lu, piv, lwork, overwrite_lu) = <fortran object>
Wrapper for dgetri.

Parameters
    lu  [input rank-2 array('d') with bounds (n,n)]
    piv  [input rank-1 array('i') with bounds (n)]

Returns
    inv_a  [rank-2 array('d') with bounds (n,n) and lu storage]
    info  [int]

Other Parameters
    overwrite_lu  [input int, optional] Default: 0
    lwork  [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.cgetri

scipy.linalg.lapack.cgetri(lu, piv, lwork, overwrite_lu) = <fortran object>
Wrapper for cgetri.

Parameters
    lu  [input rank-2 array('F') with bounds (n,n)]
    piv  [input rank-1 array('i') with bounds (n)]

Returns
    inv_a  [rank-2 array('F') with bounds (n,n) and lu storage]
    info  [int]

Other Parameters
    overwrite_lu  [input int, optional] Default: 0
    lwork  [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.zgetri

scipy.linalg.lapack.zgetri(lu, piv, lwork, overwrite_lu) = <fortran object>
Wrapper for zgetri.

Parameters
    lu  [input rank-2 array('D') with bounds (n,n)]
    piv  [input rank-1 array('i') with bounds (n)]

Returns
    inv_a  [rank-2 array('D') with bounds (n,n) and lu storage]
    info  [int]

Other Parameters

6.11. Low-level LAPACK functions (scipy.linalg.lapack) 913
overwrite_lu
    [input int, optional] Default: 0
lwork
    [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.sgetri_lwork

scipy.linalg.lapack.sgetri_lwork(n) = <fortran object>
    Wrapper for sgetri_lwork.

Parameters
    n [input int]

Returns
    work [float]
    info [int]

scipy.linalg.lapack.dgetri_lwork

scipy.linalg.lapack.dgetri_lwork(n) = <fortran object>
    Wrapper for dgetri_lwork.

Parameters
    n [input int]

Returns
    work [float]
    info [int]

scipy.linalg.lapack.cgetri_lwork

scipy.linalg.lapack.cgetri_lwork(n) = <fortran object>
    Wrapper for cgetri_lwork.

Parameters
    n [input int]

Returns
    work [complex]
    info [int]

scipy.linalg.lapack.zgetri_lwork

scipy.linalg.lapack.zgetri_lwork(n) = <fortran object>
    Wrapper for zgetri_lwork.

Parameters
    n [input int]

Returns
    work [complex]
    info [int]
SciPy Reference Guide, Release 1.2.0

**scipy.linalg.lapack.sgetrs**

```python
scipy.linalg.lapack.sgetrs(lu, piv, b[, trans, overwrite_b]) = <fortran object>
```

Wrapper for sgetrs.

**Parameters**

- **lu**  [input rank-2 array('f') with bounds (n,n)]
- **piv**  [input rank-1 array('i') with bounds (n)]
- **b**  [input rank-2 array('f') with bounds (n,nrhs)]

**Returns**

- **x**  [rank-2 array('f') with bounds (n,nrhs) and b storage]
- **info**  [int]

**Other Parameters**

- **overwrite_b**  [input int, optional] Default: 0
- **trans**  [input int, optional] Default: 0

---

**scipy.linalg.lapack.dgetrs**

```python
scipy.linalg.lapack.dgetrs(lu, piv, b[, trans, overwrite_b]) = <fortran object>
```

Wrapper for dgetrs.

**Parameters**

- **lu**  [input rank-2 array('d') with bounds (n,n)]
- **piv**  [input rank-1 array('i') with bounds (n)]
- **b**  [input rank-2 array('d') with bounds (n,nrhs)]

**Returns**

- **x**  [rank-2 array('d') with bounds (n,nrhs) and b storage]
- **info**  [int]

**Other Parameters**

- **overwrite_b**  [input int, optional] Default: 0
- **trans**  [input int, optional] Default: 0

---

**scipy.linalg.lapack.cgetrs**

```python
scipy.linalg.lapack.cgetrs(lu, piv, b[, trans, overwrite_b]) = <fortran object>
```

Wrapper for cgetrs.

**Parameters**

- **lu**  [input rank-2 array('F') with bounds (n,n)]
- **piv**  [input rank-1 array('i') with bounds (n)]
- **b**  [input rank-2 array('F') with bounds (n,nrhs)]

**Returns**

- **x**  [rank-2 array('F') with bounds (n,nrhs) and b storage]
- **info**  [int]

**Other Parameters**
 overwrite_b  [input int, optional] Default: 0
 trans  [input int, optional] Default: 0

**scipy.linalg.lapack.zgetrs**

```python
scipy.linalg.lapack.zgetrs(lu, piv, b[trans, overwrite_b]) = <fortran object>
```
Wrapper for zgetrs.

**Parameters**

- **lu**  [input rank-2 array('D') with bounds (n,n)]
- **piv**  [input rank-1 array('i') with bounds (n)]
- **b**  [input rank-2 array('D') with bounds (n, nrhs)]

**Returns**

- **x**  [rank-2 array('D') with bounds (n, nrhs) and b storage]
- **info**  [int]

**Other Parameters**

- **overwrite_b**  [input int, optional] Default: 0
- **trans**  [input int, optional] Default: 0

**scipy.linalg.lapack.sges**

```python
scipy.linalg.lapack.sges(sselect, a, b[jobvl, jobvsr, sort_t, ldvsl, ldvsr, lwork, sselect_extra_args, overwrite_a, overwrite_b]) = <fortran object>
```
Wrapper for sges.

**Parameters**

- **sselect**  [call-back function]
- **a**  [input rank-2 array('f') with bounds (lda, n)]
- **b**  [input rank-2 array('f') with bounds (ldb, n)]

**Returns**

- **a**  [rank-2 array('f') with bounds (lda, n)]
- **b**  [rank-2 array('f') with bounds (ldb, n)]
- **sdim**  [int]
- **alphar**  [rank-1 array('f') with bounds (n)]
- **alphai**  [rank-1 array('f') with bounds (n)]
- **beta**  [rank-1 array('f') with bounds (n)]
- **vsl**  [rank-2 array('f') with bounds (ldvsl, n)]
- **vsl**  [rank-2 array('f') with bounds (ldvsl, n)]
- **vsr**  [rank-2 array('f') with bounds (ldvsr, n)]
- **work**  [rank-1 array('f') with bounds (MAX(lwork,1))]
- **info**  [int]

**Other Parameters**

- **jobvl**  [input int, optional] Default: 1
- **jobvsr**  [input int, optional] Default: 1
- **sort_t**  [input int, optional] Default: 0
- **sselect_extra_args**  [input tuple, optional] Default: ()
- **overwrite_a**  [input int, optional] Default: 0
- **overwrite_b**  [input int, optional] Default: 0
Scipy Reference Guide, Release 1.2.0

overwrite_b
[input int, optional] Default: 0

ldvsl [input int, optional] Default: ((jobvsl==1)?n:1)

ldvsr [input int, optional] Default: ((jobvsr==1)?n:1)

lwork [input int, optional] Default: max(8*n+16,1)

Notes
Call-back functions:

```python
def sselect(alphar,alphai,beta): return sselect
```

Required arguments:
alphar : input float
alphai : input float
beta : input float

Return objects:
sselect : int

scipy.linalg.lapack.dgges

scipy.linalg.lapack.dgges(dselect, a, b, jobvsl, jobvsr, sort_t, ldvsl, ldvsr, lwork, 

dselect_extra_args, overwrite_a, overwrite_b) = <fortran object>

Wrapper for dgges.

Parameters

dselect [call-back function]
a [input rank-2 array('d') with bounds (lda,n)]
b [input rank-2 array('d') with bounds (ldb,n)]

Returns

a [rank-2 array('d') with bounds (lda,n)]
b [rank-2 array('d') with bounds (ldb,n)]
sdim [int]
alphar [rank-1 array('d') with bounds (n)]
alphai [rank-1 array('d') with bounds (n)]
beta [rank-1 array('d') with bounds (n)]
vsl [rank-2 array('d') with bounds (ldvsl,n)]
vsr [rank-2 array('d') with bounds (ldvsr,n)]
work [rank-1 array('d') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

jobvsl [input int, optional] Default: 1
jobvsr [input int, optional] Default: 1
sort_t [input int, optional] Default: 0
dselect_extra_args [input tuple, optional] Default: ()
overwrite_a [input int, optional] Default: 0
overwrite_b [input int, optional] Default: 0
ldvsl [input int, optional] Default: ((jobvsl==1)?n:1)
ldvsr [input int, optional] Default: ((jobvsr==1)?n:1)
lwork [input int, optional] Default: max(8*n+16,1)
Notes
Call-back functions:

```python
def dselect(alphar, alphai, beta):
    return dselect
```

Required arguments:
- `alphar` : input float
- `alphai` : input float
- `beta` : input float

Return objects:
- `dselect` : int

**scipy.linalg.lapack.cgges**

**scipy.linalg.lapack.cgges**

```python
cselect, a, b, jobvsl, jobvsr, sort_t, ldvsl, ldvsr, lwork, cselect_extra_args, overwrite_a, overwrite_b)
```

Wrapper for `cgges`.

**Parameters**
- `cselect` : [call-back function]
- `a` : [input rank-2 array('F') with bounds (lda,n)]
- `b` : [input rank-2 array('F') with bounds (ldb,n)]

**Returns**
- `a` : [rank-2 array('F') with bounds (lda,n)]
- `b` : [rank-2 array('F') with bounds (ldb,n)]
- `sdim` : [int]
- `alpha` : [rank-1 array('F') with bounds (n)]
- `beta` : [rank-1 array('F') with bounds (n)]
- `vsl` : [rank-2 array('F') with bounds (ldvsl,n)]
- `vsr` : [rank-2 array('F') with bounds (ldvsr,n)]
- `work` : [rank-1 array('F') with bounds (MAX(lwork,1))]
- `info` : [int]

**Other Parameters**
- `jobvsl` : [input int, optional] Default: 1
- `jobvsr` : [input int, optional] Default: 1
- `sort_t` : [input int, optional] Default: 0
- `cselect_extra_args` : [input tuple, optional] Default: ()
- `overwrite_a` : [input int, optional] Default: 0
- `overwrite_b` : [input int, optional] Default: 0
- `ldvsl` : [input int, optional] Default: ((jobvsl==1)?n:1)
- `ldvsr` : [input int, optional] Default: ((jobvsr==1)?n:1)
- `lwork` : [input int, optional] Default: max(2*n,1)

Notes
Call-back functions:

```python
def cselect(alpha, beta):
    return cselect
```

Required arguments:
- `alpha` : input complex

(continues on next page)
beta : input complex

Return objects:
cselect : int

### scipy.linalg.lapack.zgges

**scipy.linalg.lapack.zgges**

**scipy.linalg.lapack.zgges** *(zselect, a, b[, jobvsl, jobvsr, sort_t, ldvsl, ldvsr, lwork, zselect_extra_args, overwrite_a, overwrite_b]) = <fortran object>*

Wrapper for zgges.

**Parameters**

- **zselect** : [call-back function]
- **a** : [input rank-2 array('D') with bounds (lda,n)]
- **b** : [input rank-2 array('D') with bounds (ldb,n)]

**Returns**

- **a** : [rank-2 array('D') with bounds (lda,n)]
- **b** : [rank-2 array('D') with bounds (ldb,n)]
- **sdim** : [int]
- **alpha** : [rank-1 array('D') with bounds (n)]
- **beta** : [rank-1 array('D') with bounds (n)]
- **vsl** : [rank-2 array('D') with bounds (ldvsl,n)]
- **vsr** : [rank-2 array('D') with bounds (ldvsr,n)]
- **work** : [rank-1 array('D') with bounds (MAX(lwork,1))]  
- **info** : [int]

**Other Parameters**

- **jobvsl** : [input int, optional] Default: 1
- **jobvsr** : [input int, optional] Default: 1
- **sort_t** : [input int, optional] Default: 0
- **zselect_extra_args** : [input tuple, optional] Default: ()
- **overwrite_a** : [input int, optional] Default: 0
- **overwrite_b** : [input int, optional] Default: 0
- **ldvsl** : [input int, optional] Default: ((jobvsl==1)?n:1)
- **ldvsr** : [input int, optional] Default: ((jobvsr==1)?n:1)
- **lwork** : [input int, optional] Default: max(2*n,1)

**Notes**

Call-back functions:

```python
def zselect(alpha,beta): return zselect
```

Required arguments:
- **alpha** : input complex
- **beta** : input complex

Return objects:
- **zselect** : int

---

6.11. Low-level LAPACK functions *(scipy.linalg.lapack)* 919
scipy.linalg.lapack.sgev

scipy.linalg.lapack.sgev(a, b[, compute_vl, compute_vr, lwork, overwrite_a, overwrite_b]) =
<fortran object>

Wrapper for sgev.

Parameters

a [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (n,n)]

Returns

alphar [rank-1 array('f') with bounds (n)]
alphai [rank-1 array('f') with bounds (n)]
beta [rank-1 array('f') with bounds (n)]
vl [rank-2 array('f') with bounds (ldvl,n)]
vr [rank-2 array('f') with bounds (ldvr,n)]
work [rank-1 array('f') with bounds (MAX(lwork,1))] info [int]

Other Parameters

compute_vl [input int, optional] Default: 1
compute_vr [input int, optional] Default: 1
overwrite_a [input int, optional] Default: 0
overwrite_b [input int, optional] Default: 0
lwork [input int, optional] Default: max(8*n,1)

scipy.linalg.lapack.dgev

scipy.linalg.lapack.dgev(a, b[, compute_vl, compute_vr, lwork, overwrite_a, overwrite_b]) =
<fortran object>

Wrapper for dgev.

Parameters

a [input rank-2 array('d') with bounds (n,n)]
b [input rank-2 array('d') with bounds (n,n)]

Returns

alphar [rank-1 array('d') with bounds (n)]
alphai [rank-1 array('d') with bounds (n)]
beta [rank-1 array('d') with bounds (n)]
vl [rank-2 array('d') with bounds (ldvl,n)]
vr [rank-2 array('d') with bounds (ldvr,n)]
work [rank-1 array('d') with bounds (MAX(lwork,1))] info [int]

Other Parameters

compute_vl [input int, optional] Default: 1
compute_vr [input int, optional] Default: 1
```python
overwrite_a
   [input int, optional] Default: 0
overwrite_b
   [input int, optional] Default: 0
lwork   [input int, optional] Default: max(8*n,1)
```

```
scipy.linalg.lapack.cggev
```

```
scipy.linalg.lapack.cggev(a, b, [compute_vl, compute_vr, lwork, overwrite_a, overwrite_b]) = <fortran object>
```

Wrapper for cggev.

**Parameters**

- **a**  [input rank-2 array(‘F’) with bounds (n,n)]
- **b**  [input rank-2 array(‘F’) with bounds (n,n)]

**Returns**

- **alpha**  [rank-1 array(‘F’) with bounds (n)]
- **beta**  [rank-1 array(‘F’) with bounds (n)]
- **vl**  [rank-2 array(‘F’) with bounds (ldvl,n)]
- **vr**  [rank-2 array(‘F’) with bounds (ldvr,n)]
- **work**  [rank-1 array(‘F’) with bounds (MAX(lwork,1))]
- **info**  [int]

**Other Parameters**

- **compute_vl**
  [input int, optional] Default: 1
- **compute_vr**
  [input int, optional] Default: 1
- **overwrite_a**
  [input int, optional] Default: 0
- **overwrite_b**
  [input int, optional] Default: 0
- **lwork**
  [input int, optional] Default: max(2*n,1)

```
scipy.linalg.lapack.zggev
```

```
scipy.linalg.lapack.zggev(a, b, [compute_vl, compute_vr, lwork, overwrite_a, overwrite_b]) = <fortran object>
```

Wrapper for zggev.

**Parameters**

- **a**  [input rank-2 array(‘D’) with bounds (n,n)]
- **b**  [input rank-2 array(‘D’) with bounds (n,n)]

**Returns**

- **alpha**  [rank-1 array(‘D’) with bounds (n)]
- **beta**  [rank-1 array(‘D’) with bounds (n)]
- **vl**  [rank-2 array(‘D’) with bounds (ldvl,n)]
- **vr**  [rank-2 array(‘D’) with bounds (ldvr,n)]
- **work**  [rank-1 array(‘D’) with bounds (MAX(lwork,1))]
- **info**  [int]

**Other Parameters**

6.11. Low-level LAPACK functions (scipy.linalg.lapack)
compute_vl
   [input int, optional] Default: 1
compute_vr
   [input int, optional] Default: 1
overwrite_a
   [input int, optional] Default: 0
overwrite_b
   [input int, optional] Default: 0
lwork
   [input int, optional] Default: max(2*n,1)

scipy.linalg.lapack.chbevd

scipy.linalg.lapack.chbevd(ab, compute_v, lower, ldab, lrwork, liwork, overwrite_ab) =
   <fortran object>

Parameters

   ab   [input rank-2 array('F') with bounds (ldab,n)]

Returns

   w    [rank-1 array('f') with bounds (n)]
   z    [rank-2 array('F') with bounds (ldz,ldz)]
   info [int]

Other Parameters

   overwrite_ab
      [input int, optional] Default: 1
   compute_v
      [input int, optional] Default: 1
   lower
      [input int, optional] Default: 0
   ldab
      [input int, optional] Default: shape(ab,0)
   lrwork
      [input int, optional] Default: (compute_v?1+5*n+2*n*n:n)
   liwork
      [input int, optional] Default: (compute_v?3+5*n:1)

scipy.linalg.lapack.zhbevd

scipy.linalg.lapack.zhbevd(ab, compute_v, lower, ldab, lrwork, liwork, overwrite_ab) =
   <fortran object>

Parameters

   ab   [input rank-2 array('D') with bounds (ldab,n)]

Returns

   w    [rank-1 array('d') with bounds (n)]
   z    [rank-2 array('D') with bounds (ldz,ldz)]
   info [int]

Other Parameters

   overwrite_ab
      [input int, optional] Default: 1
   compute_v
      [input int, optional] Default: 1
   lower
      [input int, optional] Default: 0
scipy.linalg.lapack.chbevx

scipy.linalg.lapack.chbevx(ab, vl, vu, il, iu[, ldab, compute_v, range, lower, abstol, mmax, overwrite_ab]) = <fortran object>

Wrapper for chbevx.

Parameters

- **ab** [input rank-2 array('F') with bounds (ldab,n)]
- **vl** [input float]
- **vu** [input float]
- **il** [input int]
- **iu** [input int]

Returns

- **w** [rank-1 array('f') with bounds (n)]
- **z** [rank-2 array('F') with bounds (ldz,mmax)]
- **m** [int]
- **ifail** [rank-1 array('i') with bounds ((compute_v?n:1))]
- **info** [int]

Other Parameters

- **overwrite_ab** [input int, optional] Default: 1
- **ldab** [input int, optional] Default: shape(ab,0)
- **compute_v** [input int, optional] Default: shape(ab,0)
- **range** [input int, optional] Default: 0
- **lower** [input int, optional] Default: 0
- **abstol** [input float, optional] Default: 0.0
- **mmax** [input int, optional] Default: (compute_v?(range==2?(iu-il+1):n):1)

scipy.linalg.lapack.zhbevx

scipy.linalg.lapack.zhbevx(ab, vl, vu, il, iu[, ldab, compute_v, range, lower, abstol, mmax, overwrite_ab]) = <fortran object>

Wrapper for zhbevx.

Parameters

- **ab** [input rank-2 array('D') with bounds (ldab,n)]
- **vl** [input float]
- **vu** [input float]
- **il** [input int]
- **iu** [input int]

Returns

- **w** [rank-1 array('d') with bounds (n)]
- **z** [rank-2 array('D') with bounds (ldz,mmax)]
- **m** [int]
- **ifail** [rank-1 array('i') with bounds ((compute_v?n:1))]
info  [int]

Other Parameters

overwrite_ab
 [input int, optional] Default: 1
ldab  [input int, optional] Default: shape(ab,0)
compute_v
 [input int, optional] Default: 1
range  [input int, optional] Default: 0
lower  [input int, optional] Default: 0
abstol  [input float, optional] Default: 0.0
mmax  [input int, optional] Default: (compute_v?(range==2?(iu-il+1):n):1)

scipy.linalg.lapack.cheev

scipy.linalg.lapack.cheev(a, compute_v, lower, lwork, overwrite_a) = <fortran object>
Wrapper for cheev.

Parameters

a  [input rank-2 array(‘F’) with bounds (n,n)]

Returns

w  [rank-1 array(‘f’) with bounds (n)]
v  [rank-2 array(‘F’) with bounds (n,n) and a storage]
info  [int]

Other Parameters

compute_v
 [input int, optional] Default: 1
lower  [input int, optional] Default: 0
overwrite_a
 [input int, optional] Default: 0
lwork  [input int, optional] Default: max(2*n-1,1)

scipy.linalg.lapack.zheev

scipy.linalg.lapack.zheev(a, compute_v, lower, lwork, overwrite_a) = <fortran object>
Wrapper for zheev.

Parameters

a  [input rank-2 array(‘D’) with bounds (n,n)]

Returns

w  [rank-1 array(‘d’) with bounds (n)]
v  [rank-2 array(‘D’) with bounds (n,n) and a storage]
info  [int]

Other Parameters

compute_v
 [input int, optional] Default: 1
lower  [input int, optional] Default: 0
overwrite_a
 [input int, optional] Default: 0
lwork  [input int, optional] Default: max(2*n-1,1)
scipy.linalg.lapack.cheevd

scipy.linalg.lapack.cheevd(a[, compute_v, lower, lwork, overwrite_a]) = <fortran object>

Wrapper for cheevd.

Parameters

- a [input rank-2 array('F') with bounds (n,n)]

Returns

- w [rank-1 array('f') with bounds (n)]
- v [rank-2 array('F') with bounds (n,n) and a storage]
- info [int]

Other Parameters

- compute_v [input int, optional] Default: 1
- lower [input int, optional] Default: 0
- overwrite_a [input int, optional] Default: 0
- lwork [input int, optional] Default: max((compute_v?2*n+n*n:n+1),1)

scipy.linalg.lapack.zheevd

scipy.linalg.lapack.zheevd(a[, compute_v, lower, lwork, overwrite_a]) = <fortran object>

Wrapper for zheevd.

Parameters

- a [input rank-2 array('D') with bounds (n,n)]

Returns

- w [rank-1 array('d') with bounds (n)]
- v [rank-2 array('D') with bounds (n,n) and a storage]
- info [int]

Other Parameters

- compute_v [input int, optional] Default: 1
- lower [input int, optional] Default: 0
- overwrite_a [input int, optional] Default: 0
- lwork [input int, optional] Default: max((compute_v?2*n+n*n:n+1),1)

scipy.linalg.lapack.cheevr

scipy.linalg.lapack.cheevr(a[, jobz, range, uplo, il, iu, lwork, overwrite_a]) = <fortran object>

Wrapper for cheevr.

Parameters

- a [input rank-2 array('F') with bounds (n,n)]

Returns

- w [rank-1 array('f') with bounds (n)]
- z [rank-2 array('F') with bounds (n,m)]
info [int]

Other Parameters

jobz [input string(len=1), optional] Default: ‘V’
range [input string(len=1), optional] Default: ‘A’
uplo [input string(len=1), optional] Default: ‘L’
overwrite_a [input int, optional] Default: 0
il [input int, optional] Default: 1
iu [input int, optional] Default: n
lwork [input int, optional] Default: max(18*n,1)

scipy.linalg.lapack.zheevr

scipy.linalg.lapack.zheevr(a[, jobz, range, uplo, il, iu, lwork, overwrite_a]) = <fortran object>

Wrapper for zheevr.

Parameters

a [input rank-2 array(‘D’) with bounds (n,n)]

Returns

w [rank-1 array(‘d’) with bounds (n)]
z [rank-2 array(‘D’) with bounds (n,m)]
info [int]

Other Parameters

jobz [input string(len=1), optional] Default: ‘V’
range [input string(len=1), optional] Default: ‘A’
uplo [input string(len=1), optional] Default: ‘L’
overwrite_a [input int, optional] Default: 0
il [input int, optional] Default: 1
iu [input int, optional] Default: n
lwork [input int, optional] Default: max(18*n,1)

scipy.linalg.lapack.chegv

scipy.linalg.lapack.chegv(a, b[, itype, jobz, uplo, overwrite_a, overwrite_b]) = <fortran object>

Wrapper for chegv.

Parameters

a [input rank-2 array(‘F’) with bounds (n,n)]
b [input rank-2 array(‘F’) with bounds (n,n)]

Returns

a [rank-2 array(‘F’) with bounds (n,n)]
w [rank-1 array(‘f’) with bounds (n)]
info [int]

Other Parameters

itype [input int, optional] Default: 1
jobz [input string(len=1), optional] Default: ‘V’
uplo     [input string(len=1), optional] Default: ‘L’
overwrite_a  [input int, optional] Default: 0
overwrite_b  [input int, optional] Default: 0

scipy.linalg.lapack.zhegv

scipy.linalg.lapack.zhegv(a, b[, itype, jobz, uplo, overwrite_a, overwrite_b]) = <fortran object>

Wrapper for zhegv.

Parameters

a         [input rank-2 array('D') with bounds (n,n)]
b         [input rank-2 array('D') with bounds (n,n)]

Returns

a         [rank-2 array('D') with bounds (n,n)]
w         [rank-1 array('d') with bounds (n)]
info      [int]

Other Parameters

itype     [input int, optional] Default: 1
jobz      [input string(len=1), optional] Default: ‘V’
uplo      [input string(len=1), optional] Default: ‘L’
overwrite_a  [input int, optional] Default: 0
overwrite_b  [input int, optional] Default: 0

scipy.linalg.lapack.chegvd

scipy.linalg.lapack.chegvd(a, b[, itype, jobz, uplo, overwrite_a, overwrite_b, lwork]) = <fortran object>

Wrapper for chegvd.

Parameters

a         [input rank-2 array('F') with bounds (n,n)]
b         [input rank-2 array('F') with bounds (n,n)]

Returns

a         [rank-2 array('F') with bounds (n,n)]
w         [rank-1 array('f') with bounds (n)]
info      [int]

Other Parameters

itype     [input int, optional] Default: 1
jobz      [input string(len=1), optional] Default: ‘V’
uplo      [input string(len=1), optional] Default: ‘L’
overwrite_a  [input int, optional] Default: 0
overwrite_b  [input int, optional] Default: 0
lwork     [input int, optional] Default: max(2*n+n*n,1)
scipy.linalg.lapack.zhegvd

scipy.linalg.lapack.zhegvd(a, b[, itype, jobz, uplo, lwork, overwrite_a, overwrite_b]) = <fortran object>

Wrapper for zhegvd.

Parameters
- a [input rank-2 array('D') with bounds (n,n)]
- b [input rank-2 array('D') with bounds (n,n)]

Returns
- a [rank-2 array('D') with bounds (n,n)]
- w [rank-1 array('d') with bounds (n)]
- info [int]

Other Parameters
- itype [input int, optional] Default: 1
- jobz [input string(len=1), optional] Default: 'V'
- uplo [input string(len=1), optional] Default: 'L'
- overwrite_a [input int, optional] Default: 0
- overwrite_b [input int, optional] Default: 0
- lwork [input int, optional] Default: max(2*n+n*n,1)

scipy.linalg.lapack.chegvx

scipy.linalg.lapack.chegvx(a, b, iu[, itype, jobz, uplo, il, lwork, overwrite_a, overwrite_b]) = <fortran object>

Wrapper for chegvx.

Parameters
- a [input rank-2 array('F') with bounds (n,n)]
- b [input rank-2 array('F') with bounds (n,n)]
- iu [input int]

Returns
- w [rank-1 array('f') with bounds (n)]
- z [rank-2 array('F') with bounds (n,m)]
- ifail [rank-1 array('i') with bounds (n)]
- info [int]

Other Parameters
- itype [input int, optional] Default: 1
- jobz [input string(len=1), optional] Default: 'V'
- uplo [input string(len=1), optional] Default: 'L'
- overwrite_a [input int, optional] Default: 0
- overwrite_b [input int, optional] Default: 0
- il [input int, optional] Default: 1
- lwork [input int, optional] Default: max(18*n-1,1)
**scipy.linalg.lapack.zhegvx**

`scipy.linalg.lapack.zhegvx(a, b, iu[, itype, jobz, uplo, il, lwork, overwrite_a, overwrite_b]) = <fortran object>`

Wrapper for zhegvx.

**Parameters**

- `a` [input rank-2 array('D') with bounds (n,n)]
- `b` [input rank-2 array('D') with bounds (n,n)]
- `iu` [input int]

**Returns**

- `w` [rank-1 array('d') with bounds (n)]
- `z` [rank-2 array('D') with bounds (n,m)]
- `ifail` [rank-1 array('i') with bounds (n)]
- `info` [int]

**Other Parameters**

- `itype` [input int, optional] Default: 1
- `jobz` [input string(len=1), optional] Default: ‘V’
- `uplo` [input string(len=1), optional] Default: ‘L’
- `overwrite_a` [input int, optional] Default: 0
- `overwrite_b` [input int, optional] Default: 0
- `il` [input int, optional] Default: 1
- `lwork` [input int, optional] Default: max(18*n-1,1)

**scipy.linalg.lapack.slarf**

`scipy.linalg.lapack.slarf(v, tau, c[, side, incv, overwrite_c]) = <fortran object>`

Wrapper for slarf.

**Parameters**

- `v` [input rank-1 array('f') with bounds ((side[0]=='L'?(1 + (m-1)*abs(incv)):1 + (n-1)*abs(incv)))]
- `tau` [input float]
- `c` [input rank-2 array('f') with bounds (m,n)]
- `work` [input rank-1 array('f') with bounds (lwork)]

**Returns**

- `c` [rank-2 array('f') with bounds (m,n)]

**Other Parameters**

- `side` [input string(len=1), optional] Default: ‘L’
- `incv` [input int, optional] Default: 1
- `overwrite_c` [input int, optional] Default: 0
scipy.linalg.lapack.dlarf

scipy.linalg.lapack.dlarf(v, tau, c, work[, side, incv, overwrite_c]) = <fortran object>
Wrapper for dlarf.

Parameters
- **v** [input rank-1 array('d') with bounds ((side[0]=='L'?1+(m-1)*abs(incv)):1+(n-1)*abs(incv)))]
- **tau** [input float]
- **c** [input rank-2 array('d') with bounds (m,n)]
- **work** [input rank-1 array('d') with bounds (lwork)]

Returns
- **c** [rank-2 array('d') with bounds (m,n)]

Other Parameters
- **side** [input string(len=1), optional] Default: ‘L’
- **incv** [input int, optional] Default: 1
- **overwrite_c** [input int, optional] Default: 0

scipy.linalg.lapack.clarf

scipy.linalg.lapack.clarf(v, tau, c, work[, side, incv, overwrite_c]) = <fortran object>
Wrapper for clarf.

Parameters
- **v** [input rank-1 array('F') with bounds ((side[0]=='L'?1+(m-1)*abs(incv)):1+(n-1)*abs(incv)))]
- **tau** [input complex]
- **c** [input rank-2 array('F') with bounds (m,n)]
- **work** [input rank-1 array('F') with bounds (lwork)]

Returns
- **c** [rank-2 array('F') with bounds (m,n)]

Other Parameters
- **side** [input string(len=1), optional] Default: ‘L’
- **incv** [input int, optional] Default: 1
- **overwrite_c** [input int, optional] Default: 0

scipy.linalg.lapack.zlarf

scipy.linalg.lapack.zlarf(v, tau, c, work[, side, incv, overwrite_c]) = <fortran object>
Wrapper for zlarf.

Parameters
- **v** [input rank-1 array('D') with bounds ((side[0]=='L'?1+(m-1)*abs(incv)):1+(n-1)*abs(incv)))]
- **tau** [input complex]
- **c** [input rank-2 array('D') with bounds (m,n)]
- **work** [input rank-1 array('D') with bounds (lwork)]

Returns
- **c** [rank-2 array('D') with bounds (m,n)]
c       [rank-2 array('D') with bounds (m,n)]

**Other Parameters**

- `side`       [input string(len=1), optional] Default: ‘L’
- `incv`       [input int, optional] Default: 1
- `overwrite_c`       [input int, optional] Default: 0

scipy.linalg.lapack.slarfg

scipy.linalg.lapack.slarfg(n, alpha, x[:, incx, overwrite_x]) = <fortran object>
Wrapper for slarfg.

**Parameters**

- `n`       [input int]
- `alpha`       [input float]
- `x`       [input rank-1 array('f') with bounds (lx)]

**Returns**

- `alpha`       [float]
- `x`       [rank-1 array('f') with bounds (lx)]
- `tau`       [float]

**Other Parameters**

- `overwrite_x`       [input int, optional] Default: 0
- `incx`       [input int, optional] Default: 1

scipy.linalg.lapack.dlarfg

scipy.linalg.lapack.dlarfg(n, alpha, x[:, incx, overwrite_x]) = <fortran object>
Wrapper for dlarfg.

**Parameters**

- `n`       [input int]
- `alpha`       [input float]
- `x`       [input rank-1 array('d') with bounds (lx)]

**Returns**

- `alpha`       [float]
- `x`       [rank-1 array('d') with bounds (lx)]
- `tau`       [float]

**Other Parameters**

- `overwrite_x`       [input int, optional] Default: 0
- `incx`       [input int, optional] Default: 1
scipy.linalg.lapack.clarfg

`scipy.linalg.lapack.clarfg(n, alpha, x[, incx, overwrite_x]) = <fortran object>`

Wrapper for `clarfg`.

**Parameters**

- `n` [input int]
- `alpha` [input complex]
- `x` [input rank-1 array('F') with bounds (lx)]

**Returns**

- `alpha` [complex]
- `x` [rank-1 array('F') with bounds (lx)]
- `tau` [complex]

**Other Parameters**

- `overwrite_x` [input int, optional] Default: 0
- `incx` [input int, optional] Default: 1

scipy.linalg.lapack.zlarfg

`scipy.linalg.lapack.zlarfg(n, alpha, x[, incx, overwrite_x]) = <fortran object>`

Wrapper for `zlarfg`.

**Parameters**

- `n` [input int]
- `alpha` [input complex]
- `x` [input rank-1 array('D') with bounds (lx)]

**Returns**

- `alpha` [complex]
- `x` [rank-1 array('D') with bounds (lx)]
- `tau` [complex]

**Other Parameters**

- `overwrite_x` [input int, optional] Default: 0
- `incx` [input int, optional] Default: 1

scipy.linalg.lapack.slartg

`scipy.linalg.lapack.slartg(f, g) = <fortran object>`

Wrapper for `slartg`.

**Parameters**

- `f` [input float]
- `g` [input float]

**Returns**

- `cs` [float]
- `sn` [float]
- `r` [float]
scipy.linalg.lapack.dlartg

scipy.linalg.lapack.dlartg(f, g) = <fortran object>
Wrapper for dlartg.

Parameters
  f [input float]
  g [input float]

Returns
  cs [float]
  sn [float]
  r [float]

scipy.linalg.lapack.clartg

scipy.linalg.lapack.clartg(f, g) = <fortran object>
Wrapper for clartg.

Parameters
  f [input complex]
  g [input complex]

Returns
  cs [float]
  sn [complex]
  r [complex]

scipy.linalg.lapack.zlartg

scipy.linalg.lapack.zlartg(f, g) = <fortran object>
Wrapper for zlartg.

Parameters
  f [input complex]
  g [input complex]

Returns
  cs [float]
  sn [complex]
  r [complex]

scipy.linalg.lapack.slasd4

scipy.linalg.lapack.slasd4(i, d, z[, rho]) = <fortran object>
Wrapper for slasd4.

Parameters
  i [input int]
  d [input rank-1 array('f') with bounds (n)]
  z [input rank-1 array('f') with bounds (n)]

Returns
  delta [rank-1 array('f') with bounds (n)]
  sigma [float]
work  [rank-1 array('f') with bounds (n)]
info  [int]

Other Parameters
rho  [input float, optional] Default: 1.0

scipy.linalg.lapack.dlasd4

scipy.linalg.lapack.dlasd4(i, d, z[, rho]) = <fortran object>
Wrapper for dlasd4.

Parameters
i  [input int]
d  [input rank-1 array('d') with bounds (n)]
z  [input rank-1 array('d') with bounds (n)]

Returns
delta  [rank-1 array('d') with bounds (n)]
sigma  [float]
work  [rank-1 array('d') with bounds (n)]
info  [int]

Other Parameters
rho  [input float, optional] Default: 1.0

scipy.linalg.lapack.slaswp

scipy.linalg.lapack.slaswp(a, piv[, k1, k2, off, inc, overwrite_a]) = <fortran object>
Wrapper for slaswp.

Parameters
a  [input rank-2 array('f') with bounds (nrows,n)]
piv  [input rank-1 array('i') with bounds (npiv)]

Returns
a  [rank-2 array('f') with bounds (nrows,n)]

Other Parameters
overwrite_a  [input int, optional] Default: 0
k1  [input int, optional] Default: 0
k2  [input int, optional] Default: npiv-1
off  [input int, optional] Default: 0
inc  [input int, optional] Default: 1

scipy.linalg.lapack.dlaswp

scipy.linalg.lapack.dlaswp(a, piv[, k1, k2, off, inc, overwrite_a]) = <fortran object>
Wrapper for dlaswp.

Parameters
a  [input rank-2 array('d') with bounds (nrows,n)]
piv  [input rank-1 array('i') with bounds (npiv)]
Returns

\[ \text{a} \quad \text{[rank-2 array('d') with bounds (nrows,n)]} \]

Other Parameters

\[
\begin{align*}
\text{overwrite}_\text{a} & \quad \text{[input int, optional] Default: 0} \\
\text{k1} & \quad \text{[input int, optional] Default: 0} \\
\text{k2} & \quad \text{[input int, optional] Default: npiv-1} \\
\text{off} & \quad \text{[input int, optional] Default: 0} \\
\text{inc} & \quad \text{[input int, optional] Default: 1}
\end{align*}
\]

\text{scipy.linalg.lapack.claswp}

\[
\text{scipy.linalg.lapack.claswp} (a, \text{piv}, \text{k1, k2, off, inc, overwrite}_\text{a}) = \text{<fortran object>}
\]

Wrapper for \text{claswp}.

Parameters

\[
\begin{align*}
\text{a} & \quad \text{[input rank-2 array('F') with bounds (nrows,n)]} \\
\text{piv} & \quad \text{[input rank-1 array('i') with bounds (npiv)]}
\end{align*}
\]

Returns

\[ \text{a} \quad \text{[rank-2 array('F') with bounds (nrows,n)]} \]

Other Parameters

\[
\begin{align*}
\text{overwrite}_\text{a} & \quad \text{[input int, optional] Default: 0} \\
\text{k1} & \quad \text{[input int, optional] Default: 0} \\
\text{k2} & \quad \text{[input int, optional] Default: npiv-1} \\
\text{off} & \quad \text{[input int, optional] Default: 0} \\
\text{inc} & \quad \text{[input int, optional] Default: 1}
\end{align*}
\]

\text{scipy.linalg.lapack.zlaswp}

\[
\text{scipy.linalg.lapack.zlaswp} (a, \text{piv}, \text{k1, k2, off, inc, overwrite}_\text{a}) = \text{<fortran object>}
\]

Wrapper for \text{zlaswp}.

Parameters

\[
\begin{align*}
\text{a} & \quad \text{[input rank-2 array('D') with bounds (nrows,n)]} \\
\text{piv} & \quad \text{[input rank-1 array('i') with bounds (npiv)]}
\end{align*}
\]

Returns

\[ \text{a} \quad \text{[rank-2 array('D') with bounds (nrows,n)]} \]

Other Parameters

\[
\begin{align*}
\text{overwrite}_\text{a} & \quad \text{[input int, optional] Default: 0} \\
\text{k1} & \quad \text{[input int, optional] Default: 0} \\
\text{k2} & \quad \text{[input int, optional] Default: npiv-1} \\
\text{off} & \quad \text{[input int, optional] Default: 0} \\
\text{inc} & \quad \text{[input int, optional] Default: 1}
\end{align*}
\]
scipy.linalg.lapack.slaum

scipy.linalg.lapack.slaum(c, lower, overwrite_c) = <fortran object>
Wrapper for slaum.

**Parameters**
- c [input rank-2 array('f') with bounds (n,n)]

**Returns**
- a [rank-2 array('f') with bounds (n,n) and c storage]
- info [int]

**Other Parameters**
- overwrite_c [input int, optional] Default: 0
- lower [input int, optional] Default: 0

scipy.linalg.lapack.dlaum

scipy.linalg.lapack.dlaum(c, lower, overwrite_c) = <fortran object>
Wrapper for dlaum.

**Parameters**
- c [input rank-2 array('d') with bounds (n,n)]

**Returns**
- a [rank-2 array('d') with bounds (n,n) and c storage]
- info [int]

**Other Parameters**
- overwrite_c [input int, optional] Default: 0
- lower [input int, optional] Default: 0

scipy.linalg.lapack.claum

scipy.linalg.lapack.claum(c, lower, overwrite_c) = <fortran object>
Wrapper for clauum.

**Parameters**
- c [input rank-2 array('F') with bounds (n,n)]

**Returns**
- a [rank-2 array('F') with bounds (n,n) and c storage]
- info [int]

**Other Parameters**
- overwrite_c [input int, optional] Default: 0
- lower [input int, optional] Default: 0
scipy.linalg.lapack.zlaumu

scipy.linalg.lapack.zlaumu(c[, lower, overwrite_c]) = <fortran object>
Wrapper for zlaumu.

Parameters

- **c** [input rank-2 array(‘D’) with bounds (n,n)]

Returns

- **a** [rank-2 array(‘D’) with bounds (n,n) and c storage]
- **info** [int]

Other Parameters

- **overwrite_c** [input int, optional] Default: 0
- **lower** [input int, optional] Default: 0

scipy.linalg.lapack.spbsv

scipy.linalg.lapack.spbsv(ab, b[, lower, ldab, overwrite_ab, overwrite_b]) = <fortran object>
Wrapper for spbsv.

Parameters

- **ab** [input rank-2 array(‘f’) with bounds (ldab,n)]
- **b** [input rank-2 array(‘f’) with bounds (ldb,nrhs)]

Returns

- **c** [rank-2 array(‘f’) with bounds (ldab,n) and ab storage]
- **x** [rank-2 array(‘f’) with bounds (ldb,nrhs) and b storage]
- **info** [int]

Other Parameters

- **lower** [input int, optional] Default: 0
- **overwrite_ab** [input int, optional] Default: 0
- **ldab** [input int, optional] Default: shape(ab,0)
- **overwrite_b** [input int, optional] Default: 0

scipy.linalg.lapack.dpbsv

scipy.linalg.lapack.dpbsv(ab, b[, lower, ldab, overwrite_ab, overwrite_b]) = <fortran object>
Wrapper for dpbsv.

Parameters

- **ab** [input rank-2 array(‘d’) with bounds (ldab,n)]
- **b** [input rank-2 array(‘d’) with bounds (ldb,nrhs)]

Returns

- **c** [rank-2 array(‘d’) with bounds (ldab,n) and ab storage]
- **x** [rank-2 array(‘d’) with bounds (ldb,nrhs) and b storage]
- **info** [int]

Other Parameters

- **lower** [input int, optional] Default: 0
- **overwrite_ab** [input int, optional] Default: 0
- **ldab** [input int, optional] Default: shape(ab,0)
- **overwrite_b** [input int, optional] Default: 0
scipy.linalg.lapack.cpbsv

scipy.linalg.lapack.cpbsv(ab, b[, lower, ldab, overwrite_ab, overwrite_b]) = <fortran object>
Wrapper for cpbsv.

Parameters

- **ab** [input rank-2 array('F') with bounds (ldab,n)]
- **b** [input rank-2 array('F') with bounds (ldb, nrhs)]

Returns

- **c** [rank-2 array('F') with bounds (ldab,n) and ab storage]
- **x** [rank-2 array('F') with bounds (ldb, nrhs) and b storage]
- **info** [int]

Other Parameters

- **lower** [input int, optional] Default: 0
- **overwrite_ab** [input int, optional] Default: 0
- **ldab** [input int, optional] Default: shape(ab,0)
- **overwrite_b** [input int, optional] Default: 0

scipy.linalg.lapack.zpbsv

scipy.linalg.lapack.zpbsv(ab, b[, lower, ldab, overwrite_ab, overwrite_b]) = <fortran object>
Wrapper for zpbsv.

Parameters

- **ab** [input rank-2 array('D') with bounds (ldab,n)]
- **b** [input rank-2 array('D') with bounds (ldb, nrhs)]

Returns

- **c** [rank-2 array('D') with bounds (ldab,n) and ab storage]
- **x** [rank-2 array('D') with bounds (ldb, nrhs) and b storage]
- **info** [int]

Other Parameters

- **lower** [input int, optional] Default: 0
- **overwrite_ab** [input int, optional] Default: 0
- **ldab** [input int, optional] Default: shape(ab,0)
- **overwrite_b** [input int, optional] Default: 0
scipy.linalg.lapack.spbtrf

scipy.linalg.lapack.spbtrf(ab[, lower, ldab, overwrite_ab]) = <fortran object>

Wrapper for spbtrf.

Parameters

ab [input rank-2 array('f') with bounds (ldab,n)]

Returns

c [rank-2 array('f') with bounds (ldab,n) and ab storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_ab [input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)

scipy.linalg.lapack.dpbtrf

scipy.linalg.lapack.dpbtrf(ab[, lower, ldab, overwrite_ab]) = <fortran object>

Wrapper for dpbtrf.

Parameters

ab [input rank-2 array('d') with bounds (ldab,n)]

Returns

c [rank-2 array('d') with bounds (ldab,n) and ab storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_ab [input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)

scipy.linalg.lapack.cpbtrf

scipy.linalg.lapack.cpbtrf(ab[, lower, ldab, overwrite_ab]) = <fortran object>

Wrapper for cpbtrf.

Parameters

ab [input rank-2 array('F') with bounds (ldab,n)]

Returns

c [rank-2 array('F') with bounds (ldab,n) and ab storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_ab [input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)
scipy.linalg.lapack.zpbtrf

scipy.linalg.lapack.zpbtrf(ab, lower, ldab, overwrite_ab) = <fortran object>

Wrapper for zpbtrf.

Parameters
- ab: [input rank-2 array('D') with bounds (ldab,n)]
- lower: [input int, optional] Default: 0
- overwrite_ab: [input int, optional] Default: 0
- ldab: [input int, optional] Default: shape(ab,0)

Returns
- c: [rank-2 array('D') with bounds (ldab,n) and ab storage]
- info: [int]

Other Parameters
- overwrite_ab: [input int, optional] Default: 0

scipy.linalg.lapack.spbtrs

scipy.linalg.lapack.spbtrs(ab, b, lower, ldab, overwrite_b) = <fortran object>

Wrapper for spbtrs.

Parameters
- ab: [input rank-2 array('f') with bounds (ldab,n)]
- b: [input rank-2 array('f') with bounds (ldb,nrhs)]
- lower: [input int, optional] Default: 0
- overwrite_b: [input int, optional] Default: 0
- ldab: [input int, optional] Default: shape(ab,0)

Returns
- x: [rank-2 array('f') with bounds (ldb,nrhs) and b storage]
- info: [int]

Other Parameters
- overwrite_b: [input int, optional] Default: 0

scipy.linalg.lapack.dpbtrs

scipy.linalg.lapack.dpbtrs(ab, b, lower, ldab, overwrite_b) = <fortran object>

Wrapper for dpbtrs.

Parameters
- ab: [input rank-2 array('d') with bounds (ldab,n)]
- b: [input rank-2 array('d') with bounds (ldb,nrhs)]
- lower: [input int, optional] Default: 0
- ldab: [input int, optional] Default: shape(ab,0)

Returns
- x: [rank-2 array('d') with bounds (ldb,nrhs) and b storage]
- info: [int]

Other Parameters
- overwrite_b: [input int, optional] Default: 0
overwrite_b
   [input int, optional] Default: 0

scipy.linalg.lapack.cpbtrs

scipy.linalg.lapack.cpbtrs(ab, b[, lower, ldab, overwrite_b]) = <fortran object>
Wrapper for cpbtrs.

Parameters
   ab   [input rank-2 array('F') with bounds (ldab,n)]
   b    [input rank-2 array('F') with bounds (ldb,nrhs)]

Returns
   x    [rank-2 array('F') with bounds (ldb,nrhs) and b storage]
   info [int]

Other Parameters
   lower [input int, optional] Default: 0
   ldab  [input int, optional] Default: shape(ab,0)
   overwrite_b [input int, optional] Default: 0

scipy.linalg.lapack.zpbtrs

scipy.linalg.lapack.zpbtrs(ab, b[, lower, ldab, overwrite_b]) = <fortran object>
Wrapper for zpbtrs.

Parameters
   ab   [input rank-2 array('D') with bounds (ldab,n)]
   b    [input rank-2 array('D') with bounds (ldb,nrhs)]

Returns
   x    [rank-2 array('D') with bounds (ldb,nrhs) and b storage]
   info [int]

Other Parameters
   lower [input int, optional] Default: 0
   ldab  [input int, optional] Default: shape(ab,0)
   overwrite_b [input int, optional] Default: 0

scipy.linalg.lapack.sposv

scipy.linalg.lapack.sposv(a, b[, lower, overwrite_a, overwrite_b]) = <fortran object>
Wrapper for sposv.

Parameters
   a    [input rank-2 array('f') with bounds (n,n)]
   b    [input rank-2 array('f') with bounds (n,nrhs)]

Returns
   c    [rank-2 array('f') with bounds (n,n) and a storage]
   x    [rank-2 array('f') with bounds (n,nrhs) and b storage]
   info [int]
Other Parameters

overwrite_a
  [input int, optional] Default: 0

overwrite_b
  [input int, optional] Default: 0

lower
  [input int, optional] Default: 0

scipy.linalg.lapack.dposv

scipy.linalg.lapack.dposv(a, b[, lower, overwrite_a, overwrite_b]) = <fortran object>
Wrapper for dposv.

Parameters

a
  [input rank-2 array('d') with bounds (n,n)]
b
  [input rank-2 array('d') with bounds (n,nrhs)]

Returns

c
  [rank-2 array('d') with bounds (n,n) and a storage]
x
  [rank-2 array('d') with bounds (n,nrhs) and b storage]
info
  [int]

Other Parameters

overwrite_a
  [input int, optional] Default: 0

overwrite_b
  [input int, optional] Default: 0

lower
  [input int, optional] Default: 0

scipy.linalg.lapack.cposv

scipy.linalg.lapack.cposv(a, b[, lower, overwrite_a, overwrite_b]) = <fortran object>
Wrapper for cposv.

Parameters

a
  [input rank-2 array('F') with bounds (n,n)]
b
  [input rank-2 array('F') with bounds (n,nrhs)]

Returns

c
  [rank-2 array('F') with bounds (n,n) and a storage]
x
  [rank-2 array('F') with bounds (n,nrhs) and b storage]
info
  [int]

Other Parameters

overwrite_a
  [input int, optional] Default: 0

overwrite_b
  [input int, optional] Default: 0

lower
  [input int, optional] Default: 0
scipy.linalg.lapack.zposv

scipy.linalg.lapack.zposv(a, b[, lower, overwrite_a, overwrite_b]) = <fortran object>
Wrapper for zposv.

Parameters
a [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (n,nrhs)]

Returns
c [rank-2 array('D') with bounds (n,n) and a storage]
x [rank-2 array('D') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters
overwrite_a [input int, optional] Default: 0
overwrite_b [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.sposvx

scipy.linalg.lapack.sposvx(a, b[, fact, af, equed, s, lower, overwrite_a, overwrite_b]) = <fortran object>
Wrapper for sposvx.

Parameters
a [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (n,nrhs)]

Returns
a_s [rank-2 array('f') with bounds (n,n) and a storage]
lu [rank-2 array('f') with bounds (n,n) and af storage]
equed [string(len=1)]
s [rank-1 array('f') with bounds (n)]
b_s [rank-2 array('f') with bounds (n,nrhs) and b storage]
x [rank-2 array('f') with bounds (n,nrhs)]
rcnd [float]
ferr [rank-1 array('f') with bounds (nrhs)]
berr [rank-1 array('f') with bounds (nrhs)]
info [int]

Other Parameters
fact [input string(len=1), optional] Default: ‘E’
overwrite_a [input int, optional] Default: 0
af [input rank-2 array('f') with bounds (n,n)]
equed [input string(len=1), optional] Default: ‘Y’
s [input rank-1 array('f') with bounds (n)]
overwrite_b [input int, optional] Default: 0
lower [input int, optional] Default: 0
scipy.linalg.lapack.dposvx

```python
scipy.linalg.lapack.dposvx(a, b[, fact, af, equed, s, lower, overwrite_a, overwrite_b]) =
<fortran object>
```

Wrapper for dposvx.

**Parameters**

- **a** [input rank-2 array('d') with bounds (n,n)]
- **b** [input rank-2 array('d') with bounds (n,nrhs)]

**Returns**

- **a_s** [rank-2 array('d') with bounds (n,n) and a storage]
- **lu** [rank-2 array('d') with bounds (n,n) and af storage]
- **equed** [string(len=1)]
- **s** [rank-1 array('d') with bounds (n)]
- **b_s** [rank-2 array('d') with bounds (n,nrhs) and b storage]
- **x** [rank-2 array('d') with bounds (n,nrhs)]
- **rcond** [float]
- **ferr** [rank-1 array('d') with bounds (nrhs)]
- **berr** [rank-1 array('d') with bounds (nrhs)]
- **info** [int]

**Other Parameters**

- **fact** [input string(len=1), optional] Default: ‘E’
- **overwrite_a** [input int, optional] Default: 0
- **af** [input rank-2 array('d') with bounds (n,n)]
- **equed** [input string(len=1), optional] Default: ‘Y’
- **s** [input rank-1 array('d') with bounds (n)]
- **overwrite_b** [input int, optional] Default: 0
- **lower** [input int, optional] Default: 0

scipy.linalg.lapack.cposvx

```python
scipy.linalg.lapack.cposvx(a, b[, fact, af, equed, s, lower, overwrite_a, overwrite_b]) =
<fortran object>
```

Wrapper for cposvx.

**Parameters**

- **a** [input rank-2 array('F') with bounds (n,n)]
- **b** [input rank-2 array('F') with bounds (n,nrhs)]

**Returns**

- **a_s** [rank-2 array('F') with bounds (n,n) and a storage]
- **lu** [rank-2 array('F') with bounds (n,n) and af storage]
- **equed** [string(len=1)]
- **s** [rank-1 array('F') with bounds (n)]
- **b_s** [rank-2 array('F') with bounds (n,nrhs) and b storage]
- **x** [rank-2 array('F') with bounds (n,nrhs)]
- **rcond** [float]
- **ferr** [rank-1 array('F') with bounds (nrhs)]
- **berr** [rank-1 array('F') with bounds (nrhs)]
- **info** [int]
**Other Parameters**

- **fact** [input string(len=1), optional] Default: ‘E’
- **overwrite_a** [input int, optional] Default: 0
- **af** [input rank-2 array(‘F’) with bounds (n,n)]
- **equed** [input string(len=1), optional] Default: ‘Y’
- **s** [input rank-1 array(‘f’) with bounds (n)]
- **overwrite_b** [input int, optional] Default: 0
- **lower** [input int, optional] Default: 0

**scipy.linalg.lapack.zposvx**

```python
scipy.linalg.lapack.zposvx(a, b[, fact, af, equed, s, lower, overwrite_a, overwrite_b]) =
<fortran object>
```

Wrapper for zposvx.

**Parameters**

- **a** [input rank-2 array(‘D’) with bounds (n,n)]
- **b** [input rank-2 array(‘D’) with bounds (n,nrhs)]

**Returns**

- **a_s** [rank-2 array(‘D’) with bounds (n,n) and a storage]
- **lu** [rank-2 array(‘D’) with bounds (n,n) and af storage]
- **equed** [string(len=1)]
- **s** [rank-1 array(‘d’) with bounds (n)]
- **b_s** [rank-2 array(‘D’) with bounds (n,nrhs) and b storage]
- **x** [rank-2 array(‘D’) with bounds (n,nrhs)]
- **rcond** [float]
- **ferr** [rank-1 array(‘d’) with bounds (nrhs)]
- **berr** [rank-1 array(‘d’) with bounds (nrhs)]
- **info** [int]

**Other Parameters**

- **fact** [input string(len=1), optional] Default: ‘E’
- **overwrite_a** [input int, optional] Default: 0
- **af** [input rank-2 array(‘D’) with bounds (n,n)]
- **equed** [input string(len=1), optional] Default: ‘Y’
- **s** [input rank-1 array(‘d’) with bounds (n)]
- **overwrite_b** [input int, optional] Default: 0
- **lower** [input int, optional] Default: 0

**scipy.linalg.lapack.spocon**

```python
scipy.linalg.lapack.spocon(a, anorm[, uplo]) = <fortran object>
```

Wrapper for spocon.

**Parameters**

- **a** [input rank-2 array(‘F’) with bounds (n,n)]
- **anorm** [input float]

**Returns**
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rcond  [float]
info   [int]

Other Parameters
uplo   [input string(len=1), optional] Default: ‘U’

scipy.linalg.lapack.dpocon

scipy.linalg.lapack.dpocon(a, anorm[, uplo]) = <fortran object>
Wrapper for dpocon.

Parameters
a      [input rank-2 array('d') with bounds (n,n)]
anorm  [input float]

Returns
rcond  [float]
info   [int]

Other Parameters
uplo   [input string(len=1), optional] Default: ‘U’

scipy.linalg.lapack.cpocon

scipy.linalg.lapack.cpocon(a, anorm[, uplo]) = <fortran object>
Wrapper for cpocon.

Parameters
a      [input rank-2 array('F') with bounds (n,n)]
anorm  [input float]

Returns
rcond  [float]
info   [int]

Other Parameters
uplo   [input string(len=1), optional] Default: ‘U’

scipy.linalg.lapack.zpocon

scipy.linalg.lapack.zpocon(a, anorm[, uplo]) = <fortran object>
Wrapper for zpocon.

Parameters
a      [input rank-2 array('D') with bounds (n,n)]
anorm  [input float]

Returns
rcond  [float]
info   [int]

Other Parameters
uplo   [input string(len=1), optional] Default: ‘U’
scipy.linalg.lapack.spotrf

scipy.linalg.lapack.spotrf(a[, lower, clean, overwrite_a]) = <fortran object>

Wrapper for spotrf.

Parameters

a [input rank-2 array('f') with bounds (n,n)]

Returns

c [rank-2 array('f') with bounds (n,n) and a storage]
info [int]

Other Parameters

overwrite_a [input int, optional] Default: 0
lower [input int, optional] Default: 0
clean [input int, optional] Default: 1

scipy.linalg.lapack.dpotrf

scipy.linalg.lapack.dpotrf(a[, lower, clean, overwrite_a]) = <fortran object>

Wrapper for dpotrf.

Parameters

a [input rank-2 array('d') with bounds (n,n)]

Returns

c [rank-2 array('d') with bounds (n,n) and a storage]
info [int]

Other Parameters

overwrite_a [input int, optional] Default: 0
lower [input int, optional] Default: 0
clean [input int, optional] Default: 1

scipy.linalg.lapack.cpotrf

scipy.linalg.lapack.cpotrf(a[, lower, clean, overwrite_a]) = <fortran object>

Wrapper for cpotrf.

Parameters

a [input rank-2 array('F') with bounds (n,n)]

Returns

c [rank-2 array('F') with bounds (n,n) and a storage]
info [int]

Other Parameters

overwrite_a [input int, optional] Default: 0
lower [input int, optional] Default: 0
clean [input int, optional] Default: 1
**scipy.linalg.lapack.zpotrf**

```
scipy.linalg.lapack.zpotrf(a[, lower, clean, overwrite_a]) = <fortran object>
```

Wrapper for zpotrf.

**Parameters**

- `a` [input rank-2 array('D') with bounds (n,n)]

**Returns**

- `c` [rank-2 array('D') with bounds (n,n) and a storage]
- `info` [int]

**Other Parameters**

- `overwrite_a` [input int, optional] Default: 0
- `lower` [input int, optional] Default: 0
- `clean` [input int, optional] Default: 1

**scipy.linalg.lapack.spotri**

```
scipy.linalg.lapack.spotri(c[, lower, overwrite_c]) = <fortran object>
```

Wrapper for spotri.

**Parameters**

- `c` [input rank-2 array('f') with bounds (n,n)]

**Returns**

- `inv_a` [rank-2 array('f') with bounds (n,n) and c storage]
- `info` [int]

**Other Parameters**

- `overwrite_c` [input int, optional] Default: 0
- `lower` [input int, optional] Default: 0

**scipy.linalg.lapack.dpotri**

```
scipy.linalg.lapack.dpotri(c[, lower, overwrite_c]) = <fortran object>
```

Wrapper for dpotri.

**Parameters**

- `c` [input rank-2 array('d') with bounds (n,n)]

**Returns**

- `inv_a` [rank-2 array('d') with bounds (n,n) and c storage]
- `info` [int]

**Other Parameters**

- `overwrite_c` [input int, optional] Default: 0
- `lower` [input int, optional] Default: 0
scipy.linalg.lapack.cpotri

scipy.linalg.lapack.cpotri(c[, lower, overwrite_c]) = <fortran object>
Wrapper for cpotri.

Parameters

  c          [input rank-2 array(‘F’) with bounds (n,n)]

Returns

  inv_a      [rank-2 array(‘F’) with bounds (n,n) and c storage]
  info       [int]

Other Parameters

  overwrite_c
    [input int, optional] Default: 0
  lower      [input int, optional] Default: 0

scipy.linalg.lapack.zpotri

scipy.linalg.lapack.zpotri(c[, lower, overwrite_c]) = <fortran object>
Wrapper for zpotri.

Parameters

  c          [input rank-2 array(‘D’) with bounds (n,n)]

Returns

  inv_a      [rank-2 array(‘D’) with bounds (n,n) and c storage]
  info       [int]

Other Parameters

  overwrite_c
    [input int, optional] Default: 0
  lower      [input int, optional] Default: 0

scipy.linalg.lapack.spotrs

scipy.linalg.lapack.spotrs(c, b[, lower, overwrite_b]) = <fortran object>
Wrapper for spotrs.

Parameters

  c          [input rank-2 array(‘f’) with bounds (n,n)]
  b          [input rank-2 array(‘f’) with bounds (n,nrhs)]

Returns

  x          [rank-2 array(‘f’) with bounds (n,nrhs) and b storage]
  info       [int]

Other Parameters

  overwrite_b
    [input int, optional] Default: 0
  lower      [input int, optional] Default: 0
scipy.linalg.lapack.dpotrs

`scipy.linalg.lapack.dpotrs(c, b[, lower, overwrite_b]) = <fortran object>`

Wrapper for `dpotrs`.

**Parameters**
- `c` [input rank-2 array('d') with bounds (n,n)]
- `b` [input rank-2 array('d') with bounds (n,nrhs)]

**Returns**
- `x` [rank-2 array('d') with bounds (n,nrhs) and b storage]
- `info` [int]

**Other Parameters**
- `overwrite_b` [input int, optional] Default: 0
- `lower` [input int, optional] Default: 0

scipy.linalg.lapack.cpotrs

`scipy.linalg.lapack.cpotrs(c, b[, lower, overwrite_b]) = <fortran object>`

Wrapper for `cpotrs`.

**Parameters**
- `c` [input rank-2 array('F') with bounds (n,n)]
- `b` [input rank-2 array('F') with bounds (n,nrhs)]

**Returns**
- `x` [rank-2 array('F') with bounds (n,nrhs) and b storage]
- `info` [int]

**Other Parameters**
- `overwrite_b` [input int, optional] Default: 0
- `lower` [input int, optional] Default: 0

scipy.linalg.lapack.zpotrs

`scipy.linalg.lapack.zpotrs(c, b[, lower, overwrite_b]) = <fortran object>`

Wrapper for `zpotrs`.

**Parameters**
- `c` [input rank-2 array('D') with bounds (n,n)]
- `b` [input rank-2 array('D') with bounds (n,nrhs)]

**Returns**
- `x` [rank-2 array('D') with bounds (n,nrhs) and b storage]
- `info` [int]

**Other Parameters**
- `overwrite_b` [input int, optional] Default: 0
- `lower` [input int, optional] Default: 0
scipy.linalg.lapack.crot

```python
scipy.linalg.lapack.crot(x, y, c, s, n, offx, incx, offy, incy, overwrite_x, overwrite_y) =
<fortran object>
```

Wrapper for crot.

**Parameters**

- `x` : [input] rank-1 array('F') with bounds (lx)
- `y` : [input] rank-1 array('F') with bounds (ly)
- `c` : [input] float
- `s` : [input] complex

**Returns**

- `x` : rank-1 array('F') with bounds (lx)
- `y` : rank-1 array('F') with bounds (ly)

**Other Parameters**

- `n` : [input int, optional] Default: (lx-1-offx)/abs(incx)+1
- `overwrite_x` : [input int, optional] Default: 0
- `offx` : [input int, optional] Default: 0
- `incx` : [input int, optional] Default: 1
- `overwrite_y` : [input int, optional] Default: 0
- `offy` : [input int, optional] Default: 0
- `incy` : [input int, optional] Default: 1

scipy.linalg.lapack.zrot

```python
scipy.linalg.lapack.zrot(x, y, c, s, n, offx, incx, offy, incy, overwrite_x, overwrite_y) =
<fortran object>
```

Wrapper for zrot.

**Parameters**

- `x` : [input] rank-1 array('D') with bounds (lx)
- `y` : [input] rank-1 array('D') with bounds (ly)
- `c` : [input] float
- `s` : [input] complex

**Returns**

- `x` : rank-1 array('D') with bounds (lx)
- `y` : rank-1 array('D') with bounds (ly)

**Other Parameters**

- `n` : [input int, optional] Default: (lx-1-offx)/abs(incx)+1
- `overwrite_x` : [input int, optional] Default: 0
- `offx` : [input int, optional] Default: 0
- `incx` : [input int, optional] Default: 1
- `overwrite_y` : [input int, optional] Default: 0
- `offy` : [input int, optional] Default: 0
- `incy` : [input int, optional] Default: 1
scipy.linalg.lapack.strsyl

scipy.linalg.lapack.strsyl(a, b, c[, trana, tranb, isgn, overwrite_c]) = <fortran object>
Wrapper for strsyl.

Parameters
---
a [input rank-2 array('f') with bounds (m,m)]
b [input rank-2 array('f') with bounds (n,n)]
c [input rank-2 array('f') with bounds (m,n)]

Returns
---
x [rank-2 array('f') with bounds (m,n) and c storage]
scale [float]
info [int]

Other Parameters
---
trana [input string(len=1), optional] Default: ‘N’
tranb [input string(len=1), optional] Default: ‘N’
isgn [input int, optional] Default: 1
overwrite_c [input int, optional] Default: 0

scipy.linalg.lapack.dtrsyl

scipy.linalg.lapack.dtrsyl(a, b, c[, trana, tranb, isgn, overwrite_c]) = <fortran object>
Wrapper for dtrsyl.

Parameters
---
a [input rank-2 array('d') with bounds (m,m)]
b [input rank-2 array('d') with bounds (n,n)]
c [input rank-2 array('d') with bounds (m,n)]

Returns
---
x [rank-2 array('d') with bounds (m,n) and c storage]
scale [float]
info [int]

Other Parameters
---
trana [input string(len=1), optional] Default: ‘N’
tranb [input string(len=1), optional] Default: ‘N’
isgn [input int, optional] Default: 1
overwrite_c [input int, optional] Default: 0

scipy.linalg.lapack.ctrsyl

scipy.linalg.lapack.ctrsyl(a, b, c[, trana, tranb, isgn, overwrite_c]) = <fortran object>
Wrapper for ctrsyl.

Parameters
---
a [input rank-2 array('F') with bounds (m,m)]
b [input rank-2 array('F') with bounds (n,n)]
c [input rank-2 array('F') with bounds (m,n)]

Returns
---

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x [rank-2 array('F') with bounds (m,n) and c storage]
scale [float]
info [int]

**Other Parameters**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
<th>Default</th>
</tr>
</thead>
<tbody>
<tr>
<td>trana</td>
<td>[input string(len=1), optional] Default: ‘N’</td>
<td></td>
</tr>
<tr>
<td>tranb</td>
<td>[input string(len=1), optional] Default: ‘N’</td>
<td></td>
</tr>
<tr>
<td>isgn</td>
<td>[input int, optional] Default: 1</td>
<td></td>
</tr>
<tr>
<td>overwrite_c</td>
<td>[input int, optional] Default: 0</td>
<td></td>
</tr>
</tbody>
</table>

scipy.linalg.lapack.ztrsyl

```python
scipy.linalg.lapack.ztrsyl(a, b, c[, trana, tranb, isgn, overwrite_c]) = <fortran object>
```

Wrapper for ztrsyl.

**Parameters**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
<th>Default</th>
</tr>
</thead>
<tbody>
<tr>
<td>a</td>
<td>[input rank-2 array('D') with bounds (m,m)]</td>
<td></td>
</tr>
<tr>
<td>b</td>
<td>[input rank-2 array('D') with bounds (n,n)]</td>
<td></td>
</tr>
<tr>
<td>c</td>
<td>[input rank-2 array('D') with bounds (m,n)]</td>
<td></td>
</tr>
</tbody>
</table>

**Returns**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
<th>Default</th>
</tr>
</thead>
<tbody>
<tr>
<td>x</td>
<td>[rank-2 array('D') with bounds (m,n) and c storage]</td>
<td></td>
</tr>
<tr>
<td>scale</td>
<td>[float]</td>
<td></td>
</tr>
<tr>
<td>info</td>
<td>[int]</td>
<td></td>
</tr>
</tbody>
</table>

**Other Parameters**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
<th>Default</th>
</tr>
</thead>
<tbody>
<tr>
<td>trana</td>
<td>[input string(len=1), optional] Default: ‘N’</td>
<td></td>
</tr>
<tr>
<td>tranb</td>
<td>[input string(len=1), optional] Default: ‘N’</td>
<td></td>
</tr>
<tr>
<td>isgn</td>
<td>[input int, optional] Default: 1</td>
<td></td>
</tr>
<tr>
<td>overwrite_c</td>
<td>[input int, optional] Default: 0</td>
<td></td>
</tr>
</tbody>
</table>

scipy.linalg.lapack.strtri

```python
scipy.linalg.lapack.strtri(c[, lower, unitdiag, overwrite_c]) = <fortran object>
```

Wrapper for strtri.

**Parameters**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
<th>Default</th>
</tr>
</thead>
<tbody>
<tr>
<td>c</td>
<td>[input rank-2 array('F') with bounds (n,n)]</td>
<td></td>
</tr>
</tbody>
</table>

**Returns**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
<th>Default</th>
</tr>
</thead>
<tbody>
<tr>
<td>inv_c</td>
<td>[rank-2 array('F') with bounds (n,n) and c storage]</td>
<td></td>
</tr>
<tr>
<td>info</td>
<td>[int]</td>
<td></td>
</tr>
</tbody>
</table>

**Other Parameters**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
<th>Default</th>
</tr>
</thead>
<tbody>
<tr>
<td>overwrite_c</td>
<td>[input int, optional] Default: 0</td>
<td></td>
</tr>
<tr>
<td>lower</td>
<td>[input int, optional] Default: 0</td>
<td></td>
</tr>
<tr>
<td>unitdiag</td>
<td>[input int, optional] Default: 0</td>
<td></td>
</tr>
</tbody>
</table>

6.11. Low-level LAPACK functions (scipy.linalg.lapack)
scipy.linalg.lapack.dtrtri

Wrapper for dtrtri.

Parameters
---

- **c** : [input rank-2 array('d') with bounds (n,n)]

Returns
---

- **inv_c** : [rank-2 array('d') with bounds (n,n) and c storage]
- **info** : [int]

Other Parameters
---

- **overwrite_c** : [input int, optional] Default: 0
- **lower** : [input int, optional] Default: 0
- **unitdiag** : [input int, optional] Default: 0

scipy.linalg.lapack.ctrtri

Wrapper for ctrtri.

Parameters
---

- **c** : [input rank-2 array('F') with bounds (n,n)]

Returns
---

- **inv_c** : [rank-2 array('F') with bounds (n,n) and c storage]
- **info** : [int]

Other Parameters
---

- **overwrite_c** : [input int, optional] Default: 0
- **lower** : [input int, optional] Default: 0
- **unitdiag** : [input int, optional] Default: 0

scipy.linalg.lapack.ztrtri

Wrapper for ztrtri.

Parameters
---

- **c** : [input rank-2 array('D') with bounds (n,n)]

Returns
---

- **inv_c** : [rank-2 array('D') with bounds (n,n) and c storage]
- **info** : [int]

Other Parameters
---

- **overwrite_c** : [input int, optional] Default: 0
- **lower** : [input int, optional] Default: 0
- **unitdiag** : [input int, optional] Default: 0
scipy.linalg.lapack.strtrs

scipy.linalg.lapack.strtrs(a, b[ , lower, trans, unitdiag, lda, overwrite_b]) = <fortran object>

Wrapper for strtrs.

Parameters

a  [input rank-2 array('f') with bounds (lda,n)]
b  [input rank-2 array('f') with bounds (ldb,nrhs)]

Returns

x  [rank-2 array('f') with bounds (ldb,nrhs) and b storage]
info  [int]

Other Parameters

lower  [input int, optional] Default: 0
trans  [input int, optional] Default: 0
unitdiag  [input int, optional] Default: 0
lda  [input int, optional] Default: shape(a,0)
overwrite_b  [input int, optional] Default: 0

scipy.linalg.lapack.dtrtrs

scipy.linalg.lapack.dtrtrs(a, b[ , lower, trans, unitdiag, lda, overwrite_b]) = <fortran object>

Wrapper for dtrtrs.

Parameters

a  [input rank-2 array('d') with bounds (lda,n)]
b  [input rank-2 array('d') with bounds (ldb,nrhs)]

Returns

x  [rank-2 array('d') with bounds (ldb,nrhs) and b storage]
info  [int]

Other Parameters

lower  [input int, optional] Default: 0
trans  [input int, optional] Default: 0
unitdiag  [input int, optional] Default: 0
lda  [input int, optional] Default: shape(a,0)
overwrite_b  [input int, optional] Default: 0

scipy.linalg.lapack.ctrtrs

scipy.linalg.lapack.ctrtrs(a, b[ , lower, trans, unitdiag, lda, overwrite_b]) = <fortran object>

Wrapper for ctrtrs.

Parameters

a  [input rank-2 array('F') with bounds (lda,n)]
b  [input rank-2 array('F') with bounds (ldb,nrhs)]

Returns

x  [rank-2 array('F') with bounds (ldb,nrhs) and b storage]
info  [int]

6.11. Low-level LAPACK functions (scipy.linalg.lapack)
Other Parameters

lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
unitdiag [input int, optional] Default: 0
lda [input int, optional] Default: shape(a,0)
overwrite_b [input int, optional] Default: 0

scipy.linalg.lapack.ztrtrs

scipy.linalg.lapack.ztrtrs(a, b[, lower, trans, unitdiag, lda, overwrite_b]) = <fortran object>
Wrapper for ztrtrs.

Parameters

a [input rank-2 array('D') with bounds (lda,n)]
b [input rank-2 array('D') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('D') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
unitdiag [input int, optional] Default: 0
lda [input int, optional] Default: shape(a,0)
overwrite_b [input int, optional] Default: 0

scipy.linalg.lapack.spftrf

scipy.linalg.lapack.spftrf(n, a[, transr, uplo, overwrite_a]) = <fortran object>
Wrapper for spftrf.

Parameters

n [input int]
a [input rank-1 array('f') with bounds (nt)]

Returns

achol [rank-1 array('f') with bounds (nt) and a storage]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: ‘N’
uplo [input string(len=1), optional] Default: ‘U’
overwrite_a [input int, optional] Default: 0
scipy.linalg.lapack.dpftrf

scipy.linalg.lapack.dpftrf(n, a[, transr, uplo, overwrite_a]) = <fortran object>
Wrapper for dpftrf.

Parameters

- n [input int]
- a [input rank-1 array('d') with bounds (nt)]

Returns

- achol [rank-1 array('d') with bounds (nt) and a storage]
- info [int]

Other Parameters

- transr [input string(len=1), optional] Default: ‘N’
- uplo [input string(len=1), optional] Default: ‘U’
- overwrite_a [input int, optional] Default: 0

scipy.linalg.lapack.cpftrf

scipy.linalg.lapack.cpftrf(n, a[, transr, uplo, overwrite_a]) = <fortran object>
Wrapper for cpftrf.

Parameters

- n [input int]
- a [input rank-1 array('F') with bounds (nt)]

Returns

- achol [rank-1 array('F') with bounds (nt) and a storage]
- info [int]

Other Parameters

- transr [input string(len=1), optional] Default: ‘N’
- uplo [input string(len=1), optional] Default: ‘U’
- overwrite_a [input int, optional] Default: 0

scipy.linalg.lapack.zpftrf

scipy.linalg.lapack.zpftrf(n, a[, transr, uplo, overwrite_a]) = <fortran object>
Wrapper for zpftrf.

Parameters

- n [input int]
- a [input rank-1 array('D') with bounds (nt)]

Returns

- achol [rank-1 array('D') with bounds (nt) and a storage]
- info [int]

Other Parameters

- transr [input string(len=1), optional] Default: ‘N’
- uplo [input string(len=1), optional] Default: ‘U’
overwrite_a
    [input int, optional] Default: 0

scipy.linalg.lapack.spftri

scipy.linalg.lapack.spftri(n, a[, transr, uplo, overwrite_a]) = <fortran object>
Wrapper for spftri.

Parameters

n       [input int]
a       [input rank-1 array('f') with bounds (nt)]

Returns

ainv    [rank-1 array('f') with bounds (nt) and a storage]
info    [int]

Other Parameters

transr  [input string(len=1), optional] Default: ‘N’
uplo    [input string(len=1), optional] Default: ‘U’
overwrite_a
        [input int, optional] Default: 0

scipy.linalg.lapack.dpftri

scipy.linalg.lapack.dpftri(n, a[, transr, uplo, overwrite_a]) = <fortran object>
Wrapper for dpftri.

Parameters

n       [input int]
a       [input rank-1 array('d') with bounds (nt)]

Returns

ainv    [rank-1 array('d') with bounds (nt) and a storage]
info    [int]

Other Parameters

transr  [input string(len=1), optional] Default: ‘N’
uplo    [input string(len=1), optional] Default: ‘U’
overwrite_a
        [input int, optional] Default: 0

scipy.linalg.lapackcpftri

scipy.linalg.lapackcpftri(n, a[, transr, uplo, overwrite_a]) = <fortran object>
Wrapper for cpftri.

Parameters

n       [input int]
a       [input rank-1 array('F') with bounds (nt)]

Returns

ainv    [rank-1 array('F') with bounds (nt) and a storage]
info    [int]
Other Parameters

- transr [input string(len=1), optional] Default: ‘N’
- uplo [input string(len=1), optional] Default: ‘U’
- overwrite_a [input int, optional] Default: 0

scipy.linalg.lapack.zpftri

scipy.linalg.lapack.zpftri(n, a[, transr, uplo, overwrite_a]) = <fortran object>

Wrapper for zpftri.

Parameters

- n [input int]
- a [input rank-1 array('D') with bounds (nt)]

Returns

- ainv [rank-1 array('D') with bounds (nt) and a storage]
- info [int]

Other Parameters

- transr [input string(len=1), optional] Default: ‘N’
- uplo [input string(len=1), optional] Default: ‘U’
- overwrite_a [input int, optional] Default: 0

scipy.linalg.lapack.spftrs

scipy.linalg.lapack.spftrs(n, a, b[, transr, uplo, overwrite_b]) = <fortran object>

Wrapper for spftrs.

Parameters

- n [input int]
- a [input rank-1 array('F') with bounds (nt)]
- b [input rank-2 array('F') with bounds (ldb,nhrs)]

Returns

- x [rank-2 array('F') with bounds (ldb,nhrs) and b storage]
- info [int]

Other Parameters

- transr [input string(len=1), optional] Default: ‘N’
- uplo [input string(len=1), optional] Default: ‘U’
- overwrite_b [input int, optional] Default: 0

scipy.linalg.lapack.dpftrs

scipy.linalg.lapack.dpftrs(n, a, b[, transr, uplo, overwrite_b]) = <fortran object>

Wrapper for dpftrs.

Parameters

- n [input int]
- a [input rank-1 array('D') with bounds (nt)]
 Returns

\[ x \text{ [rank-2 array('d') with bounds (ldb,nhrs) and b storage]} \]

\[ \text{info [int]} \]

Other Parameters

\[ \text{transr [input string(len=1), optional] Default: ‘N’} \]
\[ \text{uplo [input string(len=1), optional] Default: ‘U’} \]
\[ \text{overwrite\_b [input int, optional] Default: 0} \]

scipy.linalg.lapack.cpftrs

scipy.linalg.lapack.cpftrs\((n, a, b, transr, uplo, overwrite\_b)\) = <fortran object>

Wrapper for cpftrs.

 Parameters

\[ n \text{ [input int]} \]
\[ a \text{ [input rank-1 array('F') with bounds (nt)]} \]
\[ b \text{ [input rank-2 array('F') with bounds (ldb,nhrs)]} \]

 Returns

\[ x \text{ [rank-2 array('F') with bounds (ldb,nhrs) and b storage]} \]
\[ \text{info [int]} \]

Other Parameters

\[ \text{transr [input string(len=1), optional] Default: ‘N’} \]
\[ \text{uplo [input string(len=1), optional] Default: ‘U’} \]
\[ \text{overwrite\_b [input int, optional] Default: 0} \]

scipy.linalg.lapack.zpftrs

scipy.linalg.lapack.zpftrs\((n, a, b, transr, uplo, overwrite\_b)\) = <fortran object>

Wrapper for zpftrs.

 Parameters

\[ n \text{ [input int]} \]
\[ a \text{ [input rank-1 array('D') with bounds (nt)]} \]
\[ b \text{ [input rank-2 array('D') with bounds (ldb,nhrs)]} \]

 Returns

\[ x \text{ [rank-2 array('D') with bounds (ldb,nhrs) and b storage]} \]
\[ \text{info [int]} \]

Other Parameters

\[ \text{transr [input string(len=1), optional] Default: ‘N’} \]
\[ \text{uplo [input string(len=1), optional] Default: ‘U’} \]
\[ \text{overwrite\_b [input int, optional] Default: 0} \]
scipy.linalg.lapack.cunghr

scipy.linalg.lapack.cunghr(a, tau[, lo, hi, lwork, overwrite_a]) = <fortran object>
Wrapper for cunghr.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
tau [input rank-1 array('F') with bounds (n - 1)]

Returns

ht [rank-2 array('F') with bounds (n,n) and a storage]
info [int]

Other Parameters

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1
overwrite_a [input int, optional] Default: 0
lwork [input int, optional] Default: max(hi-lo,1)

scipy.linalg.lapack.zunghr

scipy.linalg.lapack.zunghr(a, tau[, lo, hi, lwork, overwrite_a]) = <fortran object>
Wrapper for zunghr.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
tau [input rank-1 array('D') with bounds (n - 1)]

Returns

ht [rank-2 array('D') with bounds (n,n) and a storage]
info [int]

Other Parameters

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1
overwrite_a [input int, optional] Default: 0
lwork [input int, optional] Default: max(hi-lo,1)

scipy.linalg.lapack.cungqr

scipy.linalg.lapack.cungqr(a, tau[, lwork, overwrite_a]) = <fortran object>
Wrapper for cungqr.

Parameters

a [input rank-2 array('F') with bounds (m,n)]
tau [input rank-1 array('F') with bounds (k)]

Returns

q [rank-2 array('F') with bounds (m,n) and a storage]
work [rank-1 array('F') with bounds (MAX(lwork,1))]
info [int]

Other Parameters
overwrite_a  [input int, optional] Default: 0
lwork   [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.zungqr

scipy.linalg.lapack.zungqr(a, tau[, lwork, overwrite_a]) = <fortran object>
Wrapper for zungqr.

Parameters
a        [input rank-2 array('D') with bounds (m,n)]
tau      [input rank-1 array('D') with bounds (k)]

Returns
q        [rank-2 array('D') with bounds (m,n) and a storage]
work     [rank-1 array('D') with bounds (MAX(lwork,1))]
info     [int]

Other Parameters
overwrite_a  [input int, optional] Default: 0
lwork       [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.cungrq

scipy.linalg.lapack.cungrq(a, tau[, lwork, overwrite_a]) = <fortran object>
Wrapper for cungrq.

Parameters
a        [input rank-2 array('F') with bounds (m,n)]
tau      [input rank-1 array('F') with bounds (k)]

Returns
q        [rank-2 array('F') with bounds (m,n) and a storage]
work     [rank-1 array('F') with bounds (MAX(lwork,1))]
info     [int]

Other Parameters
overwrite_a  [input int, optional] Default: 0
lwork       [input int, optional] Default: max(3*m,1)

scipy.linalg.lapack.zungrq

scipy.linalg.lapack.zungrq(a, tau[, lwork, overwrite_a]) = <fortran object>
Wrapper for zungrq.

Parameters
a        [input rank-2 array('D') with bounds (m,n)]
tau      [input rank-1 array('D') with bounds (k)]

Returns
q        [rank-2 array('D') with bounds (m,n) and a storage]
work     [rank-1 array('D') with bounds (MAX(lwork,1))]

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info [int]

**Other Parameters**

overwrite_a

[input int, optional] Default: 0

lwork

[input int, optional] Default: max(3*m,1)

**scipy.linalg.lapack.cunmqr**

scipy.linalg.lapack.cunmqr(side, trans, a, tau, c, lwork[, overwrite_c]) = <fortran object>

Wrapper for cunmqr.

**Parameters**

side [input string(len=1)]

trans [input string(len=1)]

a [input rank-2 array('F') with bounds (lda,k)]

tau [input rank-1 array('F') with bounds (k)]

c [input rank-2 array('F') with bounds (ldc,n)]

lwork [input int]

**Returns**

cq [rank-2 array('F') with bounds (ldc,n) and c storage]

work [rank-1 array('F') with bounds (MAX(lwork,1))]

info [int]

**Other Parameters**

overwrite_c

[input int, optional] Default: 0

**scipy.linalg.lapack.zunmqr**

scipy.linalg.lapack.zunmqr(side, trans, a, tau, c, lwork[, overwrite_c]) = <fortran object>

Wrapper for zunmqr.

**Parameters**

side [input string(len=1)]

trans [input string(len=1)]

a [input rank-2 array('D') with bounds (lda,k)]

tau [input rank-1 array('D') with bounds (k)]

c [input rank-2 array('D') with bounds (ldc,n)]

lwork [input int]

**Returns**

cq [rank-2 array('D') with bounds (ldc,n) and c storage]

work [rank-1 array('D') with bounds (MAX(lwork,1))]

info [int]

**Other Parameters**

overwrite_c

[input int, optional] Default: 0
scipy.linalg.lapack.cunmrz

scipy.linalg.lapack.cunmrz(a, tau[, side, trans, lwork, overwrite_c]) = <fortran object>
Wrapper for cunmrz.

Parameters

- a [input rank-2 array('F') with bounds (k,nt)]
- tau [input rank-1 array('F') with bounds (k)]
- c [input rank-2 array('F') with bounds (m,n)]

Returns

- cq [rank-2 array('F') with bounds (m,n) and c storage]
- info [int]

Other Parameters

- side [input string(len=1), optional] Default: ‘L’
- trans [input string(len=1), optional] Default: ‘N’
- overwrite_c [input int, optional] Default: 0
- lwork [input int, optional] Default: MAX((side[0]=='L'?n:m),1)

scipy.linalg.lapack.zunmrz

scipy.linalg.lapack.zunmrz(a, tau[, side, trans, lwork, overwrite_c]) = <fortran object>
Wrapper for zunmrz.

Parameters

- a [input rank-2 array('D') with bounds (k,nt)]
- tau [input rank-1 array('D') with bounds (k)]
- c [input rank-2 array('D') with bounds (m,n)]

Returns

- cq [rank-2 array('D') with bounds (m,n) and c storage]
- info [int]

Other Parameters

- side [input string(len=1), optional] Default: ‘L’
- trans [input string(len=1), optional] Default: ‘N’
- overwrite_c [input int, optional] Default: 0
- lwork [input int, optional] Default: MAX((side[0]=='L'?n:m),1)

scipy.linalg.lapack.cunmrz_lwork

scipy.linalg.lapack.cunmrz_lwork(m, n[, side, trans]) = <fortran object>
Wrapper for cunmrz_lwork.

Parameters

- m [input int]
- n [input int]

Returns

- work [complex]
- info [int]
**Other Parameters**

- **side**  
  [input string(len=1), optional] Default: ‘L’

- **trans**  
  [input string(len=1), optional] Default: ‘N’

---

**scipy.linalg.lapack.zunmrz_lwork**

`scipy.linalg.lapack.zunmrz_lwork(m, n, side, trans) = <fortran object>`

Wrapper for `zunmrz_lwork`.

**Parameters**

- **m**  
  [input int]

- **n**  
  [input int]

**Returns**

- **work**  
  [complex]

- **info**  
  [int]

---

**Other Parameters**

- **side**  
  [input string(len=1), optional] Default: ‘L’

- **trans**  
  [input string(len=1), optional] Default: ‘N’

---

**scipy.linalg.lapack.sgtsv**

`scipy.linalg.lapack.sgtsv(dl, d, du, b, overwrite_dl, overwrite_d, overwrite_du, overwrite_b) = <fortran object>`

Wrapper for `sgtsv`.

**Parameters**

- **dl**  
  [input rank-1 array('f') with bounds (n - 1)]

- **d**  
  [input rank-1 array('f') with bounds (n)]

- **du**  
  [input rank-1 array('f') with bounds (n - 1)]

- **b**  
  [input rank-2 array('f') with bounds (n,nrhs)]

**Returns**

- **du2**  
  [rank-1 array('f') with bounds (n - 1) and dl storage]

- **d**  
  [rank-1 array('f') with bounds (n)]

- **du**  
  [rank-1 array('f') with bounds (n - 1)]

- **x**  
  [rank-2 array('f') with bounds (n,nrhs) and b storage]

- **info**  
  [int]

**Other Parameters**

- **overwrite_dl**  
  [input int, optional] Default: 0

- **overwrite_d**  
  [input int, optional] Default: 0

- **overwrite_du**  
  [input int, optional] Default: 0

- **overwrite_b**  
  [input int, optional] Default: 0
scipy.linalg.lapack.dgtsv

`scipy.linalg.lapack.dgtsv(dl, d, du, b[, overwrite_dl, overwrite_d, overwrite_du, overwrite_b])` = <fortran object>

Wrapper for `dgtsv`.

**Parameters**

- `dl` [input rank-1 array('d') with bounds (n - 1)]
- `d` [input rank-1 array('d') with bounds (n)]
- `du` [input rank-1 array('d') with bounds (n - 1)]
- `b` [input rank-2 array('d') with bounds (n,nrhs)]

**Returns**

- `du2` [rank-1 array('d') with bounds (n - 1) and dl storage]
- `d` [rank-1 array('d') with bounds (n)]
- `du` [rank-1 array('d') with bounds (n - 1)]
- `x` [rank-2 array('d') with bounds (n,nrhs) and b storage]
- `info` [int]

**Other Parameters**

- `overwrite_dl` [input int, optional] Default: 0
- `overwrite_d` [input int, optional] Default: 0
- `overwrite_du` [input int, optional] Default: 0
- `overwrite_b` [input int, optional] Default: 0

scipy.linalg.lapack.cgtsv

`scipy.linalg.lapack.cgtsv(dl, d, du, b[, overwrite_dl, overwrite_d, overwrite_du, overwrite_b])` = <fortran object>

Wrapper for `cgtsv`.

**Parameters**

- `dl` [input rank-1 array('F') with bounds (n - 1)]
- `d` [input rank-1 array('F') with bounds (n)]
- `du` [input rank-1 array('F') with bounds (n - 1)]
- `b` [input rank-2 array('F') with bounds (n,nrhs)]

**Returns**

- `du2` [rank-1 array('F') with bounds (n - 1) and dl storage]
- `d` [rank-1 array('F') with bounds (n)]
- `du` [rank-1 array('F') with bounds (n - 1)]
- `x` [rank-2 array('F') with bounds (n,nrhs) and b storage]
- `info` [int]

**Other Parameters**

- `overwrite_dl` [input int, optional] Default: 0
- `overwrite_d` [input int, optional] Default: 0
overwrite_du
[optional int] Default: 0

overwrite_b
[optional int] Default: 0

scipy.linalg.lapack.zgtsv

scipy.linalg.lapack.zgtsv(dl, d, du, b[, overwrite__du, overwrite_d, overwrite__du, overwrite_b])
= <fortran object>

Wrapper for zgtsv.

Parameters

- dl
  [input rank-1 array('D') with bounds (n - 1)]
- d
  [input rank-1 array('D') with bounds (n)]
- du
  [input rank-1 array('D') with bounds (n - 1)]
- b
  [input rank-2 array('D') with bounds (n,nrhs)]

Returns

- du2
  [rank-1 array('D') with bounds (n - 1) and dl storage]
- d
  [rank-1 array('D') with bounds (n)]
- du
  [rank-1 array('D') with bounds (n - 1)]
- x
  [rank-2 array('D') with bounds (n,nrhs) and b storage]
- info
  [int]

Other Parameters

- overwrite__du
  [optional int] Default: 0
- overwrite_d
  [optional int] Default: 0
- overwrite__du
  [optional int] Default: 0
- overwrite_b
  [optional int] Default: 0

scipy.linalg.lapack.sptsv

scipy.linalg.lapack.sptsv(d, e, b[, overwrite_d, overwrite_e, overwrite_b])
= <fortran object>

Wrapper for sptsv.

Parameters

- d
  [input rank-1 array('f') with bounds (n)]
- e
  [input rank-1 array('f') with bounds (n - 1)]
- b
  [input rank-2 array('f') with bounds (n,nrhs)]

Returns

- d
  [rank-1 array('f') with bounds (n)]
- du
  [rank-1 array('f') with bounds (n - 1) and e storage]
- x
  [rank-2 array('f') with bounds (n,nrhs) and b storage]
- info
  [int]

Other Parameters

- overwrite_d
  [optional int] Default: 0
overwrite_e

[input int, optional] Default: 0

overwrite_b

[input int, optional] Default: 0

**scipy.linalg.lapack.dptsv**

```python
scipy.linalg.lapack.dptsv(d, e, b[, overwrite_d, overwrite_e, overwrite_b]) = <fortran object>
```

Wrapper for dptsv.

**Parameters**

- **d** [input rank-1 array('d') with bounds (n)]
- **e** [input rank-1 array('d') with bounds (n - 1)]
- **b** [input rank-2 array('d') with bounds (n,nrhs)]

**Returns**

- **d** [rank-1 array('d') with bounds (n)]
- **du** [rank-1 array('d') with bounds (n - 1) and e storage]
- **x** [rank-2 array('d') with bounds (n,nrhs) and b storage]
- **info** [int]

**Other Parameters**

- **overwrite_d** [input int, optional] Default: 0
- **overwrite_e** [input int, optional] Default: 0
- **overwrite_b** [input int, optional] Default: 0

**scipy.linalg.lapack.cptsv**

```python
scipy.linalg.lapack.cptsv(d, e, b[, overwrite_d, overwrite_e, overwrite_b]) = <fortran object>
```

Wrapper for cptsv.

**Parameters**

- **d** [input rank-1 array('f') with bounds (n)]
- **e** [input rank-1 array('F') with bounds (n - 1)]
- **b** [input rank-2 array('F') with bounds (n,nrhs)]

**Returns**

- **d** [rank-1 array('f') with bounds (n)]
- **du** [rank-1 array('F') with bounds (n - 1) and e storage]
- **x** [rank-2 array('F') with bounds (n,nrhs) and b storage]
- **info** [int]

**Other Parameters**

- **overwrite_d** [input int, optional] Default: 0
- **overwrite_e** [input int, optional] Default: 0
- **overwrite_b** [input int, optional] Default: 0
scipy.linalg.lapack.zptsv

```python
scipy.linalg.lapack.zptsv(d, e, b[, overwrite_d, overwrite_e, overwrite_b]) = <fortran object>
```

Wrapper for zptsv.

**Parameters**
- `d` [input rank-1 array('d') with bounds (n)]
- `e` [input rank-1 array('D') with bounds (n - 1)]
- `b` [input rank-2 array('D') with bounds (n,nrhs)]

**Returns**
- `d` [rank-1 array('d') with bounds (n)]
- `du` [rank-2 array('D') with bounds (n - 1) and e storage]
- `x` [rank-2 array('D') with bounds (n,nrhs) and b storage]
- `info` [int]

**Other Parameters**
- `overwrite_d` [input int, optional] Default: 0
- `overwrite_e` [input int, optional] Default: 0
- `overwrite_b` [input int, optional] Default: 0

scipy.linalg.lapack.slamch

```python
scipy.linalg.lapack.slamch(cmach) = <fortran slamch>
```

Wrapper for slamch.

**Parameters**
- `cmach` [input string(len=1)]

**Returns**
- `slamch` [float]

scipy.linalg.lapack.dlamch

```python
scipy.linalg.lapack.dlamch(cmach) = <fortran dlamch>
```

Wrapper for dlamch.

**Parameters**
- `cmach` [input string(len=1)]

**Returns**
- `dlamch` [float]

scipy.linalg.lapack.sorghr

```python
scipy.linalg.lapack.sorghr(a, tau[, lo, hi, lwork, overwrite_a]) = <fortran object>
```

Wrapper for sorghr.

**Parameters**
- `a` [input rank-2 array('f') with bounds (n,n)]
- `tau` [input rank-1 array('f') with bounds (n - 1)]
Returns
ht  [rank-2 array('f') with bounds (n,n) and a storage]
info  [int]

Other Parameters
lo  [input int, optional] Default: 0
hi  [input int, optional] Default: n-1
overwrite_a  [input int, optional] Default: 0
lwork  [input int, optional] Default: max(hi-lo,1)

scipy.linalg.lapack.dorghr
scipy.linalg.lapack.dorghr(a, tau[, lo, hi, lwork, overwrite_a]) = <fortran object>
Wrapper for dorghr.

Parameters
a  [input rank-2 array('d') with bounds (n,n)]
tau  [input rank-1 array('d') with bounds (n - 1)]

Returns
ht  [rank-2 array('d') with bounds (n,n) and a storage]
info  [int]

Other Parameters
lo  [input int, optional] Default: 0
hi  [input int, optional] Default: n-1
overwrite_a  [input int, optional] Default: 0
lwork  [input int, optional] Default: max(hi-lo,1)

scipy.linalg.lapack.sorgqr
scipy.linalg.lapack.sorgqr(a, tau[, lwork, overwrite_a]) = <fortran object>
Wrapper for sorgqr.

Parameters
a  [input rank-2 array('f') with bounds (m,n)]
tau  [input rank-1 array('f') with bounds (k)]

Returns
q  [rank-2 array('f') with bounds (m,n) and a storage]
work  [rank-1 array('f') with bounds (MAX(lwork,1))]
info  [int]

Other Parameters
overwrite_a  [input int, optional] Default: 0
lwork  [input int, optional] Default: max(3*n,1)
scipy.linalg.lapack.dorgqr

scipy.linalg.lapack.dorgqr(a, tau[, overwrite_a]) = <fortran object>

Wrapper for dorgqr.

Parameters
- a [input rank-2 array('d') with bounds (m,n)]
- tau [input rank-1 array('d') with bounds (k)]

Returns
- q [rank-2 array('d') with bounds (m,n) and a storage]
- work [rank-1 array('d') with bounds (MAX(lwork,1))]
- info [int]

Other Parameters
- overwrite_a [input int, optional] Default: 0
- lwork [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.sorgrq

scipy.linalg.lapack.sorgrq(a, tau[, overwrite_a]) = <fortran object>

Wrapper for sorgrq.

Parameters
- a [input rank-2 array('f') with bounds (m,n)]
- tau [input rank-1 array('f') with bounds (k)]

Returns
- q [rank-2 array('f') with bounds (m,n) and a storage]
- work [rank-1 array('f') with bounds (MAX(lwork,1))]
- info [int]

Other Parameters
- overwrite_a [input int, optional] Default: 0
- lwork [input int, optional] Default: max(3*m,1)

scipy.linalg.lapack.dorgrq

scipy.linalg.lapack.dorgrq(a, tau[, lwork, overwrite_a]) = <fortran object>

Wrapper for dorgrq.

Parameters
- a [input rank-2 array('d') with bounds (m,n)]
- tau [input rank-1 array('d') with bounds (k)]

Returns
- q [rank-2 array('d') with bounds (m,n) and a storage]
- work [rank-1 array('d') with bounds (MAX(lwork,1))]
- info [int]

Other Parameters
overwrite_a
          [input int, optional] Default: 0
lwork          [input int, optional] Default: max(3*m,1)

scipy.linalg.lapack.sormqr
scipy.linalg.lapack.sormqr(side, trans, a, tau, c, lwork[, overwrite_c]) = <fortran object>
Wrapper for sormqr.

Parameters
side          [input string(len=1)]
trans         [input string(len=1)]
a          [input rank-2 array('f') with bounds (lda,k)]
tau          [input rank-1 array('f') with bounds (k)]
c          [input rank-2 array('f') with bounds (ldc,n)]
lwork         [input int]

Returns
cq          [rank-2 array('f') with bounds (ldc,n) and c storage]
work         [rank-1 array('f') with bounds (MAX(lwork,1))]
info         [int]

Other Parameters
overwrite_c
          [input int, optional] Default: 0

scipy.linalg.lapack.dormqr
scipy.linalg.lapack.dormqr(side, trans, a, tau, c, lwork[, overwrite_c]) = <fortran object>
Wrapper for dormqr.

Parameters
side          [input string(len=1)]
trans         [input string(len=1)]
a          [input rank-2 array('d') with bounds (lda,k)]
tau          [input rank-1 array('d') with bounds (k)]
c          [input rank-2 array('d') with bounds (ldc,n)]
lwork         [input int]

Returns
cq          [rank-2 array('d') with bounds (ldc,n) and c storage]
work         [rank-1 array('d') with bounds (MAX(lwork,1))]
info         [int]

Other Parameters
overwrite_c
          [input int, optional] Default: 0
scipy.linalg.lapack.sormrz

scipy.linalg.lapack.sormrz(a, tau, c[, side, trans, lwork, overwrite_c]) = <fortran object>

Wrapper for sormrz.

Parameters

a [input rank-2 array('f') with bounds (k,nt)]
tau [input rank-1 array('f') with bounds (k)]
c [input rank-2 array('f') with bounds (m,n)]

Returns

cq [rank-2 array('f') with bounds (m,n) and c storage]
info [int]

Other Parameters

side [input string(len=1), optional] Default: ‘L’
trans [input string(len=1), optional] Default: ‘N’
overwrite_c [input int, optional] Default: 0
lwork [input int, optional] Default: MAX((side[0]=='L'?n:m),1)

scipy.linalg.lapack.dormrz

scipy.linalg.lapack.dormrz(a, tau, c[, side, trans, lwork, overwrite_c]) = <fortran object>

Wrapper for dormrz.

Parameters

a [input rank-2 array('d') with bounds (k,nt)]
tau [input rank-1 array('d') with bounds (k)]
c [input rank-2 array('d') with bounds (m,n)]

Returns

cq [rank-2 array('d') with bounds (m,n) and c storage]
info [int]

Other Parameters

side [input string(len=1), optional] Default: ‘L’
trans [input string(len=1), optional] Default: ‘N’
overwrite_c [input int, optional] Default: 0
lwork [input int, optional] Default: MAX((side[0]=='L'?n:m),1)

scipy.linalg.lapack.sormrz_lwork

scipy.linalg.lapack.sormrz_lwork(m, n[, side, trans]) = <fortran object>

Wrapper for sormrz_lwork.

Parameters

m [input int]
n [input int]

Returns

work [float]
info [int]

6.11. Low-level LAPACK functions (scipy.linalg.lapack)
Other Parameters

side [input string(len=1), optional] Default: ‘L’
trans [input string(len=1), optional] Default: ‘N’

scipy.linalg.lapack.dormrz_lwork

scipy.linalg.lapack.dormrz_lwork(m, n[, side, trans]) = <fortran object>
Wrapper for dormrz_lwork.

Parameters

m [input int]
n [input int]

Returns

work [float]
info [int]

Other Parameters

side [input string(len=1), optional] Default: ‘L’
trans [input string(len=1), optional] Default: ‘N’

scipy.linalg.lapack.ssbev

scipy.linalg.lapack.ssbev(ab[, compute_v, lower, ldab, overwrite_ab]) = <fortran object>
Wrapper for ssbev.

Parameters

ab [input rank-2 array(‘f’) with bounds (ldab,n)]

Returns

w [rank-1 array(‘f’) with bounds (n)]
z [rank-2 array(‘f’) with bounds (ldz,ldz)]
info [int]

Other Parameters

overwrite_ab [input int, optional] Default: 1
compute_v [input int, optional] Default: 1
lower [input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)

scipy.linalg.lapack.dsbev

scipy.linalg.lapack.dsbev(ab[, compute_v, lower, ldab, overwrite_ab]) = <fortran object>
Wrapper for dsbev.

Parameters

ab [input rank-2 array(‘d’) with bounds (ldab,n)]

Returns

w [rank-1 array(‘d’) with bounds (n)]
z [rank-2 array(‘d’) with bounds (ldz,ldz)]
```python
info [int]

Other Parameters

overwrite_ab
[input int, optional] Default: 1
compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)

scipy.linalg.lapack.ssbevd

scipy.linalg.lapack.ssbevd(ab[, compute_v, lower, ldab, liwork, overwrite_ab]) = <fortran object>
Wrapper for ssbevd.

Parameters

ab [input rank-2 array('f') with bounds (ldab,n)]

Returns

w [rank-1 array('f') with bounds (n)]
z [rank-2 array('f') with bounds (ldz,ldz)]
info [int]

Other Parameters

overwrite_ab
[input int, optional] Default: 1
compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)
liwork [input int, optional] Default: (compute_v?3+5*n:1)

scipy.linalg.lapack.dsbevd

scipy.linalg.lapack.dsbevd(ab[, compute_v, lower, ldab, liwork, overwrite_ab]) = <fortran object>
Wrapper for dsbevd.

Parameters

ab [input rank-2 array('d') with bounds (ldab,n)]

Returns

w [rank-1 array('d') with bounds (n)]
z [rank-2 array('d') with bounds (ldz,ldz)]
info [int]

Other Parameters

overwrite_ab
[input int, optional] Default: 1
compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)
```

6.11. Low-level LAPACK functions (`scipy.linalg.lapack`)
liwork  [input int, optional] Default: (compute_v?3+5*n:1)

scipy.linalg.lapack.ssbevx

scipy.linalg.lapack.ssbevx(ab, vl, vu, il, iu, ldab, compute_v, range, lower, abstol, mmax, overwrite_ab) = <fortran object>

Wrapper for ssbevx.

Parameters

ab  [input rank-2 array('f') with bounds (ldab,n)]
vl  [input float]
vu  [input float]
il  [input int]
iu  [input int]

Returns

w  [rank-1 array('f') with bounds (n)]
z  [rank-2 array('f') with bounds (ldz,mmax)]
m  [int]
ifail  [rank-1 array('i') with bounds ((compute_v?n:1))]
info  [int]

Other Parameters

overwrite_ab  [input int, optional] Default: 1
ldab  [input int, optional] Default: shape(ab,0)
compute_v

range  [input int, optional] Default: 0
lower  [input int, optional] Default: 0
abstol  [input float, optional] Default: 0.0
mmax  [input int, optional] Default: (compute_v?(range==2?(iu-il+1):n):1)

scipy.linalg.lapack.dsbevx

scipy.linalg.lapack.dsbevx(ab, vl, vu, il, iu, ldab, compute_v, range, lower, abstol, mmax, overwrite_ab) = <fortran object>

Wrapper for dsbevx.

Parameters

ab  [input rank-2 array('d') with bounds (ldab,n)]
vl  [input float]
vu  [input float]
il  [input int]
iu  [input int]

Returns

w  [rank-1 array('d') with bounds (n)]
z  [rank-2 array('d') with bounds (ldz,mmax)]
m  [int]
ifail  [rank-1 array('i') with bounds ((compute_v?n:1))]
info  [int]

Other Parameters
overwrite_ab
[input int, optional] Default: 1

ldb
[input int, optional] Default: shape(ab,0)

compute_v
[input int, optional] Default: 1

range
[input int, optional] Default: 0

lower
[input int, optional] Default: 0

abstol
[input float, optional] Default: 0.0

mmax
[input int, optional] Default: (compute_v?(range==2?(iu-il+1):n):1)

scipy.linalg.lapack.sstebz

scipy.linalg.lapack.sstebz(d, e, range, vl, vu, il, iu, tol, order) = <fortran object>
Wrapper for sstebz.

Parameters

d [input rank-1 array('f') with bounds (n)]
e [input rank-1 array('f') with bounds (n - 1)]
range [input int]
vl [input float]
vu [input float]
il [input int]
iu [input int]
tol [input float]
order [input string(len=1)]

Returns

m [int]
w [rank-1 array('f') with bounds (n)]
iblock [rank-1 array('i') with bounds (n)]
isplit [rank-1 array('i') with bounds (n)]
info [int]

scipy.linalg.lapack.dstebz

scipy.linalg.lapack.dstebz(d, e, range, vl, vu, il, iu, tol, order) = <fortran object>
Wrapper for dstebz.

Parameters

d [input rank-1 array('d') with bounds (n)]
e [input rank-1 array('d') with bounds (n - 1)]
range [input int]
vl [input float]
vu [input float]
il [input int]
iu [input int]
tol [input float]
order [input string(len=1)]

Returns

m [int]
w [rank-1 array('d') with bounds (n)]
iblock [rank-1 array('i') with bounds (n)]
isplit [rank-1 array('i') with bounds (n)]
Wrapper for `sstemr`.

**Parameters**

- \(d\) [input rank-1 array('f') with bounds (n)]
- \(e\) [input rank-1 array('f') with bounds (n)]
- `range` [input int]
- \(vl\) [input float]
- \(vu\) [input float]
- `il` [input int]
- `iu` [input int]

**Returns**

- \(m\) [int]
- \(w\) [rank-1 array('f') with bounds (n)]
- \(z\) [rank-2 array('f') with bounds (n,n)]
- `info` [int]

**Other Parameters**

- `overwrite_d` [input int, optional] Default: 0
- `compute_v` [input int, optional] Default: 1
- `lwork` [input int, optional] Default: max((compute_v?18*n:12*n),1)
- `liwork` [input int, optional] Default: (compute_v?10*n:8*n)

Wrapper for `dstemr`.

**Parameters**

- \(d\) [input rank-1 array('d') with bounds (n)]
- \(e\) [input rank-1 array('d') with bounds (n)]
- `range` [input int]
- \(vl\) [input float]
- \(vu\) [input float]
- `il` [input int]
- `iu` [input int]

**Returns**

- \(m\) [int]
- \(w\) [rank-1 array('d') with bounds (n)]
- \(z\) [rank-2 array('d') with bounds (n,n)]
- `info` [int]

**Other Parameters**
overwrite_d
[input int, optional] Default: 0

compute_v
[input int, optional] Default: 1

lwork
[input int, optional] Default: max((compute_v?18*n:12*n),1)

liwork
[input int, optional] Default: (compute_v?10*n:8*n)

scipy.linalg.lapack.ssterf

scipy.linalg.lapack.ssterf(d, e, overwrite_d, overwrite_e) = <fortran object>
Wrapper for ssterf.

Parameters

d [input rank-1 array('f') with bounds (n)]
e [input rank-1 array('f') with bounds (n - 1)]

Returns

vals [rank-1 array('f') with bounds (n) and d storage]
info [int]

Other Parameters

overwrite_d
[input int, optional] Default: 0

overwrite_e
[input int, optional] Default: 0

scipy.linalg.lapack.dsterf

scipy.linalg.lapack.dsterf(d, e, overwrite_d, overwrite_e) = <fortran object>
Wrapper for dsterf.

Parameters

d [input rank-1 array('d') with bounds (n)]
e [input rank-1 array('d') with bounds (n - 1)]

Returns

vals [rank-1 array('d') with bounds (n) and d storage]
info [int]

Other Parameters

overwrite_d
[input int, optional] Default: 0

overwrite_e
[input int, optional] Default: 0

scipy.linalg.lapack.sstein

scipy.linalg.lapack.sstein(d, e, w, iblock, isplit) = <fortran object>
Wrapper for sstein.

Parameters

d [input rank-1 array('f') with bounds (n)]
e [input rank-1 array('f') with bounds (n - 1)]
w [input rank-1 array('f') with bounds (m)]
iblock  [input rank-1 array('i') with bounds (n)]
isplit  [input rank-1 array('i') with bounds (n)]

Returns

z  [rank-2 array('f') with bounds (ldz,m)]
info  [int]

scipy.linalg.lapack.dstein

scipy.linalg.lapack.dstein(d, e, iblock, isplit) = <fortran object>
Wrapper for dstein.

Parameters

d  [input rank-1 array('d') with bounds (n)]
e  [input rank-1 array('d') with bounds (n - 1)]
w  [input rank-1 array('d') with bounds (m)]
iblock  [input rank-1 array('i') with bounds (n)]
isplit  [input rank-1 array('i') with bounds (n)]

Returns

z  [rank-2 array('d') with bounds (ldz,m)]
info  [int]

scipy.linalg.lapack.sstev

scipy.linalg.lapack.sstev(d, e[, compute_v, overwrite_d, overwrite_e]) = <fortran object>
Wrapper for sstev.

Parameters

d  [input rank-1 array('f') with bounds (n)]
e  [input rank-1 array('f') with bounds (MAX(n-1,1))]

Returns

vals  [rank-1 array('f') with bounds (n) and d storage]
z  [rank-2 array('f') with bounds (ldz,(compute_v?n:1))]
info  [int]

Other Parameters

overwrite_d  [input int, optional] Default: 0
overwrite_e  [input int, optional] Default: 0
compute_v  [input int, optional] Default: 1

scipy.linalg.lapack.dstev

scipy.linalg.lapack.dstev(d, e[, compute_v, overwrite_d, overwrite_e]) = <fortran object>
Wrapper for dstev.

Parameters

d  [input rank-1 array('d') with bounds (n)]
e  [input rank-1 array('d') with bounds (MAX(n-1,1))]

Returns
vals  [rank-1 array(‘d’) with bounds (n) and d storage]
z     [rank-2 array(‘d’) with bounds (ldz,(compute_v?n:1))]
info [int]

**Other Parameters**

overwrite_d  [input int, optional] Default: 0
overwrite_e  [input int, optional] Default: 0
compute_v    [input int, optional] Default: 1

scipy.linalg.lapack.ssyev

scipy.linalg.lapack.ssyev(a[, compute_v, lower, lwork, overwrite_a]) = <fortran object>
Wrapper for ssyev.

**Parameters**

a     [input rank-2 array(‘f’) with bounds (n,n)]

**Returns**

w     [rank-1 array(‘f’) with bounds (n)]
v     [rank-2 array(‘f’) with bounds (n,n) and a storage]
info  [int]

**Other Parameters**

compute_v    [input int, optional] Default: 1
lower         [input int, optional] Default: 0
overwrite_a   [input int, optional] Default: 0
lwork         [input int, optional] Default: max(3*n-1,1)

scipy.linalg.lapack.dsyev

scipy.linalg.lapack.dsyev(a[, compute_v, lower, lwork, overwrite_a]) = <fortran object>
Wrapper for dsyev.

**Parameters**

a     [input rank-2 array(‘d’) with bounds (n,n)]

**Returns**

w     [rank-1 array(‘d’) with bounds (n)]
v     [rank-2 array(‘d’) with bounds (n,n) and a storage]
info  [int]

**Other Parameters**

compute_v    [input int, optional] Default: 1
lower         [input int, optional] Default: 0
overwrite_a   [input int, optional] Default: 0
lwork         [input int, optional] Default: max(3*n-1,1)
scipy.linalg.lapack.ssyevd

scipy.linalg.lapack.ssyevd(a, compute_v, lower, lwork, overwrite_a) = <fortran object>
Wrapper for ssyevd.

Parameters
- a [input rank-2 array('f') with bounds (n,n)]

Returns
- w [rank-1 array('f') with bounds (n)]
- v [rank-2 array('f') with bounds (n,n) and a storage]
- info [int]

Other Parameters
- compute_v [input int, optional] Default: 1
- lower [input int, optional] Default: 0
- overwrite_a [input int, optional] Default: 0
- lwork [input int, optional] Default: max((compute_v?1+6*n+2*n*n:2*n+1),1)

scipy.linalg.lapack.dsyevd

scipy.linalg.lapack.dsyevd(a, compute_v, lower, lwork, overwrite_a) = <fortran object>
Wrapper for dsyevd.

Parameters
- a [input rank-2 array('d') with bounds (n,n)]

Returns
- w [rank-1 array('d') with bounds (n)]
- v [rank-2 array('d') with bounds (n,n) and a storage]
- info [int]

Other Parameters
- compute_v [input int, optional] Default: 1
- lower [input int, optional] Default: 0
- overwrite_a [input int, optional] Default: 0
- lwork [input int, optional] Default: max((compute_v?1+6*n+2*n*n:2*n+1),1)

scipy.linalg.lapack.ssyevr

scipy.linalg.lapack.ssyevr(a, jobz, range, uplo, il, iu, lwork, overwrite_a) = <fortran object>
Wrapper for ssyevr.

Parameters
- a [input rank-2 array('f') with bounds (n,n)]

Returns
- w [rank-1 array('f') with bounds (n)]
- z [rank-2 array('f') with bounds (n,m)]
**info**  [int]

**Other Parameters**
- **jobz**  [input string(len=1), optional] Default: ‘V’
- **range**  [input string(len=1), optional] Default: ‘A’
- **uplo**  [input string(len=1), optional] Default: ‘L’
- **overwrite_a**  [input int, optional] Default: 0
- **il**  [input int, optional] Default: 1
- **iu**  [input int, optional] Default: n
- **lwork**  [input int, optional] Default: max(26*n,1)

**scipy.linalg.lapack.dsyevr**

**scipy.linalg.lapack.dsyevr**(`a`, `jobz`, `range`, `uplo`, `il`, `iu`, `lwork`, `overwrite_a`) = <fortran object>

Wrapper for `dsyevr`.

**Parameters**
- **a**  [input rank-2 array('d') with bounds (n,n)]

**Returns**
- **w**  [rank-1 array('d') with bounds (n)]
- **z**  [rank-2 array('d') with bounds (n,m)]
- **info**  [int]

**Other Parameters**
- **jobz**  [input string(len=1), optional] Default: ‘V’
- **range**  [input string(len=1), optional] Default: ‘A’
- **uplo**  [input string(len=1), optional] Default: ‘L’
- **overwrite_a**  [input int, optional] Default: 0
- **il**  [input int, optional] Default: 1
- **iu**  [input int, optional] Default: n
- **lwork**  [input int, optional] Default: max(26*n,1)

**scipy.linalg.lapack.ssygv**

**scipy.linalg.lapack.ssygv**(`a`, `b`, `itype`, `jobz`, `uplo`, `overwrite_a`, `overwrite_b`) = <fortran object>

Wrapper for `ssygv`.

**Parameters**
- **a**  [input rank-2 array('f') with bounds (n,n)]
- **b**  [input rank-2 array('f') with bounds (n,n)]

**Returns**
- **a**  [rank-2 array('f') with bounds (n,n)]
- **w**  [rank-1 array('f') with bounds (n)]
- **info**  [int]

**Other Parameters**
- **itype**  [input int, optional] Default: 1
- **jobz**  [input string(len=1), optional] Default: ‘V’
uplo    [input string(len=1), optional] Default: ‘L’
overwrite_a    [input int, optional] Default: 0
overwrite_b    [input int, optional] Default: 0

scipy.linalg.lapack.dsygv

scipy.linalg.lapack.dsygv(a, b[, itype, jobz, uplo, overwrite_a, overwrite_b]) = <fortran object>
Wrapper for dsygv.

Parameters

a    [input rank-2 array('d') with bounds (n,n)]
b    [input rank-2 array('d') with bounds (n,n)]

Returns

a    [rank-2 array('d') with bounds (n,n)]
w    [rank-1 array('d') with bounds (n)]
info    [int]

Other Parameters

itype    [input int, optional] Default: 1
jobz    [input string(len=1), optional] Default: ‘V’
uplo    [input string(len=1), optional] Default: ‘L’
overwrite_a    [input int, optional] Default: 0
overwrite_b    [input int, optional] Default: 0

scipy.linalg.lapack.ssygvd

scipy.linalg.lapack.ssygvd(a, b[, itype, jobz, uplo, lwork, overwrite_a, overwrite_b]) = <fortran object>
Wrapper for ssygvd.

Parameters

a    [input rank-2 array('f') with bounds (n,n)]
b    [input rank-2 array('f') with bounds (n,n)]

Returns

a    [rank-2 array('f') with bounds (n,n)]
w    [rank-1 array('f') with bounds (n)]
info    [int]

Other Parameters

itype    [input int, optional] Default: 1
jobz    [input string(len=1), optional] Default: ‘V’
uplo    [input string(len=1), optional] Default: ‘L’
overwrite_a    [input int, optional] Default: 0
overwrite_b    [input int, optional] Default: 0
lwork    [input int, optional] Default: max(1+6*n+2*n*n,1)
**scipy.linalg.lapack.dsygvd**

```python
scipy.linalg.lapack.dsygvd(a, b, itype, jobz, uplo, lwork, overwrite_a, overwrite_b) = <fortran object>
```

Wrapper for dsygvd.

**Parameters**

- `a` [input rank-2 array('d') with bounds (n,n)]
- `b` [input rank-2 array('d') with bounds (n,n)]

**Returns**

- `a` [rank-2 array('d') with bounds (n,n)]
- `w` [rank-1 array('d') with bounds (n)]
- `info` [int]

**Other Parameters**

- `itype` [input int, optional] Default: 1
- `jobz` [input string(len=1), optional] Default: ‘V’
- `uplo` [input string(len=1), optional] Default: ‘L’
- `overwrite_a` [input int, optional] Default: 0
- `overwrite_b` [input int, optional] Default: 0
- `lwork` [input int, optional] Default: max(1+6*n+2*n*n,1)

**scipy.linalg.lapack.ssygvx**

```python
scipy.linalg.lapack.ssygvx(a, b, iu, itype, jobz, uplo, il, lwork, overwrite_a, overwrite_b) = <fortran object>
```

Wrapper for ssygvx.

**Parameters**

- `a` [input rank-2 array('f') with bounds (n,n)]
- `b` [input rank-2 array('f') with bounds (n,n)]
- `iu` [input int]

**Returns**

- `w` [rank-1 array('f') with bounds (n)]
- `z` [rank-2 array('f') with bounds (n,m)]
- `ifail` [rank-1 array('i') with bounds (n)]
- `info` [int]

**Other Parameters**

- `itype` [input int, optional] Default: 1
- `jobz` [input string(len=1), optional] Default: ‘V’
- `uplo` [input string(len=1), optional] Default: ‘L’
- `overwrite_a` [input int, optional] Default: 0
- `overwrite_b` [input int, optional] Default: 0
- `il` [input int, optional] Default: 1
- `lwork` [input int, optional] Default: max(8*n,1)
scipy.linalg.lapack.dsygvx

scipy.linalg.lapack.dsygvx(a, b, iu, itype, jobz, uplo, il, lwork, overwrite_a, overwrite_b) = <fortran object>

Wrapper for dsygvx.

Parameters
a [input rank-2 array('d') with bounds (n,n)]
b [input rank-2 array('d') with bounds (n,n)]
iu [input int]

Returns
w [rank-1 array('d') with bounds (n)]
z [rank-2 array('d') with bounds (n,m)]
ifail [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters
itype [input int, optional] Default: 1
jobz [input string(len=1), optional] Default: 'V'
uplo [input string(len=1), optional] Default: 'L'
overwrite_a [input int, optional] Default: 0
overwrite_b [input int, optional] Default: 0
il [input int, optional] Default: 1
lwork [input int, optional] Default: max(8*n,1)

scipy.linalg.lapack.ssfrk

scipy.linalg.lapack.ssfrk(n, k, alpha, a, beta, c, transr, uplo, trans, overwrite_c) = <fortran object>

Wrapper for ssfrk.

Parameters
n [input int]
k [input int]
alpha [input float]
a [input rank-2 array('f') with bounds (lda,ka)]
beta [input float]
c [input rank-1 array('f') with bounds (nt)]

Returns
cout [rank-1 array('f') with bounds (nt) and c storage]

Other Parameters
transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'
trans [input string(len=1), optional] Default: 'N'
overwrite_c [input int, optional] Default: 0
SciPy Reference Guide, Release 1.2.0

scipy.linalg.lapack.dsfrk

scipy.linalg.lapack.dsfrk(n, k, alpha, a, beta[, transr, uplo, trans, overwrite_c]) = <fortran object>

Wrapper for dsfrk.

Parameters

n [input int]
k [input int]
alphas [input float]
a [input rank-2 array('d') with bounds (lda,ka)]
betas [input float]
c [input rank-1 array('d') with bounds (nt)]

Returns
cout [rank-1 array('d') with bounds (nt) and c storage]

Other Parameters

transr [input string(len=1), optional] Default: ‘N’
uplo [input string(len=1), optional] Default: ‘U’
trans [input string(len=1), optional] Default: ‘N’
overwrite_c [input int, optional] Default: 0

scipy.linalg.lapack.chfrk

scipy.linalg.lapack.chfrk(n, k, alpha, a, beta[, transr, uplo, trans, overwrite_c]) = <fortran object>

Wrapper for chfrk.

Parameters

n [input int]
k [input int]
alphas [input float]
a [input rank-2 array('F') with bounds (lda,ka)]
betas [input float]
c [input rank-1 array('F') with bounds (nt)]

Returns
cout [rank-1 array('F') with bounds (nt) and c storage]

Other Parameters

transr [input string(len=1), optional] Default: ‘N’
uplo [input string(len=1), optional] Default: ‘U’
trans [input string(len=1), optional] Default: ‘N’
overwrite_c [input int, optional] Default: 0

6.11. Low-level LAPACK functions (scipy.linalg.lapack)
scipy.linalg.lapack.zhfrk

```
scipy.linalg.lapack.zhfrk(n, k, alpha, a, beta, c[, transr, uplo, trans, overwrite_c]) = <fortran object>
```

Wrapper for zhfrk.

**Parameters**

- `n` [input int]
- `k` [input int]
- `alpha` [input float]
- `a` [input rank-2 array('D') with bounds (lda,ka)]
- `beta` [input float]
- `c` [input rank-1 array('D') with bounds (nt)]

**Returns**

- `cout` [rank-1 array('D') with bounds (nt) and c storage]

**Other Parameters**

- `transr` [input string(len=1), optional] Default: ‘N’
- `uplo` [input string(len=1), optional] Default: ‘U’
- `trans` [input string(len=1), optional] Default: ‘N’
- `overwrite_c` [input int, optional] Default: 0

scipy.linalg.lapack.stfsm

```
scipy.linalg.lapack.stfsm(alpha, a, b[, transr, side, uplo, trans, diag, overwrite_b]) = <fortran object>
```

Wrapper for stfsm.

**Parameters**

- `alpha` [input float]
- `a` [input rank-1 array('f') with bounds (nt)]
- `b` [input rank-2 array('f') with bounds (m,n)]

**Returns**

- `x` [rank-2 array('f') with bounds (m,n) and b storage]

**Other Parameters**

- `transr` [input string(len=1), optional] Default: ‘N’
- `side` [input string(len=1), optional] Default: ‘L’
- `uplo` [input string(len=1), optional] Default: ‘U’
- `trans` [input string(len=1), optional] Default: ‘N’
- `diag` [input string(len=1), optional] Default: ‘N’
- `overwrite_b` [input int, optional] Default: 0

scipy.linalg.lapack.dtfsm

```
scipy.linalg.lapack.dtfsm(alpha, a, b[, transr, side, uplo, trans, diag, overwrite_b]) = <fortran object>
```

Wrapper for dtfsm.

**Parameters**

- `alpha` [input float]
a  [input rank-1 array('d') with bounds (nt)]

b  [input rank-2 array('d') with bounds (m,n)]

**Returns**

x  [rank-2 array('d') with bounds (m,n) and b storage]

**Other Parameters**

transr  [input string(len=1), optional] Default: ‘N’

trans  [input string(len=1), optional] Default: ‘N’

side  [input string(len=1), optional] Default: ‘L’

uplo  [input string(len=1), optional] Default: ‘U’

diag  [input string(len=1), optional] Default: ‘N’

overwrite_b  [input int, optional] Default: 0

```python
scipy.linalg.lapack.ctfsm(alpha, a, b[, transr, side, uplo, trans, diag, overwrite_b]) = <fortran object>
```

Wrapper for `ctfsm`.

**Parameters**

alpha  [input complex]

a  [input rank-1 array('F') with bounds (nt)]

b  [input rank-2 array('F') with bounds (m,n)]

**Returns**

x  [rank-2 array('F') with bounds (m,n) and b storage]

**Other Parameters**

transr  [input string(len=1), optional] Default: ‘N’

side  [input string(len=1), optional] Default: ‘L’

uplo  [input string(len=1), optional] Default: ‘U’

trans  [input string(len=1), optional] Default: ‘N’

diag  [input string(len=1), optional] Default: ‘N’

overwrite_b  [input int, optional] Default: 0

```python
scipy.linalg.lapack.ztfsm(alpha, a, b[, transr, side, uplo, trans, diag, overwrite_b]) = <fortran object>
```

Wrapper for `ztfsm`.

**Parameters**

alpha  [input complex]

a  [input rank-1 array('D') with bounds (nt)]

b  [input rank-2 array('D') with bounds (m,n)]

**Returns**

x  [rank-2 array('D') with bounds (m,n) and b storage]

**Other Parameters**

transr  [input string(len=1), optional] Default: ‘N’
side [input string(len=1), optional] Default: ‘L’
uplo [input string(len=1), optional] Default: ‘U’
trans [input string(len=1), optional] Default: ‘N’
diag [input string(len=1), optional] Default: ‘N’
overwrite_b [input int, optional] Default: 0

\texttt{scipy.linalg.lapack.stpttf}

\texttt{scipy.linalg.lapack.stpttf}(n, ap[, transr, uplo]) = <fortran object>
Wrapper for stpttf.

\textit{Parameters}

\begin{itemize}
  \item \texttt{n} [input int]
  \item \texttt{ap} [input rank-1 array('f') with bounds (nt)]
\end{itemize}

\textit{Returns}

\begin{itemize}
  \item \texttt{arf} [rank-1 array('f') with bounds (nt)]
  \item \texttt{info} [int]
\end{itemize}

\textit{Other Parameters}

\begin{itemize}
  \item \texttt{transr} [input string(len=1), optional] Default: ‘N’
  \item \texttt{uplo} [input string(len=1), optional] Default: ‘U’
\end{itemize}

\texttt{scipy.linalg.lapack.dtpttf}

\texttt{scipy.linalg.lapack.dtpttf}(n, ap[, transr, uplo]) = <fortran object>
Wrapper for dtpttf.

\textit{Parameters}

\begin{itemize}
  \item \texttt{n} [input int]
  \item \texttt{ap} [input rank-1 array('d') with bounds (nt)]
\end{itemize}

\textit{Returns}

\begin{itemize}
  \item \texttt{arf} [rank-1 array('d') with bounds (nt)]
  \item \texttt{info} [int]
\end{itemize}

\textit{Other Parameters}

\begin{itemize}
  \item \texttt{transr} [input string(len=1), optional] Default: ‘N’
  \item \texttt{uplo} [input string(len=1), optional] Default: ‘U’
\end{itemize}

\texttt{scipy.linalg.lapack.ctpttf}

\texttt{scipy.linalg.lapack.ctpttf}(n, ap[, transr, uplo]) = <fortran object>
Wrapper for ctpttf.

\textit{Parameters}

\begin{itemize}
  \item \texttt{n} [input int]
  \item \texttt{ap} [input rank-1 array('F') with bounds (nt)]
\end{itemize}

\textit{Returns}

\begin{itemize}
  \item \texttt{arf} [rank-1 array('F') with bounds (nt)]
  \item \texttt{info} [int]
Other Parameters

\begin{itemize}
\item transr \ [input string(len=1), optional] Default: ‘N’
\item uplo \ [input string(len=1), optional] Default: ‘U’
\end{itemize}

\texttt{scipy.linalg.lapack.ztpttf}

\texttt{scipy.linalg.lapack.ztpttf(n, ap[, transr, uplo]) = <fortran object>}

Wrapper for \texttt{ztpttf}.

\begin{itemize}
\item \texttt{n} \ [input int]
\item \texttt{ap} \ [input rank-1 array(‘D’) with bounds (nt)]
\end{itemize}

Returns

\begin{itemize}
\item \texttt{arf} \ [rank-1 array(‘D’) with bounds (nt)]
\item \texttt{info} \ [int]
\end{itemize}

Other Parameters

\begin{itemize}
\item transr \ [input string(len=1), optional] Default: ‘N’
\item uplo \ [input string(len=1), optional] Default: ‘U’
\end{itemize}

\texttt{scipy.linalg.lapack.stfttp}

\texttt{scipy.linalg.lapack.stfttp(n, arf[, transr, uplo]) = <fortran object>}

Wrapper for \texttt{stfttp}.

\begin{itemize}
\item \texttt{n} \ [input int]
\item \texttt{arf} \ [input rank-1 array(‘F’) with bounds (nt)]
\end{itemize}

Returns

\begin{itemize}
\item \texttt{ap} \ [rank-1 array(‘F’) with bounds (nt)]
\item \texttt{info} \ [int]
\end{itemize}

Other Parameters

\begin{itemize}
\item transr \ [input string(len=1), optional] Default: ‘N’
\item uplo \ [input string(len=1), optional] Default: ‘U’
\end{itemize}

\texttt{scipy.linalg.lapack.dtfttp}

\texttt{scipy.linalg.lapack.dtfttp(n, arf[, transr, uplo]) = <fortran object>}

Wrapper for \texttt{dtfttp}.

\begin{itemize}
\item \texttt{n} \ [input int]
\item \texttt{arf} \ [input rank-1 array(‘D’) with bounds (nt)]
\end{itemize}

Returns

\begin{itemize}
\item \texttt{ap} \ [rank-1 array(‘D’) with bounds (nt)]
\item \texttt{info} \ [int]
\end{itemize}

Other Parameters

\begin{itemize}
\item transr \ [input string(len=1), optional] Default: ‘N’
\item uplo \ [input string(len=1), optional] Default: ‘U’
\end{itemize}
scipy.linalg.lapack.ctfttp

scipy.linalg.lapack.ctfttp(n, arf[, transr, uplo]) = <fortran object>
Wrapper for ctfttp.

Parameters

- n [input int]
- arf [input rank-1 array('F') with bounds (nt)]

Returns

- ap [rank-1 array('F') with bounds (nt)]
- info [int]

Other Parameters

- transr [input string(len=1), optional] Default: ‘N’
- uplo [input string(len=1), optional] Default: ‘U’

scipy.linalg.lapack.ztfttp

scipy.linalg.lapack.ztfttp(n, arf[, transr, uplo]) = <fortran object>
Wrapper for ztfttp.

Parameters

- n [input int]
- arf [input rank-1 array('D') with bounds (nt)]

Returns

- ap [rank-1 array('D') with bounds (nt)]
- info [int]

Other Parameters

- transr [input string(len=1), optional] Default: ‘N’
- uplo [input string(len=1), optional] Default: ‘U’

scipy.linalg.lapack.stfttr

scipy.linalg.lapack.stfttr(n, arf[, transr, uplo]) = <fortran object>
Wrapper for stfttr.

Parameters

- n [input int]
- arf [input rank-1 array('f') with bounds (nt)]

Returns

- a [rank-2 array('f') with bounds (lda,n)]
- info [int]

Other Parameters

- transr [input string(len=1), optional] Default: ‘N’
- uplo [input string(len=1), optional] Default: ‘U’
scipy.linalg.lapack.dtfttr

scipy.linalg.lapack.dtfttr(n, arf[, transr, uplo]) = <fortran object>
Wrapper for dtfttr.

Parameters
n [input int]
arf [input rank-1 array('d') with bounds (nt)]

Returns
a [rank-2 array('d') with bounds (lda,n)]
info [int]

Other Parameters
transr [input string(len=1), optional] Default: ‘N’
uplo [input string(len=1), optional] Default: ‘U’

scipy.linalg.lapack.ctfttr

scipy.linalg.lapack.ctfttr(n, arf[, transr, uplo]) = <fortran object>
Wrapper for ctfttr.

Parameters
n [input int]
arf [input rank-1 array('F') with bounds (nt)]

Returns
a [rank-2 array('F') with bounds (lda,n)]
info [int]

Other Parameters
transr [input string(len=1), optional] Default: ‘N’
uplo [input string(len=1), optional] Default: ‘U’

scipy.linalg.lapack.ztfttr

scipy.linalg.lapack.ztfttr(n, arf[, transr, uplo]) = <fortran object>
Wrapper for ztfttr.

Parameters
n [input int]
arf [input rank-1 array('D') with bounds (nt)]

Returns
a [rank-2 array('D') with bounds (lda,n)]
info [int]

Other Parameters
transr [input string(len=1), optional] Default: ‘N’
uplo [input string(len=1), optional] Default: ‘U’
scipy.linalg.lapack.strttf

scipy.linalg.lapack.strttf(a[, transr, uplo]) = <fortran object>
Wrapper for strttf.

Parameters

- a [input rank-2 array('f') with bounds (lda,n)]

Returns

- arf [rank-1 array('f') with bounds (n*(n+1)/2)]
- info [int]

Other Parameters

- transr [input string(len=1), optional] Default: ‘N’
- uplo [input string(len=1), optional] Default: ‘U’

scipy.linalg.lapack.dtrttf

scipy.linalg.lapack.dtrttf(a[, transr, uplo]) = <fortran object>
Wrapper for dtrttf.

Parameters

- a [input rank-2 array('d') with bounds (lda,n)]

Returns

- arf [rank-1 array('d') with bounds (n*(n+1)/2)]
- info [int]

Other Parameters

- transr [input string(len=1), optional] Default: ‘N’
- uplo [input string(len=1), optional] Default: ‘U’

scipy.linalg.lapack.ctrttf

scipy.linalg.lapack.ctrttf(a[, transr, uplo]) = <fortran object>
Wrapper for ctrttf.

Parameters

- a [input rank-2 array('F') with bounds (lda,n)]

Returns

- arf [rank-1 array('F') with bounds (n*(n+1)/2)]
- info [int]

Other Parameters

- transr [input string(len=1), optional] Default: ‘N’
- uplo [input string(len=1), optional] Default: ‘U’
scipy.linalg.lapack.ztrttf

scipy.linalg.lapack.ztrttf(a[, transr, uplo]) = <fortran object>
Wrapper for ztrttf.

Parameters:
- a [input rank-2 array('D') with bounds (lda,n)]

Returns:
- arf [rank-1 array('D') with bounds (n*(n+1)/2)]
- info [int]

Other Parameters:
- transr [input string(len=1), optional] Default: ‘N’
- uplo [input string(len=1), optional] Default: ‘U’

scipy.linalg.lapack.stpttr

scipy.linalg.lapack.stpttr(n, ap[, uplo]) = <fortran object>
Wrapper for stpttr.

Parameters:
- n [input int]
- ap [input rank-1 array('f') with bounds (nt)]

Returns:
- a [rank-2 array('f') with bounds (n,n)]
- info [int]

Other Parameters:
- uplo [input string(len=1), optional] Default: ‘U’

scipy.linalg.lapack.dtpttr

scipy.linalg.lapack.dtpttr(n, ap[, uplo]) = <fortran object>
Wrapper for dtpttr.

Parameters:
- n [input int]
- ap [input rank-1 array('d') with bounds (nt)]

Returns:
- a [rank-2 array('d') with bounds (n,n)]
- info [int]

Other Parameters:
- uplo [input string(len=1), optional] Default: ‘U’
scipy.linalg.lapack.ctpttr

```
scipy.linalg.lapack.ctpttr(n, ap[, uplo]) = <fortran object>
```

Wrapper for ctpttr.

**Parameters**
- `n` [input int]
- `ap` [input rank-1 array('F') with bounds (nt)]

**Returns**
- `a` [rank-2 array('F') with bounds (n,n)]
- `info` [int]

**Other Parameters**
- `uplo` [input string(len=1), optional] Default: ‘U’

scipy.linalg.lapack.ztpttr

```
scipy.linalg.lapack.ztpttr(n, ap[, uplo]) = <fortran object>
```

Wrapper for ztpttr.

**Parameters**
- `n` [input int]
- `ap` [input rank-1 array('D') with bounds (nt)]

**Returns**
- `a` [rank-2 array('D') with bounds (n,n)]
- `info` [int]

**Other Parameters**
- `uplo` [input string(len=1), optional] Default: ‘U’

scipy.linalg.lapack.strttp

```
scipy.linalg.lapack.strttp(a[, uplo]) = <fortran object>
```

Wrapper for strttp.

**Parameters**
- `a` [input rank-2 array('f') with bounds (lda,n)]

**Returns**
- `ap` [rank-1 array('f') with bounds (n*(n+1)/2)]
- `info` [int]

**Other Parameters**
- `uplo` [input string(len=1), optional] Default: ‘U’
scipy.linalg.lapack.dtrttp

scipy.linalg.lapack.dtrttp(a[, uplo]) = <fortran object>
Wrapper for dtrttp.

Parameters
a         [input rank-2 array('d') with bounds (lda,n)]

Returns
ap       [rank-1 array('d') with bounds (n*(n+1)/2)]
info     [int]

Other Parameters
uplo     [input string(len=1), optional] Default: ‘U’

scipy.linalg.lapack ctrttp

scipy.linalg.lapack.ctrttp(a[, uplo]) = <fortran object>
Wrapper for ctrttp.

Parameters
a         [input rank-2 array('F') with bounds (lda,n)]

Returns
ap       [rank-1 array('F') with bounds (n*(n+1)/2)]
info     [int]

Other Parameters
uplo     [input string(len=1), optional] Default: ‘U’

scipy.linalg.lapack.ztrttp

scipy.linalg.lapack.ztrttp(a[, uplo]) = <fortran object>
Wrapper for ztrttp.

Parameters
a         [input rank-2 array('D') with bounds (lda,n)]

Returns
ap       [rank-1 array('D') with bounds (n*(n+1)/2)]
info     [int]

Other Parameters
uplo     [input string(len=1), optional] Default: ‘U’

scipy.linalg.lapack.stzrzf

scipy.linalg.lapack.stzrzf(a[, lwork, overwrite_a]) = <fortran object>
Wrapper for stzrzf.

Parameters
a         [input rank-2 array('f') with bounds (m,n)]

Returns
**scipy.linalg.lapack.dtzrzf**

`scipy.linalg.lapack.dtzrzf(a[, lwork, overwrite_a]) = <fortran object>`

Wrapper for `dtzrzf`.

**Parameters**

- `a` [input rank-2 array('d') with bounds (m,n)]

**Returns**

- `rz` [rank-2 array('d') with bounds (m,n) and a storage]
- `tau` [rank-1 array('d') with bounds (m)]
- `info` [int]

**Other Parameters**

- `overwrite_a` [input int, optional] Default: 0
- `lwork` [input int, optional] Default: MAX(m,1)

**scipy.linalg.lapack.ctzrzf**

`scipy.linalg.lapack.ctzrzf(a[, lwork, overwrite_a]) = <fortran object>`

Wrapper for `ctzrzf`.

**Parameters**

- `a` [input rank-2 array('F') with bounds (m,n)]

**Returns**

- `rz` [rank-2 array('F') with bounds (m,n) and a storage]
- `tau` [rank-1 array('F') with bounds (m)]
- `info` [int]

**Other Parameters**

- `overwrite_a` [input int, optional] Default: 0
- `lwork` [input int, optional] Default: MAX(m,1)

**scipy.linalg.lapack.ztzrzf**

`scipy.linalg.lapack.ztzrzf(a[, lwork, overwrite_a]) = <fortran object>`

Wrapper for `ztzrzf`.

**Parameters**

- `a` [input rank-2 array('D') with bounds (m,n)]

**Returns**

- `[input rank-2 array('D') with bounds (m,n)]

**Other Parameters**

- `overwrite_a` [input int, optional] Default: 0
- `lwork` [input int, optional] Default: MAX(m,1)

---

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rz  [rank-2 array('D') with bounds (m,n) and a storage]
tau [rank-1 array('D') with bounds (m)]
info [int]

Other Parameters

overwrite_a  [input int, optional] Default: 0
lwork  [input int, optional] Default: MAX(m,1)

scipy.linalg.lapack.stzrzf_lwork

scipy.linalg.lapack.stzrzf_lwork(m, n) = <fortran object>
Wrapper for stzrzf_lwork.

Parameters

m [input int]
n [input int]

Returns

work [float]
info [int]

scipy.linalg.lapack.dtzrzf_lwork

scipy.linalg.lapack.dtzrzf_lwork(m, n) = <fortran object>
Wrapper for dtzrzf_lwork.

Parameters

m [input int]
n [input int]

Returns

work [float]
info [int]

scipy.linalg.lapack.ctzrzf_lwork

scipy.linalg.lapack.ctzrzf_lwork(m, n) = <fortran object>
Wrapper for ctzrzf_lwork.

Parameters

m [input int]
n [input int]

Returns

work [complex]
info [int]
scipy.linalg.lapack.ztzrzf_lwork

scipy.linalg.lapack.ztzrzf_lwork(m, n) = <fortran object>
Wrapper for ztzrzf_lwork.

Parameters
- m [input int]
- n [input int]

Returns
- work [complex]
- info [int]

scipy.linalg.lapack.slange

scipy.linalg.lapack.slange(norm, a) = <fortran slange>
Wrapper for slange.

Parameters
- norm [input string(len=1)]
- a [input rank-2 array('f') with bounds (m,n)]

Returns
- n2 [float]

scipy.linalg.lapack.dlange

scipy.linalg.lapack.dlange(norm, a) = <fortran dlange>
Wrapper for dlange.

Parameters
- norm [input string(len=1)]
- a [input rank-2 array('d') with bounds (m,n)]

Returns
- n2 [float]

scipy.linalg.lapack.clange

scipy.linalg.lapack.clange(norm, a) = <fortran clange>
Wrapper for clange.

Parameters
- norm [input string(len=1)]
- a [input rank-2 array('F') with bounds (m,n)]

Returns
- n2 [float]
scipy.linalg.lapack.zlange

scipy.linalg.lapack.zlange(norm, a) = <fortran zlange>
Wrapper for zlange.

Parameters

- norm [input string(len=1)]
- a [input rank-2 array('D') with bounds (m,n)]

Returns

- n2 [float]

scipy.linalg.lapack.ilaver

scipy.linalg.lapack.ilaver = <fortran object>
Wrapper for ilaver.

Returns

- major [int]
- minor [int]
- patch [int]

6.12 BLAS Functions for Cython

Usable from Cython via:

```python
cimport scipy.linalg.cython_blas
```

These wrappers do not check for alignment of arrays. Alignment should be checked before these wrappers are used.

Raw function pointers (Fortran-style pointer arguments):

- caxpy
- ccopy
- cdotc
- cdotu
- cgbmv
- cgemm
- cgemv
- cgerc
- cgeru
- chbmv
- chemm
- chemv
- cher
- cher2
- cher2k
- cherk
- chpmv
- chpr
- chpr2
- crotg
- cscal
- csrot
- csscal
- cswap
- csymm
- csyr2k
- csyrk
- ctbmv
- ctbvk
- ctbsv
- ctbmv
- ctbsv
- ctpmv
- ctpsv
- ctrmm
- ctrmv
- ctrsm
- ctrsv
- dasum
- daxpy
- dcabs1
- dcopy
- ddot
- dgbmv
- dgemm
- dgemv
- dger
- dnrm2
- drot
- drotg
- drotm
- drotmg
- dsbmv
- dscal
• dsdot
• dspmv
• dspr
• dspr2
• dswap
• dsymm
• dsymv
• dsyr
• dsyr2
• dsyr2k
• dsyrk
• dtbmv
• dtbsv
• dtpmv
• dtpsv
• dtrmm
• dtrmv
• dtrsm
• dtrsv
• dzasum
• dznrm2
• icamax
• idamax
• isamax
• izamax
• lsame
• sasum
• saxpy
• scasum
• scnrm2
• scopy
• sdot
• sdsdot
• sgbmv
• sgemm
• sgemv
- sger
- snrm2
- srot
- srotg
- srotm
- srotmg
- ssbmv
- sscl
- ssMV
- sspr
- sspr2
- ssswap
- ssymmm
- ssMV
- ssyr
- ssyr2
- ssyr2k
- ssyrk
- stbmv
- stbsv
- stpmv
- stpsv
- strmm
- strmv
- strms
- strsv
- zaxpy
- zcopy
- zdotc
- zdotu
- zdot
- zdscal
- zgbmv
- zgemm
- zgemv
- zgerc
• zgeru
• zhbmv
• zhemm
• zhemv
• zher
• zher2
• zher2k
• zherk
• zhpmv
• zhpr
• zhpr2
• zrotg
• zscal
• zswap
• zsyrmm
• zsyr2k
• zsyrk
• ztbmv
• ztbsv
• ztpmv
• ztpsv
• ztrmm
• ztrmv
• ztrsm
• ztrsv

6.13 LAPACK functions for Cython

Usable from Cython via:

```python
import scipy.linalg.cython_lapack
```

This module provides Cython-level wrappers for all primary routines included in LAPACK 3.4.0 except for `zgesv` since its interface is not consistent from LAPACK 3.4.0 to 3.6.0. It also provides some of the fixed-api auxiliary routines.

These wrappers do not check for alignment of arrays. Alignment should be checked before these wrappers are used.

Raw function pointers (Fortran-style pointer arguments):
• cbbcsd
• cbdsqr
• cgbbrd
• cgbcon
• cgbequ
• cgbequb
• cgbrfs
• cgbsv
• cgbsvx
• cgbtf2
• cgbtrf
• cgbtrs
• cgebak
• cgebal
• cgebd2
• cgebrd
• cgecon
• cgeequ
• cgeequb
• cgees
• cgeesx
• cgeev
• cgeevx
• cgehd2
• cgehrd
• cgelq2
• cgelqf
• cgels
• cgelsd
• cgelss
• cgelsy
• cgemqrt
• cgeql2
• cgeqlf
• cgeqp3
• cgeqr2
• cgeqr2p
- cgeqrf
- cgeqrfp
- cgeqrt
- cgeqrt2
- cgeqrt3
- cgerfs
- cgerq2
- cgerqf
- cgesc2
- cgescvd
- cgesv
- cgesvd
- cgesvx
- cgetc2
- cgetf2
- cgetrf
- cgetri
- cgetrs
- cggbak
- cggbal
- cgges
- cggesx
- cggev
- cggevx
- cgglm
- cgghrd
- cgglse
- cggqrf
- cggrqf
- cgtrcon
- cgtrfs
- cgtsv
- cgtsvx
- cgttref
- cgtrrs
- cgttts2
• chbev
• chbevd
• chbevx
• chbgst
• chbgv
• chbgvd
• chbgvx
• chbtrd
• checon
• cheequb
• cheev
• cheevd
• cheevr
• cheevx
• chegs2
• chegst
• chegy
• chegvd
• chegvy
• chegvd
• chegvy
• cherfs
• chesv
• chesvx
• cheswapr
• chetd2
• chetf2
• chetrd
• chetrf
• chetri
• chetri2
• chetri2x
• chetrs
• chetrs2
• chfrk
• chgeqz
• chla_transtype
• chipcon
- chpev
- chpevd
- chpevx
- chpevx
- chpgst
- chpgv
- chpgvd
- chpgvx
- chprfs
- chpsv
- chpsvx
- chptrd
- chptrf
- chptri
- chptrs
- chsein
- chseqr
- clabrd
- clacgv
- clacn2
- clacon
- clacp2
- clacpy
- clacrm
- clacr
- cladiv
- claed0
- claed7
- claed8
- claein
- claesy
- claev2
- clag2z
- clags2
- clagtm
- clahef
- clahqr
• clahr2
• claic1
• clals0
• clalsa
• clalsd
• clangb
• clange
• clangt
• clanhb
• clanhe
• clanhf
• clanhp
• clanhb
• clanht
• clansb
• clansp
• clansy
• clantb
• clantp
• clantr
• clapll
• clapmr
• clapmt
• claqgb
• claqge
• claqhb
• claqhe
• claqhp
• claqp2
• claqps
• claqr0
• claqr1
• claqr2
• claqr3
• claqr4
• claqr5
6.13. LAPACK functions for Cython
• cpbrfs
• cpbstf
• cpbsv
• cpbsvx
• cpbsvx
• cpbtf2
• cpbtrf
• cpbtrs
• cpftri
• cpftrs
• cpocon
• cpoequ
• cpoequb
• cporfs
• cposv
• cposvx
• cpotf2
• cpotrf
• cpotri
• cpotrs
• cppcon
• cppequ
• cpprfs
• cppsv
• cppsvx
• cpptrf
• cpptri
• cpptrs
• cpstf2
• cpstrf
• cptcon
• cpteqr
• cptrfs
• cpts
• cpts
• cpts
• cpttrf
• cptrs
• cptts2
• crot
• cspscon
• cspsmv
• cspr
• csprfs
• cspsv
• cspsvx
• csptrf
• csptri
• csptrs
• csrscl
• cstedc
• csteqr
• cstein
• cstemr
• csteqf
• csycon
• csyconv
• csyequb
• csynv
• csyr
• csyrfs
• csyev
• csyevx
• csyswapr
• csytf2
• csytrf
• csytri
• csytrf2
• csytri2x
• csytrs
• csytrs2
• cthcon
• cthbfs

6.13. LAPACK functions for Cython
• cunbdb
• cuncsd
• cung2l
• cung2r
• cungbr
• cunghr
• cungl2
• cunglq
• cungql
• cungqr
• cungr2
• cungrq
• cungtr
• cunm2l
• cunm2r
• cunnbr
• cunnhr
• cunnml2
• cunnmlq
• cunnmlq
• cunnqr
• cunnmr2
• cunnmr3
• cunnmrq
• cunnmrz
• cunnmtr
• cupgtr
• cupmtr
• dbbcsd
• dbdsdc
• dbdsdc
• ddisna
• dgbbrd
• dgbccon
• dgbequ
• dgbequb
• dgbtrfs
• dgbsv
• dgbsvx
• dgbsvx
• dgbtf2
• dgbtrf
• dgbtrs
• dgebak
• dgebal
• dgebd2
• dgebrd
• dgecon
• dgeeqqu
• dgeequb
• dgees
• dgeesx
• dgeev
• dgeevx
• dgehd2
• dgehrd
• dgejsv
• dgelq2
• dgelqf
• dgels
• dgelsd
• dgelss
• dgelsy
• dgemqrt
• dgeql2
• dgeqlf
• dgeqpf
• dgeqpf
• dgeqrt
• dgeqrt2
- dgeqrt3
- dgerfs
- dgerq2
- dgerqf
- dgesc2
- dgesdd
- dgesv
- dgesvd
- dgesvj
- dgesvx
- dgetc2
- dgetf2
- dgetrf
- dgetri
- dgetrs
- dggbak
- dggbal
- dggges
- dgggesx
- dgggev
- dgggevx
- dggglm
- dggghrd
- dgglse
- dggqrf
- dggqrqf
- dgsvj0
- dgsvj1
- dgtcon
- dgtrfs
- dgtsv
- dgtsvx
- dgttrf
- dgttrs
- dgtts2
- dhgeqz
• dhsein
• dhseqr
• disnan
• dlabad
• dlabrd
• dlacn2
• dlacon
• dlacpy
• dladiv
• dlae2
• dlaebz
• dlaed0
• dlaed1
• dlaed2
• dlaed3
• dlaed4
• dlaed5
• dlaed6
• dlaed7
• dlaed8
• dlaed9
• dlaeda
• dlaein
• dlaev2
• dlaexc
• dlag2
• dlag2s
• dlags2
• dlagtf
• dlagtm
• dlagts
• dlav2
• dlaqr
• dlaqr2
• dlaic1
• dlaic2
• dlaib
- dlals0
- dlalsa
- dlalsd
- dlamch
- dlamrg
- dlaneq
- dlangb
- dlange
- dlangt
- dlans
- dlansb
- dlansf
- dlansp
- dlansr
- dlansy
- dlantb
- dlantp
- dlansr
- dlansv2
- dlapll
- dlapmr
- dlapmt
- dlapy2
- dlapy3
- dlaqgb
- dlaque
- dlaqp2
- dlaqps
- dlahaq0
- dlahaq1
- dlahaq2
- dlahaq3
- dlahaq4
- dlahaq5
- dlahaqsb
- dlahaqsp

6.13. LAPACK functions for Cython
- dlaqsy
- dlaqtr
- dlar1v
- dlar2v
- dlarf
- dlarfb
- dlarfg
- dlarfgp
- dlarft
- dlarfx
- dlargv
- dlarnv
- dlarra
- dlarrb
- dlarrc
- dlarrd
- dlarre
- dlarrf
- dlarrj
- dlarrk
- dlarrr
- dlarrv
- dlartg
- dlartgp
- dlartgs
- dlartv
- dlaruv
- dlarz
- dlarzb
- dlarzt
- dlas2
- dlascl
- dlasd0
- dlasd1
- dlasd2
- dlasd3
• dlasd4
• dlasd5
• dlasd6
• dlasd7
• dlasd8
• dlaseda
• dlasdq
• dlasdt
• dlaset
• dlasq1
• dlasq2
• dlasq3
• dlasq4
• dlasq6
• dlasr
• dlasrt
• dllassq
• dlasv2
• dlaswp
• dlasv2
• dlasv2
• dlasyf
• dlat2s
• dlatsb
• dlatdf
• dlatps
• dlattrd
• dlattr
• dlattrz
• dlaunu2
• dlauum
• dopgtr
• dopmtr
• dorbdb
• dorcsd
• dorg2l
• dorg2r
• dorgbr
• dorghr
• dorgl2
• dorglq
• dorgql
• dorgqr
• dorgr2
• dorgrq
• dorgtr
• dorm2l
• dorm2r
• dormbr
• dorshr
• dorml2
• dormlq
• dormql
• dormqr
• dormr2
• dormr3
• dormrq
• dormrz
• dormtr
• dpbcon
• dpbequ
• dpbrfs
• dpbutf
• dpbstrf
• dpbsv
• dpbsvx
• dpbstf2
• dpbtrf
• dpbtrs
• dpftrf
• dpftri
• dpftrs
• dpocon
• dpoequ
• dpoequb
• dpors
• dpsov
• dpsov
• dpotf2
• dpotrf
• dpotri
• dpotrs
• dppequ
• dppequ
• dpprfs
• dppsv
• dppsv
• dpptrf
• dpptri
• dpptrs
• dpstf2
• dpstf2
• dptcon
• dptcon
• dppteqr
• dppteqr
• dpptfs
• dpptsv
• dpptsv
• dppttrf
• dppttrs
• dpptts2
• drscl
• dsbev
• dsbev
• dsbev
• dsbev
• dsbev
• dsbevd
• dsbevd
• dsbev
• dsbev
• dsbev
• dsbev
• dsbtrd
• dsfrk

6.13. LAPACK functions for Cython
- dsgesv
- dspcon
- dspev
- dspevd
- dspevx
- dspgst
- dspgv
- dspgvd
- dspgvx
- dsposv
- dsprfs
- dspsv
- dspsvx
- dsptrd
- dsptrf
- dsptri
- dsptrs
- dstebz
- dstedc
- dstegr
- dstein
- dstemr
- dsteqr
- dsterf
- dstev
- dstevd
- dstevr
- dstevx
- dsycon
- dsyconv
- dsyequb
- dsyev
- dsyevd
- dsyevr
- dsyevx
- dsygs2
• dsygst
• dsygv
• dsygvd
• dsygvx
• dsyrfs
• dsyev
• dsyevx
• dsyevapr
• dsyevd2
• dsyevf2
• dsyevrd
• dsyevrf
• dsyevri
• dsyevri2
• dsyevri2x
• dsyevrs
• dsyevrs2
• dtbcon
• dtbrfs
• dtbtrs
• dtbsm
• dtbtri
• dtfttp
• dtfttr
• dtgevc
• dtgex2
• dtgexc
• dtgense
• dtgjsja
• dtgjsna
• dtgjsy2
• dtgjsyl
• dtptcon
• dtptmqrt
• dtptqrt
• dtptqrt2
• dtprfb
• dtprfs
• dtptri
• dtptrs
• dtpttf
• dtpttr
• dtrcon
• dtrevc
• dtrexc
• dtrrfs
• dtrrsen
• dtrrsna
• dtrsy1
• dtrtri2
• dtrtri
• dtrtrs
• dtrtff
• dtrttf
• dtrttp
• dtzrzf
• dzsum1
• icmax1
• ieeeck
• ilaelc
• ilaelr
• iladiag
• iladlc
• iladlr
• ilaprec
• ilaslc
• ilasl1r
• ilatrans
• ilauplo
• ilaver
• ilaz1c
• ilaz1r
• izmax1
6.13. LAPACK functions for Cython

- sbbcsd
- sbdsdc
- sbdsqrc
- scsum1
- sdisna
- sghbrd
- sghcon
- sghbequ
- sghbequb
- sghbrfs
- sghsv
- sghsvx
- sghbtf2
- sghbtrf
- sghbtrs
- sgebak
- sgebal
- sgebd2
- sgebrd
- sgecon
- sgeeqeu
- sgeequb
- sgees
- sgeesx
- sgeev
- sgeevx
- sgeehd2
- sgehrd
- sgejsv
- sgelq2
- sgelqf
- sgels
- sgelsd
- sgelsq
- sgelsy
- sgemqrt
- sgeql2
- sgeqlf
- sgeqp3
- sgeqr2
- sgeqr2p
- sgeqrf
- sgeqrfp
- sgeqrt
- sgeqrt2
- sgeqrt3
- sgerfs
- sgerq2
- sgerqf
- sgesc2
- sgesdd
- sgescv
- sgescvd
- sgescvj
- sgescvx
- sgetc2
- sgetf2
- sgetrf
- sgetri
- sgetrs
- sggbak
- sggbal
- sgges
- sggesx
- sggesx
- sggev
- sggevfx
- sggevd
- sggevvx
- sggevdx
- sggglm
- sgghrd
- sggldc
- sggqr
- sggqrf
- sgqrqf
6.13. LAPACK functions for Cython

- sgsvj1
- sgtcon
- sgtrfs
- sgtsv
- sgtsvx
- sgttrf
- sgttrs
- sgtts2
- shgeqz
- shsein
- shseqr
- slabad
- slabrd
- slacn2
- slacon
- slacpy
- sladiv
- slae2
- slaebz
- slaed0
- slaed1
- slaed2
- slaed3
- slaed4
- slaed5
- slaed6
- slaed7
- slaed8
- slaed9
- slaeda
- slaein
- slaev2
- slaexc
- slag2
- slag2d
- slags2
• slagtf
• slagtm
• slagt5
• slagt6
• slagv2
• slahqr
• slahr2
• slaic1
• slahlr2
• slals0
• slalsa
• slalsd
• slamch
• slamrg
• slangb
• slange
• slangt
• slanhs
• slansb
• slansf
• slansp
• slanst
• slansy
• slantb
• slantp
• slantr
• slanv2
• slapll
• slapmr
• slapnt
• slapy2
• slapy3
• slaqgb
• slaqge
• slaqp2
• slaqps
• slaqr0
- slaqr1
- slaqr2
- slaqr3
- slaqr4
- slaqr5
- slaqsb
- slaqsp
- slaqsy
- slaqr
- slar1v
- slar2v
- slarf
- slarfb
- slarf
- slarf
- slarft
- slarfx
- slargv
- slarnv
- slarra
- slarrb
- slarrc
- slarrd
- slarre
- slarrf
- slarrj
- slarrk
- slarr
- slarrv
- slartg
- slartgp
- slartgs
- slartv
- slaruv
- slarz
- slarzb

6.13. LAPACK functions for Cython
• slarzt
• slas2
• slasc1
• slasd0
• slasd1
• slasd2
• slasd3
• slasd4
• slasd5
• slasd6
• slasd7
• slasd8
• slasda
• slasdq
• slasd1t
• slaset
• slaq1
• slaq2
• slaq3
• slaq4
• slaq6
• slasr
• slasrt
• slassq
• slasv2
• slaswp
• slasy2
• slasyf
• slatbs
• slatdf
• slatps
• slatrd
• slatrs
• slatrz
• slauu2
• slauum
- sopgtr
- sopmtr
- sorbdb
- sorcsd
- sorg2l
- sorg2r
- sorgbr
- sorghr
- sorgl2
- sorglq
- sorgql
- sorgqr
- sorg2r
- sorgrq
- sorgtr
- sorm2l
- sorm2r
- sormbr
- sormhr
- sorml2
- sormlq
- sormql
- sormqr
- sormr2
- sormr3
- sormrq
- sormrz
- sormtr
- spbcon
- spbequ
- spbrfs
- spbstf
- spbsv
- spbsvx
- spbtf2
- spbtrf
• ssbgst
• ssbgv
• ssbgvd
• ssbgvx
• ssbtrd
• ssfrk
• sspcon
• sspev
• sspevd
• sspevx
• sspgst
• sspgv
• sspgvd
• sspgvx
• ssprfs
• sspsv
• sspsvx
• ssprtrd
• ssprtrf
• ssprtri
• ssprtrs
• ssstebz
• ssstedc
• ssstegr
• ssstein
• ssstemr
• sssteqr
• ssstef
• ssstev
• ssstevd
• ssstevr
• ssstevx
• ssycon
• ssyconv
• ssyequb
• ssyev
- ssyevd
- ssyevr
- ssyevx
- ssygs2
- ssygst
- ssygv
- ssygvd
- ssygvx
- ssyrfs
- ssysv
- ssysvx
- ssyswapr
- ssytd2
- ssytf2
- ssytrd
- ssytrf
- ssytri
- ssytri2
- ssytri2x
- ssytrs
- ssytrs2
- stbcon
- stbtrfs
- stbtrrs
- stfsn
- stftri
- stfttp
- stfttr
- stgevc
- stgex2
- stgexc
- stgsen
- stgsja
- stgsna
- stgsy2
- stgsyl
- stpcon
- stpmqrt
- stpqrt
- stpqrt2
- stprfb
- stprfs
- stptri
- stptrs
- stpttf
- stpttr
- strocon
- strevc
- strexc
- strrfs
- strsen
- strsna
- strsyl
- strti2
- strtri
- strtrs
- strttf
- strttp
- strzrf
- xerbla_array
- zbbcsd
- zbdbsqr
- zcgesv
- zcposv
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- zgbbrd
- zgbdcon
- zgbequ
- zgbequb
- zgbrfs
- zgbsv
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- zgbtf2
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- zgbtrs
- zgebak
- zgebal
- zgebd2
- zgebrd
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• ztgexc
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• ztpcon
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• zunglq
• zungql
6.14 Interpolative matrix decomposition (scipy.linalg.interpolative)

New in version 0.13.

An interpolative decomposition (ID) of a matrix $A \in \mathbb{C}^{m \times n}$ of rank $k \leq \min\{m, n\}$ is a factorization

$$A \Pi = \begin{bmatrix} A \Pi_1 & A \Pi_2 \end{bmatrix} = A \Pi_1 \begin{bmatrix} I & T \end{bmatrix},$$

where $\Pi = [\Pi_1, \Pi_2]$ is a permutation matrix with $\Pi_1 \in \{0, 1\}^{n \times k}$, i.e., $A \Pi_2 = A \Pi_1 T$. This can equivalently be written as $A = BP$, where $B = A \Pi_1$ and $P = [I, T] \Pi^T$ are the skeleton and interpolation matrices, respectively.

If $A$ does not have exact rank $k$, then there exists an approximation in the form of an ID such that $A = BP + E$, where $\|E\| \sim \sigma_{k+1}$ is on the order of the $(k+1)$-th largest singular value of $A$. Note that $\sigma_{k+1}$ is the best possible error for a rank-$k$ approximation and, in fact, is achieved by the singular value decomposition (SVD) $A \approx U S V^*$, where $U \in \mathbb{C}^{m \times k}$ and $V \in \mathbb{C}^{n \times k}$ have orthonormal columns and $S = \text{diag}(\sigma_i) \in \mathbb{C}^{k \times k}$ is diagonal with nonnegative entries. The principal advantages of using an ID over an SVD are that:

- it is cheaper to construct;
- it preserves the structure of $A$; and
- it is more efficient to compute with in light of the identity submatrix of $P$. 
6.14.1 Routines

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<td>Estimate matrix rank to a specified relative</td>
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```
scipy.linalg.interpolative.interp_decomp

scipy.linalg.interpolative.interp_decomp(A, eps_or_k, rand=True)
```

Compute ID of a matrix.

An ID of a matrix $A$ is a factorization defined by a rank $k$, a column index array $idx$, and interpolation coefficients $proj$ such that:

```
numpy.dot(A[:,idx[:k]], proj) = A[:,idx[k:]]
```

The original matrix can then be reconstructed as:

```
numpy.hstack([A[:,idx[:k]],
              numpy.dot(A[:,idx[:k]], proj)])[:,numpy.argsort(idx)]
```

or via the routine `reconstruct_matrix_from_id`. This can equivalently be written as:

```
numpy.dot(A[:,idx[:k]],
              numpy.hstack([numpy.eye(k), proj]))[:,np.argsort(idx)]
```

in terms of the skeleton and interpolation matrices:

```
B = A[:,idx[:k]]
```

and:

```
P = numpy.hstack([numpy.eye(k), proj])[:,np.argsort(idx)]
```

respectively. See also `reconstruct_interp_matrix` and `reconstruct_skel_matrix`.

The ID can be computed to any relative precision or rank (depending on the value of `eps_or_k`). If a precision is specified ($eps_or_k < 1$), then this function has the output signature:

```
k, idx, proj = interp_decomp(A, eps_or_k)
```

Otherwise, if a rank is specified ($eps_or_k >= 1$), then the output signature is:
idx, proj = interp_decomp(A, eps_or_k)

**Parameters**

- **A** [numpy.ndarray or scipy.sparse.linalg.LinearOperator with rmatvec] Matrix to be factored.
- **eps_or_k** [float or int] Relative error (if eps_or_k < 1) or rank (if eps_or_k >= 1) of approximation.
- **rand** [bool, optional] Whether to use random sampling if A is of type numpy.ndarray (randomized algorithms are always used if A is of type scipy.sparse.linalg.LinearOperator).

**Returns**

- **k** [int] Rank required to achieve specified relative precision if eps_or_k < 1.
- **idx** [numpy.ndarray] Column index array.
- **proj** [numpy.ndarray] Interpolation coefficients.

**scipy.linalg.interpolative.reconstruct_matrix_from_id**

scipy.linalg.interpolative.reconstruct_matrix_from_id(B, idx, proj)
Reconstruct matrix from its ID.

A matrix A with skeleton matrix B and ID indices and coefficients idx and proj, respectively, can be reconstructed as:

```
numpy.hstack([B, numpy.dot(B, proj)])[::numpy.argsort(idx)]
```

See also `reconstruct_interp_matrix` and `reconstruct_skel_matrix`.

**Parameters**

- **B** [numpy.ndarray] Skeleton matrix.
- **idx** [numpy.ndarray] Column index array.
- **proj** [numpy.ndarray] Interpolation coefficients.

**Returns**

:func:`numpy.ndarray`
Reconstructed matrix.

**scipy.linalg.interpolative.reconstruct_interp_matrix**

scipy.linalg.interpolative.reconstruct_interp_matrix(idx, proj)
Reconstruct interpolation matrix from ID.

The interpolation matrix can be reconstructed from the ID indices and coefficients idx and proj, respectively, as:

```
P = numpy.hstack([numpy.eye(proj.shape[0]), proj])[::numpy.argsort(idx)]
```

The original matrix can then be reconstructed from its skeleton matrix B via:

```
numpy.dot(B, P)
```

See also `reconstruct_matrix_from_id` and `reconstruct_skel_matrix`.

**Parameters**
idx  [numpy.ndarray] Column index array.
proj [numpy.ndarray] Interpolation coefficients.

Returns

:class:`numpy.ndarray`
Interpolation matrix.

**scipy.linalg.interpolative.reconstruct_skel_matrix**

**scipy.linalg.interpolative.reconstruct_skel_matrix(A, k, idx)**

Reconstruct skeleton matrix from ID.

The skeleton matrix can be reconstructed from the original matrix $A$ and its ID rank and indices $k$ and $idx$, respectively, as:

$$B = A[:, idx[:k]]$$

The original matrix can then be reconstructed via:

```python
numpy.hstack([B, numpy.dot(B, proj)])[numpy.argsort(idx)]
```

See also *reconstruct_matrix_from_id* and *reconstruct_interp_matrix*.

**Parameters**

- **A** [numpy.ndarray] Original matrix.
- **k** [int] Rank of ID.
- **idx** [numpy.ndarray] Column index array.

**Returns**

:class:`numpy.ndarray`
Skeleton matrix.

**scipy.linalg.interpolative.id_to_svd**

**scipy.linalg.interpolative.id_to_svd(B, idx, proj)**

Convert ID to SVD.

The SVD reconstruction of a matrix with skeleton matrix $B$ and ID indices and coefficients $idx$ and $proj$, respectively, is:

$$U, S, V = id_to_svd(B, idx, proj)$$

$$A = numpy.dot(U, numpy.dot(numpy.diag(S), V.conj().T))$$

See also *svd*.

**Parameters**

- **B** [numpy.ndarray] Skeleton matrix.
- **idx** [numpy.ndarray] Column index array.
- **proj** [numpy.ndarray] Interpolation coefficients.

**Returns**

- **U** [numpy.ndarray] Left singular vectors.
- **S** [numpy.ndarray] Singular values.
- **V** [numpy.ndarray] Right singular vectors.
scipy.linalg.interpolative.svd

scipy.linalg.interpolative.svd(A, eps_or_k, rand=True)
Compute SVD of a matrix via an ID.

An SVD of a matrix $A$ is a factorization:

$$A = \text{numpy}.\dot{\text{dot}}(U, \text{numpy}.\dot{\text{dot}}(\text{numpy}.\text{diag}(S), V.\text{conj}.T))$$

where $U$ and $V$ have orthonormal columns and $S$ is nonnegative.

The SVD can be computed to any relative precision or rank (depending on the value of $eps_or_k$).

See also interp_decomp and id_to_svd.

Parameters

- **A**: [numpy.ndarray or scipy.sparse.linalg.LinearOperator] Matrix to be factored, given as either a numpy.ndarray or a scipy.sparse.linalg.LinearOperator with the matvec and rmatvec methods (to apply the matrix and its adjoint).
- **eps_or_k**: [float or int] Relative error (if $eps_or_k < 1$) or rank (if $eps_or_k \geq 1$) of approximation.
- **rand**: [bool, optional] Whether to use random sampling if $A$ is of type numpy.ndarray (randomized algorithms are always used if $A$ is of type scipy.sparse.linalg.LinearOperator).

Returns

- **U**: [numpy.ndarray] Left singular vectors.
- **S**: [numpy.ndarray] Singular values.
- **V**: [numpy.ndarray] Right singular vectors.

scipy.linalg.interpolative.estimate_spectral_norm

scipy.linalg.interpolative.estimate_spectral_norm(A, its=20)
Estimate spectral norm of a matrix by the randomized power method.

Parameters

- **A**: [scipy.sparse.linalg.LinearOperator] Matrix given as a scipy.sparse.linalg.LinearOperator with the matvec and rmatvec methods (to apply the matrix and its adjoint).
- **its**: [int, optional] Number of power method iterations.

Returns

- **float**: Spectral norm estimate.

scipy.linalg.interpolative.estimate_spectral_norm_diff

scipy.linalg.interpolative.estimate_spectral_norm_diff(A, B, its=20)
Estimate spectral norm of the difference of two matrices by the randomized power method.

Parameters

- **A**: [scipy.sparse.linalg.LinearOperator] First matrix given as a scipy.sparse.linalg.LinearOperator with the matvec and rmatvec methods (to apply the matrix and its adjoint).
Second matrix given as a `scipy.sparse.linalg.LinearOperator` with the `matvec` and `rmatvec` methods (to apply the matrix and its adjoint).

**Returns**

- `float`: Spectral norm estimate of matrix difference.

### scipy.linalg.interpolative.estimate_rank

**scipy.linalg.interpolative.estimate_rank**

Estimate matrix rank to a specified relative precision using randomized methods.

The matrix $A$ can be given as either a `numpy.ndarray` or a `scipy.sparse.linalg.LinearOperator`, with different algorithms used for each case. If $A$ is of type `numpy.ndarray`, then the output rank is typically about 8 higher than the actual numerical rank.

**Parameters**

- `A`: `numpy.ndarray` or `scipy.sparse.linalg.LinearOperator` Matrix whose rank is to be estimated, given as either a `numpy.ndarray` or a `scipy.sparse.linalg.LinearOperator` with the `rmatvec` method (to apply the matrix adjoint).
- `eps`: [float] Relative error for numerical rank definition.

**Returns**

- `int`: Estimated matrix rank.

### Support functions:

#### scipy.linalg.interpolative.seed

**scipy.linalg.interpolative.seed**

Seed the internal random number generator used in this ID package.

The generator is a lagged Fibonacci method with 55-element internal state.

**Parameters**

- `seed` [int, sequence, ‘default’, optional] If ‘default’, the random seed is reset to a default value. If `seed` is a sequence containing 55 floating-point numbers in range [0,1], these are used to set the internal state of the generator. If the value is an integer, the internal state is obtained from `numpy.random.RandomState` (MT19937) with the integer used as the initial seed. If `seed` is omitted (None), `numpy.random` is used to initialize the generator.

#### scipy.linalg.interpolative.rand

**scipy.linalg.interpolative.rand**

Generate standard uniform pseudorandom numbers via a very efficient lagged Fibonacci method.

This routine is used for all random number generation in this package and can affect ID and SVD results.
Parameters

- shape: Shape of output array

6.14.2 References

This module uses the ID software package [R5a82238cdab4-1] by Martinsson, Rokhlin, Shkolnisky, and Tygert, which is a Fortran library for computing IDs using various algorithms, including the rank-revealing QR approach of [R5a82238cdab4-2] and the more recent randomized methods described in [R5a82238cdab4-3], [R5a82238cdab4-4], and [R5a82238cdab4-5]. This module exposes its functionality in a way convenient for Python users. Note that this module does not add any functionality beyond that of organizing a simpler and more consistent interface.

We advise the user to consult also the documentation for the ID package.

6.14.3 Tutorial

Initializing

The first step is to import `scipy.linalg.interpolative` by issuing the command:

```python
>>> import scipy.linalg.interpolative as sli
```

Now let’s build a matrix. For this, we consider a Hilbert matrix, which is well known to have low rank:

```python
>>> from scipy.linalg import hilbert
>>> n = 1000
>>> A = hilbert(n)
```

We can also do this explicitly via:

```python
>>> import numpy as np
>>> n = 1000
>>> A = np.empty((n, n), order='F')
>>> for j in range(n):
...     for i in range(m):
...         A[i, j] = 1. / (i + j + 1)
```

Note the use of the flag `order='F'` in `numpy.empty`. This instantiates the matrix in Fortran-contiguous order and is important for avoiding data copying when passing to the backend.

We then define multiplication routines for the matrix by regarding it as a `scipy.sparse.linalg.LinearOperator`:

```python
>>> from scipy.sparse.linalg import aslinearoperator
>>> L = aslinearoperator(A)
```

This automatically sets up methods describing the action of the matrix and its adjoint on a vector.

Computing an ID

We have several choices of algorithm to compute an ID. These fall largely according to two dichotomies:

1. how the matrix is represented, i.e., via its entries or via its action on a vector; and
2. whether to approximate it to a fixed relative precision or to a fixed rank.
We step through each choice in turn below.

In all cases, the ID is represented by three parameters:

1. a rank \( k \);
2. an index array \( \text{idx} \); and
3. interpolation coefficients \( \text{proj} \).

The ID is specified by the relation \( \text{np.dot}(A[:, \text{idx}[:k]], \text{proj}) == A[:, \text{idx}[k:]] \).

**From matrix entries**

We first consider a matrix given in terms of its entries.

To compute an ID to a fixed precision, type:

```python
>>> k, idx, proj = sli.interp_decomp(A, eps)
```

where \( \text{eps} < 1 \) is the desired precision.

To compute an ID to a fixed rank, use:

```python
>>> idx, proj = sli.interp_decomp(A, k)
```

where \( k \geq 1 \) is the desired rank.

Both algorithms use random sampling and are usually faster than the corresponding older, deterministic algorithms, which can be accessed via the commands:

```python
>>> k, idx, proj = sli.interp_decomp(A, eps, rand=False)
```

and:

```python
>>> idx, proj = sli.interp_decomp(A, k, rand=False)
```

respectively.

**From matrix action**

Now consider a matrix given in terms of its action on a vector as a `scipy.sparse.linalg.LinearOperator`.

To compute an ID to a fixed precision, type:

```python
>>> k, idx, proj = sli.interp_decomp(L, eps)
```

To compute an ID to a fixed rank, use:

```python
>>> idx, proj = sli.interp_decomp(L, k)
```

These algorithms are randomized.

**Reconstructing an ID**

The ID routines above do not output the skeleton and interpolation matrices explicitly but instead return the relevant information in a more compact (and sometimes more useful) form. To build these matrices, write:

```python
>>> B = sli.reconstruct_skel_matrix(A, k, idx)
```

for the skeleton matrix and:
for the interpolation matrix. The ID approximation can then be computed as:

```python
>>> C = np.dot(B, P)
```

This can also be constructed directly using:

```python
>>> C = sli.reconstruct_matrix_from_id(B, idx, proj)
```

without having to first compute P. Alternatively, this can be done explicitly as well using:

```python
>>> B = A[:,idx[:k]]
>>> P = np.hstack([np.eye(k), proj])[:,np.argsort(idx)]
>>> C = np.dot(B, P)
```

### Computing an SVD

An ID can be converted to an SVD via the command:

```python
>>> U, S, V = sli.id_to_svd(B, idx, proj)
```

The SVD approximation is then:

```python
>>> C = np.dot(U, np.dot(np.diag(S), np.dot(V.conj().T)))
```

The SVD can also be computed “fresh” by combining both the ID and conversion steps into one command. Following the various ID algorithms above, there are correspondingly various SVD algorithms that one can employ.

#### From matrix entries

We consider first SVD algorithms for a matrix given in terms of its entries.

To compute an SVD to a fixed precision, type:

```python
>>> U, S, V = sli.svd(A, eps)
```

To compute an SVD to a fixed rank, use:

```python
>>> U, S, V = sli.svd(A, k)
```

Both algorithms use random sampling; for the deterministic versions, issue the keyword `rand=False` as above.

#### From matrix action

Now consider a matrix given in terms of its action on a vector.

To compute an SVD to a fixed precision, type:

```python
>>> U, S, V = sli.svd(L, eps)
```

To compute an SVD to a fixed rank, use:

```python
>>> U, S, V = sli.svd(L, k)
```
Utility routines

Several utility routines are also available.

To estimate the spectral norm of a matrix, use:

```python
>>> snorm = sli.estimate_spectral_norm(A)
```

This algorithm is based on the randomized power method and thus requires only matrix-vector products. The number of iterations to take can be set using the keyword `its` (default: `its=20`). The matrix is interpreted as a `scipy.sparse.linalg.LinearOperator`, but it is also valid to supply it as a `numpy.ndarray`, in which case it is trivially converted using `scipy.sparse.linalg.aslinearoperator`.

The same algorithm can also estimate the spectral norm of the difference of two matrices $A_1$ and $A_2$ as follows:

```python
>>> diff = sli.estimate_spectral_norm_diff(A1, A2)
```

This is often useful for checking the accuracy of a matrix approximation.

Some routines in `scipy.linalg.interpolative` require estimating the rank of a matrix as well. This can be done with either:

```python
>>> k = sli.estimate_rank(A, eps)
```

or:

```python
>>> k = sli.estimate_rank(L, eps)
```

depending on the representation. The parameter `eps` controls the definition of the numerical rank.

Finally, the random number generation required for all randomized routines can be controlled via `scipy.linalg.interpolative.seed`. To reset the seed values to their original values, use:

```python
>>> sli.seed('default')
```

To specify the seed values, use:

```python
>>> sli.seed(s)
```

where `s` must be an integer or array of 55 floats. If an integer, the array of floats is obtained by using `np.random.rand` with the given integer seed.

To simply generate some random numbers, type:

```python
>>> sli.rand(n)
```

where `n` is the number of random numbers to generate.

Remarks

The above functions all automatically detect the appropriate interface and work with both real and complex data types, passing input arguments to the proper backend routine.

6.15 Miscellaneous routines (scipy.misc)

Various utilities that don’t have another home.
Note that Pillow (https://python-pillow.org/) is not a dependency of SciPy, but the image manipulation functions indicated in the list below are not available without it.

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### 6.15.1 scipy.misc.ascent

**scipy.misc.ascent()**

Get an 8-bit grayscale bit-depth, 512 x 512 derived image for easy use in demos

The image is derived from ascent-to-the-top.jpg at http://www.public-domain-image.com/people-public-domain-images-pictures/

**Parameters**

None

**Returns**

ascent [ndarray] convenient image to use for testing and demonstration

**Examples**

```python
>>> import scipy.misc
>>> ascent = scipy.misc.ascent()
>>> ascent.shape
(512, 512)
>>> ascent.max()
255
```

```python
>>> import matplotlib.pyplot as plt
>>> plt.gray()
>>> plt.imshow(ascent)
>>> plt.show()
```

### 6.15.2 scipy.misc.central_diff_weights

**scipy.misc.central_diff_weights(Np, ndiv=1)**

Return weights for an Np-point central derivative.

Assumes equally-spaced function points.

If weights are in the vector w, then derivative is $w[0] \cdot f(x-h_0\cdot dx) + \ldots + w[-1] \cdot f(x+h_0\cdot dx)$

**Parameters**

- **Np**  [int] Number of points for the central derivative.
- **ndiv**  [int, optional] Number of divisions. Default is 1.

**Notes**

Can be inaccurate for large number of points.
6.15.3 scipy.misc.derivative

scipy.misc.derivative(func, x0, dx=1.0, n=1, args=(), order=3)

Find the n-th derivative of a function at a point.

Given a function, use a central difference formula with spacing dx to compute the n-th derivative at x0.

Parameters

- **func**: [function] Input function.
- **x0**: [float] The point at which n-th derivative is found.
- **dx**: [float, optional] Spacing.
- **n**: [int, optional] Order of the derivative. Default is 1.
- **args**: [tuple, optional] Arguments
- **order**: [int, optional] Number of points to use, must be odd.

Notes

Decreasing the step size too small can result in round-off error.

Examples

```python
>>> from scipy.misc import derivative
>>> def f(x):
...     return x**3 + x**2
>>> derivative(f, 1.0, dx=1e-6)
4.9999999999217337
```

6.15.4 scipy.misc.face

scipy.misc.face(gray=False)

Get a 1024 x 768, color image of a raccoon face.

raccoon-procyon-lotor.jpg at http://www.public-domain-image.com

Parameters

- **gray**: [bool, optional] If True return 8-bit grey-scale image, otherwise return a color image

Returns
SciPy Reference Guide, Release 1.2.0

face  [ndarray] image of a raccoon face

Examples

```python
>>> import scipy.misc
>>> face = scipy.misc.face()
>>> face.shape
(768, 1024, 3)
>>> face.max()
255
>>> face.dtype
dtype('uint8')
```

```python
>>> import matplotlib.pyplot as plt
>>> plt.gray()
>>> plt.imshow(face)
>>> plt.show()
```

6.15.5 scipy.misc.electrocardiogram

scipy.misc.electrocardiogram()

Load an electrocardiogram as an example for a one-dimensional signal.

The returned signal is a 5 minute long electrocardiogram (ECG), a medical recording of the heart’s electrical activity, sampled at 360 Hz.

**Returns**

ecg  [ndarray] The electrocardiogram in millivolt (mV) sampled at 360 Hz.

**Notes**

The provided signal is an excerpt (19:35 to 24:35) from the record 208 (lead MLII) provided by the MIT-BIH Arrhythmia Database [1] on PhysioNet [2]. The excerpt includes noise induced artifacts, typical heartbeats as well as pathological changes.

New in version 1.1.0.

**References**

[1], [2]
Examples

```python
>>> from scipy.misc import electrocardiogram
>>> ecg = electrocardiogram()
>>> ecg
array([-0.245, -0.215, -0.185, ..., -0.405, -0.395, -0.385])
>>> ecg.shape, ecg.mean(), ecg.std()
((108000,), -0.16510875, 0.5992473991177294)
```

As stated the signal features several areas with a different morphology. E.g. the first few seconds show the electrical activity of a heart in normal sinus rhythm as seen below.

```python
>>> import matplotlib.pyplot as plt
>>> fs = 360
>>> time = np.arange(ecg.size) / fs
>>> plt.plot(time, ecg)
>>> plt.xlabel("time in s")
>>> plt.ylabel("ECG in mV")
>>> plt.xlim(9, 10.2)
>>> plt.ylim(-1, 1.5)
>>> plt.show()
```

![](chart.png)

After second 16 however, the first premature ventricular contractions, also called extrasystoles, appear. These have a different morphology compared to typical heartbeats. The difference can easily be observed in the following plot.

```python
>>> plt.plot(time, ecg)
>>> plt.xlabel("time in s")
>>> plt.ylabel("ECG in mV")
>>> plt.xlim(46.5, 50)
>>> plt.ylim(-2, 1.5)
>>> plt.show()
```

At several points large artifacts disturb the recording, e.g.:
Finally, examining the power spectrum reveals that most of the biosignal is made up of lower frequencies. At 60 Hz the noise induced by the mains electricity can be clearly observed.

```python
>>> from scipy.signal import welch
>>> f, Pxx = welch(ecg, fs=fs, nperseg=2048, scaling="spectrum")
>>> plt.semilogy(f, Pxx)
>>> plt.xlabel("Frequency in Hz")
```
>>> plt.ylabel("Power spectrum of the ECG in mV**2")
>>> plt.xlim(f[[0, -1]])
>>> plt.show()

![Power Spectrum of the ECG in mV**2](image)

```
6.15.6 scipy.misc.bytescale

scipy.misc.bytescale(*args, **kwds)

bytescale is deprecated! bytescale is deprecated in SciPy 1.0.0, and will be removed in 1.2.0.
```

Byte scales an array (image).

Byte scaling means converting the input image to uint8 dtype and scaling the range to \((\text{low}, \text{high})\) (default 0-255). If the input image already has dtype uint8, no scaling is done.

```
```
This function is only available if Python Imaging Library (PIL) is installed.

**Parameters**

- `data` [ndarray]
  PIL image data array.
- `cmin` [scalar, optional]
  Bias scaling of small values. Default is `data.min()`.
- `cmax` [scalar, optional]
  Bias scaling of large values. Default is `data.max()`.
- `high` [scalar, optional]
  Scale max value to `high`. Default is 255.
- `low` [scalar, optional]
  Scale min value to `low`. Default is 0.

**Returns**

- `img_array` [uint8 ndarray]
  The byte-scaled array.

**Examples**

```python
>>> from scipy.misc import bytescale

>>> img = np.array([[91.06794177, 3.39058326, 84.4221549],
                  ...
                  [73.88003259, 80.91433048, 4.88878881],
                  ...
                  [51.53875334, 34.45808177, 27.5873488]])

>>> bytescale(img)
array([[255,   0, 236],
       [205, 225,   4],
       [140, 90,  70]], dtype=uint8)

>>> bytescale(img, high=200, low=100)
array([[200, 100, 192],
       [180, 188, 102],
       [155, 135, 128]], dtype=uint8)

>>> bytescale(img, cmin=0, cmax=255)
array([[91, 3, 84],
       [74, 81, 5],
       [52, 34, 28]], dtype=uint8)
```

### 6.15.7 scipy.misc.fromimage

`scipy.misc.fromimage(*args, **kwds)`

*fromimage* is deprecated! *fromimage* is deprecated in SciPy 1.0.0. and will be removed in 1.2.0. Use `np.asarray(im)` instead.

Return a copy of a PIL image as a numpy array.

This function is only available if Python Imaging Library (PIL) is installed.

**Parameters**

- `im` [PIL image]
  Input image.
- `flatten` [bool]
  If true, convert the output to grey-scale.
- `mode` [str, optional]
  Mode to convert image to, e.g. 'RGB'. See the Notes of the `imread` docstring for more details.

**Returns**
fromimage
[ndarray] The different colour bands/channels are stored in the third dimension, such that a grey-image is MxN, an RGB-image MxNx3 and an RGBA-image MxNx4.

6.15.8 scipy.misc.imfilter

scipy.misc.imfilter(*args, **kwds)
imfilter is deprecated! imfilter is deprecated in SciPy 1.0.0, and will be removed in 1.2.0. Use Pillow filtering functionality directly.

Simple filtering of an image.
This function is only available if Python Imaging Library (PIL) is installed.

**Warning:** This function uses bytescale under the hood to rescale images to use the full (0, 255) range if mode is one of None, ‘L’, ‘P’, ‘1’. It will also cast data for 2-D images to uint32 for mode=None (which is the default).

**Parameters**

- **arr** [ndarray] The array of Image in which the filter is to be applied.

**Returns**

- **imfilter** [ndarray] The array with filter applied.

**Raises**

- **ValueError** Unknown filter type. If the filter you are trying to apply is unsupported.

6.15.9 scipy.misc.imread

scipy.misc.imread(*args, **kwds)
imread is deprecated! imread is deprecated in SciPy 1.0.0, and will be removed in 1.2.0. Use imageio.imread instead.

Read an image from a file as an array.
This function is only available if Python Imaging Library (PIL) is installed.

**Parameters**

- **name** [str or file object] The file name or file object to be read.
- **flatten** [bool, optional] If True, flattens the color layers into a single gray-scale layer.
- **mode** [str, optional] Mode to convert image to, e.g. ‘RGB’. See the Notes for more details.

**Returns**

- **imread** [ndarray] The array obtained by reading the image.
Notes

`imread` uses the Python Imaging Library (PIL) to read an image. The following notes are from the PIL documentation.

`mode` can be one of the following strings:

- ‘L’ (8-bit pixels, black and white)
- ‘P’ (8-bit pixels, mapped to any other mode using a color palette)
- ‘RGB’ (3x8-bit pixels, true color)
- ‘RGBA’ (4x8-bit pixels, true color with transparency mask)
- ‘CMYK’ (4x8-bit pixels, color separation)
- ‘YCbCr’ (3x8-bit pixels, color video format)
- ‘I’ (32-bit signed integer pixels)
- ‘F’ (32-bit floating point pixels)

PIL also provides limited support for a few special modes, including ‘LA’ (‘L’ with alpha), ‘RGBX’ (true color with padding) and ‘RGBa’ (true color with premultiplied alpha).

When translating a color image to black and white (mode ‘L’, ‘I’ or ‘F’), the library uses the ITU-R 601-2 luma transform:

\[
L = R \times \frac{299}{1000} + G \times \frac{587}{1000} + B \times \frac{114}{1000}
\]

When `flatten` is True, the image is converted using mode ‘F’. When `mode` is not None and `flatten` is True, the image is first converted according to `mode`, and the result is then flattened using mode ‘F’.

6.15.10 scipy.misc.imresize

`scipy.misc.imresize(*args, **kwargs)`  
`imresize` is deprecated! `imresize` is deprecated in SciPy 1.0.0, and will be removed in 1.3.0. Use Pillow instead: `numpy.array(Image.fromarray(arr).resize())`.

Resize an image.
This function is only available if Python Imaging Library (PIL) is installed.

**Warning:** This function uses `bytescale` under the hood to rescale images to use the full (0, 255) range if `mode` is one of `None`, ‘L’, ‘P’, ‘I’. It will also cast data for 2-D images to `uint32` for `mode=None` (which is the default).

**Parameters**

- `arr` [ndarray] The array of image to be resized.
- `size` [int, float or tuple]  
  - int - Percentage of current size.
  - float - Fraction of current size.
  - tuple - Size of the output image (height, width).
- `interp` [str, optional] Interpolation to use for re-sizing (‘nearest’, ‘lanczos’, ‘bilinear’, ‘bicubic’ or ‘cubic’).
mode  [str, optional] The PIL image mode (‘P’, ‘L’, etc.) to convert arr before resizing. If mode=None (the default), 2-D images will be treated like mode='L', i.e. casting to long integer. For 3-D and 4-D arrays, mode will be set to ‘RGB’ and ‘RGBA’ respectively.

Returns

imresize  [ndarray] The resized array of image.

See also:

toimage
Implicitly used to convert arr according to mode.

scipy.ndimage.zoom
More generic implementation that does not use PIL.

6.15.11 scipy.misc.imrotate

scipy.misc.imrotate(*args, **kwds)
imrotate is deprecated! imrotate is deprecated in SciPy 1.0.0, and will be removed in 1.2.0. Use skimage.transform.rotate instead.

Rotate an image counter-clockwise by angle degrees.
This function is only available if Python Imaging Library (PIL) is installed.

Warning: This function uses bytescale under the hood to rescale images to use the full (0, 255) range if mode is one of None, ‘L’, ‘P’, ‘1’. It will also cast data for 2-D images to uint32 for mode=None (which is the default).

Parameters

arr  [ndarray] Input array of image to be rotated.

angle  [float] The angle of rotation.

interp  [str, optional] Interpolation

- ‘nearest’ : for nearest neighbor
- ‘bilinear’ : for bilinear
- ‘lanczos’ : for lanczos
- ‘cubic’ : for bicubic
- ‘bicubic’ : for bicubic

Returns

imrotate  [ndarray] The rotated array of image.

6.15.12 scipy.misc.imsave

scipy.misc.imsave(*args, **kwds)
imsave is deprecated! imsave is deprecated in SciPy 1.0.0, and will be removed in 1.2.0. Use imageio. imwrite instead.

Save an array as an image.
This function is only available if Python Imaging Library (PIL) is installed.
**Warning:** This function uses `bytescale` under the hood to rescale images to use the full (0, 255) range if `mode` is one of `None`, `'L'`, `'P'`, `'1'`. It will also cast data for 2-D images to `uint32` for `mode=None` (which is the default).

**Parameters**
- `name` [str or file object]
  - Output file name or file object.
- `arr` [ndarray, MxN or MxNx3 or MxNx4]
  - Array containing image values. If the shape is MxN, the array represents a grey-level image. Shape MxNx3 stores the red, green and blue bands along the last dimension. An alpha layer may be included, specified as the last colour band of an MxNx4 array.
- `format` [str]
  - Image format. If omitted, the format to use is determined from the file name extension. If a file object was used instead of a file name, this parameter should always be used.

**Examples**

Construct an array of gradient intensity values and save to file:

```python
from scipy.misc import imsave
x = np.zeros((255, 255))
x = np.zeros((255, 255), dtype=np.uint8)
x[:,:] = np.arange(255)
imsave('gradient.png', x)
```

Construct an array with three colour bands (R, G, B) and store to file:

```python
rgb = np.zeros((255, 255, 3), dtype=np.uint8)
rgb[... , 0] = np.arange(255)
gr[... , 1] = 55
rgb[... , 2] = 1 - np.arange(255)
imsave('rgb_gradient.png', rgb)
```

### 6.15.13 `scipy.misc.imshow`

`scipy.misc.imshow(*args, **kwds)`

`imshow` is deprecated! `imshow` is deprecated in SciPy 1.0.0, and will be removed in 1.2.0. Use `matplotlib.pyplot.imshow` instead.

Simple showing of an image through an external viewer.

This function is only available if Python Imaging Library (PIL) is installed.

Uses the image viewer specified by the environment variable `SCIPY_PIL_IMAGE_VIEWER`, or if that is not defined then `see`, to view a temporary file generated from array data.

**Warning:** This function uses `bytescale` under the hood to rescale images to use the full (0, 255) range if `mode` is one of `None`, `'L'`, `'P'`, `'1'`. It will also cast data for 2-D images to `uint32` for `mode=None` (which is the default).

**Parameters**
- `arr` [ndarray]
  - Array of image data to show.
Returns
None

Examples
```python
>>> a = np.tile(np.arange(255), (255,1))
>>> from scipy import misc
>>> misc.imshow(a)
```

6.15.14 scipy.misc.toimage

```
scipy.misc.toimage(*args, **kwds)

.. deprecated::
   toimage is deprecated! toimage is deprecated in SciPy 1.0.0, and will be removed in 1.2.0. Use Pillow’s Image.fromarray directly instead.

Takes a numpy array and returns a PIL image.

This function is only available if Python Imaging Library (PIL) is installed. The mode of the PIL image depends on the array shape and the pal and mode keywords. For 2-D arrays, if pal is a valid (N,3) byte-array giving the RGB values (from 0 to 255) then mode='P', otherwise mode='L', unless mode is given as ‘F’ or ‘I’ in which case a float and/or integer array is made.

Warning: This function uses bytescale under the hood to rescale images to use the full (0, 255) range if mode is one of None, 'L', 'P', 'I'. It will also cast data for 2-D images to uint32 for mode= None (which is the default).
```

Notes

For 3-D arrays, the channel_axis argument tells which dimension of the array holds the channel data. For 3-D arrays if one of the dimensions is 3, the mode is ‘RGB’ by default or ‘YCbCr’ if selected.

The numpy array must be either 2 dimensional or 3 dimensional.

Deprecated aliases:

```
comb(*args, **kwds)

comb is deprecated! Importing comb from scipy.misc is deprecated in scipy 1.0.0.
```

```
factorial(*args, **kwds)

factorial is deprecated! Importing factorial from scipy.misc is deprecated in scipy 1.0.0.
```

```
factorial2(*args, **kwds)

factorial2 is deprecated! Importing factorial2 from scipy.misc is deprecated in scipy 1.0.0.
```

```
factorialk(*args, **kwds)

factorialk is deprecated! Importing factorialk from scipy.misc is deprecated in scipy 1.0.0.
```

```
logsumexp(*args, **kwds)

logsumexp is deprecated! Importing logsumexp from scipy.misc is deprecated in scipy 1.0.0.
```

```
pade(*args, **kwds)

pade is deprecated! Importing pade from scipy.misc is deprecated in scipy 1.0.0.
```

```
info(*args, **kwds)

Get help information for a function, class, or module.
```

```
source(*args, **kwds)

source is deprecated! Importing source from scipy.misc is deprecated in scipy 1.0.0.
```

```
who(*args, **kwds)

who is deprecated! Importing who from scipy.misc is deprecated in scipy 1.0.0.
```
6.15.15 scipy.misc.comb

scipy.misc.comb(*args, **kwds)

comb is deprecated! Importing comb from scipy.misc is deprecated in scipy 1.0.0. Use scipy.special.comb instead.

The number of combinations of \( N \) things taken \( k \) at a time.

This is often expressed as “\( N \) choose \( k \)”.

**Parameters**

- \( N \) [int, ndarray] Number of things.
- \( k \) [int, ndarray] Number of elements taken.
- `exact` [bool, optional] If `exact` is False, then floating point precision is used, otherwise exact long integer is computed.
- `repetition` [bool, optional] If `repetition` is True, then the number of combinations with repetition is computed.

**Returns**

- `val` [int, float, ndarray] The total number of combinations.

See also:

- `binom`
  Binomial coefficient ufunc

**Notes**

- Array arguments accepted only for `exact=False` case.
- If \( k > N \), \( N < 0 \), or \( k < 0 \), then a 0 is returned.

**Examples**

```python
>>> from scipy.special import comb
>>> k = np.array([3, 4])
>>> n = np.array([10, 10])
>>> comb(n, k, exact=False)
array([ 120., 210.])
>>> comb(10, 3, exact=True)
120L
>>> comb(10, 3, exact=True, repetition=True)
220L
```

6.15.16 scipy.misc.factorial

scipy.misc.factorial(*args, **kwds)

factorial is deprecated! Importing factorial from scipy.misc is deprecated in scipy 1.0.0. Use scipy.special.factorial instead.

The factorial of a number or array of numbers.

The factorial of non-negative integer \( n \) is the product of all positive integers less than or equal to \( n \):
\[ n! = n \times (n - 1) \times (n - 2) \times \ldots \times 1 \]

**Parameters**

- **n** [int or array_like of ints]
  Input values. If \( n < 0 \), the return value is 0.
- **exact** [bool, optional] If True, calculate the answer exactly using long integer arithmetic. If False, result is approximated in floating point rapidly using the \textit{gamma} function. Default is False.

**Returns**

- **nf** [float or int or ndarray] Factorial of \( n \), as integer or float depending on \textit{exact}.

**Notes**

For arrays with \textit{exact=True}, the factorial is computed only once, for the largest input, with each other result computed in the process. The output dtype is increased to \texttt{int64} or \texttt{object} if necessary.

With \textit{exact=False} the factorial is approximated using the gamma function:

\[ n! = \Gamma(n + 1) \]

**Examples**

```python
>>> from scipy.special import factorial
>>> arr = np.array([3, 4, 5])
>>> factorial(arr, exact=False)
array([ 6., 24., 120.])
>>> factorial(arr, exact=True)
array([ 6, 24, 120])
>>> factorial(5, exact=True)
120L
```

### 6.15.17 scipy.misc.factorial2

\texttt{scipy.misc.factorial2(*args, **kwds)}

\textit{factorial2} is deprecated! Importing \textit{factorial2} from scipy.misc is deprecated in scipy 1.0.0. Use \texttt{scipy.special.factorial2} instead.

Double factorial.

This is the factorial with every second value skipped. E.g., \( 7!! = 7 \times 5 \times 3 \times 1 \). It can be approximated numerically as:

\[
\begin{align*}
n!! &= \text{special.gamma}(n/2+1) \times 2^{(m+1)/2} / \sqrt{\pi} & \text{n odd} \\
&= 2^{(n/2)} \times (n/2)! & \text{n even}
\end{align*}
\]

**Parameters**

- **n** [int or array_like]
  Calculate n!!. Arrays are only supported with \textit{exact} set to False. If \( n < 0 \), the return value is 0.
- **exact** [bool, optional] The result can be approximated rapidly using the gamma-formula above (default). If \textit{exact} is set to True, calculate the answer exactly using integer arithmetic.
Returns
nff [float or int] Double factorial of n, as an int or a float depending on exact.

Examples
>>> from scipy.special import factorial2
>>> factorial2(7, exact=False)
array(105.00000000000001)
>>> factorial2(7, exact=True)
105L

6.15.18 scipy.misc.factorialk

scipy.misc.factorialk(*args, **kwds)

factorialk is deprecated! Importing factorialk from scipy.misc is deprecated in scipy 1.0.0. Use scipy.special.factorialk instead.

Multifactorial of n of order k, n(!!...!).

This is the multifactorial of n skipping k values. For example,
factorialk(17, 4) = 17!!!! = 17 * 13 * 9 * 5 * 1
In particular, for any integer n, we have
factorialk(n, 1) = factorial(n)
factorialk(n, 2) = factorial2(n)

Parameters
n [int] Calculate multifactorial. If n < 0, the return value is 0.
k [int] Order of multifactorial.
exact [bool, optional] If exact is set to True, calculate the answer exactly using integer arithmetic.

Returns

Raises
NotImplementedError Raises when exact is False

Examples
>>> from scipy.special import factorialk
>>> factorialk(5, 1, exact=True)
120L
>>> factorialk(5, 3, exact=True)
10L

6.15.19 scipy.misc.logsumexp

scipy.misc.logsumexp(*args, **kwds)

logsumexp is deprecated! Importing logsumexp from scipy.misc is deprecated in scipy 1.0.0. Use scipy.special.logsumexp instead.

Compute the log of the sum of exponentials of input elements.
**Parameters**

- **a** [array_like]
  Input array.
- **axis** [None or int or tuple of ints, optional]
  Axis or axes over which the sum is taken. By default `axis` is None, and all elements are summed. New in version 0.11.0.
- **keepdims** [bool, optional]
  If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original array. New in version 0.15.0.
- **b** [array-like, optional]
  Scaling factor for `exp(a)` must be of the same shape as `a` or broadcastable to `a`. These values may be negative in order to implement subtraction. New in version 0.12.0.
- **return_sign** [bool, optional]
  If this is set to True, the result will be a pair containing sign information; if False, results that are negative will be returned as NaN. Default is False (no sign information). New in version 0.16.0.

**Returns**

- **res** [ndarray]
  The result, `np.log(np.sum(np.exp(a)))` calculated in a numerically more stable way. If `b` is given then `np.log(np.sum(b*np.exp(a)))` is returned.
- **sgn** [ndarray]
  If `return_sign` is True, this will be an array of floating-point numbers matching `res` and +1, 0, or -1 depending on the sign of the result. If False, only one result is returned.

**Notes**

Numpy has a `logaddexp` function which is very similar to `logsumexp`, but only handles two arguments. `logaddexp.reduce` is similar to this function, but may be less stable.

**Examples**

```python
>>> from scipy.special import logsumexp
>>> a = np.arange(10)
>>> np.log(np.sum(np.exp(a)))
9.4586297444267107
>>> logsumexp(a)
9.4586297444267107
```

With weights

```python
>>> a = np.arange(10)
>>> b = np.arange(10, 0, -1)
>>> logsumexp(a, b=b)
9.9170178533034665
>>> np.log(np.sum(b*np.exp(a)))
9.9170178533034647
```

Returning a sign flag

```python
Notice that \texttt{logsumexp} does not directly support masked arrays. To use it on a masked array, convert the mask into zero weights:

```python
>>> a = np.ma.array([np.log(2), 2, np.log(3)],
                  mask=[False, True, False])
>>> b = (~a.mask).astype(int)
>>> logsumexp(a.data, b=b), np.log(5)
(1.6094379124341005, 1.6094379124341005)
```

### 6.15.20 scipy.misc.pade

\texttt{scipy.misc.pade(*args, **kwds)}

\texttt{pade} is deprecated! Importing \texttt{pade} from scipy.misc is deprecated in scipy 1.0.0. Use \texttt{scipy.interpolate.pade} instead.

Return Pade approximation to a polynomial as the ratio of two polynomials.

**Parameters**

- \texttt{an} [[N,] array_like]
  Taylor series coefficients.
- \texttt{m} [int] The order of the returned approximating polynomial \(q\).
- \texttt{n} [int, optional] The order of the returned approximating polynomial \(p\).
  By default, the order is \texttt{len(an)}-\texttt{m}.

**Returns**

- \(p, q\) [Polynomial class] The Pade approximation of the polynomial defined by \(an\) is \(p(x)/q(x)\).

**Examples**

```python
>>> from scipy.interpolate import pade
>>> e_exp = [1.0, 1.0, 1.0/2.0, 1.0/6.0, 1.0/24.0, 1.0/120.0]
>>> p, q = pade(e_exp, 2)

>>> e_exp.reverse()
>>> e_poly = np.poly1d(e_exp)

Compare \(e_{\text{poly}}(x)\) and the Pade approximation \(p(x)/q(x)\)

```python
>>> e_poly(1)
2.7166666666666668

```python
>>> p(1)/q(1)
2.7179487179487181
```

### 6.15.21 scipy.misc.info

\texttt{scipy.misc.info(*args, **kwds)}

Get help information for a function, class, or module.
Parameters

object [object or str, optional] Input object or name to get information about. If object is a numpy object, its docstring is given. If it is a string, available modules are searched for matching objects. If None, information about info itself is returned.

maxwidth [int, optional] Printing width.

output [file like object, optional] File like object that the output is written to, default is stdout. The object has to be opened in ‘w’ or ‘a’ mode.

toplevel [str, optional] Start search at this level.

See also:

source, lookfor

Notes

When used interactively with an object, np.info(obj) is equivalent to help(obj) on the Python prompt or obj? on the IPython prompt.

Examples

```python
>>> np.info(np.polyval)

polyval(p, x)
    Evaluate the polynomial p at x.
...
```

When using a string for object it is possible to get multiple results.

```python
>>> np.info('fft')

*** Found in numpy ***
Core FFT routines
...
*** Found in numpy.fft ***
fft(a, n=None, axis=-1)
...
*** Repeat reference found in numpy.fft.fftpack ***
*** Total of 3 references found. ***
```

6.15.22 scipy.misc.source

scipy.misc.source(*args, **kwds)

source is deprecated! Importing source from scipy.misc is deprecated in scipy 1.0.0. Use numpy.source instead.

Print or write to a file the source code for a NumPy object.

The source code is only returned for objects written in Python. Many functions and classes are defined in C and will therefore not return useful information.

Parameters

object [numpy object] Input object. This can be any object (function, class, module, ...).

output [file object, optional] If output not supplied then source code is printed to screen (sys.stdout). File object must be created with either write ‘w’ or append ‘a’ modes.
**Examples**

```python
>>> np.source(np.interp)
In file: /usr/lib/python2.6/dist-packages/numpy/lib/function_base.py
def interp(x, xp, fp, left=None, right=None):
    """... (full docstring printed)""
    if isinstance(x, (float, int, number)):
        return compiled_interp([x], xp, fp, left, right).item()
    else:
        return compiled_interp(x, xp, fp, left, right)
```

The source code is only returned for objects written in Python.

```python
>>> np.source(np.array)
Not available for this object.
```

### 6.15.23 scipy.misc.who

```python
scipy.misc.who(*args, **kwds)

who is deprecated! Importing who from scipy.misc is deprecated in scipy 1.0.0. Use numpy.who instead.

Print the NumPy arrays in the given dictionary. If there is no dictionary passed in or vardict is None then returns NumPy arrays in the globals() dictionary (all NumPy arrays in the namespace).

**Parameters**

- **vardict** [dict, optional] A dictionary possibly containing ndarrays. Default is globals().

**Returns**

- **out** [None] Returns ‘None’.

**Notes**

Prints out the name, shape, bytes and type of all of the ndarrays present in vardict.

**Examples**

```python
>>> a = np.arange(10)
>>> b = np.ones(20)
>>> np.who()
Name Shape Bytes Type
-------------------------------
a 10 40 int32
b 20 160 float64
Upper bound on total bytes = 200
```

```python
>>> d = {'x': np.arange(2.0), 'y': np.arange(3.0), 'txt': 'Some str',
... 'idx':5}
>>> np.who(d)
Name Shape Bytes Type
-------------------------------
y 3 24 float64
x 2 16 float64
Upper bound on total bytes = 40
```
### 6.16 Multi-dimensional image processing (scipy.ndimage)

This package contains various functions for multi-dimensional image processing.

#### 6.16.1 Filters

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**scipy.ndimage.convolve**

`scipy.ndimage.convolve(input, weights, output=None, mode='reflect', cval=0.0, origin=0)`  
Multidimensional convolution.

The array is convolved with the given kernel.

**Parameters**

- `input` [array_like] The input array.
- `weights` [array_like] Array of weights, same number of dimensions as input.
output  [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode  [str or sequence, optional] The mode parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is 'reflect'. The valid values and their behavior is as follows:

- 'reflect' (d c b a / a b c d / d c b a)
  The input is extended by reflecting about the edge of the last pixel.

- 'constant' (k k k k / a b c d / k k k k)
  The input is extended by filling all values beyond the edge with the same constant value, defined by the cval parameter.

- 'nearest' (a a a a / a b c d / d d d d)
  The input is extended by replicating the last pixel.

- 'mirror' (d c b / a b c d / c b a)
  The input is extended by reflecting about the center of the last pixel.

- 'wrap' (a b c d / a b c d / a b c d)
  The input is extended by wrapping around to the opposite edge.

cval  [scalar, optional] Value to fill past edges of input if mode is 'constant'. Default is 0.0

origin  [int or sequence, optional] Controls the placement of the filter on the input array’s pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right. By passing a sequence of origins with length equal to the number of dimensions of the input array, different shifts can be specified along each axis.

Returns

result  [ndarray] The result of convolution of input with weights.

See also:

correlate

Correlate an image with a kernel.

Notes

Each value in result is \( C_k = \sum_j I_{i+k-j} W_j \), where \( W \) is the weights kernel, \( j \) is the n-D spatial index over \( W \), \( I \) is the input and \( k \) is the coordinate of the center of \( W \), specified by origin in the input parameters.

Examples

Perhaps the simplest case to understand is mode='constant', cval=0.0, because in this case borders (i.e. where the weights kernel, centered on any one value, extends beyond an edge of input) are treated as zeros.

```python
>>> a = np.array([[1, 2, 0, 0],
...               [5, 3, 0, 4],
...               [0, 0, 0, 7],
...               [9, 3, 0, 0]])
>>> k = np.array([[1,1,1],[1,0,0],[1,0,0]])
>>> from scipy import ndimage
>>> ndimage.convolve(a, k, mode='constant', cval=0.0)
array([[11, 10,  7,  4],
       [10,  3, 11, 11]])
```

(continues on next page)
Setting `cval=1.0` is equivalent to padding the outer edge of `input` with 1.0’s (and then extracting only the original region of the result).

```python
>>> ndimage.convolve(a, k, mode='constant', cval=1.0)
array([[13, 11, 8, 7],
       [11, 3, 11, 14],
       [16, 12, 14, 10],
       [15, 6, 10, 5]],
      dtype=int)
```

With `mode='reflect'` (the default), outer values are reflected at the edge of `input` to fill in missing values.

```python
>>> b = np.array([[2, 0, 0],
                 ... [1, 0, 0],
                 ... [0, 0, 0]])
>>> k = np.array([[0,1,0], [0,1,0], [0,1,0]])
>>> ndimage.convolve(b, k, mode='reflect')
array([[5, 0, 1],
       [3, 0, 0],
       [1, 0, 0]],
      dtype=int)
```

This includes diagonally at the corners.

```python
>>> k = np.array([[1,0,0],[0,1,0],[0,0,1]])
>>> ndimage.convolve(b, k)
array([[4, 2, 0],
       [3, 2, 0],
       [1, 1, 0]],
      dtype=int)
```

With `mode='nearest'`, the single nearest value in to an edge in `input` is repeated as many times as needed to match the overlapping `weights`.

```python
>>> c = np.array([[2, 0, 1],
                 ... [1, 0, 0],
                 ... [0, 0, 0]])
>>> k = np.array([[0, 1, 0],
                 ... [0, 1, 0],
                 ... [0, 1, 0],
                 ... [0, 1, 0]])
>>> ndimage.convolve(c, k, mode='nearest')
array([[7, 0, 3],
       [5, 0, 2],
       [3, 0, 1]],
      dtype=int)
```

**scipy.ndimage.convolve1d**

`scipy.ndimage.convolve1d(input, weights, axis=-1, output=None, mode='reflect', cval=0.0, origin=0)`

Calculate a one-dimensional convolution along the given axis.
The lines of the array along the given axis are convolved with the given weights.

**Parameters**

- **input** [array_like] The input array.
- **weights** [ndarray] One-dimensional sequence of numbers.
- **axis** [int, optional] The axis of `input` along which to calculate. Default is -1.
- **output** [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
- **mode** [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The `mode` parameter determines how the input array is extended beyond its boundaries. Default is ‘reflect’. Behavior for each valid value is as follows:
  - ‘reflect’ ([d c b a / a b c d / d c b a])
    The input is extended by reflecting about the edge of the last pixel.
  - ‘constant’ ([k k k k / a b c d / k k k k])
    The input is extended by filling all values beyond the edge with the same constant value, defined by the `cval` parameter.
  - ‘nearest’ ([a a a a / a b c d / d d d d])
    The input is extended by replicating the last pixel.
  - ‘mirror’ ([d c b / a b c d / c b a])
    The input is extended by reflecting about the center of the last pixel.
  - ‘wrap’ ([a b c d / a b c d / a b c d])
    The input is extended by wrapping around to the opposite edge.
- **cval** [scalar, optional] Value to fill past edges of input if `mode` is ‘constant’. Default is 0.0.
- **origin** [int, optional] Controls the placement of the filter on the input array’s pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right.

**Returns**

- **convolve1d** [ndarray] Convolved array with same shape as input

**Examples**

```python
>>> from scipy.ndimage import convolve1d
>>> convolve1d([[2, 8, 0, 4, 1, 9, 9, 0], weights=[1, 3])
array([[14, 24,  4, 13, 12, 36, 27,  0]])
```

**scipy.ndimage.correlate**

**scipy.ndimage.correlate**(input, weights, output=None, mode='reflect', cval=0.0, origin=0)

Multi-dimensional correlation.

The array is correlated with the given kernel.

**Parameters**

- **input** [array_like] The input array.
- **weights** [ndarray] array of weights, same number of dimensions as input
- **output** [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
- **mode** [str or sequence, optional] The `mode` parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is ‘reflect’. The valid values and their behavior is as follows:
‘reflect’ (d c b a / a b c d / d c b a)
   The input is extended by reflecting about the edge of the last pixel.
‘constant’ (k k k k / a b c d / k k k k)
   The input is extended by filling all values beyond the edge with the
   same constant value, defined by the cval parameter.
‘nearest’ (a a a a / a b c d / d d d d)
   The input is extended by replicating the last pixel.
‘mirror’ (d c b | a b c d | c b a)
   The input is extended by reflecting about the center of the last pixel.
‘wrap’ (a b c d / a b c d / a b c d)
   The input is extended by wrapping around to the opposite edge.

cval [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is
   0.0.
origin [int or sequence, optional] Controls the placement of the filter on the input array’s
   pixels. A value of 0 (the default) centers the filter over the pixel, with positive
   values shifting the filter to the left, and negative ones to the right. By passing
   a sequence of origins with length equal to the number of dimensions of the input
   array, different shifts can be specified along each axis.

See also:

convolve

Convolve an image with a kernel.

scipy.ndimage.correlate1d

scipy.ndimage.correlate1d(input, weights, axis=-1, output=None, mode='reflect', cval=0.0, origin=0)

Calculate a one-dimensional correlation along the given axis.

The lines of the array along the given axis are correlated with the given weights.

Parameters

input [array_like] The input array.
weights [array] One-dimensional sequence of numbers.
axis [int, optional] The axis of input along which to calculate. Default is -1.
output [array or dtype, optional] The array in which to place the output, or the dtype of
   the returned array. By default an array of the same dtype as input will be created.
determines how the input array is extended beyond its boundaries. Default is
   ‘reflect’. Behavior for each valid value is as follows:
   ‘reflect’ (d c b a / a b c d / d c b a)
      The input is extended by reflecting about the edge of the last pixel.
   ‘constant’ (k k k k / a b c d / k k k k)
      The input is extended by filling all values beyond the edge with the
      same constant value, defined by the cval parameter.
   ‘nearest’ (a a a a / a b c d / d d d d)
      The input is extended by replicating the last pixel.
   ‘mirror’ (d c b / a b c d / c b a)
      The input is extended by reflecting about the center of the last pixel.
   ‘wrap’ (a b c d / a b c d / a b c d)
      The input is extended by wrapping around to the opposite edge.
cval [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is
   0.0.
origin [int, optional] Controls the placement of the filter on the input array’s pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right.

Examples

```python
>>> from scipy.ndimage import correlate1d
>>> correlate1d([2, 8, 0, 4, 1, 9, 9], weights=[1, 3])
array([ 8, 26, 8, 12, 7, 28, 36, 9])
```

scipy.ndimage.gaussian_filter

`scipy.ndimage.gaussian_filter(input, sigma, order=0, output=None, mode='reflect', cval=0.0, truncate=4.0)`

Multidimensional Gaussian filter.

**Parameters**

- `input` [array_like] The input array.
- `sigma` [scalar or sequence of scalars] Standard deviation for Gaussian kernel. The standard deviations of the Gaussian filter are given for each axis as a sequence, or as a single number, in which case it is equal for all axes.
- `order` [int or sequence of ints, optional] The order of the filter along each axis is given as a sequence of integers, or as a single number. An order of 0 corresponds to convolution with a Gaussian kernel. A positive order corresponds to convolution with that derivative of a Gaussian.
- `output` [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
- `mode` [str or sequence, optional] The `mode` parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is ‘reflect’. The valid values and their behavior is as follows:
  - ‘reflect’ (d c b a / a b c d / d c b a)
    The input is extended by reflecting about the edge of the last pixel.
  - ‘constant’ (k k k k / a b c d / k k k k)
    The input is extended by filling all values beyond the edge with the same constant value, defined by the `cval` parameter.
  - ‘nearest’ (a a a a / a b c d / d d d d)
    The input is extended by replicating the last pixel.
  - ‘mirror’ (d c b / a b c d / c b a)
    The input is extended by reflecting about the center of the last pixel.
  - ‘wrap’ (a b c d / a b c d / a b c d)
    The input is extended by wrapping around to the opposite edge.
- `cval` [scalar, optional] Value to fill past edges of input if `mode` is ‘constant’. Default is 0.0.
- `truncate` [float] Truncate the filter at this many standard deviations. Default is 4.0.

**Returns**

`gaussian_filter` [ndarray] Returned array of same shape as `input`.

**Notes**

The multidimensional filter is implemented as a sequence of one-dimensional convolution filters. The intermediate arrays are stored in the same data type as the output. Therefore, for output types with a limited precision, the results may be imprecise because intermediate results may be stored with insufficient precision.
Examples

```python
>>> from scipy.ndimage import gaussian_filter
>>> a = np.arange(50, step=2).reshape((5,5))
>>> a
array([[ 0,  2,  4,  6,  8],
       [10, 12, 14, 16, 18],
       [20, 22, 24, 26, 28],
       [30, 32, 34, 36, 38],
       [40, 42, 44, 46, 48]])
>>> gaussian_filter(a, sigma=1)
array([[ 4,  6,  8,  9, 11],
       [10, 12, 14, 15, 17],
       [20, 22, 24, 25, 27],
       [29, 31, 33, 34, 36],
       [35, 37, 39, 40, 42]])
```

```python
>>> from scipy import misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.gray() # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121) # left side
>>> ax2 = fig.add_subplot(122) # right side
>>> ascent = misc.ascent()
>>> result = gaussian_filter(ascent, sigma=5)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```

`scipy.ndimage.gaussian_filter1d`

`scipy.ndimage.gaussian_filter1d(input, sigma, axis=-1, order=0, output=None, mode='reflect', cval=0.0, truncate=4.0)`

One-dimensional Gaussian filter.

**Parameters**
input  [array_like] The input array.
sigma  [scalar] standard deviation for Gaussian kernel
axis  [int, optional] The axis of input along which to calculate. Default is -1.
order  [int, optional] An order of 0 corresponds to convolution with a Gaussian kernel. A positive order corresponds to convolution with that derivative of a Gaussian.
output  [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
mode  [('reflect', 'constant', 'nearest', 'mirror', 'wrap'), optional] The mode parameter determines how the input array is extended beyond its boundaries. Default is 'reflect'. Behavior for each valid value is as follows:
    'reflect' (d c b a / a b c d / d c b a)
        The input is extended by reflecting about the edge of the last pixel.
    'constant' (k k k k / a b c d / k k k k)
        The input is extended by filling all values beyond the edge with the same constant value, defined by the cval parameter.
    'nearest' (a a a a / a b c d / d d d d)
        The input is extended by replicating the last pixel.
    'mirror' (d c b / a b c d / c b a)
        The input is extended by reflecting about the center of the last pixel.
    'wrap' (a b c d / a b c d / a b c d)
        The input is extended by wrapping around to the opposite edge.
cval  [scalar, optional] Value to fill past edges of input if mode is 'constant'. Default is 0.0.
truncate  [float, optional] Truncate the filter at this many standard deviations. Default is 4.0.

Returns

    gaussian_filter1d  [ndarray]

Examples

```python
>>> from scipy.ndimage import gaussian_filter1d
>>> gaussian_filter1d([1.0, 2.0, 3.0, 4.0, 5.0], 1)
array([1.42704095, 2.06782203, 3. , 3.93217797, 4.57295905])
```

```
>>> gaussian_filter1d([[1.0, 2.0, 3.0, 4.0, 5.0], 1])
array([1.42704095, 2.06782203, 3. , 3.93217797, 4.57295905])
```

```
>>> import matplotlib.pyplot as plt
>>> np.random.seed(280490)
>>> x = np.random.randn(101).cumsum()
>>> y3 = gaussian_filter1d(x, 3)
>>> y6 = gaussian_filter1d(x, 6)
>>> plt.plot(x, 'k', label='original data')
>>> plt.plot(y3, '--', label='filtered, sigma=3')
>>> plt.plot(y6, ':', label='filtered, sigma=6')
>>> plt.legend()
>>> plt.grid()
>>> plt.show()
```
input    [array_like] The input array.
sigma    [scalar or sequence of scalars] The standard deviations of the Gaussian filter are
given for each axis as a sequence, or as a single number, in which case it is equal
for all axes..
output   [array or dtype, optional] The array in which to place the output, or the dtype of
the returned array. By default an array of the same dtype as input will be created.
mode     [str or sequence, optional] The mode parameter determines how the input array is
extended when the filter overlaps a border. By passing a sequence of modes with
length equal to the number of dimensions of the input array, different modes can
be specified along each axis. Default value is ‘reflect’. The valid values and their
behavior is as follows:
   ‘reflect’ (d c b a / a b c d / d c b a)
The input is extended by reflecting about the edge of the last pixel.
   ‘constant’ (k k k k / a b c d / k k k k)
The input is extended by filling all values beyond the edge with the
same constant value, defined by the cval parameter.
   ‘nearest’ (a a a a / a b c d / d d d d)
The input is extended by replicating the last pixel.
   ‘mirror’ (d c b / a b c d / c b a)
The input is extended by reflecting about the center of the last pixel.
   ‘wrap’ (a b c d / a b c d / a b c d)
The input is extended by wrapping around to the opposite edge.
cval     [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is
0.0.

Extra keyword arguments will be passed to gaussian_filter().

Returns

    gaussian_gradient_magnitude

[ndarray] Filtered array. Has the same shape as input.

Examples

```python
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
```
```python
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = ndimage.gaussian_gradient_magnitude(ascent, sigma=5)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```

`scipy.ndimage.gaussian_laplace`

`scipy.ndimage.gaussian_laplace(input, sigma, output=None, mode='reflect', cval=0.0, **kwargs)`

Multidimensional Laplace filter using gaussian second derivatives.

**Parameters**

- `input` [array_like] The input array.
- `sigma` [scalar or sequence of scalars] The standard deviations of the Gaussian filter are given for each axis as a sequence, or as a single number, in which case it is equal for all axes.
- `output` [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
- `mode` [str or sequence, optional] The mode parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is 'reflect'. The valid values and their behavior is as follows:
  - 'reflect' (d c b a / a b c d / d c b a)
    The input is extended by reflecting about the edge of the last pixel.
  - 'constant' (k k k k / a b c d / k k k k)
    The input is extended by filling all values beyond the edge with the same constant value, defined by the cval parameter.
  - 'nearest' (a a a a / a b c d / d d d d)
    The input is extended by replicating the last pixel.
'mirror' \((d \ c \ b \ a \ b \ c \ d \ c \ b\ a)\)
   The input is extended by reflecting about the center of the last pixel.
'wrap' \((a \ b \ c \ d \ a \ b \ c \ d \ a \ b \ c \ d)\)
   The input is extended by wrapping around to the opposite edge.

cval [scalar, optional] Value to fill past edges of input if mode is 'constant'. Default is 0.0.

Extra keyword arguments will be passed to gaussian_filter().

Examples

```python
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> ascent = misc.ascent()

>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side

>>> result = ndimage.gaussian_laplace(ascent, sigma=1)
>>> ax1.imshow(result)

>>> result = ndimage.gaussian_laplace(ascent, sigma=3)
>>> ax2.imshow(result)

>>> plt.show()
```

scipy.ndimage.generic_filter

`scipy.ndimage.generic_filter(input, function, size=None, footprint=None, output=None, mode='reflect', cval=0.0, origin=0, extra_arguments=(), extra_keywords=None)`

Calculate a multi-dimensional filter using the given function.

At each element the provided function is called. The input values within the filter footprint at that element are passed to the function as a 1D array of double values.
**Parameters**

- **input** [array_like] The input array.
- **function** [{callable, scipy.LowLevelCallable}] Function to apply at each element.
- **size** [scalar or tuple, optional] See footprint, below. Ignored if footprint is given.
- **footprint** [array, optional] Either size or footprint must be defined. size gives the shape that is taken from the input array, at every element position, to define the input to the filter function. footprint is a boolean array that specifies (implicitly) a shape, but also which of the elements within this shape will get passed to the filter function. Thus size=(n,m) is equivalent to footprint=np.ones((n,m)). We adjust size to the number of dimensions of the input array, so that, if the input array is shape (10,10,10), and size is 2, then the actual size used is (2,2,2). When footprint is given, size is ignored.
- **output** [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
- **mode** [str or sequence, optional] The mode parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is ‘reflect’. The valid values and their behavior is as follows:
  - ‘reflect’ (d c b a / a b c d / d c b a)
    The input is extended by reflecting about the edge of the last pixel.
  - ‘constant’ (k k k k / a b c d / k k k k)
    The input is extended by filling all values beyond the edge with the same constant value, defined by the cval parameter.
  - ‘nearest’ (a a a a / a b c d / d d d d)
    The input is extended by replicating the last pixel.
  - ‘mirror’ (d c b / a b c d / c b a)
    The input is extended by reflecting about the center of the last pixel.
  - ‘wrap’ (a b c d / a b c d / a b c d)
    The input is extended by wrapping around to the opposite edge.
- **cval** [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is 0.0.
- **origin** [int or sequence, optional] Controls the placement of the filter on the input array’s pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right. By passing a sequence of origins with length equal to the number of dimensions of the input array, different shifts can be specified along each axis.
- **extra_arguments** [sequence, optional] Sequence of extra positional arguments to pass to passed function.
- **extra_keywords** [dict, optional] dict of extra keyword arguments to pass to passed function.

**Notes**

This function also accepts low-level callback functions with one of the following signatures and wrapped in scipy.LowLevelCallable:

```c
int callback(double *buffer, npy_intp filter_size,
              double *return_value, void *user_data)
int callback(double *buffer, intptr_t filter_size,
              double *return_value, void *user_data)
```

The calling function iterates over the elements of the input and output arrays, calling the callback function at each element. The elements within the footprint of the filter at the current element
are passed through the `buffer` parameter, and the number of elements within the footprint through `filter_size`. The calculated value is returned in `return_value`. `user_data` is the data pointer provided to `scipy.LowLevelCallable` as-is.

The callback function must return an integer error status that is zero if something went wrong and one otherwise. If an error occurs, you should normally set the python error status with an informative message before returning, otherwise a default error message is set by the calling function.

In addition, some other low-level function pointer specifications are accepted, but these are for backward compatibility only and should not be used in new code.

**`scipy.ndimage.generic_filter1d`**

```
scipy.ndimage.generic_filter1d(input, function, filter_size, axis=-1, output=None,  
    mode='reflect', cval=0.0, origin=0, extra_arguments=(),  
    extra_keywords=None)
```

Calculate a one-dimensional filter along the given axis.

generic_filter1d iterates over the lines of the array, calling the given function at each line. The arguments of the line are the input line, and the output line. The input and output lines are 1D double arrays. The input line is extended appropriately according to the filter size and origin. The output line must be modified in-place with the result.

**Parameters**

- `input` [array_like] The input array.
- `function` [{callable, scipy.LowLevelCallable}] Function to apply along given axis.
- `filter_size` [scalar] Length of the filter.
- `axis` [int, optional] The axis of `input` along which to calculate. Default is -1.
- `output` [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
- `mode` [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The `mode` parameter determines how the input array is extended beyond its boundaries. Default is `reflect`. Behavior for each valid value is as follows:
  - **reflect** (`d c b a | a b c d | d c b a`)  
    The input is extended by reflecting about the edge of the last pixel.
  - **constant** (`k k k k | a b c d | k k k k`)  
    The input is extended by filling all values beyond the edge with the same constant value, defined by the `cval` parameter.
  - **nearest** (`a a a a | a b c d | d d d d`)  
    The input is extended by replicating the last pixel.
  - **mirror** (`d c b | a b c d | c b a`)  
    The input is extended by reflecting about the center of the last pixel.
  - **wrap** (`a b c d | a b c d | a b c d`)  
    The input is extended by wrapping around to the opposite edge.
- `cval` [scalar, optional] Value to fill past edges of input if `mode` is `constant`. Default is 0.0.
- `origin` [int, optional] Controls the placement of the filter on the input array’s pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right.
- `extra_arguments` [sequence, optional] Sequence of extra positional arguments to pass to passed function.
- `extra_keywords` [dict, optional] dict of extra keyword arguments to pass to passed function.
Notes
This function also accepts low-level callback functions with one of the following signatures and wrapped in `scipy.LowLevelCallable`:

```python
int function(double *input_line, npy_intp input_length, double *output_line, npy_intp output_length, void *user_data)
int function(double *input_line, intptr_t input_length, double *output_line, intptr_t output_length, void *user_data)
```

The calling function iterates over the lines of the input and output arrays, calling the callback function at each line. The current line is extended according to the border conditions set by the calling function, and the result is copied into the array that is passed through `input_line`. The length of the input line (after extension) is passed through `input_length`. The callback function should apply the filter and store the result in the array passed through `output_line`. The length of the output line is passed through `output_length`. `user_data` is the data pointer provided to `scipy.LowLevelCallable` as-is.

The callback function must return an integer error status that is zero if something went wrong and one otherwise. If an error occurs, you should normally set the python error status with an informative message before returning, otherwise a default error message is set by the calling function.

In addition, some other low-level function pointer specifications are accepted, but these are for backward compatibility only and should not be used in new code.

`scipy.ndimage.generic_gradient_magnitude`

`scipy.ndimage.generic_gradient_magnitude(input, derivative, output=None, mode='reflect', cval=0.0, extra_arguments=(), extra_keywords=None)`

Gradient magnitude using a provided gradient function.

**Parameters**

- `input` [array_like] The input array.
- `derivative` [callable] Callable with the following signature:
  ```python
derivative(input, axis, output, mode, cval, *extra_arguments, **extra_keywords)
  ```
  See `extra_arguments`, `extra_keywords` below. `derivative` can assume that `input` and `output` are ndarrays. Note that the output from `derivative` is modified inplace; be careful to copy important inputs before returning them.
- `output` [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
- `mode` [str or sequence, optional] The `mode` parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is ‘reflect’. The valid values and their behavior is as follows:
  - ‘reflect’ (*d c b a / a b c d / d c b a*)
    The input is extended by reflecting about the edge of the last pixel.
  - ‘constant’ (*k k k k / a b c d / k k k k*)
    The input is extended by filling all values beyond the edge with the same constant value, defined by the `cval` parameter.
The input is extended by replicating the last pixel.

‘mirror’ (d c b / a b c d / c b a)

The input is extended by reflecting about the center of the last pixel.

‘wrap’ (a b c d / a b c d / a b c d)

The input is extended by wrapping around to the opposite edge.

cval [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is 0.0.

extra_keywords [dict, optional] dict of extra keyword arguments to pass to passed function.

extra_arguments [sequence, optional] Sequence of extra positional arguments to pass to passed function.

scipy.ndimage.generic_laplace

scipy.ndimage.generic_laplace(input, derivative2, output=None, mode=‘reflect’, cval=0.0, extra_arguments=(), extra_keywords=None)

N-dimensional Laplace filter using a provided second derivative function.

Parameters

input [array_like] The input array.

derivative2 [callable] Callable with the following signature:

derivative2(input, axis, output, mode, cval, *extra_arguments, **extra_keywords)

See extra_arguments, extra_keywords below.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [str or sequence, optional] The mode parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is ‘reflect’. The valid values and their behavior is as follows:

‘reflect’ (d c b a / a b c d / d c b a)

The input is extended by reflecting about the edge of the last pixel.

‘constant’ (k k k k / a b c d / k k k k)

The input is extended by filling all values beyond the edge with the same constant value, defined by the cval parameter.

‘nearest’ (a a a a / a b c d / d d d d)

The input is extended by replicating the last pixel.

‘mirror’ (d c b / a b c d / c b a)

The input is extended by reflecting about the center of the last pixel.

‘wrap’ (a b c d / a b c d / a b c d)

The input is extended by wrapping around to the opposite edge.

cval [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is 0.0.

extra_keywords [dict, optional] dict of extra keyword arguments to pass to passed function.

extra_arguments [sequence, optional] Sequence of extra positional arguments to pass to passed function.
scipy.ndimage.laplace

scipy.ndimage.laplace(input, output=None, mode='reflect', cval=0.0)
N-dimensional Laplace filter based on approximate second derivatives.

Parameters

input [array_like] The input array.
output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
mode [str or sequence, optional] The mode parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is ‘reflect’. The valid values and their behavior is as follows:
‘reflect’ (d c b a / a b c d / d c b a)
The input is extended by reflecting about the edge of the last pixel.
‘constant’ (k k k k / a b c d / k k k k)
The input is extended by filling all values beyond the edge with the same constant value, defined by the cval parameter.
‘nearest’ (a a a a / a b c d / d d d d)
The input is extended by replicating the last pixel.
‘mirror’ (d c b a / a b c d / c b a)
The input is extended by reflecting about the center of the last pixel.
‘wrap’ (a b c d / a b c d / a b c d)
The input is extended by wrapping around to the opposite edge.
cval [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is 0.0.

Examples

```python
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = ndimage.laplace(ascent)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```

scipy.ndimage.maximum_filter

scipy.ndimage.maximum_filter(input, size=None, footprint=None, output=None, mode='reflect', cval=0.0, origin=0)
Calculate a multi-dimensional maximum filter.

Parameters

input [array_like] The input array.
size [scalar or tuple, optional] See footprint, below. Ignored if footprint is given.
footprint [array, optional] Either size or footprint must be defined. size gives the shape that is taken from the input array, at every element position, to define the input to the filter function. footprint is a boolean array that specifies (implicitly) a shape, but also which of the elements within this shape will get passed to the filter function. Thus size=(n,m) is equivalent to footprint=np.ones((n,m)). We adjust size to
the number of dimensions of the input array, so that, if the input array is shape
(10,10,10), and size is 2, then the actual size used is (2,2,2). When footprint is
given, size is ignored.

output [array or dtype, optional] The array in which to place the output, or the dtype of
the returned array. By default an array of the same dtype as input will be created.

mode [str or sequence, optional] The mode parameter determines how the input array is
extended when the filter overlaps a border. By passing a sequence of modes with
length equal to the number of dimensions of the input array, different modes can
be specified along each axis. Default value is ‘reflect’. The valid values and their
behavior is as follows:

‘reflect’ (d c b a / a b c d / d c b a)
  The input is extended by reflecting about the edge of the last pixel.

‘constant’ (k k k k / a b c d / k k k k)
  The input is extended by filling all values beyond the edge with the
  same constant value, defined by the cval parameter.

‘nearest’ (a a a a / a b c d / d d d d)
  The input is extended by replicating the last pixel.

‘mirror’ (d c b / a b c d / c b a)
  The input is extended by reflecting about the center of the last pixel.

‘wrap’ (a b c d / a b c d / a b c d)
  The input is extended by wrapping around to the opposite edge.

cval [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is
0.0.

origin [int or sequence, optional] Controls the placement of the filter on the input array’s
pixels. A value of 0 (the default) centers the filter over the pixel, with positive
values shifting the filter to the left, and negative ones to the right. By passing
a sequence of origins with length equal to the number of dimensions of the input
array, different shifts can be specified along each axis.

Returns

maximum_filter [ndarray] Filtered array. Has the same shape as input.
Examples

```python
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = ndimage.maximum_filter(ascent, size=20)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```

scipy.ndimage.maximum_filter1d

**scipy.ndimage.maximum_filter1d**(`input`, `size=-1`, `output=None`, `mode=’reflect’`, `cval=0.0`, `origin=0``)

Calculate a one-dimensional maximum filter along the given axis.

The lines of the array along the given axis are filtered with a maximum filter of given size.

**Parameters**

- `input` [array_like] The input array.
- `size` [int] Length along which to calculate the 1-D maximum.
- `axis` [int, optional] The axis of `input` along which to calculate. Default is -1.
- `output` [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
- `mode` [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The `mode` parameter determines how the input array is extended beyond its boundaries. Default is 'reflect'. Behavior for each valid value is as follows:
  - **‘reflect’** (`d c b a | a b c d | d c b a `)
    The input is extended by reflecting about the edge of the last pixel.
  - **‘constant’** (`k k k k / a b c d / k k k k``)
    The input is extended by filling all values beyond the edge with the same constant value, defined by the `cval` parameter.
`'nearest' (a a a a / a b c d / d d d d)``
The input is extended by replicating the last pixel.

`'mirror' (d c b / a b c d / c b a)``
The input is extended by reflecting about the center of the last pixel.

`'wrap' (a b c d / a b c d / a b c d)``
The input is extended by wrapping around to the opposite edge.

cval [scalar, optional] Value to fill past edges of input if `mode` is ‘constant’. Default is 0.0.

origin [int, optional] Controls the placement of the filter on the input array’s pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right.

**Returns**

`maximum1d` [ndarray, None] Maximum-filtered array with same shape as input. None if `output` is not None.

**Notes**

This function implements the MAXLIST algorithm [1], as described by Richard Harter [2], and has a guaranteed O(n) performance, n being the `input` length, regardless of filter size.

**References**

[1], [2]

**Examples**

```python
>>> from scipy.ndimage import maximum_filter1d
>>> maximum_filter1d([2, 8, 0, 4, 1, 9, 9, 0], size=3)
array([8, 8, 8, 4, 9, 9, 9, 9])
```

```
scipy.ndimage.median_filter
```

Calculate a multidimensional median filter.

**Parameters**

input [array_like] The input array.

size [scalar or tuple, optional] See footprint, below. Ignored if footprint is given.

footprint [array, optional] Either `size` or `footprint` must be defined. `size` gives the shape that is taken from the input array, at every element position, to define the input to the filter function. `footprint` is a boolean array that specifies (implicitly) a shape, but also which of the elements within this shape will get passed to the filter function. Thus `size=(n,m)` is equivalent to `footprint=np.ones((n,m))`. We adjust `size` to the number of dimensions of the input array, so that, if the input array is shape (10,10,10), and `size` is 2, then the actual size used is (2,2,2). When `footprint` is given, `size` is ignored.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [str or sequence, optional] The `mode` parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is ‘reflect’. The valid values and their behavior is as follows:

`'reflect' (d c b a / a b c d / d c b a)``
The input is extended by reflecting about the edge of the last pixel.
The input is extended by filling all values beyond the edge with the same constant value, defined by the cval parameter.

The input is extended by replicating the last pixel.

The input is extended by reflecting about the center of the last pixel.

The input is extended by wrapping around to the opposite edge.

cval [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is 0.0.

origin [int or sequence, optional] Controls the placement of the filter on the input array’s pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right. By passing a sequence of origins with length equal to the number of dimensions of the input array, different shifts can be specified along each axis.

Returns

median_filter [ndarray] Filtered array. Has the same shape as input.

Examples

```
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = ndimage.median_filter(ascent, size=20)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```
scipy.ndimage.minimum_filter

scipy.ndimage.minimum_filter(input, size=None, footprint=None, output=None, mode='reflect', cval=0.0, origin=0)

Calculate a multi-dimensional minimum filter.

Parameters

- **input** [array_like] The input array.
- **size** [scalar or tuple, optional] See footprint, below. Ignored if footprint is given.
- **footprint** [array, optional] Either size or footprint must be defined. size gives the shape that is taken from the input array, at every element position, to define the input to the filter function. footprint is a boolean array that specifies (implicitly) a shape, but also which of the elements within this shape will get passed to the filter function. Thus size=(n,m) is equivalent to footprint=np.ones((n,m)). We adjust size to the number of dimensions of the input array, so that, if the input array is shape (10,10,10), and size is 2, then the actual size used is (2,2,2). When footprint is given, size is ignored.
- **output** [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
- **mode** [str or sequence, optional] The mode parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is ‘reflect’. The valid values and their behavior is as follows:
  - ‘reflect’ (d c b a / a b c d / d c b a)
    The input is extended by reflecting about the edge of the last pixel.
  - ‘constant’ (k k k k / a b c d / k k k k)
    The input is extended by filling all values beyond the edge with the same constant value, defined by the cval parameter.
  - ‘nearest’ (a a a a / a b c d / d d d d)
    The input is extended by replicating the last pixel.
  - ‘mirror’ (d c b / a b c d / c b a)
    The input is extended by reflecting about the center of the last pixel.
  - ‘wrap’ (a b c d / a b c d / a b c d)
    The input is extended by wrapping around to the opposite edge.
- **cval** [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is 0.0.
- **origin** [int or sequence, optional] Controls the placement of the filter on the input array’s pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right. By passing a sequence of origins with length equal to the number of dimensions of the input array, different shifts can be specified along each axis.

Returns

minimum_filter [ndarray] Filtered array. Has the same shape as input.

Examples

```python
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
```
```python
>>> ascent = misc.ascent()
>>> result = ndimage.minimum_filter(ascent, size=20)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```

**scipy.ndimage.minimum_filter1d**

`scipy.ndimage.minimum_filter1d(input, size=-1, output=None, mode='reflect', cval=0.0, origin=0)`

Calculate a one-dimensional minimum filter along the given axis.

The lines of the array along the given axis are filtered with a minimum filter of given size.

**Parameters**

- **input** [array_like] The input array.
- **size** [int] length along which to calculate 1D minimum
- **axis** [int, optional] The axis of `input` along which to calculate. Default is -1.
- **output** [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
- **mode** [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The `mode` parameter determines how the input array is extended beyond its boundaries. Default is 'reflect'. Behavior for each valid value is as follows:
  - **reflect** (`d c b a / a b c d / d c b a`)  
    The input is extended by reflecting about the edge of the last pixel.
  - **constant** (`k k k k / a b c d / k k k k`)  
    The input is extended by filling all values beyond the edge with the same constant value, defined by the `cval` parameter.
  - **nearest** (`a a a a / a b c d / d d d d`)  
    The input is extended by replicating the last pixel.
  - **mirror** (`d c b / a b c d / c b a`)  
    The input is extended by reflecting about the center of the last pixel.
  - **wrap** (`a b c d / a b c d / a b c d`)  
    The input is extended by wrapping around to the opposite edge.
cval  [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is 0.0.
origin  [int, optional] Controls the placement of the filter on the input array’s pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right.

Notes
This function implements the MINLIST algorithm [1], as described by Richard Harter [2], and has a guaranteed O(n) performance, n being the input length, regardless of filter size.

References
[1], [2]

Examples
```python
>>> from scipy.ndimage import minimum_filter1d
>>> minimum_filter1d([2, 8, 0, 4, 1, 9, 9, 0], size=3)
array([2, 0, 0, 0, 1, 1, 0, 0])
```

scipy.ndimage.percentile_filter

```
scipy.ndimage.percentile_filter(input, percentile, size=None, footprint=None, output=None, mode='reflect', cval=0.0, origin=0)
```

Calculate a multi-dimensional percentile filter.

Parameters

- **input** [array_like] The input array.
- **percentile** [scalar] The percentile parameter may be less than zero, i.e., percentile = -20 equals percentile = 80
- **size** [scalar or tuple, optional] See footprint, below. Ignored if footprint is given.
- **footprint** [array, optional] Either size or footprint must be defined. size gives the shape that is taken from the input array, at every element position, to define the input to the filter function. footprint is a boolean array that specifies (implicitly) a shape, but also which of the elements within this shape will get passed to the filter function. Thus size=(n,m) is equivalent to footprint=np.ones((n,m)). We adjust size to the number of dimensions of the input array, so that, if the input array is shape (10,10,10), and size is 2, then the actual size used is (2,2,2). When footprint is given, size is ignored.
- **output** [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
- **mode** [str or sequence, optional] The mode parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is ‘reflect’. The valid values and their behavior is as follows:
  - ‘reflect’  \( (d \ c \ b \ a / a \ b \ c \ d / d \ c \ b \ a) \)
    The input is extended by reflecting about the edge of the last pixel.
  - ‘constant’  \( (k \ k \ k \ k / a \ b \ c \ d / k \ k \ k \ k) \)
    The input is extended by filling all values beyond the edge with the same constant value, defined by the cval parameter.
  - ‘nearest’  \( (a \ a \ a \ a / a \ b \ c \ d / d \ d \ d \ d) \)
    The input is extended by replicating the last pixel.
  - ‘mirror’  \( (d \ c \ b / a \ b \ c \ d / c \ b \ a) \)
    The input is extended by reflecting about the center of the last pixel.
  - ‘wrap’  \( (a \ b \ c \ d / a \ b \ c \ d / a \ b \ c \ d) \)
    The input is extended by wrapping around to the opposite edge.
cval  [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is 0.0.

origin  [int or sequence, optional] Controls the placement of the filter on the input array’s pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right. By passing a sequence of origins with length equal to the number of dimensions of the input array, different shifts can be specified along each axis.

Returns

percentile_filter  [ndarray] Filtered array. Has the same shape as input.

Examples

```python
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt

>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side

>>> ascent = misc.ascent()
>>> result = ndimage.percentile_filter(ascent, percentile=20, size=20)

>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```

scipy.ndimage.prewitt

scipy.ndimage.prewitt(input, axis=-1, output=None, mode='reflect', cval=0.0)

Calculate a Prewitt filter.

Parameters

input  [array_like] The input array.
axis  [int, optional] The axis of input along which to calculate. Default is -1.
output  [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
mode [str or sequence, optional] The *mode* parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is ‘reflect’. The valid values and their behavior is as follows:

'reflect' (d c b a / a b c d / d c b a)
The input is extended by reflecting about the edge of the last pixel.

'constant' (k k k k / a b c d / k k k k)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (a a a a / a b c d / d d d d)
The input is extended by replicating the last pixel.

'mirror' (d c b / a b c d / c b a)
The input is extended by reflecting about the center of the last pixel.

'wrap' (a b c d / a b c d / a b c d)
The input is extended by wrapping around to the opposite edge.

cval [scalar, optional] Value to fill past edges of input if *mode* is ‘constant’. Default is 0.0.

Examples

```python
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = ndimage.prewitt(ascent)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```
scipy.ndimage.rank_filter

scipy.ndimage.rank_filter(input, rank, size=None, footprint=None, output=None, mode='reflect', cval=0.0, origin=0)

Calculate a multi-dimensional rank filter.

Parameters

- **input** [array_like] The input array.
- **rank** [int] The rank parameter may be less than zero, i.e., rank = -1 indicates the largest element.
- **size** [scalar or tuple, optional] See footprint, below. Ignored if footprint is given.
- **footprint** [array, optional] Either size or footprint must be defined. size gives the shape that is taken from the input array, at every element position, to define the input to the filter function. footprint is a boolean array that specifies (implicitly) a shape, but also which of the elements within this shape will get passed to the filter function. Thus size=(n,m) is equivalent to footprint=np.ones((n,m)). We adjust size to the number of dimensions of the input array, so that, if the input array is shape (10,10,10), and size is 2, then the actual size used is (2,2,2). When footprint is given, size is ignored.
- **output** [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
- **mode** [str or sequence, optional] The mode parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is 'reflect'. The valid values and their behavior is as follows:
  - 'reflect' (d c b a / a b c d / d c b a)
    The input is extended by reflecting about the edge of the last pixel.
  - 'constant' (k k k k / a b c d / k k k k)
    The input is extended by filling all values beyond the edge with the same constant value, defined by the cval parameter.
  - 'nearest' (a a a a / a b c d / d d d d)
    The input is extended by replicating the last pixel.
  - 'mirror' (d c b / a b c d / c b a)
    The input is extended by reflecting about the center of the last pixel.
  - 'wrap' (a b c d / a b c d / a b c d)
    The input is extended by wrapping around to the opposite edge.
- **cval** [scalar, optional] Value to fill past edges of input if mode is 'constant'. Default is 0.0.
- **origin** [int or sequence, optional] Controls the placement of the filter on the input array's pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right. By passing a sequence of origins with length equal to the number of dimensions of the input array, different shifts can be specified along each axis.

Returns

**rank_filter** [ndarray] Filtered array. Has the same shape as input.

Examples

```python
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.gray() # show the filtered result in grayscale
```
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = ndimage.rank_filter(ascent, rank=42, size=20)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()

scipy.ndimage.sobel

`scipy.ndimage.sobel(input, axis=-1, output=None, mode='reflect', cval=0.0)`

Calculate a Sobel filter.

**Parameters**

- **input** [array_like] The input array.
- **axis** [int, optional] The axis of `input` along which to calculate. Default is -1.
- **output** [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
- **mode** [str or sequence, optional] The `mode` parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is ‘reflect’. The valid values and their behavior is as follows:
  - ‘reflect’ \((d\ c\ b\ a\ /\ a\ b\ c\ d\ /\ d\ c\ b\ a)\)
    The input is extended by reflecting about the edge of the last pixel.
  - ‘constant’ \((k\ k\ k\ k\ /\ a\ b\ c\ d\ /\ k\ k\ k\ k)\)
    The input is extended by filling all values beyond the edge with the same constant value, defined by the `cval` parameter.
  - ‘nearest’ \((a\ a\ a\ a\ /\ a\ b\ c\ d\ /\ d\ d\ d\ d)\)
    The input is extended by replicating the last pixel.
  - ‘mirror’ \((d\ c\ b\ /\ a\ b\ c\ d\ /\ c\ b\ a)\)
    The input is extended by reflecting about the center of the last pixel.
The input is extended by wrapping around to the opposite edge.

\texttt{cval} \quad \text{[scalar, optional]} \quad \text{Value to fill past edges of input if \textit{mode} is ‘constant’. Default is 0.0.}

\textbf{Examples}

```python
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt

>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side

>>> ascent = misc.ascent()
>>> result = ndimage.sobel(ascent)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)

>>> plt.show()
```

\texttt{scipy.ndimage.uniform\_filter} \quad \text{\texttt{scipy.ndimage.uniform\_filter}(input, size=3, output=None, mode='reflect', cval=0.0, origin=0)}

\textbf{Parameters}

\begin{itemize}
  \item \texttt{input} \quad \text{[array\_like]} \text{The input array.}
  \item \texttt{size} \quad \text{[int or sequence of ints, optional]} \text{The sizes of the uniform filter are given for each axis as a sequence, or as a single number, in which case the size is equal for all axes.}
  \item \texttt{output} \quad \text{[array or dtype, optional]} \text{The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.}
  \item \texttt{mode} \quad \text{[str or sequence, optional]} \text{The \textit{mode} parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is ‘reflect’. The valid values and their behavior is as follows:}
\end{itemize}
The input is extended by reflecting about the edge of the last pixel.

The input is extended by filling all values beyond the edge with the same constant value, defined by the `cval` parameter.

The input is extended by replicating the last pixel.

The input is extended by reflecting about the center of the last pixel.

The input is extended by wrapping around to the opposite edge.

The multi-dimensional filter is implemented as a sequence of one-dimensional uniform filters. The intermediate arrays are stored in the same data type as the output. Therefore, for output types with a limited precision, the results may be imprecise because intermediate results may be stored with insufficient precision.

The lines of the array along the given axis are filtered with a uniform filter of given size.

Parameters

- `input` [array_like] The input array.
- `size` [int] length of uniform filter
- `axis` [int, optional] The axis of `input` along which to calculate. Default is -1.
output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [{‘reflect’, ‘constant’, ‘nearest’, ‘mirror’, ‘wrap’}, optional] The mode parameter determines how the input array is extended beyond its boundaries. Default is ‘reflect’. Behavior for each valid value is as follows:

‘reflect’ (d c b a / a b c d / d c b a)
The input is extended by reflecting about the edge of the last pixel.

‘constant’ (k k k k / a b c d / k k k k)
The input is extended by filling all values beyond the edge with the same constant value, defined by the cval parameter.

‘nearest’ (a a a a / a b c d / d d d d)
The input is extended by replicating the last pixel.

‘mirror’ (d c b / a b c d / c b a)
The input is extended by reflecting about the center of the last pixel.

‘wrap’ (a b c d / a b c d / a b c d)
The input is extended by wrapping around to the opposite edge.

cval [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is 0.0.

origin [int, optional] Value to fill past edges of input if mode is ‘constant’. Default is 0.0.

Example

```python
>>> from scipy.ndimage import uniform_filter1d
>>> uniform_filter1d([2, 8, 0, 4, 1, 9, 9, 0], size=3)
aarray([4, 3, 4, 1, 4, 6, 6, 3])
```

6.16.2 Fourier filters

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**scipy.ndimage.fourier_ellipsoid**

**scipy.ndimage.fourier_ellipsoid**(input, size, n=-1, axis=-1, output=None)

Multi-dimensional ellipsoid fourier filter.

The array is multiplied with the fourier transform of a ellipsoid of given sizes.

**Parameters**

- **input**: array_like. The input array.
- **size**: float or sequence. The size of the box used for filtering. If a float, size is the same for all axes. If a sequence, size has to contain one value for each axis.
- **n**: int, optional. If n is negative (default), then the input is assumed to be the result of a complex fft. If n is larger than or equal to zero, the input is assumed to be the result of a real fft, and n gives the length of the array before transformation along the real transform direction.
- **axis**: int, optional. The axis of the real transform.
- **output**: ndarray, optional. If given, the result of filtering the input is placed in this array. None is returned in this case.

**Returns**

- **fourier_ellipsoid**: ndarray. The filtered input.

**Notes**

This function is implemented for arrays of rank 1, 2, or 3.

**Examples**

```python
>>> from scipy import ndimage, misc
>>> import numpy.fft
>>> import matplotlib.pyplot as plt
>>> fig, (ax1, ax2) = plt.subplots(1, 2)
>>> plt.gray() # show the filtered result in grayscale
>>> ascent = misc.ascent()
>>> input_ = numpy.fft.fft2(ascent)
>>> result = ndimage.fourier_ellipsoid(input_, size=20)
>>> result = numpy.fft.ifft2(result)
>>> ax1.imshow(result.real) # the imaginary part is an artifact
>>> ax2.imshow(result.real) # the imaginary part is an artifact
>>> plt.show()
```

**scipy.ndimage.fourier_gaussian**

**scipy.ndimage.fourier_gaussian**(input, sigma, n=-1, axis=-1, output=None)

Multi-dimensional Gaussian fourier filter.

The array is multiplied with the fourier transform of a Gaussian kernel.

**Parameters**

- **input**: array_like. The input array.
- **sigma**: float or sequence. The sigma of the Gaussian kernel. If a float, sigma is the same for all axes. If a sequence, sigma has to contain one value for each axis.
n [int, optional] If \( n \) is negative (default), then the input is assumed to be the result of a complex fft. If \( n \) is larger than or equal to zero, the input is assumed to be the result of a real fft, and \( n \) gives the length of the array before transformation along the real transform direction.

axis [int, optional] The axis of the real transform.

output [ndarray, optional] If given, the result of filtering the input is placed in this array. None is returned in this case.

Returns

fourier_gaussian [ndarray] The filtered input.

Examples

```python
>>> from scipy import ndimage, misc
>>> import numpy.fft
>>> import matplotlib.pyplot as plt
>>> fig, (ax1, ax2) = plt.subplots(1, 2)
>>> plt.gray()  # show the filtered result in grayscale
>>> ascent = misc.ascent()
>>> input_ = numpy.fft.fft2(ascent)
>>> result = ndimage.fourier_gaussian(input_, sigma=4)
>>> result = numpy.fft.ifft2(result)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result.real)  # the imaginary part is an artifact
>>> plt.show()
```

scipy.ndimage.fourier_shift

scipy.ndimage.fourier_shift(input, shift, n=-1, axis=-1, output=None)

Multi-dimensional fourier shift filter.

The array is multiplied with the fourier transform of a shift operation.

Parameters

- input [array_like] The input array.
scipy.ndimage.fourier_shift

scipy.ndimage.fourier_shift(input, shift, n=-1, axis=-1, output=None)

Multi-dimensional uniform fourier filter.

The array is multiplied with the fourier transform of a box of given size.

Examples

```python
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> import numpy.fft
>>> fig, (ax1, ax2) = plt.subplots(1, 2)
>>> plt.gray()  # show the filtered result in grayscale
>>> ascent = misc.ascent()
>>> input_ = numpy.fft.fft2(ascent)
>>> result = ndimage.fourier_shift(input_, shift=200)
>>> result = numpy.fft.ifft2(result)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result.real)  # the imaginary part is an artifact
>>> plt.show()
```
Parameters

- **input**: [array_like] The input array.
- **size**: [float or sequence] The size of the box used for filtering. If a float, size is the same for all axes. If a sequence, size has to contain one value for each axis.
- **n**: [int, optional] If n is negative (default), then the input is assumed to be the result of a complex fft. If n is larger than or equal to zero, the input is assumed to be the result of a real fft, and n gives the length of the array before transformation along the real transform direction.
- **axis**: [int, optional] The axis of the real transform.
- **output**: [ndarray, optional] If given, the result of filtering the input is placed in this array. None is returned in this case.

Returns

- **fourier_uniform**: [ndarray] The filtered input.

Examples

```python
>>> from scipy import ndimage, misc
>>> import numpy.fft
>>> import matplotlib.pyplot as plt
>>> fig, (ax1, ax2) = plt.subplots(1, 2)
>>> plt.gray()  # show the filtered result in grayscale
>>> ascent = misc.ascent()
>>> input_ = numpy.fft.fft2(ascent)
>>> result = ndimage.fourier_uniform(input_, size=20)
>>> result = numpy.fft.ifft2(result)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result.real)  # the imaginary part is an artifact
>>> plt.show()
```

6.16.3 Interpolation
**affine_transform**

```python
affine_transform(input, matrix[, offset, ...])
```

Apply an affine transformation.

**geometric_transform**

```python
geometric_transform(input, mapping[, ...])
```

Apply an arbitrary geometric transform.

**map_coordinates**

```python
map_coordinates(input, coordinates[, ...])
```

Map the input array to new coordinates by interpolation.

**rotate**

```python
rotate(input, angle[, axes, reshape, ...])
```

Rotate an array.

**shift**

```python
shift(input, shift[, output, order, mode, ...])
```

Shift an array.

**spline_filter**

```python
spline_filter(input[, order, output, mode])
```

Multi-dimensional spline filter.

**spline_filter1d**

```python
spline_filter1d(input[, order, axis, ...])
```

Calculate a one-dimensional spline filter along the given axis.

**zoom**

```python
zoom(input, zoom[, output, order, mode, ...])
```

Zoom an array.

---

**scipy.ndimage.affine_transform**

Apply an affine transformation.

Given an output image pixel index vector `o`, the pixel value is determined from the input image at position `np.dot(matrix, o) + offset`.

**Parameters**

- `input` (array_like): The input array.
- `matrix` (ndarray): The inverse coordinate transformation matrix, mapping output coordinates to input coordinates. If `ndim` is the number of dimensions of `input`, the given matrix must have one of the following shapes:
  - `(ndim, ndim)`: the linear transformation matrix for each output coordinate.
  - `(ndim,)`: assume that the 2D transformation matrix is diagonal, with the diagonal specified by the given value. A more efficient algorithm is then used that exploits the separability of the problem.
  - `(ndim + 1, ndim + 1)`: assume that the transformation is specified using homogeneous coordinates [1]. In this case, any value passed to `offset` is ignored.
  - `(ndim, ndim + 1)`: as above, but the bottom row of a homogeneous transformation matrix is always `[0, 0, ..., 1]`, and may be omitted.
- `offset` ([float or sequence, optional]): The offset into the array where the transform is applied. If a float, `offset` is the same for each axis. If a sequence, `offset` should contain one value for each axis.
- `output_shape` ([tuple of ints, optional]): Shape tuple.
- `output` ([array or dtype, optional]): The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
- `order` ([int, optional]): The order of the spline interpolation, default is 3. The order has to be in the range 0-5.
The input is extended by wrapping around to the opposite edge.

\[
\begin{bmatrix}
  a & b & c & d \\
  a & b & c & d \\
  a & b & c & d \\
\end{bmatrix}
\]

The given matrix and offset are used to find for each point in the output the corresponding coordinates in the input by an affine transformation. The value of the input at those coordinates is determined by spline interpolation of the requested order. Points outside the boundaries of the input are filled according to the given mode.

Changed in version 0.18.0: Previously, the exact interpretation of the affine transformation depended on whether the matrix was supplied as a one-dimensional or two-dimensional array. If a one-dimensional array was supplied to the matrix parameter, the output pixel value at index \( o \) was determined from the input image at position \( \text{matrix} \times (o + \text{offset}) \).

### References

[1] scipy.ndimage.geometric_transform

**scipy.ndimage.geometric_transform**

Apply an arbitrary geometric transform.

The given mapping function is used to find, for each point in the output, the corresponding coordinates in the input. The value of the input at those coordinates is determined by spline interpolation of the requested order.

**Parameters**

- **input** [array_like] The input array.
- **mapping** [(callable, scipy.LowLevelCallable)] A callable object that accepts a tuple of length equal to the output array rank, and returns the corresponding input coordinates as a tuple of length equal to the input array rank.
- **output_shape** [tuple of ints, optional] Shape tuple.
- **output** [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
- **order** [int, optional] The order of the spline interpolation, default is 3. The order has to be in the range 0-5.
- **mode** [('reflect', 'constant', 'nearest', 'mirror', 'wrap'), optional] The mode parameter determines how the input array is extended beyond its boundaries. Default is 'constant'. Behavior for each valid value is as follows:

- **reflect** \((d \ c \ b \ a \ / \ a \ b \ c \ d \ / \ a \ b \ c \ d)\)

  The input is extended by reflecting about the edge of the last pixel.
‘constant’ \((k \ k \ k \ k \ / \ a \ b \ c \ d \ / \ k \ k \ k \ k)\)

The input is extended by filling all values beyond the edge with the same constant value, defined by the `cval` parameter.

‘nearest’ \((a \ a \ a \ a \ / \ a \ b \ c \ d \ / \ d \ d \ d \ d)\)

The input is extended by replicating the last pixel.

‘mirror’ \((d \ c \ b \ / \ a \ b \ c \ d \ / \ c \ b \ a)\)

The input is extended by reflecting about the center of the last pixel.

‘wrap’ \((a \ b \ c \ d \ / \ a \ b \ c \ d \ / \ a \ b \ c \ d)\)

The input is extended by wrapping around to the opposite edge.

cval

[scalar, optional] Value to fill past edges of input if `mode` is ‘constant’. Default is 0.0.

prefilter

[bool, optional] Determines if the input array is prefiltered with `spline_filter` before interpolation. The default is True, which will create a temporary `float64` array of filtered values if `order` > 1. If setting this to False, the output will be slightly blurred if `order` > 1, unless the input is prefiltered, i.e. it is the result of calling `spline_filter` on the original input.

extra_arguments

[tuple, optional] Extra arguments passed to `mapping`.

extra_keywords

[dict, optional] Extra keywords passed to `mapping`.

Returns

output [ndarray] The filtered input.

See also:

`map_coordinates`, `affine_transform`, `spline_filter1d`

Notes

This function also accepts low-level callback functions with one the following signatures and wrapped in `scipy.LowLevelCallable`:

```python
int mapping(npy_intp *output_coordinates, double *input_coordinates,
            int output_rank, int input_rank, void *user_data)
int mapping(intptr_t *output_coordinates, double *input_coordinates,
            int output_rank, int input_rank, void *user_data)
```

The calling function iterates over the elements of the output array, calling the callback function at each element. The coordinates of the current output element are passed through `output_coordinates`. The callback function must return the coordinates at which the input must be interpolated in `input_coordinates`. The rank of the input and output arrays are given by `input_rank` and `output_rank` respectively. `user_data` is the data pointer provided to `scipy.LowLevelCallable` as-is.

The callback function must return an integer error status that is zero if something went wrong and one otherwise. If an error occurs, you should normally set the python error status with an informative message before returning, otherwise a default error message is set by the calling function.

In addition, some other low-level function pointer specifications are accepted, but these are for backward compatibility only and should not be used in new code.

Examples

```python
>>> import numpy as np
>>> from scipy.ndimage import geometric_transform
>>> a = np.arange(12.).reshape((4, 3))
>>> def shift_func(output_coords):
...     return (output_coords[0] - 0.5, output_coords[1] - 0.5)
(continues on next page)```
...  
>>>
```
geometric_transform(a, shift_func)
array([[ 0. , 0. , 0. ],
       [ 0. , 1.362, 2.738],
       [ 0. , 4.812, 6.187],
       [ 0. , 8.263, 9.637]])
```

```python
>>> b = [1, 2, 3, 4, 5]
>>> def shift_func(output_coords):
...     return (output_coords[0] - 3,)
...  
>>> geometric_transform(b, shift_func, mode='constant')
array([0, 0, 0, 1, 2])
>>> geometric_transform(b, shift_func, mode='nearest')
array([1, 1, 1, 1, 2])
>>> geometric_transform(b, shift_func, mode='reflect')
array([3, 2, 1, 1, 2])
>>> geometric_transform(b, shift_func, mode='wrap')
array([2, 3, 4, 1, 2])
```

**scipy.ndimage.map_coordinates**

Map the input array to new coordinates by interpolation.

The array of coordinates is used to find, for each point in the output, the corresponding coordinates in the input. The value of the input at those coordinates is determined by spline interpolation of the requested order.

The shape of the output is derived from that of the coordinate array by dropping the first axis. The values of the array along the first axis are the coordinates in the input array at which the output value is found.

**Parameters**

- **input** [array_like] The input array.
- **coordinates** [array_like] The coordinates at which input is evaluated.
- **output** [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
- **order** [int, optional] The order of the spline interpolation, default is 3. The order has to be in the range 0-5.
- **mode** [‘reflect’, ‘constant’, ‘nearest’, ‘mirror’, ‘wrap’], optional] The mode parameter determines how the input array is extended beyond its boundaries. Default is ‘constant’. Behavior for each valid value is as follows:
  - ‘reflect’ (d c b a | a b c d | d c b a)
    The input is extended by reflecting about the edge of the last pixel.
  - ‘constant’ (k k k k | a b c d | k k k k)
    The input is extended by filling all values beyond the edge with the same constant value, defined by the cval parameter.
  - ‘nearest’ (a a a a | a b c d | d d d d)
    The input is extended by replicating the last pixel.
'mirror' \((d\ c\ b\ a\ b\ c\ d\ /\ c\ b\ a)\)

The input is extended by reflecting about the center of the last pixel.

'wrap' \((a\ b\ c\ d\ /\ a\ b\ c\ d\ /\ a\ b\ c\ d)\)

The input is extended by wrapping around to the opposite edge.

cval
[scalar, optional] Value to fill past edges of input if mode is 'constant'. Default is 0.0.
prefilter
[bool, optional] Determines if the input array is prefiltered with \texttt{spline\_filter} before interpolation. The default is True, which will create a temporary float64 array of filtered values if order \(>1\). If setting this to False, the output will be slightly blurred if order \(>1\), unless the input is prefiltered, i.e. it is the result of calling \texttt{spline\_filter} on the original input.

\textbf{Returns}

\texttt{map\_coordinates}
[ndarray] The result of transforming the input. The shape of the output is derived from that of \texttt{coordinates} by dropping the first axis.

\textbf{See also:}
\texttt{spline\_filter}, \texttt{geometric\_transform}, \texttt{scipy\_interpolate}

\textbf{Examples}

```python
>>> from scipy import ndimage
>>> a = np.arange(12.).reshape((4, 3))
>>> a
array([[ 0.,  1.,  2.],
       [ 3.,  4.,  5.],
       [ 6.,  7.,  8.],
       [ 9., 10., 11.]])
>>> ndimage.map_coordinates(a, [[0.5, 2], [0.5, 1]], order=1)
array([ 2.,  7.])
```

Above, the interpolated value of \(a[0.5, 0.5]\) gives output[0], while \(a[2, 1]\) is output[1].

```python
>>> inds = np.array([[0.5, 2], [0.5, 4]])
>>> ndimage.map_coordinates(a, inds, order=1, cval=-33.3)
array([ 2., -33.3])
>>> ndimage.map_coordinates(a, inds, order=1, mode='nearest')
array([ 2.,  8.])
>>> ndimage.map_coordinates(a, inds, order=1, cval=0, output=bool)
array([ True, False], dtype=bool)
```

\texttt{scipy.ndimage.rotate}

\texttt{scipy.ndimage.rotate}(\texttt{input, angle, axes=(1, 0), reshape=True, output=None, order=3, mode='constant', cval=0.0, prefilter=True})

Rotate an array.

The array is rotated in the plane defined by the two axes given by the axes parameter using spline interpolation of the requested order.

\textbf{Parameters}

- \texttt{input} [array_like] The input array.
- \texttt{angle} [float] The rotation angle in degrees.
- \texttt{axes} [tuple of 2 ints, optional] The two axes that define the plane of rotation. Default is the first two axes.
reshape [bool, optional] If reshape is true, the output shape is adapted so that the input array is contained completely in the output. Default is True.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

order [int, optional] The order of the spline interpolation, default is 3. The order has to be in the range 0-5.

mode [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The mode parameter determines how the input array is extended beyond its boundaries. Default is 'constant'. Behavior for each valid value is as follows:

- 'reflect' (d c b a / a b c d / d c b a)
  The input is extended by reflecting about the edge of the last pixel.

- 'constant' (k k k k / a b c d / k k k k)
  The input is extended by filling all values beyond the edge with the same constant value, defined by the cval parameter.

- 'nearest' (a a a a / a b c d / d d d d)
  The input is extended by replicating the last pixel.

- 'mirror' (d c b a / a b c d / c b a)
  The input is extended by reflecting about the center of the last pixel.

- 'wrap' (a b c d / a b c d / a b c d)
  The input is extended by wrapping around to the opposite edge.

cval [scalar, optional] Value to fill past edges of input if mode is 'constant'. Default is 0.0.

prefilter [bool, optional] Determines if the input array is prefiltered with spline_filter before interpolation. The default is True, which will create a temporary float64 array of filtered values if order > 1. If setting this to False, the output will be slightly blurred if order > 1, unless the input is prefiltered, i.e. it is the result of calling spline_filter on the original input.

Returns

rotate [ndarray] The rotated input.

scipy.ndimage.shift

scipy.ndimage.shift(input, shift, output=None, order=3, mode='constant', cval=0.0, prefilter=True)

Shift an array.

The array is shifted using spline interpolation of the requested order. Points outside the boundaries of the input are filled according to the given mode.

Parameters

input [array_like] The input array.
shift [float or sequence] The shift along the axes. If a float, shift is the same for each axis. If a sequence, shift should contain one value for each axis.
output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
order [int, optional] The order of the spline interpolation, default is 3. The order has to be in the range 0-5.
mode [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The mode parameter determines how the input array is extended beyond its boundaries. Default is 'constant'. Behavior for each valid value is as follows:

- 'reflect' (d c b a / a b c d / d c b a)
  The input is extended by reflecting about the edge of the last pixel.
`constant` (k k k k | a b c d | k k k k)
The input is extended by filling all values beyond the edge with the same constant value, defined by the cval parameter.

`nearest` (a a a a | a b c d | d d d d)
The input is extended by replicating the last pixel.

`mirror` (d c b | a b c d | c b a)
The input is extended by reflecting about the center of the last pixel.

`wrap` (a b c d | a b c d | a b c d)
The input is extended by wrapping around to the opposite edge.

cval [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is 0.0.

prefilter [bool, optional] Determines if the input array is prefiltered with `spline_filter` before interpolation. The default is True, which will create a temporary float64 array of filtered values if order > 1. If setting this to False, the output will be slightly blurred if order > 1, unless the input is prefiltered, i.e. it is the result of calling `spline_filter` on the original input.

Returns
shift [ndarray] The shifted input.

`scipy.ndimage.spline_filter`

`scipy.ndimage.spline_filter(input, order=3, output=<class 'numpy.float64'>, mode='mirror')`
Multi-dimensional spline filter.

For more details, see `spline_filter1d`.

See also:
`spline_filter1d`

Notes
The multi-dimensional filter is implemented as a sequence of one-dimensional spline filters. The intermediate arrays are stored in the same data type as the output. Therefore, for output types with a limited precision, the results may be imprecise because intermediate results may be stored with insufficient precision.

`scipy.ndimage.spline_filter1d`

`scipy.ndimage.spline_filter1d(input, order=3, axis=-1, output=<class 'numpy.float64'>, mode='mirror')`
Calculate a one-dimensional spline filter along the given axis.

The lines of the array along the given axis are filtered by a spline filter. The order of the spline must be >= 2 and <= 5.

Parameters
input [array_like] The input array.
order [int, optional] The order of the spline, default is 3.
axis [int, optional] The axis along which the spline filter is applied. Default is the last axis.
output [ndarray or dtype, optional] The array in which to place the output, or the dtype of the returned array. Default is numpy.float64.
mode [‘reflect’, ‘constant’, ‘nearest’, ‘mirror’, ‘wrap’], optional] The mode parameter determines how the input array is extended beyond its boundaries. Default is ‘constant’. Behavior for each valid value is as follows:
`reflect` (d c b a / a b c d / d c b a)
   The input is extended by reflecting about the edge of the last pixel.

`constant` (k k k k / a b c d / k k k k)
   The input is extended by filling all values beyond the edge with the
   same constant value, defined by the `cval` parameter.

`nearest` (a a a a / a b c d / d d d d)
   The input is extended by replicating the last pixel.

`mirror` (d c b / a b c d / c b a)
   The input is extended by reflecting about the center of the last pixel.

`wrap` (a b c d / a b c d / a b c d)
   The input is extended by wrapping around to the opposite edge.

**Returns**

`spline_filter1d`
   [ndarray] The filtered input.

**Notes**

All functions in `ndimage.interpolation` do spline interpolation of the input image. If using b-splines of
order > 1, the input image values have to be converted to b-spline coefficients first, which is done by
applying this one-dimensional filter sequentially along all axes of the input. All functions that require
b-spline coefficients will automatically filter their inputs, a behavior controllable with the `prefilter`
keyword argument. For functions that accept a `mode` parameter, the result will only be correct if it
matches the `mode` used when filtering.

`scipy.ndimage.zoom`

`scipy.ndimage.zoom`(input, zoom, output=None, order=3, mode='constant', cval=0.0, pre-filter=True)

Zoom an array.

The array is zoomed using spline interpolation of the requested order.

**Parameters**

input  [array_like] The input array.

zoom  [float or sequence] The zoom factor along the axes. If a float, `zoom` is the same for
each axis. If a sequence, `zoom` should contain one value for each axis.

output  [array or dtype, optional] The array in which to place the output, or the dtye of
the returned array. By default an array of the same dtype as input will be created.

order  [int, optional] The order of the spline interpolation, default is 3. The order has to
be in the range 0-5.

determines how the input array is extended beyond its boundaries. Default is
‘constant’. Behavior for each valid value is as follows:

`reflect` (d c b a / a b c d / d c b a)
   The input is extended by reflecting about the edge of the last pixel.

`constant` (k k k k / a b c d / k k k k)
   The input is extended by filling all values beyond the edge with the
   same constant value, defined by the `cval` parameter.

`nearest` (a a a a / a b c d / d d d d)
   The input is extended by replicating the last pixel.

`mirror` (d c b / a b c d / c b a)
   The input is extended by reflecting about the center of the last pixel.

`wrap` (a b c d / a b c d / a b c d)
   The input is extended by wrapping around to the opposite edge.

**Returns**

`spline_filter1d`
   [ndarray] The filtered input.

**Notes**

All functions in `ndimage.interpolation` do spline interpolation of the input image. If using b-splines of
order > 1, the input image values have to be converted to b-spline coefficients first, which is done by
applying this one-dimensional filter sequentially along all axes of the input. All functions that require
b-spline coefficients will automatically filter their inputs, a behavior controllable with the `prefilter`
keyword argument. For functions that accept a `mode` parameter, the result will only be correct if it
matches the `mode` used when filtering.

`scipy.ndimage.zoom`

`scipy.ndimage.zoom`(input, zoom, output=None, order=3, mode='constant', cval=0.0, pre-filter=True)

Zoom an array.

The array is zoomed using spline interpolation of the requested order.

**Parameters**

input  [array_like] The input array.

zoom  [float or sequence] The zoom factor along the axes. If a float, `zoom` is the same for
each axis. If a sequence, `zoom` should contain one value for each axis.

output  [array or dtype, optional] The array in which to place the output, or the dtye of
the returned array. By default an array of the same dtype as input will be created.

order  [int, optional] The order of the spline interpolation, default is 3. The order has to
be in the range 0-5.

determines how the input array is extended beyond its boundaries. Default is
‘constant’. Behavior for each valid value is as follows:

`reflect` (d c b a / a b c d / d c b a)
   The input is extended by reflecting about the edge of the last pixel.

`constant` (k k k k / a b c d / k k k k)
   The input is extended by filling all values beyond the edge with the
   same constant value, defined by the `cval` parameter.

`nearest` (a a a a / a b c d / d d d d)
   The input is extended by replicating the last pixel.

`mirror` (d c b / a b c d / c b a)
   The input is extended by reflecting about the center of the last pixel.

`wrap` (a b c d / a b c d / a b c d)
   The input is extended by wrapping around to the opposite edge.

**Returns**

`spline_filter1d`
   [ndarray] The filtered input.

**Notes**

All functions in `ndimage.interpolation` do spline interpolation of the input image. If using b-splines of
order > 1, the input image values have to be converted to b-spline coefficients first, which is done by
applying this one-dimensional filter sequentially along all axes of the input. All functions that require
b-spline coefficients will automatically filter their inputs, a behavior controllable with the `prefilter`
keyword argument. For functions that accept a `mode` parameter, the result will only be correct if it
matches the `mode` used when filtering.

`scipy.ndimage.zoom`

`scipy.ndimage.zoom`(input, zoom, output=None, order=3, mode='constant', cval=0.0, pre-filter=True)

Zoom an array.

The array is zoomed using spline interpolation of the requested order.

**Parameters**

input  [array_like] The input array.

zoom  [float or sequence] The zoom factor along the axes. If a float, `zoom` is the same for
each axis. If a sequence, `zoom` should contain one value for each axis.

output  [array or dtype, optional] The array in which to place the output, or the dtye of
the returned array. By default an array of the same dtype as input will be created.

order  [int, optional] The order of the spline interpolation, default is 3. The order has to
be in the range 0-5.

determines how the input array is extended beyond its boundaries. Default is
‘constant’. Behavior for each valid value is as follows:

`reflect` (d c b a / a b c d / d c b a)
   The input is extended by reflecting about the edge of the last pixel.

`constant` (k k k k / a b c d / k k k k)
   The input is extended by filling all values beyond the edge with the
   same constant value, defined by the `cval` parameter.

`nearest` (a a a a / a b c d / d d d d)
   The input is extended by replicating the last pixel.

`mirror` (d c b / a b c d / c b a)
   The input is extended by reflecting about the center of the last pixel.

`wrap` (a b c d / a b c d / a b c d)
   The input is extended by wrapping around to the opposite edge.

**Returns**

`spline_filter1d`
   [ndarray] The filtered input.

**Notes**

All functions in `ndimage.interpolation` do spline interpolation of the input image. If using b-splines of
order > 1, the input image values have to be converted to b-spline coefficients first, which is done by
applying this one-dimensional filter sequentially along all axes of the input. All functions that require
b-spline coefficients will automatically filter their inputs, a behavior controllable with the `prefilter`
keyword argument. For functions that accept a `mode` parameter, the result will only be correct if it
matches the `mode` used when filtering.

`scipy.ndimage.zoom`

`scipy.ndimage.zoom`(input, zoom, output=None, order=3, mode='constant', cval=0.0, pre-filter=True)

Zoom an array.

The array is zoomed using spline interpolation of the requested order.

**Parameters**

input  [array_like] The input array.

zoom  [float or sequence] The zoom factor along the axes. If a float, `zoom` is the same for
each axis. If a sequence, `zoom` should contain one value for each axis.

output  [array or dtype, optional] The array in which to place the output, or the dtye of
the returned array. By default an array of the same dtype as input will be created.

order  [int, optional] The order of the spline interpolation, default is 3. The order has to
be in the range 0-5.

determines how the input array is extended beyond its boundaries. Default is
‘constant’. Behavior for each valid value is as follows:

`reflect` (d c b a / a b c d / d c b a)
   The input is extended by reflecting about the edge of the last pixel.

`constant` (k k k k / a b c d / k k k k)
   The input is extended by filling all values beyond the edge with the
   same constant value, defined by the `cval` parameter.

`nearest` (a a a a / a b c d / d d d d)
   The input is extended by replicating the last pixel.

`mirror` (d c b / a b c d / c b a)
   The input is extended by reflecting about the center of the last pixel.

`wrap` (a b c d / a b c d / a b c d)
   The input is extended by wrapping around to the opposite edge.

**Returns**

`spline_filter1d`
   [ndarray] The filtered input.

**Notes**

All functions in `ndimage.interpolation` do spline interpolation of the input image. If using b-splines of
order > 1, the input image values have to be converted to b-spline coefficients first, which is done by
applying this one-dimensional filter sequentially along all axes of the input. All functions that require
b-spline coefficients will automatically filter their inputs, a behavior controllable with the `prefilter`
keyword argument. For functions that accept a `mode` parameter, the result will only be correct if it
matches the `mode` used when filtering.
prefilter  [bool, optional] Determines if the input array is prefiltered with \texttt{spline\_filter} before interpolation. The default is True, which will create a temporary \texttt{float64} array of filtered values if \texttt{order} > 1. If setting this to False, the output will be slightly blurred if \texttt{order} > 1, unless the input is prefiltered, i.e. it is the result of calling \texttt{spline\_filter} on the original input.

\textbf{Returns}

\texttt{zoom}  [ndarray] The zoomed input.

\textbf{Examples}

```python
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt

>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = ndimage.zoom(ascent, 3.0)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```

```
>>> print(ascent.shape)
(512, 512)

>>> print(result.shape)
(1536, 1536)
```

\textbf{6.16.4 Measurements}
**center_of_mass**(input[, labels, index])

Calculate the center of mass of the values of an array at labels.

**extrema**(input[, labels, index])

Calculate the minimums and maximums of the values of an array at labels, along with their positions.

**find_objects**(input[, max_label])

Find objects in a labeled array.

**histogram**(input, min, max, bins[, labels, index])

Calculate the histogram of the values of an array, optionally at labels.

**label**(input[, structure, output])

Label features in an array.

**labeled_comprehension**(input, labels, index, ...)

Roughly equivalent to [func(input[labels == i]) for i in index].

**maximum**(input[, labels, index])

Calculate the maximum of the values of an array over labeled regions.

**maximum_position**(input[, labels, index])

Find the positions of the maximums of the values of an array at labels.

**mean**(input[, labels, index])

Calculate the mean of the values of an array at labels.

**median**(input[, labels, index])

Calculate the median of the values of an array over labeled regions.

**minimum**(input[, labels, index])

Calculate the minimum of the values of an array over labeled regions.

**minimum_position**(input[, labels, index])

Find the positions of the minimums of the values of an array at labels.

**standard_deviation**(input[, labels, index])

Calculate the standard deviation of the values of an n-D image array, optionally at specified sub-regions.

**sum**(input[, labels, index])

Calculate the sum of the values of the array.

**variance**(input[, labels, index])

Calculate the variance of the values of an n-D image array, optionally at specified sub-regions.

**watershed_ift**(input, markers[, structure, ...])

Apply watershed from markers using image foresting transform algorithm.

---

### scipy.ndimage.center_of_mass

**scipy.ndimage.center_of_mass**(input, labels=None, index=None)

Calculate the center of mass of the values of an array at labels.

**Parameters**

- **input** [ndarray] Data from which to calculate center-of-mass. The masses can either be positive or negative.
- **labels** [ndarray, optional] Labels for objects in input, as generated by ndimage.label. Only used with index. Dimensions must be the same as input.
- **index** [int or sequence of ints, optional] Labels for which to calculate centers-of-mass. If not specified, all labels greater than zero are used. Only used with labels.

**Returns**

- **center_of_mass** [tuple, or list of tuples] Coordinates of center-of-mass.

**Examples**

```python
>>> a = np.array([[0,0,0,0],
...               [0,1,1,0],
...               [0,1,1,0],
...               [0,1,1,0]])
```

(continues on next page)
>> from scipy import ndimage
>>> ndimage.measurements.center_of_mass(a)
(2.0, 1.5)

Calculation of multiple objects in an image

```python
>>> b = np.array(([0,1,1,0],
...                [0,1,0,0],
...                [0,0,0,0],
...                [0,0,1,1],
...                [0,0,1,1]))
>>> lbl = ndimage.label(b)[0]
>>> ndimage.measurements.center_of_mass(b, lbl, [1,2])
[(0.33333333333333331, 1.3333333333333333), (3.5, 2.5)]
```

Negative masses are also accepted, which can occur for example when bias is removed from measured data due to random noise.

```python
>>> c = np.array(([-1,0,0,0],
...                [0,-1,-1,0],
...                [0,1,-1,0],
...                [0,1,1,0]))
>>> ndimage.measurements.center_of_mass(c)
(-4.0, 1.0)
```

If there are division by zero issues, the function does not raise an error but rather issues a RuntimeWarning before returning inf and/or NaN.

```python
>>> d = np.array([-1, 1])
>>> ndimage.measurements.center_of_mass(d)
(inf,)
```

**scipy.ndimage.extrema**

`scipy.ndimage.extrema(input, labels=None, index=None)`

Calculate the minimums and maximums of the values of an array at labels, along with their positions.

**Parameters**

- `input` : [ndarray] Nd-image data to process.
- `labels` : [ndarray, optional] Labels of features in input. If not None, must be same shape as `input`.
- `index` : [int or sequence of ints, optional] Labels to include in output. If None (default), all values where non-zero `labels` are used.

**Returns**

- `minimums`, `maximums` : [int or ndarray] Values of minimums and maximums in each feature.
- `min_positions`, `max_positions` : [tuple or list of tuples] Each tuple gives the n-D coordinates of the corresponding minimum or maximum.

**See also:**

`maximum`, `minimum`, `maximum_position`, `minimum_position`, `center_of_mass`
Examples

```python
>>> a = np.array([[1, 2, 0, 0],
...                [5, 3, 0, 4],
...                [0, 0, 0, 7],
...                [9, 3, 0, 0]])
>>> from scipy import ndimage
>>> ndimage.extrema(a)
(0, 9, (0, 2), (3, 0))
```

Features to process can be specified using labels and index:

```python
>>> lbl, n lbl = ndimage.label(a)
>>> ndimage.extrema(a, lbl, index=np.arange(1, n lbl+1))
(array([1, 4, 3]),
 array([5, 7, 9]),
 [(0, 0), (1, 3), (3, 1)],
 [(1, 0), (2, 3), (3, 0)])
```

If no index is given, non-zero labels are processed:

```python
>>> ndimage.extrema(a, lbl)
(1, 9, (0, 0), (3, 0))
```

**scipy.ndimage.find_objects**

`scipy.ndimage.find_objects(input, max_label=0)`

Find objects in a labeled array.

**Parameters**

- `input` : [ndarray of ints] Array containing objects defined by different labels. Labels with value 0 are ignored.
- `max_label` : [int, optional] Maximum label to be searched for in input. If max_label is not given, the positions of all objects are returned.

**Returns**

- `object_slices` : [list of tuples] A list of tuples, with each tuple containing N slices (with N the dimension of the input array). Slices correspond to the minimal parallelepiped that contains the object. If a number is missing, None is returned instead of a slice.

**See also:**

`label`, `center_of_mass`

**Notes**

This function is very useful for isolating a volume of interest inside a 3-D array, that cannot be “seen through”.

**Examples**

```python
>>> from scipy import ndimage
>>> a = np.zeros((6,6), dtype=int)
>>> a[2:4, 2:4] = 1
>>> a[4, 4] = 1
```

(continues on next page)
```python
>>> a[2:3] = 2
>>> a[0, 5] = 3
>>> a
array([[2, 2, 2, 0, 0, 3],
        [2, 2, 0, 0, 0, 0],
        [0, 0, 1, 1, 0, 0],
        [0, 0, 1, 1, 0, 0],
        [0, 0, 0, 0, 1, 0],
        [0, 0, 0, 0, 0, 0]])
```

```python
>>> ndimage.find_objects(a)
[(slice(2, 5, None), slice(2, 5, None)), (slice(0, 2, None), slice(0, 3, None)), (slice(0, 1, None), slice(5, 6, None))]
```

```python
>>> ndimage.find_objects(a, max_label=2)
[(slice(2, 5, None), slice(2, 5, None)), (slice(0, 2, None), slice(0, 3, None))]
```

```python
>>> ndimage.find_objects(a == 1, max_label=2)
[(slice(2, 5, None), slice(2, 5, None)), None]
```

```python
>>> loc = ndimage.find_objects(a)[0]
>>> a[loc]
array([[1, 1, 0],
        [1, 1, 0],
        [0, 0, 1]])
```

---

Scipy ndimage.histogram

**scipy.ndimage.histogram** (*input*, *min*, *max*, *bins*, *labels=None*, *index=None*)

Calculate the histogram of the values of an array, optionally at labels.

Histogram calculates the frequency of values in an array within bins determined by *min*, *max*, and *bins*. The *labels* and *index* keywords can limit the scope of the histogram to specified sub-regions within the array.

**Parameters**

- **input** [array_like] Data for which to calculate histogram.
- **min**, **max** [int] Minimum and maximum values of range of histogram bins.
- **bins** [int] Number of bins.
- **labels** [array_like, optional] Labels for objects in *input*. If not None, must be same shape as *input*.
- **index** [int or sequence of ints, optional] Label or labels for which to calculate histogram. If None, all values where label is greater than zero are used.

**Returns**

- **hist** [ndarray] Histogram counts.

**Examples**

```python
>>> a = np.array([[ 0. , 0.2146, 0.5962, 0. ],
...                [ 0. , 0.7778, 0. , 0. ],
...                [ 0. , 0. , 0. , 0. ],
...                [ 0. , 0. , 0.7181, 0.2787],
...                [ 0. , 0. , 0.6573, 0.3094]])
```

```python
>>> from scipy import ndimage
```

(continues on next page)
With labels and no indices, non-zero elements are counted:

```python
>>> lbl, nlbl = ndimage.label(a)
>>> ndimage.measurements.histogram(a, 0, 1, 10, lbl)
array([0, 0, 2, 1, 0, 1, 1, 2, 0, 0])
```

Indices can be used to count only certain objects:

```python
>>> ndimage.measurements.histogram(a, 0, 1, 10, lbl, 2)
array([0, 0, 1, 1, 0, 0, 1, 1, 0, 0])
```

**scipy.ndimage.label**

**scipy.ndimage.label**(input, structure=None, output=None)

Label features in an array.

**Parameters**

- **input** [array_like] An array-like object to be labeled. Any non-zero values in `input` are counted as features and zero values are considered the background.

- **structure** [array_like, optional] A structuring element that defines feature connections. `structure` must be symmetric. If no structuring element is provided, one is automatically generated with a squared connectivity equal to one. That is, for a 2-D `input` array, the default structuring element is:

  ```
  
  [[0,1,0],
  [1,1,1],
  [0,1,0]]
  ```

- **output** [(None, data-type, array_like), optional] If `output` is a data type, it specifies the type of the resulting labeled feature array. If `output` is an array-like object, then `output` will be updated with the labeled features from this function. This function can operate in-place, by passing `output=input`. Note that the output must be able to store the largest label, or this function will raise an Exception.

**Returns**

- **label** [ndarray or int] An integer ndarray where each unique feature in `input` has a unique label in the returned array.

- **num_features** [int] How many objects were found.

  If `output` is None, this function returns a tuple of `(labeled_array, num_features)`. If `output` is a ndarray, then it will be updated with values in `labeled_array` and only `num_features` will be returned by this function.

**See also:**

- **find_objects**

  generate a list of slices for the labeled features (or objects); useful for finding features' position or dimensions
Examples

Create an image with some features, then label it using the default (cross-shaped) structuring element:

```python
>>> from scipy.ndimage import label, generate_binary_structure
>>> a = np.array([[0, 0, 1, 1, 0],
...                [0, 0, 1, 0, 0],
...                [1, 1, 0, 1, 0],
...                [0, 0, 0, 1, 0]],
...               dtype=int)
>>> labeled_array, num_features = label(a)
```

Each of the 4 features are labeled with a different integer:

```python
>>> num_features
4
>>> labeled_array
array([[0, 0, 1, 1, 0],
        [0, 0, 1, 0, 0],
        [2, 2, 0, 0, 3],
        [0, 0, 0, 1, 0]],
       dtype=int)
```

Generate a structuring element that will consider features connected even if they touch diagonally:

```python
>>> s = generate_binary_structure(2, 2)
```

or,

```python
>>> s = [[1, 1, 1],
...       [1, 0, 1],
...       [1, 1, 1]]
```

Label the image using the new structuring element:

```python
>>> labeled_array, num_features = label(a, structure=s)
```

Show the 2 labeled features (note that features 1, 3, and 4 from above are now considered a single feature):

```python
>>> num_features
2
>>> labeled_array
array([[0, 0, 1, 1, 0],
        [0, 0, 1, 0, 0],
        [2, 2, 0, 0, 1],
        [0, 0, 0, 1, 0]],
       dtype=int)
```

### scipy.ndimage.labeled_comprehension

`scipy.ndimage.labeled_comprehension(input, labels, index, func, out_dtype, default, pass_positions=False)`

Roughly equivalent to `[func(input[labels == i]) for i in index]`.

Sequentially applies an arbitrary function (that works on array_like input) to subsets of an n-D image array specified by `labels` and `index`. The option exists to provide the function with positional parameters as the second argument.

### Parameters

- **input**: Input n-D array.
- **labels**: Labels used to index the input array, with 0 indexing.
- **index**: Labels specifying subsets of `input` to operate on.
- **func**: Function to apply to the subsets of `input` specified by `labels` and `index`.
- **out_dtype**: Data type of the output array.
- **default**: Default value to use for labels not found in `index`.
- **pass_positions**: Whether to pass positional arguments to `func`.

---

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input  [array_like] Data from which to select labels to process.
labels [array_like or None] Labels to objects in input. If not None, array must be same shape as input. If None, func is applied to raveled input.
index  [int, sequence of ints or None] Subset of labels to which to apply func. If a scalar, a single value is returned. If None, func is applied to all non-zero values of labels.
func   [callable] Python function to apply to labels from input.
out_dtype  [dtype] Dtype to use for result.
default  [int, float or None] Default return value when a element of index does not exist in labels.
pass_positions  [bool, optional] If True, pass linear indices to func as a second argument. Default is False.

Returns

result  [ndarray] Result of applying func to each of labels to input in index.

Examples

```python
>>> a = np.array([[1, 2, 0, 0],
                 ... [5, 3, 0, 4],
                 ... [0, 0, 0, 7],
                 ... [9, 3, 0, 0]])
>>> from scipy import ndimage
>>> lbl, nlbl = ndimage.label(a)
>>> lbls = np.arange(1, nlbl+1)
>>> ndimage.labeled_comprehension(a, lbl, lbls, np.mean, float, 0)
array([ 2.75, 5.5 , 6. ])  # Falling back to default:

>>> lbls = np.arange(1, nlbl+2)
>>> ndimage.labeled_comprehension(a, lbl, lbls, np.mean, float, -1)
array([ 2.75, 5.5 , 6. , -1. ])  # Passing positions:

>>> def fn(val, pos):
...     print("fn says: %s : %s" % (val, pos))
...     return (val.sum()) if (pos.sum() % 2 == 0) else (-val.sum())
...  # Not passing positions:
>>> ndimage.labeled_comprehension(a, lbl, lbls, fn, float, 0, True)
fn says: [1 2 5 3] : [0 1 4 5]
fn says: [4 7] : [ 7 11]
fn says: [9 3] : [12 13]
array([ 11., 11., -12., 0.])
```

scipy.ndimage.maximum

`scipy.ndimage.maximum(input, labels=None, index=None)`

Calculate the maximum of the values of an array over labeled regions.

Parameters

input  [array_like] Array_like of values. For each region specified by labels, the maximal values of input over the region is computed.
labels [array_like, optional] An array of integers marking different regions over which the maximum value of input is to be computed. labels must have the same shape as input. If labels is not specified, the maximum over the whole array is returned.

index [array_like, optional] A list of region labels that are taken into account for computing the maxima. If index is None, the maximum over all elements where labels is non-zero is returned.

Returns

output [float or list of floats] List of maxima of input over the regions determined by labels and whose index is in index. If index or labels are not specified, a float is returned: the maximal value of input if labels is None, and the maximal value of elements where labels is greater than zero if index is None.

See also:
label, minimum, median, maximum_position, extrema, sum, mean, variance, standard_deviation

Notes
The function returns a Python list and not a Numpy array, use np.array to convert the list to an array.

Examples

```python
>>> a = np.arange(16).reshape((4,4))
>>> a
array([[ 0,  1,  2,  3],
       [ 4,  5,  6,  7],
       [ 8,  9, 10, 11],
       [12, 13, 14, 15]])
>>> labels = np.zeros_like(a)
>>> labels[:2,:2] = 1
>>> labels[2:,1:3] = 2
>>> labels
array([[1, 1, 0, 0],
       [1, 1, 0, 0],
       [0, 2, 2, 0],
       [0, 2, 2, 0]])
>>> from scipy import ndimage
>>> ndimage.maximum(a)
15.0
>>> ndimage.maximum(a, labels=labels, index=[1,2])
[5.0, 14.0]
>>> ndimage.maximum(a, labels=labels)
14.0

>>> b = np.array([[ 1,  2,  0,  0],
                [ 5,  3,  0,  4],
                [ 0,  0,  0,  7],
                [ 9,  3,  0,  0]])
>>> labels, labels_nb = ndimage.label(b)
>>> labels
array([[1, 1, 0, 0],
       [1, 1, 0, 2],
       [0, 0, 0, 2],
       [3, 3, 0, 0]])
>>> ndimage.maximum(b, labels=labels, index=np.arange(1, labels_nb + 1))
[5.0, 7.0, 9.0]
```
scipy.ndimage.maximum_position

**scipy.ndimage.maximum_position**(input, labels=None, index=None)

Find the positions of the maximums of the values of an array at labels.

For each region specified by labels, the position of the maximum value of input within the region is returned.

**Parameters**

- **input** [array_like] Array_like of values.
- **labels** [array_like, optional] An array of integers marking different regions over which the position of the maximum value of input is to be computed. labels must have the same shape as input. If labels is not specified, the location of the first maximum over the whole array is returned.
  The labels argument only works when index is specified.
- **index** [array_like, optional] A list of region labels that are taken into account for finding the location of the maxima. If index is None, the first maximum over all elements where labels is non-zero is returned.
  The index argument only works when labels is specified.

**Returns**

- **output** [list of tuples of ints] List of tuples of ints that specify the location of maxima of input over the regions determined by labels and whose index is in index.
  If index or labels are not specified, a tuple of ints is returned specifying the location of the first maximal value of input.

**See also:**

- label, minimum, median, maximum_position, extrema, sum, mean, variance, standard_deviation

scipy.ndimage.mean

**scipy.ndimage.mean**(input, labels=None, index=None)

Calculate the mean of the values of an array at labels.

**Parameters**

- **input** [array_like] Array on which to compute the mean of elements over distinct regions.
- **labels** [array_like, optional] Array of labels of same shape, or broadcastable to the same shape as input. All elements sharing the same label form one region over which the mean of the elements is computed.
- **index** [int or sequence of ints, optional] Labels of the objects over which the mean is to be computed. Default is None, in which case the mean for all values where label is greater than 0 is calculated.

**Returns**

- **out** [list] Sequence of same length as index, with the mean of the different regions labeled by the labels in index.

**See also:**

- ndimage.variance, ndimage.standard_deviation, ndimage.minimum, ndimage.maximum, ndimage.sum, ndimage.label

**Examples**
scipy.ndimage.median

scipy.ndimage.median(input, labels=None, index=None)
Calculate the median of the values of an array over labeled regions.

Parameters

- **input** [array_like] Array_like of values. For each region specified by labels, the median value of input over the region is computed.
- **labels** [array_like, optional] An array_like of integers marking different regions over which the median value of input is to be computed. labels must have the same shape as input. If labels is not specified, the median over the whole array is returned.
- **index** [array_like, optional] A list of region labels that are taken into account for computing the medians. If index is None, the median over all elements where labels is non-zero is returned.

Returns

- **median** [float or list of floats] List of medians of input over the regions determined by labels and whose index is in index. If index or labels are not specified, a float is returned: the median value of input if labels is None, and the median value of elements where labels is greater than zero if index is None.

See also:

label, minimum, maximum, extrema, sum, mean, variance, standard_deviation

Notes

The function returns a Python list and not a Numpy array, use np.array to convert the list to an array.

Examples

```python
>>> from scipy import ndimage
>>> a = np.array([[1, 2, 0, 1],
...               [5, 3, 0, 4],
...               [0, 0, 0, 7],
...               [9, 3, 0, 0]])
>>> labels, labels_nb = ndimage.label(a)
>>> labels
array([[1, 1, 0, 2],
...       [1, 1, 0, 2],
...       [1, 1, 0, 2],
...       [1, 1, 0, 2]])
```

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scipy.ndimage.minimize

**scipy.ndimage.minimize**(*input*, *labels=None*, *index=None*)

Calculate the minimum of the values of an array over labeled regions.

**Parameters**

- **input**: [array_like] Array_like of values. For each region specified by *labels*, the minimal values of *input* over the region is computed.
- **labels**: [array_like, optional] An array_like of integers marking different regions over which the minimum value of *input* is to be computed. *labels* must have the same shape as *input*. If *labels* is not specified, the minimum over the whole array is returned.
- **index**: [array_like, optional] A list of region labels that are taken into account for computing the minima. If *index* is None, the minimum over all elements where *labels* is non-zero is returned.

**Returns**

- **minimum**: [float or list of floats] List of minima of *input* over the regions determined by *labels* and whose index is in *index*. If *index* or *labels* are not specified, a float is returned: the minimal value of *input* if *labels* is None, and the minimal value of elements where *labels* is greater than zero if *index* is None.

**See also:**

*label*, *maximum*, *median*, *minimum_position*, *extrema*, *sum*, *mean*, *variance*, *standard_deviation*

**Notes**

The function returns a Python list and not a Numpy array, use *np.array* to convert the list to an array.

**Examples**

```python
>>> from scipy import ndimage
>>> a = np.array([[1, 2, 0, 0],
...               [5, 3, 0, 4],
...               [0, 0, 0, 7],
...               [9, 3, 0, 0]])
>>> labels, labels_nb = ndimage.label(a)
>>> labels
array([[1, 1, 0, 0],  
       [1, 1, 0, 2],  
       [0, 0, 0, 2],  
       [3, 3, 0, 0]])
>>> ndimage.minimum(a, labels=labels, index=np.arange(1, labels_nb + 1))
```

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[1.0, 4.0, 3.0]
>>> ndimage.minimum(a)
0.0
>>> ndimage.minimum(a, labels=labels)
1.0

scipy.ndimage.minimum_position

scipy.ndimage.minimum_position(input, labels=None, index=None)

Find the positions of the minimums of the values of an array at labels.

**Parameters**

- **input**: [array_like] Array_like of values.
- **labels**: [array_like, optional] An array of integers marking different regions over which the position of the minimum value of `input` is to be computed. `labels` must have the same shape as `input`. If `labels` is not specified, the location of the first minimum over the whole array is returned.
- **index**: [array_like, optional] A list of region labels that are taken into account for finding the location of the minima. If `index` is None, the first minimum over all elements where `labels` is non-zero is returned.

The `labels` argument only works when `index` is specified.

The `index` argument only works when `labels` is specified.

**Returns**

- **output**: [list of tuples of ints] Tuple of ints or list of tuples of ints that specify the location of minima of `input` over the regions determined by `labels` and whose index is in `index`.

If `index` or `labels` are not specified, a tuple of ints is returned specifying the location of the first minimal value of `input`.

See also:

- label, minimum, median, maximum_position, extrema, sum, mean, variance, standard_deviation

**Examples**

```python
>>> a = np.array([[10, 20, 30],
...                [40, 80, 100],
...                [1, 100, 200]])
>>> b = np.array([[1, 2, 0, 1],
...                [5, 3, 0, 4],
...                [0, 0, 0, 7],
...                [9, 3, 0, 0]])

>>> from scipy import ndimage

>>> ndimage.minimum_position(a)
(2, 0)
>>> ndimage.minimum_position(b)
(0, 2)
```

Features to process can be specified using `labels` and `index`:
>>> label, pos = ndimage.label(a)
>>> ndimage.minimum_position(a, label, index=np.arange(1, pos+1))
[(2, 0)]

>>> label, pos = ndimage.label(b)
>>> ndimage.minimum_position(b, label, index=np.arange(1, pos+1))
[(0, 0), (0, 3), (3, 1)]

scipy.ndimage.standard_deviation

scipy.ndimage.standard_deviation(input, labels=None, index=None)
Calculate the standard deviation of the values of an n-D image array, optionally at specified sub-regions.

Parameters

input [array_like] Nd-image data to process.
lables [array_like, optional] Labels to identify sub-regions in input. If not None, must be same shape as input.
index [int or sequence of ints, optional] labels to include in output. If None (default), all values where labels is non-zero are used.

Returns

standard_deviation [float or ndarray] Values of standard deviation, for each sub-region if labels and index are specified.

See also:

label, variance, maximum, minimum, extrema

Examples

>>> a = np.array([[1, 2, 0, 0],
... [5, 3, 0, 4],
... [0, 0, 0, 7],
... [9, 3, 0, 0]])
>>> from scipy import ndimage
>>> ndimage.standard_deviation(a)
2.7585095613392387

Features to process can be specified using labels and index:

>>> lbl, nlbl = ndimage.label(a)
>>> ndimage.standard_deviation(a, lbl, index=np.arange(1, nlbl+1))
array([ 1.479, 1.5, 3.])

If no index is given, non-zero labels are processed:

>>> ndimage.standard_deviation(a, lbl)
2.4874688927665499

scipy.ndimage.sum

scipy.ndimage.sum(input, labels=None, index=None)
Calculate the sum of the values of the array.

Parameters
input  [array_like] Values of input inside the regions defined by labels are summed together.

labels  [array_like of ints, optional] Assign labels to the values of the array. Has to have the same shape as input.

index  [array_like, optional] A single label number or a sequence of label numbers of the objects to be measured.

Returns

sum  [ndarray or scalar] An array of the sums of values of input inside the regions defined by labels with the same shape as index. If ‘index’ is None or scalar, a scalar is returned.

See also:

mean, median

Examples

```python
>>> from scipy import ndimage
>>> input = [0, 1, 2, 3]
>>> labels = [1, 1, 2, 2]
>>> ndimage.sum(input, labels, index=[1, 2])
[1.0, 5.0]
>>> ndimage.sum(input, labels, index=1)
1
>>> ndimage.sum(input, labels)
6
```

scipy.ndimage.variance

scipy.ndimage.variance(input, labels=None, index=None)

Calculate the variance of the values of an n-D image array, optionally at specified sub-regions.

Parameters

input  [array_like] Nd-image data to process.

labels  [array_like, optional] Labels defining sub-regions in input. If not None, must be same shape as input.

index  [int or sequence of ints, optional] labels to include in output. If None (default), all values where labels is non-zero are used.

Returns

variance  [float or ndarray] Values of variance, for each sub-region if labels and index are specified.

See also:

label, standard_deviation, maximum, minimum, extrema

Examples

```python
>>> a = np.array([[1, 2, 0, 0],
...                [5, 3, 0, 4],
...                [0, 0, 0, 7],
...                [9, 3, 0, 1]])
>>> from scipy import ndimage
>>> ndimage.variance(a)
7.609375
```
Features to process can be specified using labels and index:

```python
>>> lbl, nlbl = ndimage.label(a)
>>> ndimage.variance(a, lbl, index=np.arange(1, nlbl+1))
array([ 2.1875,  2.25 ,  9. ])
```

If no index is given, all non-zero labels are processed:

```python
>>> ndimage.variance(a, lbl)
6.1875
```

`scipy.ndimage.watershed_ift`

`scipy.ndimage.watershed_ift(input, markers, structure=None, output=None)`

Apply watershed from markers using image foresting transform algorithm.

**Parameters**

- `input` [array_like] Input.
- `markers` [array_like] Markers are points within each watershed that form the beginning of the process. Negative markers are considered background markers which are processed after the other markers.
- `structure` [structure element, optional] A structuring element defining the connectivity of the object can be provided. If None, an element is generated with a squared connectivity equal to one.
- `output` [ndarray, optional] An output array can optionally be provided. The same shape as input.

**Returns**

`watershed_ift` [ndarray] Output. Same shape as input.

**References**

[1]

---

### 6.16.5 Morphology

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**scipy.ndimage.binary_closing**

`scipy.ndimage.binary_closing(input, structure=None, iterations=1, output=None, origin=0, mask=None, border_value=0, brute_force=False)`

Multi-dimensional binary closing with the given structuring element.

The *closing* of an input image by a structuring element is the *erosion* of the *dilation* of the image by the structuring element.

**Parameters**

- `input` [array_like] Binary array_like to be closed. Non-zero (True) elements form the subset to be closed.
- `structure` [array_like, optional] Structuring element used for the closing. Non-zero elements are considered True. If no structuring element is provided an element is generated with a square connectivity equal to one (i.e., only nearest neighbors are connected to the center, diagonally-connected elements are not considered neighbors).
- `iterations` [(int, float), optional] The dilation step of the closing, then the erosion step are each repeated `iterations` times (one, by default). If iterations is less than 1, each operation is repeated until the result does not change anymore.
- `output` [ndarray, optional] Array of the same shape as input, into which the output is placed. By default, a new array is created.
- `origin` [int or tuple of ints, optional] Placement of the filter, by default 0.
- `mask` [array_like, optional] If a mask is given, only those elements with a True value at the corresponding mask element are modified at each iteration. New in version 1.1.0.
- `border_value` [int (cast to 0 or 1), optional] Value at the border in the output array. New in version 1.1.0.
- `brute_force` [boolean, optional] Memory condition: if False, only the pixels whose value was changed in the last iteration are tracked as candidates to be updated in the current iteration; if true all pixels are considered as candidates for update, regardless of what happened in the previous iteration. False by default. New in version 1.1.0.

**Returns**
binary_closing
[ndarray of bools] Closing of the input by the structuring element.

See also:
grey_closing, binary_opening, binary_dilation, binary_erosion, generate_binary_structure

Notes
Closing [1] is a mathematical morphology operation [2] that consists in the succession of a dilation and an erosion of the input with the same structuring element. Closing therefore fills holes smaller than the structuring element.

Together with opening (binary_opening), closing can be used for noise removal.

References
[1], [2]

Examples
```python
>>> from scipy import ndimage
>>> a = np.zeros((5,5), dtype=int)
>>> a[1:-1, 1:-1] = 1; a[2,2] = 0
>>> a
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 0, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
>>> # Closing removes small holes
>>> ndimage.binary_closing(a).astype(int)
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
>>> # Closing is the erosion of the dilation of the input
>>> ndimage.binary_dilation(a).astype(int)
array([[0, 1, 1, 1, 0],
       [1, 1, 1, 1, 1],
       [1, 1, 1, 1, 1],
       [1, 1, 1, 1, 0],
       [0, 1, 1, 1, 0]])
>>> ndimage.binary_erosion(ndimage.binary_dilation(a)).astype(int)
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])

>>> a = np.zeros((7,7), dtype=int)
>>> a[1:6, 2:5] = 1; a[1:3,3] = 0
>>> a
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 0, 1, 0, 0],
       [0, 0, 1, 0, 1, 0, 0],
       [0, 0, 0, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```
>>> # In addition to removing holes, closing can also
>>> # coarsen boundaries with fine hollows.

```python
>>> ndimage.binary_closing(a).astype(int)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 0, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```
```python
>>> ndimage.binary_closing(a, structure=np.ones((2,2))).astype(int)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```

### scipy.ndimage.binary_dilation

`scipy.ndimage.binary_dilation(input, structure=None, iterations=1, mask=None, output=None, border_value=0, origin=0, brute_force=False)`

Multi-dimensional binary dilation with the given structuring element.

**Parameters**

- **input** [array_like] Binary array_like to be dilated. Non-zero (True) elements form the subset to be dilated.
- **structure** [array_like, optional] Structuring element used for the dilation. Non-zero elements are considered True. If no structuring element is provided an element is generated with a square connectivity equal to one.
- **iterations** [{int, float}, optional] The dilation is repeated `iterations` times (one, by default). If iterations is less than 1, the dilation is repeated until the result does not change anymore.
- **mask** [array_like, optional] If a mask is given, only those elements with a True value at the corresponding mask element are modified at each iteration.
- **output** [ndarray, optional] Array of the same shape as input, into which the output is placed. By default, a new array is created.
- **border_value** [int (cast to 0 or 1), optional] Value at the border in the output array.
- **origin** [int or tuple of ints, optional] Placement of the filter, by default 0.
- **brute_force** [boolean, optional] Memory condition: if False, only the pixels whose value was changed in the last iteration are tracked as candidates to be updated (dilated) in the current iteration; if True all pixels are considered as candidates for dilation, regardless of what happened in the previous iteration. False by default.

**Returns**
binary_dilation  
[ndarray of bools] Dilation of the input by the structuring element.

See also:

grey_dilation, binary_erosion, binary_closing, binary_opening, generate_binary_structure

Notes
Dilation [1] is a mathematical morphology operation [2] that uses a structuring element for expanding the shapes in an image. The binary dilation of an image by a structuring element is the locus of the points covered by the structuring element, when its center lies within the non-zero points of the image.

References
[1], [2]

Examples

```python
>>> from scipy import ndimage
>>> a = np.zeros((5, 5))
>>> a[2, 2] = 1
>>> a
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
>>> ndimage.binary_dilation(a)
array([[False, False, False, False, False],
       [False, False, True, False, False],
       [False, True, True, True, False],
       [False, False, True, False, False],
       [False, False, False, False, False]], dtype=bool)
>>> ndimage.binary_dilation(a).astype(a.dtype)
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
>>> # 3x3 structuring element with connectivity 1, used by default
>>> struct1 = ndimage.generate_binary_structure(2, 1)
>>> struct1
array([[False, True, False],
       [True, True, True],
       [False, True, False]], dtype=bool)
>>> # 3x3 structuring element with connectivity 2
>>> struct2 = ndimage.generate_binary_structure(2, 2)
>>> struct2
array([[True, True, True],
       [True, True, True],
       [True, True, True]], dtype=bool)
>>> ndimage.binary_dilation(a, structure=struct1).astype(a.dtype)
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
>>> ndimage.binary_dilation(a, structure=struct2).astype(a.dtype)
```

(continues on next page)
scipy.ndimage.binary_erosion

scipy.ndimage.binary_erosion(input, structure=None, iterations=1, mask=None, output=None, border_value=0, origin=0, brute_force=False)

Multi-dimensional binary erosion with a given structuring element.

Binary erosion is a mathematical morphology operation used for image processing.

**Parameters**

- **input** [array_like] Binary image to be eroded. Non-zero (True) elements form the subset to be eroded.
- **structure** [array_like, optional] Structuring element used for the erosion. Non-zero elements are considered True. If no structuring element is provided, an element is generated with a square connectivity equal to one.
- **iterations** [{int, float}, optional] The erosion is repeated iterations times (one, by default). If iterations is less than 1, the erosion is repeated until the result does not change anymore.
- **mask** [array_like, optional] If a mask is given, only those elements with a True value at the corresponding mask element are modified at each iteration.
- **output** [ndarray, optional] Array of the same shape as input, into which the output is placed. By default, a new array is created.
- **border_value** [int (cast to 0 or 1), optional] Value at the border in the output array.
- **origin** [int or tuple of ints, optional] Placement of the filter, by default 0.
- **brute_force** [boolean, optional] Memory condition: if False, only the pixels whose value was changed in the last iteration are tracked as candidates to be updated (eroded) in the current iteration; if True all pixels are considered as candidates for erosion, regardless of what happened in the previous iteration. False by default.

**Returns**

- **binary_erosion** [ndarray of bools] Erosion of the input by the structuring element.

See also:

grey_erosion, binary_dilation, binary_closing, binary_opening, generate_binary_structure
Notes
Erosion [1] is a mathematical morphology operation [2] that uses a structuring element for shrinking the shapes in an image. The binary erosion of an image by a structuring element is the locus of the points where a superimposition of the structuring element centered on the point is entirely contained in the set of non-zero elements of the image.

References
[1], [2]

Examples

```python
>>> from scipy import ndimage
>>> a = np.zeros((7,7), dtype=int)
>>> a[1:6, 2:5] = 1
>>> a
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```
```python
>>> ndimage.binary_erosion(a).astype(a.dtype)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 1, 0, 0, 0],
       [0, 0, 0, 1, 0, 0, 0],
       [0, 0, 0, 1, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```

```python
>>> #Erosion removes objects smaller than the structure
>>> ndimage.binary_erosion(a, structure=np.ones((5,5))).astype(a.dtype)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```
```

**scipy.ndimage.binary_fill_holes**

Fill the holes in binary objects.

**Parameters**

- **input** [array_like] n-dimensional binary array with holes to be filled
- **structure** [array_like, optional] Structuring element used in the computation; large-size elements make computations faster but may miss holes separated from the background by thin regions. The default element (with a square connectivity equal to one) yields the intuitive result where all holes in the input have been filled.
- **output** [ndarray, optional] Array of the same shape as input, into which the output is placed. By default, a new array is created.
- **origin** [int, tuple of ints, optional] Position of the structuring element.
Returns

out [ndarray] Transformation of the initial image input where holes have been filled.

See also:

`binary_dilation`, `binary_propagation`, `label`

Notes
The algorithm used in this function consists in invading the complementary of the shapes in input from the outer boundary of the image, using binary dilations. Holes are not connected to the boundary and are therefore not invaded. The result is the complementary subset of the invaded region.

References
[1]

Examples

```python
>>> from scipy import ndimage
>>> a = np.zeros((5, 5), dtype=int)
>>> a[1:4, 1:4] = 1
>>> a[2, 2] = 0
>>> a
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 0, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
>>> ndimage.binary_fill_holes(a).astype(int)
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
>>> # Too big structuring element
>>> ndimage.binary_fill_holes(a, structure=np.ones((5,5))).astype(int)
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 0, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
```

`scipy.ndimage.binary_hit_or_miss`

`scipy.ndimage.binary_hit_or_miss(input, structure1=None, structure2=None, output=None, origin1=0, origin2=None)`

Multi-dimensional binary hit-or-miss transform.

The hit-or-miss transform finds the locations of a given pattern inside the input image.

Parameters

- **input** [array_like (cast to booleans)] Binary image where a pattern is to be detected.
- **structure1** [array_like (cast to booleans), optional] Part of the structuring element to be fitted to the foreground (non-zero elements) of input. If no value is provided, a structure of square connectivity 1 is chosen.
- **structure2**
Second part of the structuring element that has to miss completely the foreground. If no value is provided, the complementary of `structure1` is taken.

**output**

- `ndarray`, optional: Array of the same shape as `input`, into which the output is placed. By default, a new array is created.

**origin1**

- `int` or `tuple of ints`, optional: Placement of the first part of the structuring element `structure1`, by default 0 for a centered structure.

**origin2**

- `int` or `tuple of ints`, optional: Placement of the second part of the structuring element `structure2`, by default 0 for a centered structure. If a value is provided for `origin1` and not for `origin2`, then `origin2` is set to `origin1`.

**Returns**

`binary_hit_or_miss`

- `ndarray`: Hit-or-miss transform of `input` with the given structuring element (`structure1`, `structure2`).

See also:

`ndimage.morphology`, `binary_erosion`

**References**

[1]

**Examples**

```python
define the zero image
>>> from scipy import ndimage
>>> a = np.zeros((7,7), dtype=int)
```
scipy.ndimage.binary_opening

**scipy.ndimage.binary_opening** *(input, structure=None, iterations=1, output=None, origin=0, mask=None, border_value=0, brute_force=False)*

Multi-dimensional binary opening with the given structuring element.

The opening of an input image by a structuring element is the dilation of the erosion of the image by the structuring element.

**Parameters**

- **input**: [array_like] Binary array_like to be opened. Non-zero (True) elements form the subset to be opened.
- **structure**: [array_like, optional] Structuring element used for the opening. Non-zero elements are considered True. If no structuring element is provided an element is generated with a square connectivity equal to one (i.e., only nearest neighbors are connected to the center, diagonally-connected elements are not considered neighbors).
- **iterations**: [{int, float}, optional] The erosion step of the opening, then the dilation step are each repeated iterations times (one, by default). If iterations is less than 1, each operation is repeated until the result does not change anymore.
- **output**: [ndarray, optional] Array of the same shape as input, into which the output is placed. By default, a new array is created.
- **origin**: [int or tuple of ints, optional] Placement of the filter, by default 0.
- **mask**: [array_like, optional] If a mask is given, only those elements with a True value at the corresponding mask element are modified at each iteration. New in version 1.1.0.
- **border_value**: [int (cast to 0 or 1), optional] Value at the border in the output array. New in version 1.1.0.
- **brute_force**: [boolean, optional] Memory condition: if False, only the pixels whose value was changed in the last iteration are tracked as candidates to be updated in the current iteration; if true all pixels are considered as candidates for update, regardless of what happened in the previous iteration. False by default. New in version 1.1.0.

**Returns**

- **binary_opening**: [ndarray of bools] Opening of the input by the structuring element.

See also:

- grey_opening, binary_closing, binary_erosion, binary_dilation, generate_binary_structure
Notes
Opening [1] is a mathematical morphology operation [2] that consists in the succession of an erosion and a dilation of the input with the same structuring element. Opening therefore removes objects smaller than the structuring element.

Together with closing (binary_closing), opening can be used for noise removal.

References
[1], [2]

Examples
```python
>>> from scipy import ndimage
>>> a = np.zeros((5,5), dtype=int)
>>> a[1:4, 1:4] = 1; a[4, 4] = 1
>>> a
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 1]])
>>> # Opening removes small objects
>>> ndimage.binary_opening(a, structure=np.ones((3,3))).astype(int)
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
>>> # Opening can also smooth corners
>>> ndimage.binary_opening(a).astype(int)
array([[0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0],
       [0, 1, 1, 0, 0],
       [0, 0, 0, 0, 0]])
>>> # Opening is the dilation of the erosion of the input
>>> ndimage.binary_erosion(a).astype(int)
array([[0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0],
       [0, 0, 0, 0, 0]])
>>> ndimage.binary_dilation(ndimage.binary_erosion(a)).astype(int)
array([[0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0],
       [0, 1, 1, 0, 0],
       [0, 0, 0, 0, 0]])
```

scipy.ndimage.binary_propagation

scipy.ndimage.binary_propagation(input, structure=None, mask=None, output=None, border_value=0, origin=0)

Multi-dimensional binary propagation with the given structuring element.

Parameters
input  [array_like] Binary image to be propagated inside mask.
structure  [array_like, optional] Structuring element used in the successive dilations. The output may depend on the structuring element, especially if mask has several connex components. If no structuring element is provided, an element is generated with a squared connectivity equal to one.
mask  [array_like, optional] Binary mask defining the region into which input is allowed to propagate.
output  [ndarray, optional] Array of the same shape as input, into which the output is placed. By default, a new array is created.
border_value  [int (cast to 0 or 1), optional] Value at the border in the output array.
origin  [int or tuple of ints, optional] Placement of the filter, by default 0.

Returns


Notes
This function is functionally equivalent to calling binary_dilation with the number of iterations less than one: iterative dilation until the result does not change anymore.

The succession of an erosion and propagation inside the original image can be used instead of an opening for deleting small objects while keeping the contours of larger objects untouched.

References
[1], [2]

Examples

```python
>>> from scipy import ndimage
>>> input = np.zeros((8, 8), dtype=int)
>>> input[2, 2] = 1
>>> mask = np.zeros((8, 8), dtype=int)
>>> input
array([[0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0]])
>>> mask
array([[0, 0, 0, 0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 0, 0, 0, 1, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 1, 1],
       [0, 0, 0, 0, 0, 0, 1, 1]])
>>> ndimage.binary_propagation(input, mask=mask).astype(int)
array([[0, 0, 0, 0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 0, 0, 0, 1, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 1, 1],
       [0, 0, 0, 0, 0, 0, 1, 1]], dtype=int32)
```
```python
>>> ndimage.binary_propagation(input, mask=mask,
... structure=np.ones((3,3))).astype(int)
array([[0, 0, 0, 0, 0, 0, 0, 0],
       [0, 1, 1, 0, 0, 0, 0, 0],
       [0, 1, 1, 0, 0, 0, 0, 0],
       [0, 1, 1, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0]])
```

```python
>>> ndimage.binary_opening(a).astype(int)
array([[0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0]])
```

```python
>>> ndimage.binary_erosion(a)
```

```python
>>> ndimage.binary_propagation(b, mask=a).astype(int)
array([[0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0]])
```
scipy.ndimage.black_tophat

scipy.ndimage.black_tophat(input, size=None, footprint=None, structure=None, output=None, mode='reflect', cval=0.0, origin=0)

Multi-dimensional black tophat filter.

Parameters

- input: [array_like] Input.
- size: [tuple of ints, optional] Shape of a flat and full structuring element used for the filter. Optional if footprint or structure is provided.
- footprint: [array of ints, optional] Positions of non-infinite elements of a flat structuring element used for the black tophat filter.
- structure: [array of ints, optional] Structuring element used for the filter. structure may be a non-flat structuring element.
- output: [array, optional] An array used for storing the output of the filter may be provided.
- mode: [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The mode parameter determines how the array borders are handled, where cval is the value when mode is equal to ‘constant’. Default is ‘reflect’.
- cval: [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is 0.0.
- origin: [scalar, optional] The origin parameter controls the placement of the filter. Default 0

Returns

- black_tophat: [ndarray] Result of the filter of input with structure.

See also:

white_tophat, grey_opening, grey_closing

scipy.ndimage.distance_transform_bf

scipy.ndimage.distance_transform_bf(input, metric='euclidean', sampling=None, return_distances=True, return_indices=False, distances=None, indices=None)

Distance transform function by a brute force algorithm.

This function calculates the distance transform of the input, by replacing each foreground (non-zero) element, with its shortest distance to the background (any zero-valued element).

In addition to the distance transform, the feature transform can be calculated. In this case the index of the closest background element is returned along the first axis of the result.

Parameters

- input: [array_like] Input
- metric: [str, optional] Three types of distance metric are supported: ‘euclidean’, ‘taxicab’ and ‘chessboard’.
- sampling: [{int, sequence of ints}, optional] This parameter is only used in the case of the euclidean metric distance transform. The sampling along each axis can be given by the sampling parameter which should be a sequence of length equal to the input rank, or a single number in which the sampling is assumed to be equal along all axes.
- return_distances: [bool, optional] The return_distances flag can be used to indicate if the distance transform is returned.
The default is True.

**return_indices**
- [bool, optional] The return_indices flags can be used to indicate if the feature transform is returned. The default is False.

**distances**
- [float64 ndarray, optional] Optional output array to hold distances (if return_distances is True).

**indices**
- [int64 ndarray, optional] Optional output array to hold indices (if return_indices is True).

**Returns**
- **distances** [ndarray] Distance array if return_distances is True.
- **indices** [ndarray] Indices array if return_indices is True.

**Notes**
This function employs a slow brute force algorithm, see also the function distance_transform_cdt for more efficient taxicab and chessboard algorithms.

**scipy.ndimage.distance_transform_cdt**

**scipy.ndimage.distance_transform_cdt**(input, metric='chessboard', return_distances=True, return_indices=False, distances=None, indices=None)

Distance transform for chamfer type of transforms.

**Parameters**
- **input** [array_like] Input
- **metric** ['chessboard', 'taxicab'], optional] The metric determines the type of chamfering that is done. If the metric is equal to 'taxicab' a structure is generated using generate_binary_structure with a squared distance equal to 1. If the metric is equal to 'chessboard', a metric is generated using generate_binary_structure with a squared distance equal to the dimensionality of the array. These choices correspond to the common interpretations of the ‘taxicab’ and the ‘chessboard’ distance metrics in two dimensions. The default for metric is ‘chessboard’.
- **return_distances, return_indices**
  - [bool, optional] The return_distances, and return_indices flags can be used to indicate if the distance transform, the feature transform, or both must be returned. If the feature transform is returned (return_indices=True), the index of the closest background element is returned along the first axis of the result. The return_distances default is True, and the return_indices default is False.
- **distances, indices**
  - [ndarrays of int32, optional] The distances and indices arguments can be used to give optional output arrays that must be the same shape as input.

**scipy.ndimage.distance_transform_edt**

**scipy.ndimage.distance_transform_edt**(input, sampling=None, return_distances=True, return_indices=False, distances=None, indices=None)

Exact euclidean distance transform.

In addition to the distance transform, the feature transform can be calculated. In this case the index of the closest background element is returned along the first axis of the result.

**Parameters**
input : [array_like] Input data to transform. Can be any type but will be converted into
binary: 1 wherever input equates to True, 0 elsewhere.
sampling : [float or int, or sequence of same, optional] Spacing of elements along each dimen-
sion. If a sequence, must be of length equal to the input rank; if a single number,
this is used for all axes. If not specified, a grid spacing of unity is implied.
return_distances : [bool, optional] Whether to return distance matrix. At least one of re-
turn_distances/return_indices must be True. Default is True.
return_indices : [bool, optional] Whether to return indices matrix. Default is False.
distances : [ndarray, optional] Used for output of distance array, must be of type float64.
indices : [ndarray, optional] Used for output of indices, must be of type int32.

Returns

distance_transform_edt
[ndarray or list of ndarrays] Either distance matrix, index matrix, or a list of the
two, depending on return_x flags and distance and indices input parameters.

Notes
The euclidean distance transform gives values of the euclidean distance:

\[
y_i = \sqrt{\sum_{i} (x[i]-b[i])^2}
\]

where b[i] is the background point (value 0) with the smallest Euclidean distance to input points x[i],
and n is the number of dimensions.

Examples

```python
>>> from scipy import ndimage
>>> a = np.array([[0,1,1,1,1],
    ...                [0,0,1,1,1],
    ...                [0,1,1,1,1],
    ...                [0,1,1,0,0],
    ...                [0,1,1,0,0]])
>>> ndimage.distance_transform_edt(a)
array([[ 0. , 1. , 1.4142, 2.2361, 3. ],
       [ 0. , 0. , 1. , 2. , 2. ],
       [ 0. , 1. , 1.4142, 1.4142, 1. ],
       [ 0. , 1. , 1.4142, 1. , 0. ],
       [ 0. , 1. , 1. , 0. , 0. ]])
```

With a sampling of 2 units along x, 1 along y:

```python
>>> ndimage.distance_transform_edt(a, sampling=[2,1])
array([[ 0. , 1. , 2. , 2.8284, 3.6056],
       [ 0. , 0. , 1. , 2. , 3. ],
       [ 0. , 1. , 2. , 2.3624, 2. ],
       [ 0. , 1. , 2. , 1. , 0. ],
       [ 0. , 1. , 1. , 0. , 0. ]])
```

Asking for indices as well:

```python
>>> ndimage.distance_transform_edt(a, sampling=[2,1])
array([[ 0. , 1. , 2. , 2.8284, 3.6056],
       [ 0. , 0. , 1. , 2. , 3. ],
       [ 0. , 1. , 2. , 2.3624, 2. ],
       [ 0. , 1. , 2. , 1. , 0. ],
       [ 0. , 1. , 1. , 0. , 0. ]])
```
```python
>>> edt, inds = ndimage.distance_transform_edt(a, return_indices=True)
```
```python
>>> inds
array([[0, 0, 1, 1, 3],
       [1, 1, 1, 1, 3],
       [2, 2, 1, 3, 3],
       [3, 3, 4, 4, 3],
       [4, 4, 4, 4, 4]],
      [[0, 0, 1, 1, 4],
       [0, 1, 1, 1, 4],
       [0, 0, 1, 4, 4],
       [0, 0, 3, 3, 4],
       [0, 0, 3, 3, 4]])
```

With arrays provided for inplace outputs:

```python
>>> indices = np.zeros(((np.ndim(a),) + a.shape), dtype=np.int32)
>>> ndimage.distance_transform_edt(a, return_indices=True, indices=indices)
array([[ 0. , 1. , 1.4142, 2.2361, 3. ]],
      [[ 0. , 0. , 1. , 2. , 2. ]],
      [[ 0. , 1. , 1.4142, 1.4142, 1. ]],
      [[ 0. , 1. , 1.4142, 1. , 0. ]],
      [[ 0. , 1. , 1. , 0. , 0. ]])
```
```python
>>> indices
array([[0, 0, 1, 1, 3],
       [1, 1, 1, 1, 3],
       [2, 2, 1, 3, 3],
       [3, 3, 4, 4, 3],
       [4, 4, 4, 4, 4]],
      [[0, 0, 1, 1, 4],
       [0, 1, 1, 1, 4],
       [0, 0, 1, 4, 4],
       [0, 0, 3, 3, 4],
       [0, 0, 3, 3, 4]])
```

`scipy.ndimage.generate_binary_structure`

`scipy.ndimage.generate_binary_structure(rank, connectivity)`

Generate a binary structure for binary morphological operations.

**Parameters**

- **rank** `[int]` Number of dimensions of the array to which the structuring element will be applied, as returned by `np.ndim`.
- **connectivity** `[int]` `connectivity` determines which elements of the output array belong to the structure, i.e. are considered as neighbors of the central element. Elements up to a squared distance of `connectivity` from the center are considered neighbors. `connectivity` may range from 1 (no diagonal elements are neighbors) to `rank` (all elements are neighbors).

**Returns**

- **output** `[ndarray of bools]` Structuring element which may be used for binary morphological operations, with `rank` dimensions and all dimensions equal to 3.
See also:

iterate_structure, binary_dilation, binary_erosion

Notes

generate_binary_structure can only create structuring elements with dimensions equal to 3, i.e. minimal dimensions. For larger structuring elements, that are useful e.g. for eroding large objects, one may either use iterate_structure, or create directly custom arrays with numpy functions such as numpy.ones.

Examples

```python
>>> from scipy import ndimage
>>> struct = ndimage.generate_binary_structure(2, 1)
>>> struct
array([[False,  True, False],
       [ True,  True,  True],
       [False,  True, False]], dtype=bool)
>>> a = np.zeros((5,5))
>>> a[2, 2] = 1
>>> a
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  1.,  0.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]], dtype=int)
>>> b = ndimage.binary_dilation(a, structure=struct).astype(a.dtype)
>>> b
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]], dtype=int)
>>> ndimage.binary_dilation(b, structure=struct).astype(a.dtype)
array([[ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 1.,  1.,  1.,  1.,  1.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.]], dtype=int)
>>> struct = ndimage.generate_binary_structure(2, 2)
>>> struct
array([[ True,  True,  True],
       [ True,  True,  True],
       [ True,  True,  True]], dtype=bool)
>>> struct = ndimage.generate_binary_structure(3, 1)
>>> struct # no diagonal elements
array([[False, False, False],
       [False, True, False],
       [False, False, False]], dtype=bool)
```
scipy.ndimage.grey_closing

Parameters

- **input** [array_like] Array over which the grayscale closing is to be computed.
- **size** [tuple of ints] Shape of a flat and full structuring element used for the grayscale closing. Optional if footprint or structure is provided.
- **footprint** [array of ints, optional] Positions of non-infinite elements of a flat structuring element used for the grayscale closing.
- **structure** [array of ints, optional] Structuring element used for the grayscale closing. structure may be a non-flat structuring element.
- **output** [array, optional] An array used for storing the output of the closing may be provided.
- **mode** [{‘reflect’, ‘constant’, ‘nearest’, ‘mirror’, ‘wrap’}, optional] The mode parameter determines how the array borders are handled, where cval is the value when mode is equal to ‘constant’. Default is ‘reflect’
- **cval** [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is 0.0.
- **origin** [scalar, optional] The origin parameter controls the placement of the filter. Default is 0

Returns

- **grey_closing** [ndarray] Result of the grayscale closing of input with structure.

See also:

- `binary_closing`, `grey_dilation`, `grey_erosion`, `grey_opening`, `generate_binary_structure`

Notes

The action of a grayscale closing with a flat structuring element amounts to smoothen deep local minima, whereas binary closing fills small holes.

References

[1]

Examples

```python
code
>>> from scipy import ndimage
>>> a = np.arange(36).reshape((6,6))
>>> a[3,3] = 0
>>> a
array([[ 0,  1,  2,  3,  4,  5],
       [ 6,  7,  8,  9, 10, 11],
       [12, 13, 14, 15, 16, 17],
       [18, 19, 20,  0, 22, 23],
       [24, 25, 26, 27, 28, 29],
       [30, 31, 32, 33, 34, 35]])
>>> ndimage.grey_closing(a, size=(3,3))
array([[ 7,  7,  8,  9, 10, 11],
       [ 7,  7,  8,  9, 10, 11],
       [13, 13, 14, 15, 16, 17],
       [13, 13, 14, 15, 16, 17],
       [13, 13, 14, 15, 16, 17],
       [13, 13, 14, 15, 16, 17]])
```
scipy.ndimage.grey_dilation

scipy.ndimage.grey_dilation(input, size=None, footprint=None, structure=None, output=None, mode='reflect', cval=0.0, origin=0)

Calculate a greyscale dilation, using either a structuring element, or a footprint corresponding to a flat structuring element.

Grayscale dilation is a mathematical morphology operation. For the simple case of a full and flat structuring element, it can be viewed as a maximum filter over a sliding window.

Parameters

input [array_like] Array over which the grayscale dilation is to be computed.
size [tuple of ints] Shape of a flat and full structuring element used for the grayscale dilation. Optional if footprint or structure is provided.
footprint [array of ints, optional] Positions of non-infinite elements of a flat structuring element used for the grayscale dilation. Non-zero values give the set of neighbors of the center over which the maximum is chosen.
structure [array of ints, optional] Structuring element used for the grayscale dilation. structure may be a non-flat structuring element.
output [array, optional] An array used for storing the output of the dilation may be provided.
mode [{‘reflect’,’constant’,’nearest’,’mirror’, ‘wrap’}, optional] The mode parameter determines how the array borders are handled, where cval is the value when mode is equal to ‘constant’. Default is ‘reflect’
cval [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is 0.0.
origin [scalar, optional] The origin parameter controls the placement of the filter. Default 0

Returns

grey_dilation [ndarray] Grayscale dilation of input.

See also:
binary_dilation, grey_erosion, grey_closing, grey_opening, generate_binary_structure, ndimage.maximum_filter

Notes
The grayscale dilation of an image input by a structuring element s defined over a domain E is given by:

$$(input+s)(x) = \max \{input(y) + s(x-y), \text{for } y \in E\}$$

In particular, for structuring elements defined as s(y) = 0 for y in E, the grayscale dilation computes the maximum of the input image inside a sliding window defined by E.

Grayscale dilation [1] is a mathematical morphology operation [2].

References
[1], [2]
Examples

```python
>>> from scipy import ndimage
>>> a = np.zeros((7,7), dtype=int)
>>> a[2:5, 2:5] = 1
>>> a[4,4] = 2; a[2,3] = 3
>>> a
array([[0, 0, 0, 0, 0, 0, 0],
        [0, 0, 0, 0, 0, 0, 0],
        [0, 0, 1, 3, 1, 0, 0],
        [0, 0, 1, 1, 1, 0, 0],
        [0, 0, 1, 2, 0, 0],
        [0, 0, 0, 0, 0, 0, 0],
        [0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.grey_dilation(a, size=(3,3))
array([[0, 0, 0, 0, 0, 0, 0],
        [0, 1, 3, 3, 3, 1, 0],
        [0, 1, 3, 3, 3, 1, 0],
        [0, 1, 1, 2, 2, 2, 0],
        [0, 1, 1, 2, 2, 2, 0],
        [0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.grey_dilation(a, footprint=np.ones((3,3)))
array([[0, 0, 0, 0, 0, 0, 0],
        [0, 1, 3, 3, 3, 1, 0],
        [0, 1, 3, 3, 3, 1, 0],
        [0, 1, 1, 2, 2, 2, 0],
        [0, 1, 1, 2, 2, 2, 0],
        [0, 0, 0, 0, 0, 0, 0]])
>>> s = ndimage.generate_binary_structure(2,1)
>>> s
array([[False,  True, False],
        [ True,  True,  True],
        [False,  True, False]], dtype=bool)
>>> ndimage.grey_dilation(a, footprint=s)
array([[0, 0, 0, 0, 0, 0, 0],
        [0, 0, 1, 3, 1, 0, 0],
        [0, 1, 3, 3, 3, 1, 0],
        [0, 1, 1, 2, 2, 2, 0],
        [0, 0, 1, 1, 2, 0, 0],
        [0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.grey_dilation(a, size=(3,3), structure=np.ones((3,3)))
array([[1, 1, 1, 1, 1, 1],
        [1, 2, 4, 4, 4, 2],
        [1, 2, 4, 4, 4, 2],
        [1, 2, 4, 4, 4, 3],
        [1, 2, 3, 3, 3],
        [1, 2, 3, 3, 3],
        [1, 1, 1, 1],])
```
scipy.ndimage.grey_erosion

scipy.ndimage.grey_erosion(input, size=None, footprint=None, structure=None, output=None,
mode='reflect', cval=0.0, origin=0)

Calculate a greyscale erosion, using either a structuring element, or a footprint corresponding to a flat
structuring element.

Grayscale erosion is a mathematical morphology operation. For the simple case of a full and flat
structuring element, it can be viewed as a minimum filter over a sliding window.

Parameters

- **input**: [array_like] Array over which the grayscale erosion is to be computed.
- **size**: [tuple of ints] Shape of a flat and full structuring element used for the grayscale
  erosion. Optional if footprint or structure is provided.
- **footprint**: [array of ints, optional] Positions of non-infinite elements of a flat structuring ele-
  ment used for the grayscale erosion. Non-zero values give the set of neighbors of
  the center over which the minimum is chosen.
- **structure**: [array of ints, optional] Structuring element used for the grayscale erosion. struc-
  ture may be a non-flat structuring element.
- **output**: [array, optional] An array used for storing the output of the erosion may be pro-
  vided.
- **mode**: [{'reflect','constant','nearest','mirror', 'wrap'}, optional] The mode parameter de-
  termines how the array borders are handled, where cval is the value when mode is
  equal to 'constant'. Default is 'reflect'
- **cval**: [scalar, optional] Value to fill past edges of input if mode is 'constant'. Default is
  0.0.
- **origin**: [scalar, optional] The origin parameter controls the placement of the filter. Default

Returns

- **output**: [ndarray] Grayscale erosion of input.

See also:

- binary_erosion, grey_dilation, grey_opening, grey_closing, generate_binary_structure,
  ndimage.minimum_filter

Notes

The grayscale erosion of an image input by a structuring element s defined over a domain E is given
by:

\[ (input+s)(x) = \min\{input(y) - s(x-y), \text{ for } y \in E \} \]

In particular, for structuring elements defined as s(y) = 0 for y in E, the grayscale erosion computes
the minimum of the input image inside a sliding window defined by E.

Grayscale erosion [1] is a mathematical morphology operation [2].

References

[1], [2]

Examples

```python
>>> from scipy import ndimage
>>> a = np.zeros((7,7), dtype=int)
>>> a[1:6, 1:6] = 3
>>> a[4,4] = 2; a[2,3] = 1
>>> a
```

(continues on next page)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 3, 3, 3, 3, 3, 0],
       [0, 3, 3, 1, 3, 3, 0],
       [0, 3, 3, 3, 3, 3, 0],
       [0, 3, 3, 3, 2, 3, 0],
       [0, 3, 3, 3, 3, 3, 0],
       [0, 0, 0, 0, 0, 0, 0]])

>>> ndimage.grey_erosion(a, size=(3,3))
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 3, 2, 2, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])

>>> footprint = ndimage.generate_binary_structure(2, 1)

>>> footprint
array([[False, True, False],
        [True, True, True],
        [False, True, False]], dtype=bool)

>>> # Diagonally-connected elements are not considered neighbors
>>> ndimage.grey_erosion(a, size=(3,3), footprint=footprint)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 3, 1, 2, 0, 0],
       [0, 0, 3, 2, 2, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])

scipy.ndimage.grey_opening

scipy.ndimage.grey_opening(input, size=None, footprint=None, structure=None, output=None, mode='reflect', cval=0.0, origin=0)

Multi-dimensional greyscale opening.

A greyscale opening consists in the succession of a greyscale erosion, and a greyscale dilation.

**Parameters**

- **input** [array_like] Array over which the greyscale opening is to be computed.
- **size** [tuple of ints] Shape of a flat and full structuring element used for the greyscale opening. Optional if footprint or structure is provided.
- **footprint** [array of ints, optional] Positions of non-infinite elements of a flat structuring element used for the greyscale opening.
- **structure** [array of ints, optional] Structuring element used for the greyscale opening. structure may be a non-flat structuring element.
- **output** [array, optional] An array used for storing the output of the opening may be provided.
- **mode** ['reflect', 'constant', 'nearest', 'mirror', 'wrap'], optional The mode parameter determines how the array borders are handled, where cval is the value when mode is equal to 'constant'. Default is 'reflect'
cval [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is 0.0.

origin [scalar, optional] The origin parameter controls the placement of the filter. Default 0

Returns

grey_opening [ndarray] Result of the grayscale opening of input with structure.

See also:

binary_opening, grey_dilation, grey_erosion, grey_closing, generate_binary_structure

Notes

The action of a grayscale opening with a flat structuring element amounts to smoothen high local maxima, whereas binary opening erases small objects.

References

[1]

Examples

```python
>>> from scipy import ndimage
>>> a = np.arange(36).reshape((6,6))
>>> a[3,3] = 50
>>> a
array([[ 0, 1, 2, 3, 4, 5],
       [ 6, 7, 8, 9, 10, 11],
       [12, 13, 14, 50, 16, 17],
       [18, 19, 20, 21, 22, 23],
       [24, 25, 26, 27, 28, 29],
       [30, 31, 32, 33, 34, 35]])
>>> ndimage.grey_opening(a, size=(3,3))
array([[ 0, 1, 2, 3, 4, 4],
       [ 6, 7, 8, 9, 10, 10],
       [12, 13, 14, 15, 16, 16],
       [18, 19, 20, 22, 22, 22],
       [24, 25, 26, 27, 28, 28],
       [24, 25, 26, 27, 28, 28]])
>>> # Note that the local maximum a[3,3] has disappeared
```

scipy.ndimage.iterate_structure

scipy.ndimage.iterate_structure(structure, iterations, origin=None)

Iterate a structure by dilating it with itself.

Parameters

structure [array_like] Structuring element (an array of bools, for example), to be dilated with itself.

iterations [int] number of dilations performed on the structure with itself

origin [optional] If origin is None, only the iterated structure is returned. If not, a tuple of the iterated structure and the modified origin is returned.

Returns

iterate_structure
A new structuring element obtained by dilating \textit{structure} \((\text{iterations} - 1)\) times with itself.

\textbf{See also:}

generate\_binary\_structure

\textbf{Examples}

```python
>>> from scipy import ndimage
>>> struct = ndimage.generate_binary_structure(2, 1)
>>> struct.astype(int)
array([[0, 1, 0],
       [1, 1, 1],
       [0, 1, 0]])
>>> ndimage.iterate_structure(struct, 2).astype(int)
array([[0, 0, 1, 0, 0],
       [0, 1, 1, 1, 0],
       [1, 1, 1, 1, 1],
       [0, 1, 1, 1, 0],
       [0, 0, 1, 0, 0]])
>>> ndimage.iterate_structure(struct, 3).astype(int)
array([[0, 0, 0, 1, 0, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [1, 1, 1, 1, 1, 1, 1],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 0, 1, 0, 0, 0]])
```

\texttt{scipy.ndimage.morphological\_gradient}

\texttt{scipy.ndimage.morphological\_gradient} \((input, size=None, footprint=None, structure=None, output=None, mode='reflect', cval=0.0, origin=0)\)

Multi-dimensional morphological gradient.

The morphological gradient is calculated as the difference between a dilation and an erosion of the input with a given structuring element.

\textbf{Parameters}

- \textit{input} [array\_like] Array over which to compute the morphological gradient.
- \textit{size} [tuple of ints] Shape of a flat and full structuring element used for the mathematical morphology operations. Optional if \textit{footprint} or \textit{structure} is provided. A larger \textit{size} yields a more blurred gradient.
- \textit{footprint} [array of ints, optional] Positions of non-infinite elements of a flat structuring element used for the morphology operations. Larger footprints give a more blurred morphological gradient.
- \textit{structure} [array of ints, optional] Structuring element used for the morphology operations. \textit{structure} may be a non-flat structuring element.
- \textit{output} [array, optional] An array used for storing the output of the morphological gradient may be provided.
- \textit{mode} [\{'reflect', 'constant', 'nearest', 'mirror', 'wrap'\}, optional] The \textit{mode} parameter determines how the array borders are handled, where \textit{cval} is the value when \textit{mode} is equal to 'constant'. Default is 'reflect'.
- \textit{cval} [scalar, optional] Value to fill past edges of input if \textit{mode} is 'constant'. Default is 0.0.
origin  [scalar, optional] The origin parameter controls the placement of the filter. Default 0

Returns


See also:
grey_dilation, grey_erosion, ndimage.gaussian_gradient_magnitude

Notes

For a flat structuring element, the morphological gradient computed at a given point corresponds to the maximal difference between elements of the input among the elements covered by the structuring element centered on the point.

References

[1]

Examples

>>> from scipy import ndimage
>>> a = np.zeros((7,7), dtype=int)
>>> a[2:6, 2:5] = 1
>>> ndimage.morphological_gradient(a, size=(3,3))
array([[0, 0, 0, 0, 0, 0, 0],
[0, 1, 1, 1, 1, 1, 0],
[0, 1, 1, 1, 1, 1, 0],
[0, 1, 1, 0, 1, 1, 0],
[0, 1, 1, 1, 1, 1, 0],
[0, 1, 1, 1, 1, 1, 0],
[0, 0, 0, 0, 0, 0, 0]])
>>> # The morphological gradient is computed as the difference
>>> # between a dilation and an erosion
>>> ndimage.grey_dilation(a, size=(3,3)) -
... ndimage.grey_erosion(a, size=(3,3))
array([[0, 0, 0, 0, 0, 0, 0],
[0, 1, 1, 1, 1, 1, 0],
[0, 1, 1, 1, 1, 1, 0],
[0, 1, 1, 0, 1, 1, 0],
[0, 1, 1, 1, 1, 1, 0],
[0, 1, 1, 1, 1, 1, 0],
[0, 0, 0, 0, 0, 0, 0]])
>>> a = np.zeros((7,7), dtype=int)
>>> a[2:6, 2:5] = 1
>>> a[4,4] = 2; a[2,3] = 3
>>> a
array([[0, 0, 0, 0, 0, 0, 0],
[0, 0, 0, 0, 0, 0, 0],
[0, 0, 1, 3, 1, 0, 0],
[0, 0, 1, 1, 1, 0, 0],
[0, 0, 1, 1, 1, 0, 0],
[0, 0, 0, 0, 0, 0, 0],
[0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.morphological_gradient(a, size=(3,3))
array([[0, 0, 0, 0, 0, 0, 0],
[0, 1, 3, 3, 3, 1, 0],
[0, 1, 3, 3, 3, 1, 0],
[0, 1, 3, 3, 3, 1, 0],
[0, 1, 3, 3, 3, 1, 0],
[0, 1, 3, 3, 3, 1, 0],
[0, 0, 0, 0, 0, 0, 0]])

{continues on next page}
scipy.ndimage.morphological_laplace

scipy.ndimage.morphological_laplace(input, size=None, footprint=None, structure=None, output=None, mode='reflect', cval=0.0, origin=0)

Multi-dimensional morphological laplace.

Parameters

- input [array_like] Input.
- size [int or sequence of ints, optional] See structure.
- footprint [bool or ndarray, optional] See structure.
- structure [structure, optional] Either size, footprint, or the structure must be provided.
- output [ndarray, optional] An output array can optionally be provided.
- mode [{‘reflect’, ‘constant’, ‘nearest’, ‘mirror’, ‘wrap’}, optional] The mode parameter determines how the array borders are handled. For ‘constant’ mode, values beyond borders are set to be cval. Default is ‘reflect’.
- cval [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is 0.0
- origin [origin, optional] The origin parameter controls the placement of the filter.

Returns

morphological_laplace [ndarray] Output

scipy.ndimage.white_tophat

scipy.ndimage.white_tophat(input, size=None, footprint=None, structure=None, output=None, mode='reflect', cval=0.0, origin=0)

Multi-dimensional white tophat filter.

Parameters

- input [array_like] Input.
- size [tuple of ints] Shape of a flat and full structuring element used for the filter. Optional if footprint or structure is provided.
- footprint [array of ints, optional] Positions of elements of a flat structuring element used for the white tophat filter.
- structure [array of ints, optional] Structuring element used for the filter. structure may be a non-flat structuring element.
- output [array, optional] An array used for storing the output of the filter may be provided.
- mode [{‘reflect’, ‘constant’, ‘nearest’, ‘mirror’, ‘wrap’}, optional] The mode parameter determines how the array borders are handled, where cval is the value when mode is equal to ‘constant’. Default is ‘reflect’.
- cval [scalar, optional] Value to fill past edges of input if mode is ‘constant’. Default is 0.0.
- origin [scalar, optional] The origin parameter controls the placement of the filter. Default is 0.
Returns

output [ndarray] Result of the filter of input with structure.

See also:

black_tophat

6.16.6 Utility

imread(*args, **kwds) imread is deprecated! imread is deprecated in SciPy 1.0.0, and will be removed in 1.2.0.

scipy.ndimage.imread

scipy.ndimage.imread(*args, **kwds)
imread is deprecated! imread is deprecated in SciPy 1.0.0, and will be removed in 1.2.0. Use imageio.imread instead.

Read an image from a file as an array.
This function is only available if Python Imaging Library (PIL) is installed.

Parameters

fname [str or file object] The file name or file object to be read.

flatten [bool, optional] If True, flattens the color layers into a single gray-scale layer.

mode [str, optional] Mode to convert image to, e.g. 'RGB'. See the Notes for more details.

Returns

imread [ndarray] The array obtained by reading the image.

Notes

imread uses the Python Imaging Library (PIL) to read an image. The following notes are from the PIL documentation.

mode can be one of the following strings:

- ‘L’ (8-bit pixels, black and white)
- ‘P’ (8-bit pixels, mapped to any other mode using a color palette)
- ‘RGB’ (3x8-bit pixels, true color)
- ‘RGBA’ (4x8-bit pixels, true color with transparency mask)
- ‘CMYK’ (4x8-bit pixels, color separation)
- ‘YCbCr’ (3x8-bit pixels, color video format)
- ‘I’ (32-bit signed integer pixels)
- ‘F’ (32-bit floating point pixels)

PIL also provides limited support for a few special modes, including ‘LA’ (‘L’ with alpha), ‘RGBX’ (true color with padding) and ‘RGBa’ (true color with premultiplied alpha).

When translating a color image to black and white (mode ‘L’, ‘I’ or ‘F’), the library uses the ITU-R 601-2 luma transform:
When `flatten` is True, the image is converted using mode ‘F’. When `mode` is not None and `flatten` is True, the image is first converted according to `mode`, and the result is then flattened using mode ‘F’.

### 6.17 Orthogonal distance regression (scipy.odr)

#### 6.17.1 Package Content

<table>
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<tr>
<th>Class</th>
<th>Description</th>
</tr>
</thead>
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<td><code>Data(x[, y, we, wd, fix, meta])</code></td>
<td>The data to fit.</td>
</tr>
<tr>
<td><code>RealData(x[, y, sx, sy, covx, covy, fix, meta])</code></td>
<td>The data, with weightings as actual standard deviations and/or covariances.</td>
</tr>
<tr>
<td><code>Model(fcn[, fjacb, fjacd, extra_args, ...])</code></td>
<td>The Model class stores information about the function you wish to fit.</td>
</tr>
<tr>
<td><code>ODR(data, model[, beta0, delta0, ifixb, ...])</code></td>
<td>The ODR class gathers all information and coordinates the running of the main fitting routine.</td>
</tr>
<tr>
<td><code>Output(output)</code></td>
<td>The Output class stores the output of an ODR run.</td>
</tr>
<tr>
<td><code>odr(fcn, beta0, y, x[, we, wd, fjacb, ...])</code></td>
<td>Low-level function for ODR.</td>
</tr>
<tr>
<td><code>OdrWarning</code></td>
<td>Warning indicating that the data passed into ODR will cause problems when passed into ‘odr’ that the user should be aware of.</td>
</tr>
<tr>
<td><code>OdrError</code></td>
<td>Exception indicating an error in fitting.</td>
</tr>
<tr>
<td><code>odr_error</code></td>
<td>alias of <code>scipy.odr.odrpack.OdrError</code></td>
</tr>
<tr>
<td><code>odr_stop</code></td>
<td>alias of <code>scipy.odr.odrpack.OdrStop</code></td>
</tr>
</tbody>
</table>

**scipy.odr.Data**

```python
class scipy.odr.Data(x, y=None, we=None, wd=None, fix=None, meta={})
The data to fit.
```

**Parameters**

- **x** [array_like] Observed data for the independent variable of the regression
- **y** [array_like, optional] If array-like, observed data for the dependent variable of the regression. A scalar input implies that the model to be used on the data is implicit.
- **we** [array_like, optional] If `we` is a scalar, then that value is used for all data points (and all dimensions of the response variable). If `we` is a rank-1 array of length `q` (the dimensionality of the response variable), then this vector is the diagonal of the covariant weighting matrix for all data points. If `we` is a rank-1 array of length `n` (the number of data points), then the i’th element is the weight for the i’th response variable observation (single-dimensional only). If `we` is a rank-2 array of shape `(q, q)`, then this is the full covariant weighting matrix broadcast to each observation. If `we` is a rank-2 array of shape `(q, n)`, then `we[:,i]` is the diagonal of the covariant weighting matrix for the i’th observation. If `we` is a rank-3 array of shape `(q, q, n)`, then `we[:,:,i]` is the full specification of the covariant weighting matrix for each observation. If the fit is implicit, then only a positive scalar value is used.
- **wd** [array_like, optional] If `wd` is a scalar, then that value is used for all data points (and all dimensions of the input variable). If `wd = 0`, then the covariant weighting matrix for each observation is set to the identity matrix (so each dimension of each observation has the same weight). If `wd` is a rank-1 array of length `m` (the dimensionality of the input variable), then this vector is the diagonal of the
covariant weighting matrix for all data points. If \( wd \) is a rank-1 array of length \( n \) (the number of data points), then the \( i \)’th element is the weight for the \( i \)’th input variable observation (single-dimensional only). If \( wd \) is a rank-2 array of shape \((m, n)\), then this is the full covariant weighting matrix broadcast to each observation. If \( wd \) is a rank-2 array of shape \((m, n)\), then \( wd[:,i] \) is the diagonal of the covariant weighting matrix for the \( i \)’th observation. If \( wd \) is a rank-3 array of shape \((m, m, n)\), then \( wd[:,:,i] \) is the full specification of the covariant weighting matrix for each observation.

**fix**
[array_like of ints, optional] The \( fix \) argument is the same as ifixx in the class ODR. It is an array of integers with the same shape as data.x that determines which input observations are treated as fixed. One can use a sequence of length \( m \) (the dimensionality of the input observations) to fix some dimensions for all observations. A value of 0 fixes the observation, a value \( > 0 \) makes it free.

**meta**

### Notes
Each argument is attached to the member of the instance of the same name. The structures of \( x \) and \( y \) are described in the Model class docstring. If \( y \) is an integer, then the Data instance can only be used to fit with implicit models where the dimensionality of the response is equal to the specified value of \( y \).

The \( we \) argument weights the effect a deviation in the response variable has on the fit. The \( wd \) argument weights the effect a deviation in the input variable has on the fit. To handle multidimensional inputs and responses easily, the structure of these arguments has the \( n \)’th dimensional axis first. These arguments heavily use the structured arguments feature of ODRPACK to conveniently and flexibly support all options. See the ODRPACK User’s Guide for a full explanation of how these weights are used in the algorithm. Basically, a higher value of the weight for a particular data point makes a deviation at that point more detrimental to the fit.

### Methods

**set_meta(**kwds**)**
Update the metadata dictionary with the keywords and data provided by keywords.

```
scipy.odr.Data.set_meta
Data.set_meta(**kwds**)
Update the metadata dictionary with the keywords and data provided by keywords.
```

**Examples**

```
data.set_meta(lab="Ph 7; Lab 26", title="Ag110 + Ag108 Decay")
```

### scipy.odr.RealData

```
class scipy.odr.RealData(x, y=None, sx=None, sy=None, covx=None, covy=None, fix=None, meta={})
The data, with weightings as actual standard deviations and/or covariances.
```

**Parameters**

- **x**
  [array_like] Observed data for the independent variable of the regression
- **y**
  [array_like, optional] If array-like, observed data for the dependent variable of the regression. A scalar input implies that the model to be used on the data is implicit.
- **sx**
  [array_like, optional] Standard deviations of \( x \). \( sx \) are standard deviations of \( x \) and are converted to weights by dividing 1.0 by their squares.
- **sy**
  [array_like, optional] Standard deviations of \( y \). \( sy \) are standard deviations of \( y \) and are converted to weights by dividing 1.0 by their squares.
- **covx**
  [array_like, optional] Covariance of \( x \). \( covx \) is an array of covariance matrices of \( x \) and are converted to weights by performing a matrix inversion on each observation’s
covy
[array_like, optional] Covariance of y. covy is an array of covariance matrices and are converted to weights by performing a matrix inversion on each observation’s covariance matrix.

fix
[array_like, optional] The argument and member fix is the same as Data.fix and ODR.ifixx: It is an array of integers with the same shape as x that determines which input observations are treated as fixed. One can use a sequence of length m (the dimensionality of the input observations) to fix some dimensions for all observations. A value of 0 fixes the observation, a value > 0 makes it free.

meta

Notes
The weights $w_d$ and $w_e$ are computed from provided values as follows:

$s_x$ and $s_y$ are converted to weights by dividing 1.0 by their squares. For example, $w_d = 1./\text{numpy.power}(\cdot s_x \cdot, 2)$.

$cov_x$ and $cov_y$ are arrays of covariance matrices and are converted to weights by performing a matrix inversion on each observation’s covariance matrix. For example, $w_e[i] = \text{numpy.linalg.inv}(cov_y[i])$.

These arguments follow the same structured argument conventions as $w_d$ and $w_e$ only restricted by their natures: $s_x$ and $s_y$ can’t be rank-3, but $cov_x$ and $cov_y$ can be.

Only set either $s_x$ or $cov_x$ (not both). Setting both will raise an exception. Same with $s_y$ and $cov_y$.

Methods

```python
set_meta(**kwds)
```
Update the metadata dictionary with the keywords and data provided by keywords.

```python
scipy.odr.RealData.set_meta
RealData.set_meta(**kwds)
```
Update the metadata dictionary with the keywords and data provided by keywords.

Examples

```python
data.set_meta(lab="Ph 7; Lab 26", title="Ag110 + Ag108 Decay")
```

scipy.odr.Model

class scipy.odr.Model(fcn, fjacb=None, fjacd=None, extra_args=None, estimate=None, implicit=0, meta=None)
The Model class stores information about the function you wish to fit.

It stores the function itself, at the least, and optionally stores functions which compute the Jacobians used during fitting. Also, one can provide a function that will provide reasonable starting values for the fit parameters possibly given the set of data.

Parameters

- fcn [function] $fcn(\beta, x) \rightarrow y$
- fjacb [function] Jacobian of fcn wrt the fit parameters beta.
  $fjacb(\beta, x) \rightarrow @f_i(x,\beta)/@\beta_j$
- fjacd [function] Jacobian of fcn wrt the (possibly multidimensional) input variable.
  $fjacd(\beta, x) \rightarrow @f_i(x,\beta)/@x_j$
- extra_args [tuple, optional] If specified, extra_args should be a tuple of extra arguments to pass to $fcn$, $fjacb$, and $fjacd$. Each will be called by $apply(fcn, (\beta, x) + extra_args)$
- estimate [array_like of rank-1] Provides estimates of the fit parameters from the data.
  estimate(data) $\rightarrow$ estbeta
implicit  [boolean] If TRUE, specifies that the model is implicit; i.e \( fcn(beta, x) = 0 \) and there is no \( y \) data to fit against.

meta  [dict, optional] freeform dictionary of metadata for the model

Notes
Note that the \( fcn, fjacb, \) and \( fjacd \) operate on NumPy arrays and return a NumPy array. The \texttt{estimate} object takes an instance of the Data class.

Here are the rules for the shapes of the argument and return arrays of the callback functions:

\textbf{x} if the input data is single-dimensional, then \( x \) is rank-1 array; i.e. \( x = array([1, 2, 3, \ldots]) \); \( x.shape = (n,) \) If the input data is multi-dimensional, then \( x \) is a rank-2 array; i.e., \( x = array([[1, 2, \ldots], [2, 4, \ldots]]) \); \( x.shape = (m, n) \). In all cases, it has the same shape as the input data array passed to \texttt{odr}. \( m \) is the dimensionality of the input data, \( n \) is the number of observations.

\textbf{y} if the response variable is single-dimensional, then \( y \) is a rank-1 array, i.e., \( y = array([2, 4, \ldots]) \); \( y.shape = (n,) \). If the response variable is multi-dimensional, then \( y \) is a rank-2 array, i.e., \( y = array([[2, 4, \ldots], [3, 6, \ldots]]) \); \( y.shape = (q, n) \) where \( q \) is the dimensionality of the response variable.

\textbf{beta}  
rank-1 array of length \( p \) where \( p \) is the number of parameters; i.e. \( \textbf{beta} = array([B_1, B_2, \ldots, B_p]) \)

\textbf{fjacb}  
if the response variable is multi-dimensional, then the return array’s shape is \( (q, p, n) \) such that \( fjacb(x, beta)[l, k, i] = d f_l(X, B) / d B_k \) evaluated at the \( i \)’th data point. If \( q == 1 \), then the return array is only rank-2 and with shape \( (p, n) \).

\textbf{fjacd}  
as with \( fjacb \), only the return array’s shape is \( (q, m, n) \) such that \( fjacd(x, beta)[l, j, i] = d f_l(X, B) / d X_j \) at the \( i \)’th data point. If \( q == 1 \), then the return array’s shape is \( (m, n) \). If \( m == 1 \), the shape is \( (q, n) \). If \( m == q == 1 \), the shape is \( (n,) \).

Methods

\begin{verbatim}
set_meta(**kwds) \hspace{1cm} Update the metadata dictionary with the key-
words and data provided here.
\end{verbatim}

\texttt{scipy.odr.Model.set_meta}

Model.set_meta(**kwds)  
Update the metadata dictionary with the keywords and data provided here.

Examples

set_meta(name="Exponential", equation="y = a \exp(b \ x) + c")

\texttt{scipy.odr.ODR}

class scipy.odr.ODR(data, model, beta0=None, delta0=None, ifixb=None, ifixx=None, job=None, iprint=None, errfile=None, rptfile=None, ndigit=None, taufac=None, sstol=None, partol=None, maxit=None, stpb=None, stpd=None, sclb=None, scld=None, work=None, iwork=None)

The ODR class gathers all information and coordinates the running of the main fitting routine.

Members of instances of the ODR class have the same names as the arguments to the initialization routine.

Parameters
<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>data</td>
<td>[Data class instance] instance of the Data class</td>
</tr>
<tr>
<td>model</td>
<td>[Model class instance] instance of the Model class</td>
</tr>
</tbody>
</table>

**Other Parameters**

- **beta0** [array_like of rank-1] a rank-1 sequence of initial parameter values. Optional if model provides an “estimate” function to estimate these values.
- **delta0** [array_like of floats of rank-1, optional] a (double-precision) float array to hold the initial values of the errors in the input variables. Must be same shape as data.x
- **ifixb** [array_like of ints of rank-1, optional] sequence of integers with the same length as beta0 that determines which parameters are held fixed. A value of 0 fixes the parameter, a value > 0 makes the parameter free.
- **ifixx** [array_like of ints with same shape as data.x, optional] an array of integers with the same shape as data.x that determines which input observations are treated as fixed. One can use a sequence of length m (the dimensionality of the input observations) to fix some dimensions for all observations. A value of 0 fixes the observation, a value > 0 makes it free.
- **job** [int, optional] an integer telling ODRPACK what tasks to perform. See p. 31 of the ODRPACK User’s Guide if you absolutely must set the value here. Use the method set_job post-initialization for a more readable interface.
- **iprint** [int, optional] an integer telling ODRPACK what to print. See pp. 33-34 of the ODRPACK User’s Guide if you absolutely must set the value here. Use the method set_iprint post-initialization for a more readable interface.
- **errfile** [str, optional] string with the filename to print ODRPACK errors to. Do Not Open This File Yourself!
- **rptfile** [str, optional] string with the filename to print ODRPACK summaries to. Do Not Open This File Yourself!
- **ndigit** [int, optional] integer specifying the number of reliable digits in the computation of the function.
- **taufac** [float, optional] float specifying the initial trust region. The default value is 1. The initial trust region is equal to taufac times the length of the first computed Gauss-Newton step. taufac must be less than 1.
- **sstol** [float, optional] float specifying the tolerance for convergence based on the relative change in the sum-of-squares. The default value is eps**(1/2) where eps is the smallest value such that 1 + eps > 1 for double precision computation on the machine. sstol must be less than 1.
- **partol** [float, optional] float specifying the tolerance for convergence based on the relative change in the estimated parameters. The default value is eps**(2/3) for explicit models and eps**(1/3) for implicit models. partol must be less than 1.
- **maxit** [int, optional] integer specifying the maximum number of iterations to perform. For first runs, maxit is the total number of iterations performed and defaults to 50. For restarts, maxit is the number of additional iterations to perform and defaults to 10.
- **stpb** [array_like, optional] sequence (len(stpb) == len(beta0)) of relative step sizes to compute finite difference derivatives wrt the parameters.
- **stpd** [optional] array (stpd.shape == data.x.shape or stpd.shape == (m,)) of relative step sizes to compute finite difference derivatives wrt the input variable errors. If stpd is a rank-1 array with length m (the dimensionality of the input variable), then the values are broadcast to all observations.
- **sclb** [array_like, optional] sequence (len(stpb) == len(beta0)) of scaling factors for the parameters. The purpose of these scaling factors are to scale all of the parameters to around unity. Normally appropriate scaling factors are computed if this argument is not specified. Specify them yourself if the automatic procedure goes awry.
scipy.odr.ODR.restart

ODR.restart(iter=None)

Restarts the run with iter more iterations.

Parameters

iter [int, optional] ODRPACK’s default for the number of new iterations is 10.

Returns

output [Output instance] This object is also assigned to the attribute .output.

scipy.odr.ODR.run

ODR.run()

Run the fitting routine with all of the information given and with full_output=1.

Returns

output [Output instance] This object is also assigned to the attribute .output.

scipy.odr.ODR.set_iprint

ODR.set_iprint(init=None, so_init=None, iter=None, so_iter=None, iter_step=None, final=None, so_final=None)

Set the iprint parameter for the printing of computation reports.

If any of the arguments are specified here, then they are set in the iprint member. If iprint is not set manually or with this method, then ODRPACK defaults to no printing. If no filename is specified with the member rptfile, then ODRPACK prints to stdout. One can tell ODRPACK to print to stdout in addition to the specified filename by setting the so_* arguments to this function, but one cannot specify to print to stdout but not a file since one can do that by not specifying a rptfile filename.

There are three reports: initialization, iteration, and final reports. They are represented by the arguments init, iter, and final respectively. The permissible values are 0, 1, and 2 representing “no report”, “short report”, and “long report” respectively.
The argument iter_step (0 <= iter_step <= 9) specifies how often to make the iteration report; the report will be made for every iter_step’th iteration starting with iteration one. If iter_step == 0, then no iteration report is made, regardless of the other arguments.

If the rptfile is None, then any so_* arguments supplied will raise an exception.

```python
scipy.odr.ODR.set_job
ODR.set_job(fit_type=None, deriv=None, var_calc=None, del_init=None, restart=None)
```
Sets the “job” parameter in a hopefully comprehensible way.

If an argument is not specified, then the value is left as is. The default value from class initialization is for all of these options set to 0.

**Parameters**

- `fit_type` [{0, 1, 2} int] 0 -> explicit ODR
  1 -> implicit ODR
  2 -> ordinary least-squares

- `deriv` [{0, 1, 2, 3} int] 0 -> forward finite differences
  1 -> central finite differences
  2 -> user-supplied derivatives (Jacobians) with results checked by ODRPACK
  3 -> user-supplied derivatives, no checking

- `var_calc` [{0, 1, 2} int] 0 -> calculate asymptotic covariance matrix and fit parameter uncertainties (V_B, s_B) using derivatives recomputed at the final solution
  1 -> calculate V_B and s_B using derivatives from last iteration
  2 -> do not calculate V_B and s_B

- `del_init` [{0, 1} int] 0 -> initial input variable offsets set to 0
  1 -> initial offsets provided by user in variable “work”

- `restart` [{0, 1} int] 0 -> fit is not a restart
  1 -> fit is a restart

**Notes**

The permissible values are different from those given on pg. 31 of the ODRPACK User’s Guide only in that one cannot specify numbers greater than the last value for each variable.

If one does not supply functions to compute the Jacobians, the fitting procedure will change deriv to 0, finite differences, as a default. To initialize the input variable offsets by yourself, set del_init to 1 and put the offsets into the “work” variable correctly.

```python
scipy.odr.Output
```

**class scipy.odr.Output(output)**

The Output class stores the output of an ODR run.

**Notes**

Takes one argument for initialization, the return value from the function `odr`. The attributes listed as “optional” above are only present if `odr` was run with `full_output=1`.

**Attributes**

- `beta` [ndarray] Estimated parameter values, of shape (q,).
- `sd_beta` [ndarray] Standard errors of the estimated parameters, of shape (p,).
- `cov_beta` [ndarray] Covariance matrix of the estimated parameters, of shape (p,p).
- `delta` [ndarray, optional] Array of estimated errors in input variables, of same shape as x.
eps [ndarray, optional] Array of estimated errors in response variables, of same shape as y.
xplus [ndarray, optional] Array of x + delta.
y [ndarray, optional] Array y = fcn(x + delta).
res_var [float, optional] Residual variance.
sum_square [float, optional] Sum of squares error.
sum_square_delta [float, optional] Sum of squares of delta error.
sum_square_eps [float, optional] Sum of squares of eps error.
inv_condnum [float, optional] Inverse condition number (cf. ODRPACK UG p. 77).
rel_error [float, optional] Relative error in function values computed within fcn.
work [ndarray, optional] Final work array.
work_ind [dict, optional] Indices into work for drawing out values (cf. ODRPACK UG p. 83).
info [int, optional] Reason for returning, as output by ODRPACK (cf. ODRPACK UG p. 38).
stopreason [list of str, optional] info interpreted into English.

Methods

pprint()

Pretty-print important results.

scipy.odr.Output.pprint

Output.pprint()

Pretty-print important results.

scipy.odr

scipy.odr(fcn, beta0, y, x, we=None, wd=None, fjacb=None, fjacd=None, extra_args=None,
ifx=None, ifzb=None, job=0, iprint=0, errfile=None, rptfile=None, ndigit=0,
taufac=0.0, sstol=-1.0, partol=-1.0, maxit=-1, stpb=None, stpd=None, sclb=None,
scld=None, work=None, iwork=None, full_output=0)

Low-level function for ODR.

See also:

ODR, Model, Data, RealData

Notes

This is a function performing the same operation as the ODR, Model and Data classes together. The parameters of this function are explained in the class documentation.

scipy.odr.OdrWarning

exception scipy.odr.OdrWarning

Warning indicating that the data passed into ODR will cause problems when passed into ‘odr’ that the user should be aware of.
scipy.odr.OdrError

exception scipy.odr.OdrError
    Exception indicating an error in fitting.
    This is raised by scipy.odr if an error occurs during fitting.

scipy.odr.OdrStop

exception scipy.odr.OdrStop
    Exception stopping fitting.
    You can raise this exception in your objective function to tell scipy.odr to stop fitting.

scipy.odr.odr_error

scipy.odr.odr_error
    alias of scipy.odr.odrpack.OdrError

scipy.odr.odr_stop

scipy.odr.odr_stop
    alias of scipy.odr.odrpack.OdrStop

Prebuilt models:

<table>
<thead>
<tr>
<th>polynomial(order)</th>
<th>Factory function for a general polynomial model.</th>
</tr>
</thead>
</table>

scipy.odr.polynomial

scipy.odr.polynomial(order)
    Factory function for a general polynomial model.

Parameters

order [int or sequence] If an integer, it becomes the order of the polynomial to fit. If a sequence of numbers, then these are the explicit powers in the polynomial. A constant term (power 0) is always included, so don’t include 0. Thus, polynomial(n) is equivalent to polynomial(range(1, n+1)).

Returns


scipy.odr.exponential
scipy.odr.multilinear
scipy.odr.unilinear
scipy.odr.quadratic
scipy.odr.polynomial

6.17.2 Usage information

Introduction

Why Orthogonal Distance Regression (ODR)? Sometimes one has measurement errors in the explanatory (a.k.a., “independent”) variable(s), not just the response (a.k.a., “dependent”) variable(s). Ordinary Least
Squares (OLS) fitting procedures treat the data for explanatory variables as fixed, i.e., not subject to error of any kind. Furthermore, OLS procedures require that the response variables be an explicit function of the explanatory variables; sometimes making the equation explicit is impractical and/or introduces errors. ODR can handle both of these cases with ease, and can even reduce to the OLS case if that is sufficient for the problem.

ODRPACK is a FORTRAN-77 library for performing ODR with possibly non-linear fitting functions. It uses a modified trust-region Levenberg-Marquardt-type algorithm to estimate the function parameters. The fitting functions are provided by Python functions operating on NumPy arrays. The required derivatives may be provided by Python functions as well, or may be estimated numerically. ODRPACK can do explicit or implicit ODR fits, or it can do OLS. Input and output variables may be multi-dimensional. Weights can be provided to account for different variances of the observations, and even covariances between dimensions of the variables.

The scipy.odr package offers an object-oriented interface to ODRPACK, in addition to the low-level odr function.

Additional background information about ODRPACK can be found in the ODRPACK User’s Guide, reading which is recommended.

Basic usage

1. Define the function you want to fit against:

```python
def f(B, x):
    # 'Linear function y = m*x + b''
    # B is a vector of the parameters.
    # x is an array of the current x values.
    # x is in the same format as the x passed to Data or RealData.
    #
    # Return an array in the same format as y passed to Data or RealData.
    return B[0]*x + B[1]
```

2. Create a Model:

```python
linear = Model(f)
```

3. Create a Data or RealData instance:

```python
mydata = Data(x, y, wd=1./power(sx,2), we=1./power(sy,2))
```

or, when the actual covariances are known:

```python
mydata = RealData(x, y, sx=sx, sy=sy)
```

4. Instantiate ODR with your data, model and initial parameter estimate:

```python
myodr = ODR(mydata, linear, beta0=[1., 2.])
```

5. Run the fit:

```python
myoutput = myodr.run()
```

6. Examine output:

```python
myoutput.pprint()
```
SciPy optimize provides functions for minimizing (or maximizing) objective functions, possibly subject to constraints. It includes solvers for nonlinear problems (with support for both local and global optimization algorithms), linear programing, constrained and nonlinear least-squares, root finding and curve fitting.

Common functions and objects, shared across different solvers, are:

- `show_options([solver, method, disp])` Show documentation for additional options of optimization solvers.
- `OptimizeResult` Represents the optimization result.
- `OptimizeWarning`

### 6.18.1 scipy.optimize.show_options

`scipy.optimize.show_options(solver=None, method=None, disp=True)`  
Show documentation for additional options of optimization solvers.

These are method-specific options that can be supplied through the `options` dict.

**Parameters**

- `method` [str, optional] If not given, shows all methods of the specified solver. Otherwise, show only the options for the specified method. Valid values corresponds to methods’ names of respective solver (e.g. ‘BFGS’ for ‘minimize’).
- `disp` [bool, optional] Whether to print the result rather than returning it.

**Returns**

- `text` Either None (for disp=False) or the text string (disp=True)

**Notes**

The solver-specific methods are:

- `scipy.optimize.minimize`
  - Nelder-Mead
  - Powell
  - CG
  - BFGS
  - Newton-CG
  - L-BFGS-B
  - TNC
  - COBYLA
  - SLSQP
  - dogleg
  - trust-ncg

- `scipy.optimize.root`
• hybr
• lm
• broyden1
• broyden2
• anderson
• linearmixing
• diagbroyden
• excitingmixing
• krylov
• df-sane

`scipy.optimize.minimize_scalar`
• brent
• golden
• bounded

`scipy.optimize.linprog`
• simplex
• interior-point

6.18.2 `scipy.optimize.OptimizeResult`

class `scipy.optimize.OptimizeResult`
Represents the optimization result.

Notes
There may be additional attributes not listed above depending on the specific solver. Since this class is essentially a subclass of dict with attribute accessors, one can see which attributes are available using the `keys()` method.

Attributes

- `x` [ndarray] The solution of the optimization.
- `success` [bool] Whether or not the optimizer exited successfully.
- `status` [int] Termination status of the optimizer. Its value depends on the underlying solver. Refer to `message` for details.
- `message` [str] Description of the cause of the termination.
- `fun`, `jac`, `hess`: [ndarray] Values of objective function, its Jacobian and its Hessian (if available). The Hessians may be approximations, see the documentation of the function in question.
- `hess_inv` [object] Inverse of the objective function’s Hessian; may be an approximation. Not available for all solvers. The type of this attribute may be either np.ndarray or scipy.sparse.linalg.LinearOperator.
- `nfev`, `njev`, `nhev` [int] Number of evaluations of the objective functions and of its Jacobian and Hessian.
- `nit` [int] Number of iterations performed by the optimizer.
- `maxcv` [float] The maximum constraint violation.
Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>clear()</code></td>
<td>Removes all items from D.</td>
</tr>
<tr>
<td><code>copy()</code></td>
<td>Returns a shallow copy of D.</td>
</tr>
<tr>
<td><code>fromkeys()</code></td>
<td>Returns a new dict with keys from iterable and values equal to value.</td>
</tr>
<tr>
<td><code>get(k[,d])</code></td>
<td>D[k] if k in D, else d. d defaults to None.</td>
</tr>
<tr>
<td><code>items()</code></td>
<td>A set-like object providing a view on D’s items</td>
</tr>
<tr>
<td><code>keys()</code></td>
<td>A set-like object providing a view on D’s keys</td>
</tr>
<tr>
<td><code>pop(k[,d])</code></td>
<td>v, remove specified key and return the corresponding value.</td>
</tr>
<tr>
<td><code>popitem()</code></td>
<td>(k, v), remove and return some (key, value) pair as a 2-tuple;</td>
</tr>
<tr>
<td></td>
<td>but raise KeyError if D is empty.</td>
</tr>
<tr>
<td><code>setdefault(k[,d])</code></td>
<td>If k in D, D[k] = v; if k not in D, D[k] = d if given, otherwise KeyError is raised</td>
</tr>
<tr>
<td><code>update([E,**F])</code></td>
<td>If E is present and has a .keys() method, then does: for k in E: D[k] = E[k] If E is present and lacks a .keys() method, then does: for k, v in E: D[k] = v In either case, this is followed by: for k in F: D[k] = F[k]</td>
</tr>
<tr>
<td><code>values()</code></td>
<td></td>
</tr>
</tbody>
</table>

**scipy.optimize.OptimizeResult.clear**

OptimizeResult.clear() → None. Remove all items from D.

**scipy.optimize.OptimizeResult.copy**

OptimizeResult.copy() → a shallow copy of D

**scipy.optimize.OptimizeResult.fromkeys**

OptimizeResult.fromkeys($type, iterable, value=None, /)

Returns a new dict with keys from iterable and values equal to value.

**scipy.optimize.OptimizeResult.get**

OptimizeResult.get(k[, d]) → D[k] if k in D, else d. d defaults to None.

**scipy.optimize.OptimizeResult.items**

OptimizeResult.items() → a set-like object providing a view on D’s items

**scipy.optimize.OptimizeResult.keys**

OptimizeResult.keys() → a set-like object providing a view on D’s keys

**scipy.optimize.OptimizeResult.pop**

OptimizeResult.pop(k[, d]) → v, remove specified key and return the corresponding value. If key is not found, d is returned if given, otherwise KeyError is raised

**scipy.optimize.OptimizeResult.popitem**

OptimizeResult.popitem() → (k, v), remove and return some (key, value) pair as a 2-tuple; but raise KeyError if D is empty.


```python
scipy.optimize.OptimizeResult.setdefault
```

```python
OptimizeResult.setdefault(k[, d]) → D.get(k,d), also set D[k]=d if k not in D
```

```python
scipy.optimize.OptimizeResult.update
```

```python
OptimizeResult.update([E], **F) → None. Update D from dict/iterable E and F.
If E is present and has a .keys() method, then does: for k in E: D[k] = E[k] If E is present and lacks a .keys() method, then does: for k, v in E: D[k] = v In either case, this is followed by: for k in F: D[k] = F[k]
```

```python
scipy.optimize.OptimizeResult.values
```

```python
OptimizeResult.values() → an object providing a view on D’s values
```

### 6.18.3 scipy.optimize.OptimizeWarning

**exception** scipy.optimize.OptimizeWarning

### 6.18.4 Optimization

**Scalar Functions Optimization**

```python
minimize_scalar(fun[, bracket, bounds, ...])  Minimization of scalar function of one variable.
```

```python
scipy.optimize.minimize_scalar
```

```python
scipy.optimize.minimize_scalar(fun, bracket=None, bounds=None, args=(), method='brent', tol=None, options=None)
```

```
Minimization of scalar function of one variable.
```

**Parameters**

- `fun` [callable] Objective function. Scalar function, must return a scalar.
- `bracket` [sequence, optional] For methods ‘brent’ and ‘golden’, `bracket` defines the bracketing interval and can either have three items (a, b, c) so that a < b < c and `fun(b) < fun(a)`, `fun(c)` or two items a and c which are assumed to be a starting interval for a downhill bracket search (see `bracket`); it doesn’t always mean that the obtained solution will satisfy `a <= x <= c`.
- `bounds` [sequence, optional] For method ‘bounded’, `bounds` is mandatory and must have two items corresponding to the optimization bounds.
- `args` [tuple, optional] Extra arguments passed to the objective function.
- `method` [str or callable, optional] Type of solver. Should be one of:
  - ‘Brent’ (see here)
  - ‘Bounded’ (see here)
  - ‘Golden’ (see here)
- `tol` [float, optional] Tolerance for termination. For detailed control, use solver-specific options.
  - `maxiter` [int] Maximum number of iterations to perform.
  - `disp` [bool] Set to True to print convergence messages.

**Returns**
res [OptimizeResult] The optimization result represented as a OptimizeResult object. Important attributes are: x the solution array, success a Boolean flag indicating if the optimizer exited successfully and message which describes the cause of the termination. See OptimizeResult for a description of other attributes.

See also:

minimize

Interface to minimization algorithms for scalar multivariate functions

show_options

Additional options accepted by the solvers

Notes

This section describes the available solvers that can be selected by the ‘method’ parameter. The default method is Brent.

Method Brent uses Brent’s algorithm to find a local minimum. The algorithm uses inverse parabolic interpolation when possible to speed up convergence of the golden section method.

Method Golden uses the golden section search technique. It uses analog of the bisection method to decrease the bracketed interval. It is usually preferable to use the Brent method.

Method Bounded can perform bounded minimization. It uses the Brent method to find a local minimum in the interval x1 < xopt < x2.

Custom minimizers

It may be useful to pass a custom minimization method, for example when using some library frontend to minimize_scalar. You can simply pass a callable as the method parameter.

The callable is called as method(fun, args, **kwarsgs, **options) where kwarsgs corresponds to any other parameters passed to minimize (such as bracket, tol, etc.), except the options dict, which has its contents also passed as method parameters pair by pair. The method shall return an OptimizeResult object.

The provided method callable must be able to accept (and possibly ignore) arbitrary parameters; the set of parameters accepted by minimize may expand in future versions and then these parameters will be passed to the method. You can find an example in the scipy.optimize tutorial.

New in version 0.11.0.

Examples

Consider the problem of minimizing the following function.

```python
>>> def f(x):
...     return (x - 2) * x * (x + 2)**2
```

Using the Brent method, we find the local minimum as:

```python
>>> from scipy.optimize import minimize_scalar
>>> res = minimize_scalar(f)
>>> res.x
1.28077640403
```

Using the Bounded method, we find a local minimum with specified bounds as:
The `minimize_scalar` function supports the following methods:

- **minimize_scalar(method='brent')**
  ```python
  scipy.optimize.minimize_scalar(f, args=(), method='brent', tol=None, options={'func': None, 'brack': None, 'xtol': 1.48e-08, 'maxiter': 500})
  ```

  See also:
  For documentation for the rest of the parameters, see `scipy.optimize.minimize_scalar`

  **Options**
  - `maxiter` [int] Maximum number of iterations to perform.
  - `xtol` [float] Relative error in solution xopt acceptable for convergence.

- **minimize_scalar(method='bounded')**
  ```python
  scipy.optimize.minimize_scalar(f, bounds=None, args=(), method='bounded', tol=None, options={'func': None, 'xatol': 1e-05, 'maxiter': 500, 'disp': 0})
  ```

  See also:
  For documentation for the rest of the parameters, see `scipy.optimize.minimize_scalar`

  **Options**
  - `maxiter` [int] Maximum number of iterations to perform.
  - `disp`: int, optional
    If non-zero, print messages.
    0: no message printing. 1: non-convergence notification messages only.
    2: print a message on convergence too. 3: print iteration results.
  - `xatol` [float] Absolute error in solution xopt acceptable for convergence.

- **minimize_scalar(method='golden')**
  ```python
  scipy.optimize.minimize_scalar(f, args=(), method='golden', tol=None, options={'func': None, 'brack': None, 'xtol': 1.4901161193847656e-08, 'maxiter': 5000})
  ```

  See also:
  For documentation for the rest of the parameters, see `scipy.optimize.minimize_scalar`

  **Options**
  - `maxiter` [int] Maximum number of iterations to perform.
  - `xtol` [float] Relative error in solution xopt acceptable for convergence.

### Local (Multivariate) Optimization
**minimize** *(fun, x0[, args, method, jac, hess, ...])*  
Minimization of scalar function of one or more variables.

**scipy.optimize.minimize** *(fun, x0, args=(), method=None, jac=None, hess=None, hessp=None, bounds=None, constraints=(), tol=None, callback=None, options=None)*

Minimization of scalar function of one or more variables.

**Parameters**

- **fun** [callable] The objective function to be minimized.
  
  `fun(x, *args) -> float`
  
  where `x` is an 1-D array with shape `(n,)` and `args` is a tuple of the fixed parameters needed to completely specify the function.

- **x0** [ndarray, shape `(n,)`] Initial guess. Array of real elements of size `(n,)`, where `n` is the number of independent variables.

- **args** [tuple, optional] Extra arguments passed to the objective function and its derivatives (`fun`, `jac` and `hess` functions).

- **method** [str or callable, optional] Type of solver. Should be one of
  
  - 'Nelder-Mead' *(see here)*
  - 'Powell' *(see here)*
  - 'CG' *(see here)*
  - 'BFGS' *(see here)*
  - 'Newton-CG' *(see here)*
  - 'L-BFGS-B' *(see here)*
  - 'TNC' *(see here)*
  - 'COBYLA' *(see here)*
  - 'SLSQP' *(see here)*
  - 'trust-constr' *(see here)*
  - 'dogleg' *(see here)*
  - 'trust-ncg' *(see here)*
  - 'trust-exact' *(see here)*
  - 'trust-krylov' *(see here)*
  - custom - a callable object (added in version 0.14.0), see below for description.

  If not given, chosen to be one of BFGS, L-BFGS-B, SLSQP, depending if the problem has constraints or bounds.

- **jac** [{callable, '2-point', '3-point', 'cs', bool}, optional] Method for computing the gradient vector. Only for CG, BFGS, Newton-CG, L-BFGS-B, TNC, SLSQP, dogleg, trust-ncg, trust-krylov, trust-exact and trust-constr. If it is a callable, it should be a function that returns the gradient vector:

  `jac(x, *args) -> array_like, shape (n,)`

  where `x` is an array with shape `(n,)` and `args` is a tuple with the fixed parameters. Alternatively, the keywords `{‘2-point’, ‘3-point’, ‘cs’}` select a finite difference scheme for numerical estimation of the gradient. Options ‘3-point’ and ‘cs’ are available only to ‘trust-constr’. If `jac` is a Boolean and is True, `fun` is assumed to return the gradient along with the objective function. If False, the gradient will be estimated using ‘2-point’ finite difference estimation.

- **hess** [{callable, '2-point', '3-point', 'cs', HessianUpdateStrategy}, optional] Method for computing the Hessian matrix. Only for Newton-CG, dogleg, trust-ncg, trust-krylov, trust-exact and trust-constr. If it is callable, it should return the Hessian matrix:

  `hess(x, *args) -> {LinearOperator, spmatrix, array}, (n, n)`
where x is a (n,) ndarray and args is a tuple with the fixed parameters. LinearOperator and sparse matrix returns are allowed only for ‘trust-constr’ method. Alternatively, the keywords {‘2-point’, ‘3-point’, ‘cs’} select a finite difference scheme for numerical estimation. Or, objects implementing HessianUpdateStrategy interface can be used to approximate the Hessian. Available quasi-Newton methods implementing this interface are:

- **BFGS**;
- **SR1**.

Whenever the gradient is estimated via finite-differences, the Hessian cannot be estimated with options {‘2-point’, ‘3-point’, ‘cs’} and needs to be estimated using one of the quasi-Newton strategies. Finite-difference options {‘2-point’, ‘3-point’, ‘cs’} and HessianUpdateStrategy are available only for ‘trust-constr’ method.

**hessp**
[callable, optional] Hessian of objective function times an arbitrary vector p. Only for Newton-CG, trust-ncg, trust-krylov, trust-constr. Only one of hessp or hess needs to be given. If hess is provided, then hessp will be ignored. hessp must compute the Hessian times an arbitrary vector:

\[
    \text{hessp}(x, p, *\text{args}) \rightarrow \text{ndarray shape (n,)}
\]

where x is a (n,) ndarray, p is an arbitrary vector with dimension (n,) and args is a tuple with the fixed parameters.

**bounds**
[sequence or Bounds, optional] Bounds on variables for L-BFGS-B, TNC, SLSQP and trust-constr methods. There are two ways to specify the bounds:
1. Instance of Bounds class.
2. Sequence of (min, max) pairs for each element in x. None is used to specify no bound.

**constraints**
[({Constraint, dict} or List of {Constraint, dict}, optional] Constraints definition (only for COBYLA, SLSQP and trust-constr). Constraints for ‘trust-constr’ are defined as a single object or a list of objects specifying constraints to the optimization problem. Available constraints are:

- **LinearConstraint**
- **NonlinearConstraint**

Constraints for COBYLA, SLSQP are defined as a list of dictionaries. Each dictionary with fields:

- **fun** [callable] The function defining the constraint.
- **jac** [callable, optional] The Jacobian of fun (only for SLSQP).
- **args** [sequence, optional] Extra arguments to be passed to the function and Jacobian.

Equality constraint means that the constraint function result is to be zero whereas inequality means that it is to be non-negative. Note that COBYLA only supports inequality constraints.

**tol** [float, optional] Tolerance for termination. For detailed control, use solver-specific options.

**options** [dict, optional] A dictionary of solver options. All methods accept the following generic options:

- **maxiter** [int] Maximum number of iterations to perform.
- **disp** [bool] Set to True to print convergence messages.

For method-specific options, see show_options.

**callback** [callable, optional] Called after each iteration. For ‘trust-constr’ it is a callable with the signature:

\[
    \text{callback}(xk, \text{OptimizeResult state}) \rightarrow \text{bool}
\]

where xk is the current parameter vector. and state is an OptimizeResult object, with the same fields as the ones from the return. If callback returns True the algorithm execution is terminated. For all the other methods, the signature is:
callback(xk)

where \(xk\) is the current parameter vector.

**Returns**

- \(res\): [OptimizeResult] The optimization result represented as a \texttt{OptimizeResult} object. Important attributes are: \texttt{x} the solution array, \texttt{success} a Boolean flag indicating if the optimizer exited successfully and \texttt{message} which describes the cause of the termination. See \texttt{OptimizeResult} for a description of other attributes.

See also:

- \texttt{minimize_scalar}
  - Interface to minimization algorithms for scalar univariate functions

- \texttt{show_options}
  - Additional options accepted by the solvers

**Notes**

This section describes the available solvers that can be selected by the ‘method’ parameter. The default method is \texttt{BFGS}.

### Unconstrained minimization

Method \texttt{Nelder-Mead} uses the Simplex algorithm [1], [2]. This algorithm is robust in many applications. However, if numerical computation of derivative can be trusted, other algorithms using the first and/or second derivatives information might be preferred for their better performance in general.

Method \texttt{Powell} is a modification of Powell’s method [3], [4] which is a conjugate direction method. It performs sequential one-dimensional minimizations along each vector of the directions set (\texttt{direc} field in \texttt{options} and \texttt{info}), which is updated at each iteration of the main minimization loop. The function need not be differentiable, and no derivatives are taken.

Method \texttt{CG} uses a nonlinear conjugate gradient algorithm by Polak and Ribiere, a variant of the Fletcher-Reeves method described in [5] pp. 120-122. Only the first derivatives are used.

Method \texttt{BFGS} uses the quasi-Newton method of Broyden, Fletcher, Goldfarb, and Shanno (BFGS) [5] pp. 136. It uses the first derivatives only. BFGS has proven good performance even for non-smooth optimizations. This method also returns an approximation of the Hessian inverse, stored as \texttt{hess_inv} in the \texttt{OptimizeResult} object.

Method \texttt{Newton-CG} uses a Newton-CG algorithm [5] pp. 168 (also known as the truncated Newton method). It uses a CG method to compute the search direction. See also \texttt{TNC} method for a box-constrained minimization with a similar algorithm. Suitable for large-scale problems.

Method \texttt{dogleg} uses the dog-leg trust-region algorithm [5] for unconstrained minimization. This algorithm requires the gradient and Hessian; furthermore the Hessian is required to be positive definite.

Method \texttt{trust-ncg} uses the Newton conjugate gradient trust-region algorithm [5] for unconstrained minimization. This algorithm requires the gradient and either the Hessian or a function that computes the product of the Hessian with a given vector. Suitable for large-scale problems.

Method \texttt{trust-krylov} uses the Newton GLTR trust-region algorithm [14], [15] for unconstrained minimization. This algorithm requires the gradient and either the Hessian or a function that computes the product of the Hessian with a given vector. Suitable for large-scale problems. On indefinite problems it requires usually less iterations than the \texttt{trust-ncg} method and is recommended for medium and large-scale problems.

Method \texttt{trust-exact} is a trust-region method for unconstrained minimization in which quadratic subproblems are solved almost exactly [13]. This algorithm requires the gradient and the Hessian (which
is not required to be positive definite). It is, in many situations, the Newton method to converge in fewer iteration and the most recommended for small and medium-size problems.

**Bound-Constrained minimization**


Method *TNC* uses a truncated Newton algorithm [5], [8] to minimize a function with variables subject to bounds. This algorithm uses gradient information; it is also called Newton Conjugate-Gradient. It differs from the Newton-CG method described above as it wraps a C implementation and allows each variable to be given upper and lower bounds.

**Constrained Minimization**

Method *COBYLA* uses the Constrained Optimization BY Linear Approximation (COBYLA) method [9], [10], [11]. The algorithm is based on linear approximations to the objective function and each constraint. The method wraps a FORTRAN implementation of the algorithm. The constraints functions ‘fun’ may return either a single number or an array or list of numbers.

Method *SLSQP* uses Sequential Least SQuares Programming to minimize a function of several variables with any combination of bounds, equality and inequality constraints. The method wraps the SLSQP Optimization subroutine originally implemented by Dieter Kraft [12]. Note that the wrapper handles infinite values in bounds by converting them into large floating values.

Method *trust-constr* is a trust-region algorithm for constrained optimization. It switches between two implementations depending on the problem definition. It is the most versatile constrained minimization algorithm implemented in SciPy and the most appropriate for large-scale problems. For equality constrained problems it is an implementation of Byrd-Omojokun Trust-Region SQP method described in [17] and in [5], p. 549. When inequality constraints are imposed as well, it switches to the trust-region interior point method described in [16]. This interior point algorithm, in turn, solves inequality constraints by introducing slack variables and solving a sequence of equality-constrained barrier problems for progressively smaller values of the barrier parameter. The previously described equality constrained SQP method is used to solve the subproblems with increasing levels of accuracy as the iterate gets closer to a solution.

**Finite-Difference Options**

For Method *trust-constr* the gradient and the Hessian may be approximated using three finite-difference schemes: ‘2-point’, ‘3-point’, ‘cs’). The scheme ‘cs’ is, potentially, the most accurate but it requires the function to correctly handle complex inputs and to be differentiable in the complex plane. The scheme ‘3-point’ is more accurate than ‘2-point’ but requires twice as much operations.

**Custom minimizers**

It may be useful to pass a custom minimization method, for example when using a frontend to this method such as *scipy.optimize.basinhopping* or a different library. You can simply pass a callable as the *method* parameter.

The callable is called as *method(fun, x0, args, **kwags, **options)* where *kwags* corresponds to any other parameters passed to *minimize* (such as *callback*, *hess*, etc.), except the *options* dict, which has its contents also passed as *method* parameters pair by pair. Also, if *jac* has been passed as a bool type, *jac* and *fun* are mangled so that *fun* returns just the function values and *jac* is converted to a function returning the Jacobian. The method shall return an *OptimizeResult* object.

The provided *method* callable must be able to accept (and possibly ignore) arbitrary parameters; the set of parameters accepted by *minimize* may expand in future versions and then these parameters will be passed to the method. You can find an example in the *scipy.optimize* tutorial.

New in version 0.11.0.

**References**

[1], [2], [3], [4], [5], [6], [7], [8], [9], [10], [11], [12], [13], [14], [15], [16], [17]
Examples
Let us consider the problem of minimizing the Rosenbrock function. This function (and its respective
derivatives) is implemented in `rosen` (resp. `rosen_der`, `rosen_hess`) in the `scipy.optimize`.

```python
>>> from scipy.optimize import minimize, rosen, rosen_der
```

A simple application of the Nelder-Mead method is:

```python
>>> x0 = [1.3, 0.7, 0.8, 1.9, 1.2]
>>> res = minimize(rosen, x0, method='Nelder-Mead', tol=1e-6)
>>> res.x
array([1., 1., 1., 1., 1.])
```

Now using the BFGS algorithm, using the first derivative and a few options:

```python
>>> res = minimize(rosen, x0, method='BFGS', jac=rosen_der,
...                 options={'gtol': 1e-6, 'disp': True})
Optimization terminated successfully.
Current function value: 0.000000
Iterations: 26
Function evaluations: 31
Gradient evaluations: 31
>>> res.x
array([1., 1., 1., 1., 1.])
>>> print(res.message)
Optimization terminated successfully.
```

```python
>>> res.hess_inv
array([[0.00749589, 0.01255155, 0.02396251, 0.04750988, 0.09495377],
       [0.01255155, 0.02510441, 0.04794055, 0.09502834, 0.18996269],
       [0.02396251, 0.04794055, 0.09631614, 0.19092151, 0.38165151],
       [0.04750988, 0.09502834, 0.19092151, 0.38341252, 0.7664427],
       [0.09495377, 0.18996269, 0.38165151, 0.7664427, 1.53713523]])
```

Next, consider a minimization problem with several constraints (namely Example 16.4 from [5]). The objective function is:

```python
>>> fun = lambda x: (x[0] - 1)**2 + (x[1] - 2.5)**2
```

There are three constraints defined as:

```python
>>> cons = ({'type': 'ineq', 'fun': lambda x: x[0] - 2 * x[1] + 2},
...          {'type': 'ineq', 'fun': lambda x: -x[0] - 2 * x[1] + 6},
...          {'type': 'ineq', 'fun': lambda x: -x[0] + 2 * x[1] + 2})
```

And variables must be positive, hence the following bounds:

```python
>>> bnds = ((0, None), (0, None))
```

The optimization problem is solved using the SLSQP method as:

```python
>>> res = minimize(fun, (2, 0), method='SLSQP', bounds=bnds,
...                 constraints=cons)
```

It should converge to the theoretical solution (1.4, 1.7).
The `minimize` function supports the following methods:

```python
minimize(method='Nelder-Mead')
```

```python
scipy.optimize.minimize(fun, x0, args=(), method='Nelder-Mead', tol=None, callback=None, options={'func': None, 'xatol': None, 'fatol': None, 'maxiter': None, 'maxfev': None, 'disp': False, 'return_all': False, 'initial_simplex': None, 'xatol': 0.0001, 'fatol': 0.0001, 'adaptive': False})
```

Minimization of scalar function of one or more variables using the Nelder-Mead algorithm.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

**Options**

- **disp** [bool] Set to True to print convergence messages.
- **maxiter, maxfev** [int] Maximum allowed number of iterations and function evaluations. Will default to N*200, where N is the number of variables, if neither `maxiter` or `maxfev` is set. If both `maxiter` and `maxfev` are set, minimization will stop at the first reached.
- **initial_simplex** [array_like of shape (N + 1, N)] Initial simplex. If given, overrides `x0`. `initial_simplex[j,:]` should contain the coordinates of the j-th vertex of the N+1 vertices in the simplex, where N is the dimension.
- **xatol** [float, optional] Absolute error in xopt between iterations that is acceptable for convergence.
- **fatol** [number, optional] Absolute error in func(xopt) between iterations that is acceptable for convergence.
- **xtol** [float] Relative error in solution xopt acceptable for convergence.
- **ftol** [float] Relative error in func(xopt) acceptable for convergence.
- **adaptive** [bool, optional] Adapt algorithm parameters to dimensionality of problem. Useful for high-dimensional minimization [1].

**References**

[1]`minimize(method='Powell')`

```python
minimize(method='Powell')
```

```python
scipy.optimize.minimize(fun, x0, args=(), method='Powell', tol=None, callback=None, options={'func': None, 'xatol': 0.0001, 'fatol': 0.0001, 'maxiter': None, 'maxfev': None, 'disp': False, 'direc': None, 'return_all': False})
```

Minimization of scalar function of one or more variables using the modified Powell algorithm.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

**Options**

- **disp** [bool] Set to True to print convergence messages.
- **xtol** [float] Relative error in solution xopt acceptable for convergence.
- **ftol** [float] Relative error in func(xopt) acceptable for convergence.
- **maxiter, maxfev** [int] Maximum allowed number of iterations and function evaluations. Will default to N*1000, where N is the number of variables, if neither `maxiter` or `maxfev` is set. If both `maxiter` and `maxfev` are set, minimization will stop at the first reached.
- **direc** [ndarray] Initial set of direction vectors for the Powell method.
SciPy Reference Guide, Release 1.2.0

minimize(method='CG')

```python
c scipy.optimize.minimize(fun, x0, args=(), method='CG', jac=None, tol=None, callback=None, options={'gtol': 1e-05, 'norm': inf, 'eps': 1.4901161193847656e-08, 'maxiter': None, 'disp': False, 'return_all': False})
```

Minimization of scalar function of one or more variables using the conjugate gradient algorithm.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

**Options**

- `disp` [bool] Set to True to print convergence messages.
- `maxiter` [int] Maximum number of iterations to perform.
- `gtol` [float] Gradient norm must be less than `gtol` before successful termination.
- `norm` [float] Order of norm (Inf is max, -Inf is min).
- `eps` [float or ndarray] If `jac` is approximated, use this value for the step size.

minimize(method='BFGS')

```python
c scipy.optimize.minimize(fun, x0, args=(), method='BFGS', jac=None, tol=None, callback=None, options={'gtol': 1e-05, 'norm': inf, 'eps': 1.4901161193847656e-08, 'maxiter': None, 'disp': False, 'return_all': False})
```

Minimization of scalar function of one or more variables using the BFGS algorithm.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

**Options**

- `disp` [bool] Set to True to print convergence messages.
- `maxiter` [int] Maximum number of iterations to perform.
- `gtol` [float] Gradient norm must be less than `gtol` before successful termination.
- `norm` [float] Order of norm (Inf is max, -Inf is min).
- `eps` [float or ndarray] If `jac` is approximated, use this value for the step size.

minimize(method='Newton-CG')

```python
c scipy.optimize.minimize(fun, x0, args=(), method='Newton-CG', jac=None, hess=None, hessp=None, tol=None, callback=None, options={'xtol': 1e-05, 'eps': 1.4901161193847656e-08, 'maxiter': None, 'disp': False, 'return_all': False})
```

Minimization of scalar function of one or more variables using the Newton-CG algorithm.

Note that the `jac` parameter (Jacobian) is required.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

**Options**

- `disp` [bool] Set to True to print convergence messages.
- `xtol` [float] Average relative error in solution `xopt` acceptable for convergence.
- `maxiter` [int] Maximum number of iterations to perform.
- `eps` [float or ndarray] If `jac` is approximated, use this value for the step size.
minimize(method='L-BFGS-B')

```
scipy.optimize.minimize(fun, x0, args=(), method='L-BFGS-B', jac=None, bounds=None, tol=None, callback=None, options={'disp': None, 'maxcor': 10, 'ftol': 2.220446049250313e-09, 'gtol': 1e-05, 'eps': 1e-08, 'maxfun': 15000, 'maxiter': 15000, 'iprint': -1, 'maxls': 20})
```

Minimize a scalar function of one or more variables using the L-BFGS-B algorithm.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

**Options**

- **disp** [None or int] If `disp` is `None` (the default), then the supplied version of `iprint` is used. If `disp` is not `None`, then it overrides the supplied version of `iprint` with the behaviour you outlined.
- **maxcor** [int] The maximum number of variable metric corrections used to define the limited memory matrix. (The limited memory BFGS method does not store the full hessian but uses this many terms in an approximation to it.)
- **ftol** [float] The iteration stops when \((f^k - f^{k+1})/\max\{|f^k|,|f^{k+1}|,1\} <= \text{ftol}\).
- **gtol** [float] The iteration will stop when \(\max\{|\text{proj } g_i | i = 1, ..., n\} <= \text{gtol}\) where \(pg_i\) is the \(i\)-th component of the projected gradient.
- **eps** [float] Step size used for numerical approximation of the jacobian.
- **maxfun** [int] Maximum number of function evaluations.
- **maxiter** [int] Maximum number of iterations.
- **maxls** [int, optional] Maximum number of line search steps (per iteration). Default is 20.

**Notes**

The option `ftol` is exposed via the `scipy.optimize.minimize` interface, but calling `scipy.optimize.fmin_l_bfgs_b` directly exposes `factr`. The relationship between the two is `ftol = factr * numpy.finfo(float).eps`. I.e., `factr` multiplies the default machine floating-point precision to arrive at `ftol`.

minimize(method='TNC')

```
scipy.optimize.minimize(fun, x0, args=(), method='TNC', jac=None, bounds=None, tol=None, callback=None, options={'eps': 1e-08, 'scale': None, 'offset': None, 'mesg_num': None, 'maxCGit': -1, 'maxiter': None, 'eta': -1, 'stepmx': 0, 'accuracy': 0, 'minfev': 0, 'ftol': -1, 'xtol': -1, 'gtol': -1, 'rescale': -1, 'disp': False})
```

Minimize a scalar function of one or more variables using a truncated Newton (TNC) algorithm.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

**Options**

- **eps** [float] Step size used for numerical approximation of the jacobian.
- **scale** [list of floats] Scaling factors to apply to each variable. If None, the factors are up-low for interval bounded variables and 1+|x| for the others. Defaults to None.
- **offset** [float] Value to subtract from each variable. If None, the offsets are (up+low)/2 for interval bounded variables and \(x\) for the others.
- **disp** [bool] Set to True to print convergence messages.
- **maxCGit** [int] Maximum number of hessian*vector evaluations per main iteration. If maxCGit == 0, the direction chosen is -gradient if maxCGit < 0, maxCGit is set to max(1,\min(50,n/2)). Defaults to -1.
maxiter [int] Maximum number of function evaluation. If None, `maxiter` is set to \(\max(100, 10^\text{len}(x0))\). Defaults to None.

eta [float] Severity of the line search. If \(< 0\) or \(> 1\), set to 0.25. Defaults to -1.

stepmx [float] Maximum step for the line search. May be increased during call. If too small, it will be set to 10.0. Defaults to 0.

accuracy [float] Relative precision for finite difference calculations. If \(\leq \text{machine\_precision}\), set to \(\sqrt{\text{machine\_precision}}\). Defaults to 0.

minfev [float] Minimum function value estimate. Defaults to 0.

ftol [float] Precision goal for the value of \(f\) in the stopping criterion. If \(ftol < 0.0\), \(ftol\) is set to 0.0 defaults to -1.

xtol [float] Precision goal for the value of \(x\) in the stopping criterion (after applying \(x\) scaling factors). If \(xtol < 0.0\), \(xtol\) is set to \(\sqrt{\text{machine\_precision}}\). Defaults to -1.

gtol [float] Precision goal for the value of the projected gradient in the stopping criterion (after applying \(x\) scaling factors). If \(gtol < 0.0\), \(gtol\) is set to \(1e-2^{*}\sqrt{\text{accuracy}}\). Setting it to 0.0 is not recommended. Defaults to -1.

rescale [float] Scaling factor (in \(\log_{10}\)) used to trigger \(f\) value rescaling. If 0, rescale at each iteration. If a large value, never rescale. If \(< 0\), rescale is set to 1.3.

```python
minimize(method='COBYLA')
```

```python
scipy.optimize.minimize(fun, x0, args=(), method='COBYLA', constraints=(), tol=None, callback=None, options={'rhobeg': 1.0, 'maxiter': 1000, 'disp': False, 'catol': 0.0002})
```

Minimize a scalar function of one or more variables using the Constrained Optimization BY Linear Approximation (COBYLA) algorithm.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

**Options**

- `rhobeg` [float] Reasonable initial changes to the variables.
- `tol` [float] Final accuracy in the optimization (not precisely guaranteed). This is a lower bound on the size of the trust region.
- `disp` [bool] Set to True to print convergence messages. If False, `verbosity` is ignored as set to 0.
- `maxiter` [int] Maximum number of function evaluations.
- `catol` [float] Tolerance (absolute) for constraint violations

```python
minimize(method='SLSQP')
```

```python
scipy.optimize.minimize(fun, x0, args=(), method='SLSQP', jac=None, bounds=None, constraints=(), tol=None, callback=None, options={'func': None, 'maxiter': 100, 'ftol': 1e-06, 'iprint': 1, 'disp': False, 'eps': 1.4901161193847656e-08})
```

Minimize a scalar function of one or more variables using Sequential Least SQUares Programming (SLSQP).

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

**Options**

- `ftol` [float] Precision goal for the value of \(f\) in the stopping criterion.
- `eps` [float] Step size used for numerical approximation of the Jacobian.
Minimize a scalar function subject to constraints.

Parameters

gtol  [float, optional] Tolerance for termination by the norm of the Lagrangian gradient. The algorithm will terminate when both the infinity norm (i.e. max abs value) of the Lagrangian gradient and the constraint violation are smaller than gtol. Default is 1e-8.

xtol  [float, optional] Tolerance for termination by the change of the independent variable. The algorithm will terminate when \( tr_radius < xtol \), where \( tr_radius \) is the radius of the trust region used in the algorithm. Default is 1e-8.

barrier_tol  [float, optional] Threshold on the barrier parameter for the algorithm termination. When inequality constraints are present the algorithm will terminate only when the barrier parameter is less than \( barrier_tol \). Default is 1e-8.

sparse_jacobian  [{bool, None}, optional] Determines how to represent Jacobians of the constraints. If bool, then Jacobians of all the constraints will be converted to the corresponding format. If None (default), then Jacobians won’t be converted, but the algorithm can proceed only if they all have the same format.

initial_tr_radius: float, optional

Initial trust radius. The trust radius gives the maximum distance between solution points in consecutive iterations. It reflects the trust the algorithm puts in the local approximation of the optimization problem. For an accurate local approximation the trust-region should be large and for an approximation valid only close to the current point it should be a small one. The trust radius is automatically updated throughout the optimization process, with \( initial_tr_radius \) being its initial value. Default is 1 (recommended in [1]_, p 19).

initial_constr_penalty  [float, optional] Initial constraints penalty parameter. The penalty parameter is used for balancing the requirements of decreasing the objective function and satisfying the constraints. It is used for defining the merit function: \( \text{merit function}(x) = \text{fun}(x) + \text{constr penalty} \times \text{constr norm}_12(x) \), where \( \text{constr norm}_12(x) \) is the l2 norm of a vector containing all the constraints. The merit function is used for accepting or rejecting trial points and \( \text{constr penalty} \) weights the two conflicting goals of reducing objective function and constraints. The penalty is automatically updated throughout the optimization process, with \( initial\_constr\_penalty \) being its initial value. Default is 1 (recommended in [1]_, p 19).

initial_barrier_parameter, initial_barrier_tolerance: float, optional

Initial barrier parameter and initial tolerance for the barrier subproblem. Both are used only when inequality constraints are present. For dealing with opti-
mization problems \( \min_x f(x) \) subject to inequality constraints \( c(x) \leq 0 \) the algorithm introduces slack variables, solving the problem \( \min_{(x,s)} f(x) + \text{barrier\_parameter} \cdot \sum \ln(s) \) subject to the equality constraints \( c(x) + s = 0 \) instead of the original problem. This subproblem is solved for increasing values of \text{barrier\_parameter} and with decreasing tolerances for the termination, starting with \text{initial\_barrier\_parameter} for the barrier parameter and \text{initial\_barrier\_tolerance} for the barrier subproblem barrier. Default is 0.1 for both values (recommended in [1] p. 19).

\texttt{factorization\_method}

[string or None, optional] Method to factorize the Jacobian of the constraints. Use None (default) for the auto selection or one of:
- ‘NormalEquation’ (requires scikit-sparse)
- ‘AugmentedSystem’
- ‘QRFactorization’
- ‘SVDFactorization’

The methods ‘NormalEquation’ and ‘AugmentedSystem’ can be used only with sparse constraints. The projections required by the algorithm will be computed using, respectively, the the normal equation and the augmented system approaches explained in [1]. ‘NormalEquation’ computes the Cholesky factorization of \( A A^T \) and ‘AugmentedSystem’ performs the LU factorization of an augmented system. They usually provide similar results. ‘AugmentedSystem’ is used by default for sparse matrices.

The methods ‘QRFactorization’ and ‘SVDFactorization’ can be used only with dense constraints. They compute the required projections using, respectively, QR and SVD factorizations. The ‘SVDFactorization’ method can cope with Jacobian matrices with deficient row rank and will be used whenever other factorization methods fail (which may imply the conversion of sparse matrices to a dense format when required). By default ‘QRFactorization’ is used for dense matrices.

\texttt{finite\_diff\_rel\_step}

[None or array_like, optional] Relative step size for the finite difference approximation.

\texttt{maxiter}

[int, optional] Maximum number of algorithm iterations. Default is 1000.

\texttt{verbose}

[{0, 1, 2}, optional] Level of algorithm’s verbosity:
- 0 (default) : work silently.
- 1 : display a termination report.
- 2 : display progress during iterations.
- 3 : display progress during iterations (more complete report).

\texttt{disp}

[bool, optional] If True (default) then \texttt{verbose} will be set to 1 if it was 0.

\texttt{Returns}

‘OptimizeResult’ with the fields documented below. Note the following:

1. All values corresponding to the constraints are ordered as they were passed to the solver. And values corresponding to \texttt{bounds} constraints are put after other constraints.

2. All numbers of function, Jacobian or Hessian evaluations correspond to numbers of actual Python function calls. It means, for example, that if a Jacobian is estimated by finite differences then the number of Jacobian evaluations will be zero and the number of function evaluations will be incremented by all calls during the finite difference estimation.

\texttt{x}

[ndarray, shape (n,)] Solution found.

\texttt{optimality}

[float] Infinity norm of the Lagrangian gradient at the solution.
<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
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<tr>
<td>constr_violation</td>
<td>Maximum constraint violation at the solution.</td>
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<tr>
<td>fun</td>
<td>Objective function at the solution.</td>
</tr>
<tr>
<td>grad</td>
<td>Gradient of the objective function at the solution.</td>
</tr>
<tr>
<td>lagrangian_grad</td>
<td>Gradient of the Lagrangian function at the solution.</td>
</tr>
<tr>
<td>nit</td>
<td>Total number of iterations.</td>
</tr>
<tr>
<td>nfev</td>
<td>Number of the objective function evaluations.</td>
</tr>
<tr>
<td>ngev</td>
<td>Number of the objective function gradient evaluations.</td>
</tr>
<tr>
<td>nhev</td>
<td>Number of the objective function Hessian evaluations.</td>
</tr>
<tr>
<td>cg_niter</td>
<td>Total number of the conjugate gradient method iterations.</td>
</tr>
<tr>
<td>method</td>
<td>Optimization method used.</td>
</tr>
<tr>
<td>constr</td>
<td>List of constraint values at the solution.</td>
</tr>
<tr>
<td>jac</td>
<td>List of the Jacobian matrices of the constraints at the solution.</td>
</tr>
<tr>
<td>v</td>
<td>List of the Lagrange multipliers for the constraints at the solution.</td>
</tr>
<tr>
<td>constr_nfev</td>
<td>Number of constraint evaluations for each of the constraints.</td>
</tr>
<tr>
<td>constr_njev</td>
<td>Number of Jacobian matrix evaluations for each of the constraints.</td>
</tr>
<tr>
<td>constr_nhev</td>
<td>Number of Hessian evaluations for each of the constraints.</td>
</tr>
<tr>
<td>tr_radius</td>
<td>Radius of the trust region at the last iteration.</td>
</tr>
<tr>
<td>constr_penalty</td>
<td>Penalty parameter at the last iteration, see initial_constr_penalty.</td>
</tr>
<tr>
<td>barrier_tolerance</td>
<td>Tolerance for the barrier subproblem at the last iteration. Only for problems with inequality constraints.</td>
</tr>
<tr>
<td>barrier_parameter</td>
<td>Barrier parameter at the last iteration. Only for problems with inequality constraints.</td>
</tr>
<tr>
<td>execution_time</td>
<td>Total execution time.</td>
</tr>
<tr>
<td>message</td>
<td>Termination message.</td>
</tr>
<tr>
<td>status</td>
<td>Termination status:</td>
</tr>
<tr>
<td></td>
<td>• 0 : The maximum number of function evaluations is exceeded.</td>
</tr>
<tr>
<td></td>
<td>• 1 : gtol termination condition is satisfied.</td>
</tr>
<tr>
<td></td>
<td>• 2 : xtol termination condition is satisfied.</td>
</tr>
<tr>
<td></td>
<td>• 3 : callback function requested termination.</td>
</tr>
<tr>
<td>cg_stop_cond</td>
<td>Reason for CG subproblem termination at the last iteration:</td>
</tr>
<tr>
<td></td>
<td>• 0 : CG subproblem not evaluated.</td>
</tr>
<tr>
<td></td>
<td>• 1 : Iteration limit was reached.</td>
</tr>
<tr>
<td></td>
<td>• 2 : Reached the trust-region boundary.</td>
</tr>
<tr>
<td></td>
<td>• 3 : Negative curvature detected.</td>
</tr>
<tr>
<td></td>
<td>• 4 : Tolerance was satisfied.</td>
</tr>
</tbody>
</table>
**minimize(method='dogleg')**

```python
scipy.optimize.minimize(fun, x0, args=(), method='dogleg', jac=None, hess=None, tol=None, callback=None, options={})
```

Minimization of scalar function of one or more variables using the dog-leg trust-region algorithm.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

**Options**

- `initial_trust_radius` [float] Initial trust-region radius.
- `max_trust_radius` [float] Maximum value of the trust-region radius. No steps that are longer than this value will be proposed.
- `eta` [float] Trust region related acceptance stringency for proposed steps.
- `gtol` [float] Gradient norm must be less than `gtol` before successful termination.

**minimize(method='trust-ncg')**

```python
scipy.optimize.minimize(fun, x0, args=(), method='trust-ncg', jac=None, hess=None, hessp=None, tol=None, callback=None, options={})
```

Minimization of scalar function of one or more variables using the Newton conjugate gradient trust-region algorithm.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

**Options**

- `initial_trust_radius` [float] Initial trust-region radius.
- `max_trust_radius` [float] Maximum value of the trust-region radius. No steps that are longer than this value will be proposed.
- `eta` [float] Trust region related acceptance stringency for proposed steps.
- `gtol` [float] Gradient norm must be less than `gtol` before successful termination.

**minimize(method='trust-krylov')**

```python
scipy.optimize.minimize(fun, x0, args=(), method='trust-krylov', jac=None, hess=None, hessp=None, tol=None, callback=None, options={'inexact': True})
```

Minimization of a scalar function of one or more variables using a nearly exact trust-region algorithm that only requires matrix vector products with the hessian matrix.

New in version 1.0.0.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.minimize`

**Options**

- `inexact` [bool, optional] Accuracy to solve subproblems. If True requires less nonlinear iterations, but more vector products.
minimize(method='trust-exact')
sparse.optimize.minimize(fun, x0, args=(), method='trust-exact', jac=None, hess=None, tol=None,
callback=None, options={})

Minimization of scalar function of one or more variables using a nearly exact trust-region algorithm.

See also:

For documentation for the rest of the parameters, see `sparse.optimize.minimize`

Options

- initial_tr_radius: Initial trust-region radius.
- max_tr_radius: Maximum value of the trust-region radius. No steps that are longer than this value will be proposed.
- eta: Trust region related acceptance stringency for proposed steps.
- gtol: Gradient norm must be less than `gtol` before successful termination.

Constraints are passed to `minimize` function as a single object or as a list of objects from the following classes:

<table>
<thead>
<tr>
<th>NonlinearConstraint(fun, lb, ub[, jac, ...])</th>
<th>Nonlinear constraint on the variables.</th>
</tr>
</thead>
<tbody>
<tr>
<td>LinearConstraint(A, lb, ub[, keep_feasible])</td>
<td>Linear constraint on the variables.</td>
</tr>
</tbody>
</table>

sparse.optimize.NonlinearConstraint
class sparse.optimize.NonlinearConstraint(fun, lb, ub, jac='2-point',
hess=<sparse.optimize._hessian_update_strategy.BFGS
object>, keep_feasible=False, finite_diff_rel_step=None,
finite_diff_jac_sparsity=None)

Nonlinear constraint on the variables.

The constraint has the general inequality form:

\[lb \leq \text{fun}(x) \leq ub\]

Here the vector of independent variables \(x\) is passed as ndarray of shape \((n,)\) and \text{fun} returns a vector with \(m\) components.

It is possible to use equal bounds to represent an equality constraint or infinite bounds to represent a one-sided constraint.

Parameters

- `fun` [callable] The function defining the constraint. The signature is \(\text{fun}(x) \rightarrow \text{array_like, shape (m,)}\).
- `lb, ub` [array_like] Lower and upper bounds on the constraint. Each array must have the shape \((m,)\) or be a scalar, in the latter case a bound will be the same for all components of the constraint. Use `np.inf` with an appropriate sign to specify an one-sided constraint. Set components of \(lb\) and \(ub\) equal to represent an equality constraint. Note that you can mix constraints of different types: interval, one-sided or equality, by setting different components of \(lb\) and \(ub\) as necessary.
- `jac` [{callable, ‘2-point’, ‘3-point’, ‘cs’}, optional] Method of computing the Jacobian matrix (an \(m\)-by-\(n\) matrix, where element \((i, j)\) is the partial derivative of \(f[j]\) with respect to \(x[i]\)). The keywords \{‘2-point’, ‘3-point’, ‘cs’\} select a finite difference
scheme for the numerical estimation. A callable must have the following signature:

\[
\text{jac}(x) \rightarrow \{\text{ndarray, sparse matrix}\}, \text{shape} (m, n). \text{Default is ‘2-point’}.
\]

\[
\text{hess} \rightarrow \{\text{callable, ‘2-point’, ‘3-point’, ‘cs’, HessianUpdateStrategy, None}, \text{optional}\}
\]

Method for computing the Hessian matrix. The keywords {'2-point', '3-point', 'cs'} select a finite difference scheme for numerical estimation. Alternatively, objects implementing HessianUpdateStrategy interface can be used to approximate the Hessian. Currently available implementations are:

- \text{BFGS} (default option)
- \text{SR1}

A callable must return the Hessian matrix of \( \text{dot}(\text{fun}, v) \) and must have the following signature:

\[
\text{hess}(x, v) \rightarrow \{\text{LinearOperator, sparse matrix, array_like}\}, \text{shape} (n, n). \text{Here} v \text{is ndarray with shape} (m,) \text{containing Lagrange multipliers}.
\]

\[
\text{keep\_feasible} \rightarrow \{\text{array\_like of bool, optional}\}
\]

Whether to keep the constraint components feasible throughout iterations. A single value set this property for all components. Default is False. Has no effect for equality constraints.

\[
\text{finite\_diff\_rel\_step: None or array\_like, optional}
\]

Relative step size for the finite difference approximation. Default is None, which will select a reasonable value automatically depending on a finite difference scheme.

\[
\text{finite\_diff\_jac\_sparsity: \{None, array\_like, sparse matrix\}, optional}
\]

Defines the sparsity structure of the Jacobian matrix for finite difference estimation, its shape must be (m, n). If the Jacobian has only few non-zero elements in each row, providing the sparsity structure will greatly speed up the computations. A zero entry means that a corresponding element in the Jacobian is identically zero. If provided, forces the use of ‘lsmr’ trust-region solver. If None (default) then dense differencing will be used.

Notes

Finite difference schemes {'2-point', '3-point', 'cs'} may be used for approximating either the Jacobian or the Hessian. We, however, do not allow its use for approximating both simultaneously. Hence whenever the Jacobian is estimated via finite-differences, we require the Hessian to be estimated using one of the quasi-Newton strategies.

The scheme ‘cs’ is potentially the most accurate, but requires the function to correctly handles complex inputs and be analytically continuable to the complex plane. The scheme ‘3-point’ is more accurate than ‘2-point’ but requires twice as many operations.

scipy.optimize.LinearConstraint
class scipy.optimize.LinearConstraint(A, lb, ub, keep_feasible=False)

Linear constraint on the variables.

The constraint has the general inequality form:

\[
\text{lb} \leq \text{A.dot(x)} \leq \text{ub}
\]

Here the vector of independent variables \( x \) is passed as ndarray of shape (n,) and the matrix \( A \) has shape (m, n).

It is possible to use equal bounds to represent an equality constraint or infinite bounds to represent a one-sided constraint.

Parameters

\[
\text{A} \rightarrow \{\text{array\_like, sparse matrix}\}, \text{shape} (m, n)\]

Matrix defining the constraint.

\[
\text{lb, ub} \rightarrow \{\text{array\_like}\}
\]

Lower and upper bounds on the constraint. Each array must have the shape (m,) or be a scalar, in the latter case a bound will be the same for all components of the constraint. Use \text{np.inf} with an appropriate sign to specify a
one-sided constraint. Set components of \( lb \) and \( ub \) equal to represent an equality constraint. Note that you can mix constraints of different types: interval, one-sided or equality, by setting different components of \( lb \) and \( ub \) as necessary.

**keep_feasible**

[array_like of bool, optional] Whether to keep the constraint components feasible throughout iterations. A single value set this property for all components. Default is False. Has no effect for equality constraints.

Simple bound constraints are handled separately and there is a special class for them:

```
Bounds(lb, ub[, keep_feasible])
```

**scipy.optimize.Bounds**

The constraint has the general inequality form:

\[
lb < x < ub
\]

It is possible to use equal bounds to represent an equality constraint or infinite bounds to represent a one-sided constraint.

**Parameters**

- **lb, ub** [array_like, optional] Lower and upper bounds on independent variables. Each array must have the same size as \( x \) or be a scalar, in which case a bound will be the same for all the variables. Set components of \( lb \) and \( ub \) equal to fix a variable. Use \( \text{np.inf} \) with an appropriate sign to disable bounds on all or some variables. Note that you can mix constraints of different types: interval, one-sided or equality, by setting different components of \( lb \) and \( ub \) as necessary.

- **keep_feasible** [array_like of bool, optional] Whether to keep the constraint components feasible throughout iterations. A single value set this property for all components. Default is False. Has no effect for equality constraints.

Quasi-Newton strategies implementing `HessianUpdateStrategy` interface can be used to approximate the Hessian in `minimize` function (available only for the ‘trust-constr’ method). Available quasi-Newton methods implementing this interface are:

```
BFGS([exception_strategy, min_curvature, ...])
```

Broyden-Fletcher-Goldfarb-Shanno (BFGS) Hessian update strategy.

```
SR1([min_denominator, init_scale])
```

Symmetric-rank-1 Hessian update strategy.

**scipy.optimize.BFGS**

Broyden-Fletcher-Goldfarb-Shanno (BFGS) Hessian update strategy.

```
BFGS(exception_strategy='skip_update', min_curvature=None, init_scale='auto')
```

Broyden-Fletcher-Goldfarb-Shanno (BFGS) Hessian update strategy.

**Parameters**

- **exception_strategy** ([‘skip_update’, ‘damp_update’], optional) Define how to proceed when the curvature condition is violated. Set it to ‘skip_update’ to just skip the update. Or, alternatively, set it to ‘damp_update’ to interpolate between the actual BFGS result and the unmodified matrix. Both exceptions strategies are explained in [1], p.536-537.
min_curvature

[float] This number, scaled by a normalization factor, defines the minimum curvature \( \text{dot}(\Delta \text{grad}, \Delta \text{x}) \) allowed to go unaffected by the exception strategy. By default is equal to 1e-8 when exception_strategy = 'skip_update' and equal to 0.2 when exception_strategy = 'damp_update'.

init_scale

[[float, 'auto']]] Matrix scale at first iteration. At the first iteration the Hessian matrix or its inverse will be initialized with init_scale•np.eye(n), where n is the problem dimension. Set it to 'auto' in order to use an automatic heuristic for choosing the initial scale. The heuristic is described in [1], p.143. By default uses 'auto'.

Notes
The update is based on the description in [1], p.140.

References
[1]

Methods

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<th>Method</th>
<th>Description</th>
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<td>dot(p)</td>
<td>Compute the product of the internal matrix with the given vector.</td>
</tr>
<tr>
<td>get_matrix()</td>
<td>Return the current internal matrix.</td>
</tr>
<tr>
<td>initialize(n, approx_type)</td>
<td>Initialize internal matrix. Allocate internal memory for storing and updating the Hessian or its inverse (depending on how approx_type was defined).</td>
</tr>
<tr>
<td>update(delta_x, delta_grad)</td>
<td>Update internal matrix.</td>
</tr>
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scipy.optimize.BFGS.dot

BFGS.dot(p)

Compute the product of the internal matrix with the given vector.

Parameters

\( p \) [array_like] 1-d array representing a vector.

Returns

\( Hp \) [array] 1-d represents the result of multiplying the approximation matrix by vector \( p \).

scipy.optimize.BFGS.get_matrix

BFGS.get_matrix()

Return the current internal matrix.

Returns

\( M \) [ndarray, shape (n, n)] Dense matrix containing either the Hessian or its inverse (depending on how approx_type was defined).

scipy.optimize.BFGS.initialize

BFGS.initialize(n, approx_type)

Initialize internal matrix.

Allocate internal memory for storing and updating the Hessian or its inverse.

Parameters

\( n \) [int] Problem dimension.
approx_type

[{'hess', 'inv_hess'}] Selects either the Hessian or the inverse Hessian. When
set to 'hess' the Hessian will be stored and updated. When set to 'inv_hess'
its inverse will be used instead.

scipy.optimize.BFGS.update

BFGS.update(delta_x, delta_grad)
Update internal matrix.
Update Hessian matrix or its inverse (depending on how 'approx_type' is defined) using information about the last evaluated points.

Parameters

delta_x [ndarray] The difference between two points the gradient function have been evaluated at: delta_x = x2 - x1.
delta_grad [ndarray] The difference between the gradients: delta_grad = grad(x2) - grad(x1).

scipy.optimize.SR1

class scipy.optimize.SR1(min_denominator=1e-08, init_scale='auto')
Symmetric-rank-1 Hessian update strategy.

Parameters

min_denominator [float] This number, scaled by a normalization factor, defines the minimum denominator magnitude allowed in the update. When the condition is violated we skip the update. By default uses 1e-8.
init_scale [float, 'auto'], optional] Matrix scale at first iteration. At the first iteration the Hessian matrix or its inverse will be initialized with init_scale*np.eye(n), where n is the problem dimension. Set it to 'auto' in order to use an automatic heuristic for choosing the initial scale. The heuristic is described in [1], p.143. By default uses 'auto'.

Notes
The update is based on the description in [1], p.144-146.

References
[1]

Methods

dot(p) Compute the product of the internal matrix with the given vector.
get_matrix() Return the current internal matrix.
initialize(n, approx_type) Initialize internal matrix.
update(delta_x, delta_grad) Update internal matrix.

scipy.optimize.SR1.dot

SR1.dot(p)
Compute the product of the internal matrix with the given vector.

Parameters

p [array_like] 1-d array representing a vector.
Returns

\( Hp \) [array] 1-d represents the result of multiplying the approximation matrix by vector \( p \).

**scipy.optimize.SR1.get_matrix**

**SR1.get_matrix()**

Return the current internal matrix.

Returns

\( M \) [ndarray, shape (n, n)] Dense matrix containing either the Hessian or its inverse (depending on how `approx_type` was defined).

**scipy.optimize.SR1.initialize**

**SR1.initialize(n, approx_type)**

Initialize internal matrix.

Allocate internal memory for storing and updating the Hessian or its inverse.

Parameters

- **n** [int] Problem dimension.
- **approx_type** [{'hess', 'inv_hess'}] Selects either the Hessian or the inverse Hessian. When set to 'hess' the Hessian will be stored and updated. When set to 'inv_hess' its inverse will be used instead.

**scipy.optimize.SR1.update**

**SR1.update(delta_x, delta_grad)**

Update internal matrix.

Update Hessian matrix or its inverse (depending on how `approx_type` is defined) using information about the last evaluated points.

Parameters

- **delta_x** [ndarray] The difference between two points the gradient function have been evaluated at: \( \Delta_x = x_2 - x_1 \).
- **delta_grad** [ndarray] The difference between the gradients: \( \Delta \text{grad} = \text{grad}(x_2) - \text{grad}(x_1) \).

Global Optimization

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<td><code>basinhopping</code></td>
<td>Find the global minimum of a function using the basin-hopping algorithm</td>
</tr>
<tr>
<td><code>brute</code></td>
<td>Minimize a function over a given range by brute force.</td>
</tr>
<tr>
<td><code>differential_evolution</code></td>
<td>Finds the global minimum of a multivariate function.</td>
</tr>
<tr>
<td><code>shgo</code></td>
<td>Finds the global minimum of a function using SHG optimization.</td>
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<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>dual_annealing(func, bounds[, args, ...])</code></td>
<td>Find the global minimum of a function using Dual Annealing.</td>
</tr>
</tbody>
</table>

**scipy.optimize.basinhopping**

```python
scipy.optimize.basinhopping(func, x0, niter=100, T=1.0, stepsize=0.5, minimizer_kwargs=None, take_step=None, accept_test=None, callback=None, interval=50, disp=False, niter_success=None, seed=None)
```

Find the global minimum of a function using the basin-hopping algorithm

Basin-hopping is a two-phase method that combines a global stepping algorithm with local minimization at each step. Designed to mimic the natural process of energy minimization of clusters of atoms, it works well for similar problems with “funnel-like, but rugged” energy landscapes [5].

As the step-taking, step acceptance, and minimization methods are all customizable, this function can also be used to implement other two-phase methods.

**Parameters**

- **func**
  - `[callable f(x, *args)]` Function to be optimized. *args* can be passed as an optional item in the dict `minimizer_kwargs`.

- **x0**
  - `[array_like]` Initial guess.

- **niter**
  - `[integer, optional]` The number of basin-hopping iterations.

- **T**
  - `[float, optional]` The “temperature” parameter for the accept or reject criterion. Higher “temperatures” mean that larger jumps in function value will be accepted. For best results T should be comparable to the separation (in function value) between local minima.

- **stepsize**

- **minimizer_kwargs**
  - `[dict, optional]` Extra keyword arguments to be passed to the local minimizer `scipy.optimize.minimize()` Some important options could be:
    - **method**
      - `[str]` The minimization method (e.g. "L-BFGS-B")
    - **args**
      - `[tuple]` Extra arguments passed to the objective function (func) and its derivatives (Jacobian, Hessian).

- **take_step**
  - `[callable take_step(x), optional]` Replace the default step-taking routine with this routine. The default step-taking routine is a random displacement of the coordinates, but other step-taking algorithms may be better for some systems. `take_step` can optionally have the attribute `take_step.stepsize`. If this attribute exists, then `basinhopping` will adjust `take_step.stepsize` in order to try to optimize the global minimum search.

- **accept_test**
  - `[callable, accept_test(f_new=f_new, x_new=x_new, f_old=fold, x_old=x_old), optional]` Define a test which will be used to judge whether or not to accept the step. This will be used in addition to the Metropolis test based on “temperature” T. The acceptable return values are True, False, or "force accept". If any of the tests return False then the step is rejected. If the latter, then this will override any other tests in order to accept the step. This can be used, for example, to forcefully escape from a local minimum that `basinhopping` is trapped in.

- **callback**
  - `[callable, callback(x, f, accept), optional]` A callback function which will be called for all minima found. x and f are the coordinates and function value of the trial minimum, and accept is whether or not that minimum was accepted. This can be used, for example, to save the lowest N minima found. Also, `callback` can be used to specify a user defined stop criterion by optionally returning True to stop the `basinhopping` routine.
interval [integer, optional] interval for how often to update the stepsize

disp [bool, optional] Set to True to print status messages

niter_success [integer, optional] Stop the run if the global minimum candidate remains the same for this number of iterations.

seed [int or np.random.RandomState, optional] If seed is not specified the np.RandomState singleton is used. If seed is an int, a new np.random.RandomState instance is used, seeded with seed. If seed is already a np.random.RandomState instance, then that np.random.RandomState instance is used. Specify seed for repeatable minimizations. The random numbers generated with this seed only affect the default Metropolis accept_test and the default take_step. If you supply your own take_step and accept_test, and these functions use random number generation, then those functions are responsible for the state of their random number generator.

Returns

res [OptimizeResult] The optimization result represented as a OptimizeResult object. Important attributes are: x the solution array, fun the value of the function at the solution, and message which describes the cause of the termination. The OptimizeResult object returned by the selected minimizer at the lowest minimum is also contained within this object and can be accessed through the lowest_optimization_result attribute. See OptimizeResult for a description of other attributes.

See also:

minimize

The local minimization function called once for each basinhopping step. minimizer_kwargs is passed to this routine.

Notes

Basin-hopping is a stochastic algorithm which attempts to find the global minimum of a smooth scalar function of one or more variables [1] [2] [3] [4]. The algorithm in its current form was described by David Wales and Jonathan Doye [2] http://www-wales.ch.cam.ac.uk/.

The algorithm is iterative with each cycle composed of the following features

1. random perturbation of the coordinates
2. local minimization
3. accept or reject the new coordinates based on the minimized function value

The acceptance test used here is the Metropolis criterion of standard Monte Carlo algorithms, although there are many other possibilities [3].

This global minimization method has been shown to be extremely efficient for a wide variety of problems in physics and chemistry. It is particularly useful when the function has many minima separated by large barriers. See the Cambridge Cluster Database http://www-wales.ch.cam.ac.uk/CCD.html for databases of molecular systems that have been optimized primarily using basin-hopping. This database includes minimization problems exceeding 300 degrees of freedom.

See the free software program GMIN (http://www-wales.ch.cam.ac.uk/GMIN) for a Fortran implementation of basin-hopping. This implementation has many different variations of the procedure described above, including more advanced step taking algorithms and alternate acceptance criterion.

For stochastic global optimization there is no way to determine if the true global minimum has actually been found. Instead, as a consistency check, the algorithm can be run from a number of different
random starting points to ensure the lowest minimum found in each example has converged to the global minimum. For this reason basinhopping will by default simply run for the number of iterations niter and return the lowest minimum found. It is left to the user to ensure that this is in fact the global minimum.

Choosing stepsize: This is a crucial parameter in basinhopping and depends on the problem being solved. The step is chosen uniformly in the region from x0-stepsize to x0+stepsize, in each dimension. Ideally it should be comparable to the typical separation (in argument values) between local minima of the function being optimized. basinhopping will, by default, adjust stepsize to find an optimal value, but this may take many iterations. You will get quicker results if you set a sensible initial value for stepsize.

Choosing T: The parameter T is the “temperature” used in the Metropolis criterion. Basinhopping steps are always accepted if \( \text{func}(x_{\text{new}}) < \text{func}(x_{\text{old}}) \). Otherwise, they are accepted with probability:

\[
\exp\left(\frac{\text{func}(x_{\text{new}}) - \text{func}(x_{\text{old}})}{T}\right)
\]

So, for best results, T should be comparable to the typical difference (in function values) between local minima. (The height of “walls” between local minima is irrelevant.)

If T is 0, the algorithm becomes Monotonic Basin-Hopping, in which all steps that increase energy are rejected.

New in version 0.12.0.

**References**

[1], [2], [3], [4], [5]

**Examples**
The following example is a one-dimensional minimization problem, with many local minima superimposed on a parabola.

```python
>>> from scipy.optimize import basinhopping
>>> func = lambda x: np.cos(14.5 * x - 0.3) + (x + 0.2) * x
>>> x0=[1.]
```

Basinhopping, internally, uses a local minimization algorithm. We will use the parameter minimizer_kwarg to tell basinhopping which algorithm to use and how to set up that minimizer. This parameter will be passed to scipy.optimize.minimize().

```python
>>> minimizer_kwargs = {"method": "BFGS"}
>>> ret = basinhopping(func, x0, minimizer_kwargs=minimizer_kwargs,
...                     niter=200)
>>> print("global minimum: x = %.4f, f(x0) = %.4f" % (ret.x, ret.fun))
global minimum: x = -0.1951, f(x0) = -1.9999
```

Next consider a two-dimensional minimization problem. Also, this time we will use gradient information to significantly speed up the search.

```python
>>> def func2d(x):
...     f = np.cos(14.5 * x[0] - 0.3) + (x[1] + 0.2) * x[1] + (x[0] +
...     0.2) * x[0]
...     df = np.zeros(2)
...     df[0] = -14.5 * np.sin(14.5 * x[0] - 0.3) + 2. * x[0] + 0.2
...     df[1] = 2. * x[1] + 0.2
...     return f, df
```
We'll also use a different local minimization algorithm. Also we must tell the minimizer that our
function returns both energy and gradient (jacobian)

```python
>>> minimizer_kwargs = {"method": "L-BFGS-B", "jac": True}
>>> x0 = [1.0, 1.0]
>>> ret = basinhopping(func2d, x0, minimizer_kwargs=minimizer_kwargs,
... niter=200)
>>> print("global minimum: x = [%+.4f, %.4f], f(x0) = %.4f" % (ret.x[0],
... ret.x[1],
... ret.fun))
global minimum: x = [-0.1951, -0.1000], f(x0) = -1.0109
```

Here is an example using a custom step-taking routine. Imagine you want the first coordinate to take
larger steps than the rest of the coordinates. This can be implemented like so:

```python
>>> class MyTakeStep(object):
...     def __init__(self, stepsize=0.5):
...         self.stepsize = stepsize
...     def __call__(self, x):
...         s = self.stepsize
...         x[0] += np.random.uniform(-2*s, 2*s)
...         x[1:] += np.random.uniform(-s, s, x[1:].shape)
...         return x
```

Since `MyTakeStep.stepsize` exists basinhopping will adjust the magnitude of `stepsize` to optimize
the search. We'll use the same 2-D function as before

```python
>>> mytakestep = MyTakeStep()
>>> ret = basinhopping(func2d, x0, minimizer_kwargs=minimizer_kwargs,
... niter=200, take_step=mytakestep)
>>> print("global minimum: x = [%+.4f, %.4f], f(x0) = %.4f" % (ret.x[0],
... ret.x[1],
... ret.fun))
global minimum: x = [-0.1951, -0.1000], f(x0) = -1.0109
```

Now let’s do an example using a custom callback function which prints the value of every minimum
found

```python
>>> def print_fun(x, f, accepted):
...     print("at minimum %.4f accepted %d" % (f, int(accepted)))
```

We'll run it for only 10 basinhopping steps this time.

```python
>>> np.random.seed(1)
>>> ret = basinhopping(func2d, x0, minimizer_kwargs=minimizer_kwargs,
... niter=10, callback=print_fun)
at minimum 0.4159 accepted 1
at minimum -0.9073 accepted 1
at minimum -0.1021 accepted 1
at minimum -0.1021 accepted 1
at minimum 0.9102 accepted 1
at minimum 0.9102 accepted 1
at minimum 2.2945 accepted 0
at minimum -0.1021 accepted 1
```

(continues on next page)
The minimum at -1.0109 is actually the global minimum, found already on the 8th iteration.

Now let’s implement bounds on the problem using a custom `accept_test`:

```python
>>> class MyBounds(object):
...     def __init__(self, xmax=[1.1,1.1], xmin=[-1.1,-1.1]):
...         self.xmax = np.array(xmax)
...         self.xmin = np.array(xmin)
...     def __call__(self, **kwargs):
...         x = kwargs['x_new']
...         tmax = bool(np.all(x <= self.xmax))
...         tmin = bool(np.all(x >= self.xmin))
...         return tmax and tmin

>>> mybounds = MyBounds()
>>> ret = basinhopping(func2d, x0, minimizer_kwargs=minimizer_kwargs,
...                     niter=10, accept_test=mybounds)
```

**scipy.optimize.brute**

`scipy.optimize.brute(func, ranges, args=(), Ns=20, full_output=0, finish=<function fmin>, disp=False)`

Minimize a function over a given range by brute force.

Uses the “brute force” method, i.e. computes the function’s value at each point of a multidimensional grid of points, to find the global minimum of the function.

The function is evaluated everywhere in the range with the datatype of the first call to the function, as enforced by the `vectorize` NumPy function. The value and type of the function evaluation returned when `full_output=True` are affected in addition by the `finish` argument (see Notes).

The brute force approach is inefficient because the number of grid points increases exponentially - the number of grid points to evaluate is $N_s^\text{len(x)}$. Consequently, even with coarse grid spacing, even moderately sized problems can take a long time to run, and/or run into memory limitations.

**Parameters**

- `func` [callable] The objective function to be minimized. Must be in the form $f(x, *args)$, where $x$ is the argument in the form of a 1-D array and *args is a tuple of any additional fixed parameters needed to completely specify the function.

- `ranges` [tuple] Each component of the `ranges` tuple must be either a “slice object” or a range tuple of the form `(low, high)`. The program uses these to create the grid of points on which the objective function will be computed. See *Note 2* for more detail.

- `args` [tuple, optional] Any additional fixed parameters needed to completely specify the function.

- `Ns` [int, optional] Number of grid points along the axes, if not otherwise specified. See *Note 2*.

- `full_output` [bool, optional] If True, return the evaluation grid and the objective function’s values on it.

- `finish` [callable, optional] An optimization function that is called with the result of brute force minimization as initial guess. `finish` should take `func` and the initial guess as positional arguments, and take `args` as keyword arguments. It may additionally
take `full_output` and/or `disp` as keyword arguments. Use None if no “polishing”
function is to be used. See Notes for more details.

```
disp
```
[bool, optional] Set to True to print convergence messages.

```
Returns
```

```
x0
```
[ndarray] A 1-D array containing the coordinates of a point at which the objective
function had its minimum value. (See Note 1 for which point is returned.)

```
fval
```
[float] Function value at the point `x0`. (Returned when `full_output` is True.)

```
grid
```
[tuple] Representation of the evaluation grid. It has the same length as `x0`. (Re-
turned when `full_output` is True.)

```
Jout
```
[ndarray] Function values at each point of the evaluation grid, i.e., `Jout = func(*grid)`.
(Returned when `full_output` is True.)

See also:

`basinhopping`, `differential_evolution`

Notes

**Note 1:** The program finds the gridpoint at which the lowest value of the objective
function occurs. If `finish` is None, that is the point returned. When the global minimum occurs within
(or not very far outside) the grid’s boundaries, and the grid is fine enough, that point will be in the neighborhood of
the global minimum.

However, users often employ some other optimization program to “polish” the gridpoint values, i.e., to
seek a more precise (local) minimum near `brute`’s best gridpoint. The `brute` function’s `finish` option
provides a convenient way to do that. Any polishing program used must take `brute`’s output as its initial
guess as a positional argument, and take `brute`’s input values for `args` as keyword arguments, otherwise
an error will be raised. It may additionally take `full_output` and/or `disp` as keyword arguments.

`brute` assumes that the `finish` function returns either an `OptimizeResult` object or a tuple in the form:
(xmin, Jmin, ..., statuscode), where xmin is the minimizing value of the argument, Jmin is the
minimum value of the objective function, “...” may be some other returned values (which are not used
by `brute`), and statuscode is the status code of the `finish` program.

Note that when `finish` is not None, the values returned are those of the `finish` program, not the gridpoint
ones. Consequently, while `brute` confines its search to the input grid points, the `finish` program’s
results usually will not coincide with any gridpoint, and may fall outside the grid’s boundary. Thus, if
a minimum only needs to be found over the provided grid points, make sure to pass in `finish=None`.

**Note 2:** The grid of points is a `numpy.mgrid` object. For `brute` the `ranges` and `Ns` inputs have the
following effect. Each component of the `ranges` tuple can be either a slice object or a two-tuple giving
a range of values, such as (0, 5). If the component is a slice object, `brute` uses it directly. If the
component is a two-tuple range, `brute` internally converts it to a slice object that interpolates `Ns`
points from its low-value to its high-value, inclusive.

Examples

We illustrate the use of `brute` to seek the global minimum of a function of two variables that is given
as the sum of a positive-definite quadratic and two deep “Gaussian-shaped” craters. Specifically, define
the objective function `f` as the sum of three other functions, `f = f1 + f2 + f3`. We suppose each of
these has a signature (z, *params), where z = (x, y), and `params` and the functions are as defined
below.

```python
>>> params = (2, 3, 7, 8, 9, 10, 44, -1, 2, 26, 1, -2, 0.5)
>>> def f1(z, *params):
...     x, y = z
...     a, b, c, d, e, f, g, h, i, j, k, l, scale = params
...     return (a * x**2 + b * x * y + c * y**2 + d*x + e*y + f)
```
```python
>>> def f2(z, *params):
...     x, y = z
...     a, b, c, d, e, f, g, h, i, j, k, l, scale = params
...     return (-g*np.exp(-(x-h)**2 + (y-i)**2) / scale)

>>> def f3(z, *params):
...     x, y = z
...     a, b, c, d, e, f, g, h, i, j, k, l, scale = params
...     return (-j*np.exp(-(x-k)**2 + (y-l)**2) / scale)

>>> def f(z, *params):
...     return f1(z, *params) + f2(z, *params) + f3(z, *params)
```

Thus, the objective function may have local minima near the minimum of each of the three functions of which it is composed. To use \texttt{fmin} to polish its gridpoint result, we may then continue as follows:

```python
>>> rranges = (slice(-4, 4, 0.25), slice(-4, 4, 0.25))
>>> from scipy import optimize
>>> resbrute = optimize.brute(f, rranges, args=params, full_output=True,
...     finish=optimize.fmin)

>>> resbrute[0]  # global minimum
array([-1.05665192, 1.80834843])
>>> resbrute[1]  # function value at global minimum
-3.4085818767
```

Note that if \texttt{finish} had been set to None, we would have gotten the gridpoint [-1.0 1.75] where the rounded function value is -2.892.

\texttt{scipy.optimize.differential_evolution}

\texttt{scipy.optimize.differential_evolution(func, bounds, args=(),
strategy='best1bin', maxiter=1000, popsize=15, tol=0.01,
mutation=(0.5, 1), recombination=0.7, seed=None, callback=None,
disp=False, polish=True, init='latinhypercube', atol=0,
updating='immediate', workers=1)}

Finds the global minimum of a multivariate function.

Differential Evolution is stochastic in nature (does not use gradient methods) to find the minimum, and can search large areas of candidate space, but often requires larger numbers of function evaluations than conventional gradient based techniques.

The algorithm is due to Storn and Price [1].

\textbf{Parameters}

\begin{itemize}
  \item \texttt{func} [callable] The objective function to be minimized. Must be in the form \texttt{f(x, \*args)}, where \texttt{x} is the argument in the form of a 1-D array and \texttt{args} is a tuple of any additional fixed parameters needed to completely specify the function.
  \item \texttt{bounds} [sequence] Bounds for variables. \texttt{(min, max)} pairs for each element in \texttt{x}, defining the lower and upper bounds for the optimizing argument of \texttt{func}. It is required to have \texttt{len(bounds) == len(x)}. \texttt{len(bounds)} is used to determine the number of parameters in \texttt{x}.
  \item \texttt{args} [tuple, optional] Any additional fixed parameters needed to completely specify the objective function.
  \item \texttt{strategy} [str, optional] The differential evolution strategy to use. Should be one of:
    \begin{itemize}
      \item \texttt{‘best1bin’}
      \item \texttt{‘best1exp’}
    \end{itemize}
\end{itemize}
maxiter [int, optional] The maximum number of generations over which the entire population is evolved. The maximum number of function evaluations (with no polishing) is: \((\text{maxiter} + 1) \times \text{popsize} \times \text{len}(x)\)

popsize [int, optional] A multiplier for setting the total population size. The population has \(\text{popsize} \times \text{len}(x)\) individuals (unless the initial population is supplied via the init keyword).

tol [float, optional] Relative tolerance for convergence, the solving stops when \(\text{np.std(pop)} \leq \text{atol + tol} \times \text{np.abs(np.mean(population_energies))}\), where and atol and tol are the absolute and relative tolerance respectively.

mutation [float or tuple(float, float), optional] The mutation constant. In the literature this is also known as differential weight, being denoted by F. If specified as a float it should be in the range \([0, 2]\). If specified as a tuple \((\text{min}, \text{max})\) dithering is employed. Dithering randomly changes the mutation constant on a generation by generation basis. The mutation constant for that generation is taken from \(U[\text{min}, \text{max})\). Dithering can help speed convergence significantly. Increasing the mutation constant increases the search radius, but will slow down convergence.

recombination [float, optional] The recombination constant, should be in the range \([0, 1]\). In the literature this is also known as the crossover probability, being denoted by CR. Increasing this value allows a larger number of mutants to progress into the next generation, but at the risk of population stability.

seed [int or \text{np.random.RandomState}, optional] If seed is not specified the np.RandomState singleton is used. If seed is an int, a new np.random.RandomState instance is used, seeded with seed. If seed is already a np.random.RandomState instance, then that np.random.RandomState instance is used. Specify seed for repeatable minimizations.

disp [bool, optional] Display status messages

callback [callable, \text{callback(xk, convergence=val)}, optional] A function to follow the progress of the minimization. xk is the current value of x0. val represents the fractional value of the population convergence. When val is greater than one the function halts. If callback returns True, then the minimization is halted (any polishing is still carried out).

polish [bool, optional] If True (default), then scipy.optimize.minimize with the L-BFGS-B method is used to polish the best population member at the end, which can improve the minimization slightly.

init [str or array-like, optional] Specify which type of population initialization is performed. Should be one of:

- ‘latinhypercube’
- ‘random’
- array specifying the initial population. The array should have shape \((M, \text{len}(x))\), where len(x) is the number of parameters. init is clipped to bounds before use.
The default is 'latinhypercube'. Latin Hypercube sampling tries to maximize coverage of the available parameter space. 'random' initializes the population randomly - this has the drawback that clustering can occur, preventing the whole of parameter space being covered. Use of an array to specify a population subset could be used, for example, to create a tight bunch of initial guesses in an location where the solution is known to exist, thereby reducing time for convergence.

**atol**
[Float, optional] Absolute tolerance for convergence, the solving stops when np.std(pop) <= atol + tol * np.abs(np.mean(population_energies)), where atol and tol are the absolute and relative tolerance respectively.

**updating**
[{'immediate', 'deferred'}, optional] If 'immediate', the best solution vector is continuously updated within a single generation [4]. This can lead to faster convergence as trial vectors can take advantage of continuous improvements in the best solution. With 'deferred', the best solution vector is updated once per generation. Only 'deferred' is compatible with parallelization, and the workers keyword can over-ride this option.

New in version 1.2.0.

**workers**
[int or map-like callable, optional] If workers is an int the population is subdivided into workers sections and evaluated in parallel (uses multiprocessing.Pool). Supply -1 to use all available CPU cores. Alternatively supply a map-like callable, such as multiprocessing.Pool.map for evaluating the population in parallel. This evaluation is carried out as workers(func, iterable). This option will override the updating keyword to updating='deferred' if workers != 1. Requires that func be pickleable.

New in version 1.2.0.

**Returns**

**res**
[OptimizeResult] The optimization result represented as a OptimizeResult object. Important attributes are: x the solution array, success a Boolean flag indicating if the optimizer exited successfully and message which describes the cause of the termination. See OptimizeResult for a description of other attributes. If polish was employed, and a lower minimum was obtained by the polishing, then OptimizeResult also contains the jac attribute.

**Notes**

Differential evolution is a stochastic population based method that is useful for global optimization problems. At each pass through the population the algorithm mutates each candidate solution by mixing with other candidate solutions to create a trial candidate. There are several strategies [2] for creating trial candidates, which suit some problems more than others. The ‘best1bin’ strategy is a good starting point for many systems. In this strategy two members of the population are randomly chosen. Their difference is used to mutate the best member (the best in best1bin), $b_0$, so far:

$$b' = b_0 + mutation \times (population[rand0] - population[rand1])$$

A trial vector is then constructed. Starting with a randomly chosen ‘i’th parameter the trial is sequentially filled (in modulo) with parameters from $b'$ or the original candidate. The choice of whether to use $b'$ or the original candidate is made with a binomial distribution (the ‘bin’ in ‘best1bin’) - a random number in $[0, 1)$ is generated. If this number is less than the recombination constant then the parameter is loaded from $b'$, otherwise it is loaded from the original candidate. The final parameter is always loaded from $b'$. Once the trial candidate is built its fitness is assessed. If the trial is better than the original candidate then it takes its place. If it is also better than the best overall candidate it also replaces that. To improve your chances of finding a global minimum use higher popsize values, with higher mutation and (dithering), but lower recombination values. This has the effect of widening the search radius, but slowing convergence. By default the best solution vector is updated continuously within a single iteration (updating='immediate'). This is a modification [4] of the original differential evolution algorithm which can lead to faster convergence as trial vectors can immediately benefit from
improved solutions. To use the original Storn and Price behaviour, updating the best solution once per iteration, set `updating='deferred'`.

New in version 0.15.0.

**References**

[1], [2], [3], [4]

**Examples**

Let us consider the problem of minimizing the Rosenbrock function. This function is implemented in `rosen` in `scipy.optimize`.

```python
>>> from scipy.optimize import rosen, differential_evolution
>>> bounds = [(0, 2), (0, 2), (0, 2), (0, 2), (0, 2)]
>>> result = differential_evolution(rosen, bounds)
>>> result.x, result.fun
(array([1., 1., 1., 1., 1.]), 1.9216496320061384e-19)
```

Now repeat, but with parallelization.

```python
>>> bounds = [(0, 2), (0, 2), (0, 2), (0, 2), (0, 2)]
>>> result = differential_evolution(rosen, bounds, updating='deferred',
...                                workers=2)
>>> result.x, result.fun
(array([1., 1., 1., 1., 1.]), 1.9216496320061384e-19)
```

Next find the minimum of the Ackley function (https://en.wikipedia.org/wiki/Test_functions_for_optimization).

```python
>>> from scipy.optimize import differential_evolution
>>> import numpy as np
>>> def ackley(x):
...     arg1 = -0.2 * np.sqrt(0.5 * (x[0] ** 2 + x[1] ** 2))
...     arg2 = 0.5 * (np.cos(2. * np.pi * x[0]) + np.cos(2. * np.pi * x[1]))
...     return -20. * np.exp(arg1) - np.exp(arg2) + 20. + np.e
>>> bounds = [(-5, 5), (-5, 5)]
>>> result = differential_evolution(ackley, bounds)
>>> result.x, result.fun
(array([ 0., 0.]), 4.4408920985006262e-16)
```

**scipy.optimize.shgo**

Finds the global minimum of a function using SHG optimization.

SHGO stands for “simplicial homology global optimization”.

**Parameters**

- `func` (callable) The objective function to be minimized. Must be in the form `f(x, *args)`, where `x` is the argument in the form of a 1-D array and `args` is a tuple of any additional fixed parameters needed to completely specify the function.

- `bounds` (sequence) Bounds for variables. (min, max) pairs for each element in x, defining the lower and upper bounds for the optimizing argument of `func`. It is required to have `len(bounds) == len(x)`. `len(bounds)` is used to determine the number of parameters in x. Use `None` for one of min or max when there is no bound in that direction. By default bounds are `(None, None)`.
args [tuple, optional] Any additional fixed parameters needed to completely specify the objective function.

constraints [dict or sequence of dict, optional] Constraints definition. Function(s) R**n in the form:

\[
g(x) \leq 0 \quad \text{applied as } g : R^n \rightarrow R^m
g(x) = 0 \quad \text{applied as } h : R^n \rightarrow R^p
\]

Each constraint is defined in a dictionary with fields:
- **fun** [callable] The function defining the constraint.
- **jac** [callable, optional] The Jacobian of fun (only for SLSQP).
- **args** [sequence, optional] Extra arguments to be passed to the function and Jacobian.

Equality constraint means that the constraint function result is to be zero whereas inequality means that it is to be non-negative. Note that COBYLA only supports inequality constraints.

**Note:** Only the COBYLA and SLSQP local minimize methods currently support constraint arguments. If the constraints sequence used in the local optimization problem is not defined in minimize_kwarg and a constrained method is used then the global constraints will be used. (Defining a constraints sequence in minimize_kwarg means that constraints will not be added so if equality constraints and so forth need to be added then the inequality functions in constraints need to be added to minimize_kwarg too).

**n** [int, optional] Number of sampling points used in the construction of the simplicial complex. Note that this argument is only used for sobol and other arbitrary sampling_methods.

**iters** [int, optional] Number of iterations used in the construction of the simplicial complex.

**callback** [callable, optional] Called after each iteration, as callback(xk), where xk is the current parameter vector.

**minimizer_kwarg** [dict, optional] Extra keyword arguments to be passed to the minimizer scipy.optimize.minimize. Some important options could be:

- **method** [str] The minimization method (e.g. SLSQP).
- **args** [tuple] Extra arguments passed to the objective function (func) and its derivatives (Jacobian, Hessian).
- **options** [dict, optional] Note that by default the tolerance is specified as tol: 1e-12

**options** [dict, optional] A dictionary of solver options. Many of the options specified for the global routine are also passed to the scipy.optimize.minimize routine. The options that are also passed to the local routine are marked with “(L)”.

Stopping criteria, the algorithm will terminate if any of the specified criteria are met. However, the default algorithm does not require any to be specified:

- **maxfev** [int (L)] Maximum number of function evaluations in the feasible domain. (Note only methods that support this option will terminate the routine at precisely exact specified value. Otherwise the criterion will only terminate during a global iteration)
- **f_min** Specify the minimum objective function value, if it is known.
- **f_tol** [float] Precision goal for the value of f in the stopping criterion. Note that the global routine will also terminate if a sampling point in the global routine is within this tolerance.
- **maxiter** [int] Maximum number of iterations to perform.
- **maxev** [int] Maximum number of sampling evaluations to perform (includes searching in infeasible points).
- **maxtime** [float] Maximum processing runtime allowed
- **minhgrd** [int] Minimum homology group rank differential. The homology group of the objective function is calculated (approximately) during every iteration. The rank of this group has a one-to-one correspondence with the number of locally convex subdomains in the objective function (after adequate sampling points each of these subdomains contain a unique global minimum). If the difference in the hgr is 0 between iterations for `maxhgrd` specified iterations the algorithm will terminate.

Objective function knowledge:
- **symmetry**
  [bool] Specify True if the objective function contains symmetric variables. The search space (and therefore performance) is decreased by O(n!).
- **jac** [bool or callable, optional] Jacobian (gradient) of objective function. Only for CG, BFGS, Newton-CG, L-BFGS-B, TNC, SLSQP, dogleg, trust-ncg. If `jac` is a boolean and is True, `fun` is assumed to return the gradient along with the objective function. If False, the gradient will be estimated numerically. `jac` can also be a callable returning the gradient of the objective. In this case, it must accept the same arguments as `fun`. (Passed to `scipy.optimize.minimize` automatically)
- **hess, hessp**
  [callable, optional] Hessian (matrix of second-order derivatives) of objective function or Hessian of objective function times an arbitrary vector p. Only for Newton-CG, dogleg, trust-ncg. Only one of `hessp` or `hess` needs to be given. If `hess` is provided, then `hessp` will be ignored. If neither `hess` nor `hessp` is provided, then the Hessian product will be approximated using finite differences on `jac`. `hessp` must compute the Hessian times an arbitrary vector. (Passed to `scipy.optimize.minimize` automatically)

Algorithm settings:
- **minimize_every_iter**
  [bool] If True then promising global sampling points will be passed to a local minimisation routine every iteration. If False then only the final minimiser pool will be run. Defaults to False.
- **local_iter**
  [int] Only evaluate a few of the best minimiser pool candidates every iteration. If False all potential points are passed to the local minimisation routine.
- **infty_constraints**: bool
  If True then any sampling points generated which are outside will the feasible domain will be saved and given an objective function value of `inf`. If False then these points will be discarded. Using this functionality could lead to higher performance with respect to function evaluations before the global minimum is found, specifying False will use less memory at the cost of a slight decrease in performance. Defaults to True.

Feedback:
- **disp** [bool (L)] Set to True to print convergence messages.
[str or function, optional] Current built in sampling method options are sobol and simplicial. The default simplicial uses less memory and provides the theoretical guarantee of convergence to the global minimum in finite time. The sobol method is faster in terms of sampling point generation at the cost of higher memory resources and the loss of guaranteed convergence. It is more appropriate for most “easier” problems where the convergence is relatively fast. User defined sampling functions must accept two arguments of n sampling points of dimension dim per call and output an array of sampling points with shape n x dim.

Returns
res [OptimizeResult] The optimization result represented as a OptimizeResult object. Important attributes are: x the solution array corresponding to the global minimum, fun the function output at the global solution, xl an ordered list of local minima solutions, ful the function output at the corresponding local solutions, success a Boolean flag indicating if the optimizer exited successfully, message which describes the cause of the termination, nfev the total number of objective function evaluations including the sampling calls, nlfev the total number of objective function evaluations culminating from all local search optimisations, nit number of iterations performed by the global routine.

Notes
Global optimization using simplicial homology global optimisation [1]. Appropriate for solving general purpose NLP and blackbox optimisation problems to global optimality (low dimensional problems).

In general, the optimization problems are of the form:

```
minimize f(x) subject to
  g_i(x) >= 0, i = 1,..,m
  h_j(x) = 0, j = 1,..,p
```

where x is a vector of one or more variables. f(x) is the objective function R^n -> R, g_i(x) are the inequality constraints, and h_j(x) are the equality constraints.

Optionally, the lower and upper bounds for each element in x can also be specified using the bounds argument.

While most of the theoretical advantages of SHGO are only proven for when f(x) is a Lipschitz smooth function. The algorithm is also proven to converge to the global optimum for the more general case where f(x) is non-continuous, non-convex and non-smooth, if the default sampling method is used [1].

The local search method may be specified using the minimizer_kwargs parameter which is passed on to scipy.optimize.minimize. By default the SLSQP method is used. In general it is recommended to use the SLSQP or COBYLA local minimization if inequality constraints are defined for the problem since the other methods do not use constraints.

The sobol method points are generated using the Sobol (1967) [2] sequence. The primitive polynomials and various sets of initial direction numbers for generating Sobol sequences is provided by [3] by Frances Kuo and Stephen Joe. The original program sobol.cc (MIT) is available and described at http://web.maths.unsw.edu.au/~fkuo/sobol/ translated to Python 3 by Carl Sandrock 2016-03-31.

References
[1], [2], [3], [4], [5]

Examples
First consider the problem of minimizing the Rosenbrock function, rosen:
```python
>>> from scipy.optimize import rosen, shgo
>>> bounds = [(0, 2), (0, 2), (0, 2), (0, 2), (0, 2)]
>>> result = shgo(rosen, bounds)
>>> result.x, result.fun
(array([ 1., 1., 1., 1., 1.]), 2.9203923741900809e-18)
```

Note that bounds determine the dimensionality of the objective function and is therefore a required input, however you can specify empty bounds using `None` or objects like `np.inf` which will be converted to large float numbers.

```python
>>> bounds = [((None, None), )]*4
>>> result = shgo(rosen, bounds)
>>> result.x
array([ 0.99999851, 0.99999704, 0.99999411, 0.9999882])
```

Next we consider the Eggholder function, a problem with several local minima and one global minimum. We will demonstrate the use of arguments and the capabilities of `shgo`. ([https://en.wikipedia.org/wiki/Test_functions_for_optimization](https://en.wikipedia.org/wiki/Test_functions_for_optimization))

```python
>>> def eggholder(x):
...     return -(x[1] + 47.0)
...         * np.sin(np.sqrt(abs(x[0] / 2.0 + (x[1] + 47.0))))
...         - x[0] * np.sin(np.sqrt(abs(x[0] - (x[1] + 47.0))))
...     
>>> bounds = [(-512, 512), (-512, 512)]

```

`shgo` has two built-in low discrepancy sampling sequences. First we will input 30 initial sampling points of the Sobol sequence:

```python
>>> result = shgo(eggholder, bounds, n=30, sampling_method='sobol')
>>> result.x, result.fun
(array([ 512. , 404.23180542]), -959.64066272085051)
```

`shgo` also has a return for any other local minima that was found, these can be called using:

```python
>>> result.xl
array([[ 512. , 404.23180542],
       [-283.07593402, -487.12566542],
       [-294.66820039, -462.01964031],
       [-105.87688985, 423.15324143],
       [-242.97923629, 274.38032063],
       [-506.25823477, 6.3131022],
       [-408.71981195, -156.10117154],
       [ 150.23210485, 301.31378508],
       [ 91.00922754, -391.28375925],
       [ 202.8966344, -269.38042147],
       [ 361.66625957, -106.96490692],
       [-219.40615102, -244.06022436],
       [ 151.59603137, -100.61082677]])
```
result =
array([-959.64066272, -718.16745962, -704.80659592, -565.99778097, 
-559.78685655, -557.36868733, -507.87385942, -493.9605115, 
-426.48799655, -421.15571437, -419.31194957, -410.98477763, 
-202.53912972])

These results are useful in applications where there are many global minima and the values of other global minima are desired or where the local minima can provide insight into the system (for example morphologies in physical chemistry [5]).

If we want to find a larger number of local minima, we can increase the number of sampling points or the number of iterations. We’ll increase the number of sampling points to 60 and the number of iterations from the default of 1 to 5. This gives us 60 x 5 = 300 initial sampling points.

result_2 = shgo(eggholder, bounds, n=60, iters=5, sampling_method='sobol')

len(result.xl), len(result_2.xl)
(13, 39)

Note the difference between, e.g., n=180, iters=1 and n=60, iters=3. In the first case the promising points contained in the minimiser pool is processed only once. In the latter case it is processed every 60 sampling points for a total of 3 times.

To demonstrate solving problems with non-linear constraints consider the following example from Hock and Schittkowski problem 73 (cattle-feed) [4]:

\[
\begin{align*}
\text{minimize: } f &= 24.55 \cdot x_1 + 26.75 \cdot x_2 + 39 \cdot x_3 + 40.50 \cdot x_4 \\
\text{subject to: } &2.3 \cdot x_1 + 5.6 \cdot x_2 + 11.1 \cdot x_3 + 1.3 \cdot x_4 - 5 \geq 0, \\
&12 \cdot x_1 + 11.9 \cdot x_2 + 41.8 \cdot x_3 + 52.1 \cdot x_4 - 21 \\
&-1.645 \cdot \sqrt{0.28 \cdot x_1 \cdot x_1 + 0.19 \cdot x_2 \cdot x_2 + 20.5 \cdot x_3 \cdot x_3 + 0.62 \cdot x_4 \cdot x_4}) \geq 0, \\
&x_1 + x_2 + x_3 + x_4 - 1 = 0, \\
&1 \geq x_i \geq 0 \text{ for all } i
\end{align*}
\]

The approximate answer given in [4] is:

\[f([0.6355216, -0.12e-11, 0.3127019, 0.05177655]) = 29.894378\]

```
>>> def f(x): # (cattle-feed)
... >>> def g1(x):
...     return 2.3*x[0] + 5.6*x[1] + 11.1*x[2] + 1.3*x[3] - 5 # >=0
... >>> def g2(x):
...     return (12*x[0] + 11.9*x[1] + 41.8*x[2] + 52.1*x[3] - 21
...             - 1.645 * np.sqrt(0.28*x[0]*x[0] + 0.19*x[1]*x[1] + 20.5*x[2]*x[2] + 0.62*x[3]*x[3])
...             ) # >=0
... >>> def h1(x):
...     (continues on next page)
```
...

>>> cons = ({'type': 'ineq', 'fun': g1},
...         {'type': 'ineq', 'fun': g2},
...         {'type': 'eq', 'fun': h1})

>>> bounds = [(0, 1.0),]*4

>>> res = shgo(f, bounds, iters=3, constraints=cons)

>>> res
fun: 29.894378159142136
funl: array([29.89437816])
message: 'Optimization terminated successfully.'
nfev: 119
nit: 3
nlfev: 40
nlhev: 0
nljev: 5
success: True
x: array([0.63552157, 1.13700271e-13, 0.31270188, 0.05177655])
xl: array([[0.63552157, 1.13700271e-13, 0.31270188, 0.05177655]])

>>> g1(res.x), g2(res.x), h1(res.x)
(-5.06261699, -2.9594105, 0.0)

scipy.optimize.dual_annealing

scipy.optimize.dual_annealing(func, bounds, args=(), maxiter=1000, local_search_options={},
initial_temp=5230.0, restart_temp_ratio=2e-05,
visit=2.62, accept=-5.0, maxfun=1000000.0, seed=None,
no_local_search=False, callback=None, x0=None)

Find the global minimum of a function using Dual Annealing.

Parameters

func  [callable] The objective function to be minimized. Must be in the form f(x, *args), where x is the argument in the form of a 1-D array and args is a tuple of any additional fixed parameters needed to completely specify the function.

bounds  [sequence, shape (n, 2)] Bounds for variables. (min, max) pairs for each element in x, defining bounds for the objective function parameter.

args  [tuple, optional] Any additional fixed parameters needed to completely specify the objective function.

maxiter  [int, optional] The maximum number of global search iterations. Default value is 1000.

local_search_options  [dict, optional] Extra keyword arguments to be passed to the local minimizer (minimize). Some important options could be: method for the minimizer method to use and args for objective function additional arguments.

initial_temp  [float, optional] The initial temperature, use higher values to facilitates a wider search of the energy landscape, allowing dual_annealing to escape local minima that it is trapped in. Default value is 5230. Range is (0.01, 5.e4].

restart_temp_ratio  [float, optional] During the annealing process, temperature is decreasing, when it reaches initial_temp * restart_temp_ratio, the reannealing process is triggered. Default value of the ratio is 2e-5. Range is (0, 1).
visit  [float, optional] Parameter for visiting distribution. Default value is 2.62. Higher values give the visiting distribution a heavier tail, this makes the algorithm jump to a more distant region. The value range is (0, 3).

accept  [float, optional] Parameter for acceptance distribution. It is used to control the probability of acceptance. The lower the acceptance parameter, the smaller the probability of acceptance. Default value is -5.0 with a range (-1e4, -5).

maxfun  [int, optional] Soft limit for the number of objective function calls. If the algorithm is in the middle of a local search, this number will be exceeded, the algorithm will stop just after the local search is done. Default value is 1e7.

seed  [(int or numpy.random.RandomState instance), optional] If seed is not specified the numpy.random.RandomState singleton is used. If seed is an int, a new RandomState instance is used, seeded with seed. If seed is already a RandomState instance, then that instance is used. Specify seed for repeatable minimizations. The random numbers generated with this seed only affect the visiting distribution function and new coordinates generation.

no_local_search  [bool, optional] If no_local_search is set to True, a traditional Generalized Simulated Annealing will be performed with no local search strategy applied.

callback  [callable, optional] A callback function with signature callback(x, f, context), which will be called for all minima found. x and f are the coordinates and function value of the latest minimum found, and context has value in [0, 1, 2], with the following meaning:
- 0: minimum detected in the annealing process.
- 1: detection occurred in the local search process.
- 2: detection done in the dual annealing process.

If the callback implementation returns True, the algorithm will stop.

x0  [ndarray, shape(n,), optional] Coordinates of a single n-dimensional starting point.

Returns

res  [OptimizeResult] The optimization result represented as an OptimizeResult object. Important attributes are: x the solution array, fun the value of the function at the solution, and message which describes the cause of the termination. See OptimizeResult for a description of other attributes.

Notes

This function implements the Dual Annealing optimization. This stochastic approach derived from [3] combines the generalization of CSA (Classical Simulated Annealing) and FSA (Fast Simulated Annealing) [1] [2] coupled to a strategy for applying a local search on accepted locations [4]. An alternative implementation of this same algorithm is described in [5] and benchmarks are presented in [6]. This approach introduces an advanced method to refine the solution found by the generalized annealing process. This algorithm uses a distorted Cauchy-Lorentz visiting distribution, with its shape controlled by the parameter $q_v$.

$$g_{q_v}(\Delta x(t)) \propto \frac{[T_{q_v}(t)]^{-\frac{D}{q_v}}}{\left[1 + (q_v - 1) \frac{(\Delta x(t))^2}{[T_{q_v}(t)]^{-1}} + \frac{D - 1}{2} \right]^{-\frac{1}{q_v(1-q_v)}}}$$

Where $t$ is the artificial time. This visiting distribution is used to generate a trial jump distance $\Delta x(t)$ of variable $x(t)$ under artificial temperature $T_{q_v}(t)$.

From the starting point, after calling the visiting distribution function, the acceptance probability is computed as follows:

$$p_{q_v} = \min \left\{ 1, \left[ 1 - (1 - q_v) \beta \Delta E \right]^{-\frac{1}{q_v}} \right\}$$
Where $q_a$ is a acceptance parameter. For $q_a < 1$, zero acceptance probability is assigned to the cases where

$$[1 - (1 - q_a)\Delta E] < 0$$

The artificial temperature $T_{q_v}(t)$ is decreased according to

$$T_{q_v}(t) = T_{q_v}(1) \frac{2^{q_v-1} - 1}{(1 + t)^{q_v-1} - 1}$$

Where $q_v$ is the visiting parameter.

New in version 1.2.0.

References
[1], [2], [3], [4], [5], [6]

Examples
The following example is a 10-dimensional problem, with many local minima. The function involved is called Rastrigin (https://en.wikipedia.org/wiki/Rastrigin_function)

```python
>>> from scipy.optimize import dual_annealing
>>> func = lambda x: np.sum(x*x - 10*np.cos(2*np.pi*x)) + 10*np.size(x)
>>> lw = [-5.12] * 10
>>> up = [5.12] * 10
>>> ret = dual_annealing(func, bounds=list(zip(lw, up)), seed=1234)
>>> print("global minimum: xmin = {0}, f(xmin) = {1:.6f}".format...
... ret.x, ret.fun))
global minimum: xmin = [-4.26437714e-09 -3.91699361e-09 -1.86149218e-09 -3.97165720e-09 -6.29151648e-09 -6.53145322e-09 -3.93616815e-09 -6.55623025e-09 -6.05775280e-09 -5.00668935e-09], f(xmin) = 0.000000
```

### 6.18.5 Least-squares and Curve Fitting

#### Nonlinear Least-Squares

<table>
<thead>
<tr>
<th><code>least_squares</code></th>
<th>Solve a nonlinear least-squares problem with bounds on the variables.</th>
</tr>
</thead>
</table>

```python
scipy.optimize.least_squares
scipy.optimize.least_squares(fun, x0, jac='2-point', bounds=(-inf, inf), method='trf',
ftol=1e-08, xtol=1e-08, gtol=1e-08, x_scale=1.0, loss='linear',
loss_scale=1.0, diff_step=None, tr_solver=None, tr_options={},
jac_sparsity=None, max_nfev=None, verbose=0, args=(),
kwargs={})
```

Solve a nonlinear least-squares problem with bounds on the variables.

Given the residuals $f(x)$ (an m-dimensional real function of n real variables) and the loss function $\rho(s)$ (a scalar function), `least_squares` finds a local minimum of the cost function $F(x)$:

```python
minimize F(x) = 0.5 * sum(rho(f_i(x)**2)), i = 0, ..., m - 1
subject to lb <= x <= ub
```

The purpose of the loss function $\rho(s)$ is to reduce the influence of outliers on the solution.

### Parameters
fun  [callable] Function which computes the vector of residuals, with the signature
fun(x, *args, **kwargs), i.e., the minimization proceeds with respect to its
first argument. The argument x passed to this function is an ndarray of shape (n,)
(never a scalar, even for n=1). It must return a 1-d array_like of shape (m,) or a
scalar. If the argument x is complex or the function fun returns complex residuals,
it must be wrapped in a real function of real arguments, as shown at the end of
the Examples section.

x0  [array_like with shape (n,) or float] Initial guess on independent variables. If float,
it will be treated as a 1-d array with one element.
jac  [{'2-point', '3-point', 'cs', callable}, optional] Method of computing the Jacobian
matrix (an m-by-n matrix, where element (i, j) is the partial derivative of f[i]
with respect to x[j]). The keywords select a finite difference scheme for numerical
estimation. The scheme ‘3-point’ is more accurate, but requires twice as many
operations as ‘2-point’ (default). The scheme ‘cs’ uses complex steps, and while
potentially the most accurate, it is applicable only when fun correctly handles
complex inputs and can be analytically continued to the complex plane. Method
‘lm’ always uses the ‘2-point’ scheme. If callable, it is used as jac(x, *args,
**kwargs) and should return a good approximation (or the exact value) for the
Jacobian as an array_like (np.atleast_2d is applied), a sparse matrix or a scipy.
sparse.linalg.LinearOperator.

bounds  [2-tuple of array_like, optional] Lower and upper bounds on independent variables.
Defaults to no bounds. Each array must match the size of x0 or be a scalar, in
the latter case a bound will be the same for all variables. Use np.inf with an
appropriate sign to disable bounds on all or some variables.

method  [{'trf', 'dogbox', 'lm'}, optional] Algorithm to perform minimization.
• ‘trf’ : Trust Region Reflective algorithm, particularly suitable for large sparse
problems with bounds. Generally robust method.
• ‘dogbox’ : dogleg algorithm with rectangular trust regions, typical use case is
small problems with bounds. Not recommended for problems with rank-deficient
Jacobian.
• ‘lm’ : Levenberg-Marquardt algorithm as implemented in MINPACK. Doesn’t
handle bounds and sparse Jacobians. Usually the most efficient method for small
unconstrained problems.
Default is ‘trf’. See Notes for more information.

ftol  [float, optional] Tolerance for termination by the change of the cost function. De-
default is 1e-8. The optimization process is stopped when dF < ftol * F, and there
was an adequate agreement between a local quadratic model and the true model
in the last step.

xtol  [float, optional] Tolerance for termination by the change of the independent vari-
ables. Default is 1e-8. The exact condition depends on the method used:
• For ‘trf’ and ‘dogbox’: norm(dx) < xtol * (xtol + norm(x))
• For ‘lm’ : Delta < xtol * norm(xs), where Delta is a trust-region radius and
  xs is the value of x scaled according to x_scale parameter (see below).

gtol  [float, optional] Tolerance for termination by the norm of the gradient. Default is
1e-8. The exact condition depends on a method used:
• For ‘trf’ : norm(g_scaled, ord=np.inf) < gtol, where g_scaled is the value of
  the gradient scaled to account for the presence of the bounds [STIR].
• For ‘dogbox’ : norm(g_free, ord=np.inf) < gtol, where g_free is the gradient
  with respect to the variables which are not in the optimal state on the
  boundary.
• For ‘lm’ : the maximum absolute value of the cosine of angles between columns
  of the Jacobian and the residual vector is less than gtol, or the residual vector is
  zero.
x_scale [array_like or ‘jac’, optional] Characteristic scale of each variable. Setting $x_{\text{scale}}$ is equivalent to reformulating the problem in scaled variables $x_s = x / x_{\text{scale}}$. An alternative view is that the size of a trust region along j-th dimension is proportional to $x_{\text{scale}}[j]$. Improved convergence may be achieved by setting $x_{\text{scale}}$ such that a step of a given size along any of the scaled variables has a similar effect on the cost function. If set to ‘jac’, the scale is iteratively updated using the inverse norms of the columns of the Jacobian matrix (as described in [JJMore]).

loss [str or callable, optional] Determines the loss function. The following keyword values are allowed:
- ‘linear’ (default) : $\rho(z) = z$. Gives a standard least-squares problem.
- ‘soft_l1’ : $\rho(z) = 2 * ((1 + z)^{0.5} - 1)$. The smooth approximation of $l_1$ (absolute value) loss. Usually a good choice for robust least squares.
- ‘huber’ : $\rho(z) = z$ if $z \leq 1$ else $2*z^{0.5} - 1$. Works similarly to ‘soft_l1’.
- ‘cauchy’ : $\rho(z) = \ln(1 + z)$. Severely weakens outliers influence, but may cause difficulties in optimization process.
- ‘arctan’ : $\rho(z) = \arctan(z)$. Limits a maximum loss on a single residual, has properties similar to ‘cauchy’.

If callable, it must take a 1-d ndarray $z=f**2$ and return an array_like with shape (3, m) where row 0 contains function values, row 1 contains first derivatives and row 2 contains second derivatives. Method ‘lm’ supports only ‘linear’ loss.

f_scale [float, optional] Value of soft margin between inlier and outlier residuals, default is 1.0. The loss function is evaluated as follows $\rho_\text{(f**2)} = C^2 * \rho(f**2 / C^2)$, where $C$ is $f_{\text{scale}}$, and $\rho$ is determined by loss parameter. This parameter has no effect with loss=’linear’, but for other loss values it is of crucial importance.

max_nfev [None or int, optional] Maximum number of function evaluations before the termination. If None (default), the value is chosen automatically:
- For ‘trf’ and ‘dogbox’ : 100 * n.
- For ‘lm’ : 100 * n if jac is callable and 100 * n * (n + 1) otherwise (because ‘lm’ counts function calls in Jacobian estimation).

diff_step [None or array_like, optional] Determines the relative step size for the finite difference approximation of the Jacobian. The actual step is computed as $x *$ diff_step. If None (default), then diff_step is taken to be a conventional “optimal” power of machine epsilon for the finite difference scheme used [NR].

- ‘exact’ is suitable for not very large problems with dense Jacobian matrices. The computational complexity per iteration is comparable to a singular value decomposition of the Jacobian matrix.
- ‘lsmr’ is suitable for problems with sparse and large Jacobian matrices. It uses the iterative procedure scipy.sparse.linalg.lsmr for finding a solution of a linear least-squares problem and only requires matrix-vector product evaluations. If None (default) the solver is chosen based on the type of Jacobian returned on the first iteration.

tr_options [dict, optional] Keyword options passed to trust-region solver.
- tr_solver='exact': tr_options are ignored.
- tr_solver='lsmr': options for scipy.sparse.linalg.lsmr. Additionally method='trf' supports ‘regularize’ option (bool, default is True) which adds...
a regularization term to the normal equation, which improves convergence if the
Jacobian is rank-deficient [Byrd] (eq. 3.4).

jac_sparsity

[None, array_like, sparse matrix], optional] Defines the sparsity structure of the
Jacobian matrix for finite difference estimation, its shape must be \(m, n\). If
the Jacobian has only few non-zero elements in each row, providing the sparsity
structure will greatly speed up the computations [Curtis]. A zero entry means that
a corresponding element in the Jacobian is identically zero. If provided, forces the
use of ‘lsmr’ trust-region solver. If None (default) then dense differencing will be
used. Has no effect for ‘lm’ method.

verbose

[0, 1, 2], optional] Level of algorithm’s verbosity:
• 0 (default) : work silently.
• 1 : display a termination report.
• 2 : display progress during iterations (not supported by ‘lm’ method).

args, kwargs

tuple and dict, optional] Additional arguments passed to \(\text{fun}\) and \(\text{jac}\). Both empty
by default. The calling signature is \(\text{fun}(x, \ast \text{args}, \ast\ast \text{kwargs})\) and the same for
\(\text{jac}\).

Returns

‘OptimizeResult’ with the following fields defined:

\(x\) [ndarray, shape \((n,)\)] Solution found.
\(cost\) [float] Value of the cost function at the solution.
\(fun\) [ndarray, shape \((m,)\)] Vector of residuals at the solution.
\(jac\) [ndarray, sparse matrix or LinearOperator, shape \((m, n)\)] Modified Jacobian matrix
at the solution, in the sense that \(J^T J\) is a Gauss-Newton approximation of the
Hessian of the cost function. The type is the same as the one used by the algorithm.
\(grad\) [ndarray, shape \((m,)\)] Gradient of the cost function at the solution.

optimality

[float] First-order optimality measure. In unconstrained problems, it is always the
uniform norm of the gradient. In constrained problems, it is the quantity which
was compared with \(\text{gtol}\) during iterations.

active_mask

[ndarray of int, shape \((n,)\)] Each component shows whether a corresponding con-
straint is active (that is, whether a variable is at the bound):
• 0 : a constraint is not active.
• -1 : a lower bound is active.
• 1 : an upper bound is active.

Might be somewhat arbitrary for ‘trf’ method as it generates a sequence of strictly
feasible iterates and \(active\_mask\) is determined within a tolerance threshold.

nfev

[int] Number of function evaluations done. Methods ‘trf’ and ‘dogbox’ do not count
function calls for numerical Jacobian approximation, as opposed to ‘lm’ method.

njev

[int or None] Number of Jacobian evaluations done. If numerical Jacobian approx-
imation is used in ‘lm’ method, it is set to None.

status

[int] The reason for algorithm termination:
• -1 : improper input parameters status returned from MINPACK.
• 0 : the maximum number of function evaluations is exceeded.
• 1 : \(\text{gtol}\) termination condition is satisfied.
• 2 : \(\text{ftol}\) termination condition is satisfied.
• 3 : \(\text{xtol}\) termination condition is satisfied.
• 4 : Both \(\text{ftol}\) and \(\text{xtol}\) termination conditions are satisfied.

message

[str] Verbal description of the termination reason.

success

[bool] True if one of the convergence criteria is satisfied \((\text{status} > 0)\).
See also:

leastsq

A legacy wrapper for the MINPACK implementation of the Levenberg-Marquadt algorithm.

curve_fit

Least-squares minimization applied to a curve fitting problem.

Notes
Method ‘lm’ (Levenberg-Marquardt) calls a wrapper over least-squares algorithms implemented in MINPACK (lmder, lmdif). It runs the Levenberg-Marquardt algorithm formulated as a trust-region type algorithm. The implementation is based on paper [JJMore], it is very robust and efficient with a lot of smart tricks. It should be your first choice for unconstrained problems. Note that it doesn’t support bounds. Also it doesn’t work when m < n.

Method ‘trf’ (Trust Region Reflective) is motivated by the process of solving a system of equations, which constitute the first-order optimality condition for a bound-constrained minimization problem as formulated in [STIR]. The algorithm iteratively solves trust-region subproblems augmented by a special diagonal quadratic term and with trust-region shape determined by the distance from the bounds and the direction of the gradient. This enhancements help to avoid making steps directly into bounds and efficiently explore the whole space of variables. To further improve convergence, the algorithm considers search directions reflected from the bounds. To obey theoretical requirements, the algorithm keeps iterates strictly feasible. With dense Jacobians trust-region subproblems are solved by an exact method very similar to the one described in [JJMore] (and implemented in MINPACK). The difference from the MINPACK implementation is that a singular value decomposition of a Jacobian matrix is done once per iteration, instead of a QR decomposition and series of Givens rotation eliminations. For large sparse Jacobians a 2-d subspace approach of solving trust-region subproblems is used [STIR], [Byrd]. The subspace is spanned by a scaled gradient and an approximate Gauss-Newton solution delivered by scipy.sparse.linalg.lsmr. When no constraints are imposed the algorithm is very similar to MINPACK and has generally comparable performance. The algorithm works quite robust in unbounded and bounded problems, thus it is chosen as a default algorithm.

Method ‘dogbox’ operates in a trust-region framework, but considers rectangular trust regions as opposed to conventional ellipsoids [Voglis]. The intersection of a current trust region and initial bounds is again rectangular, so on each iteration a quadratic minimization problem subject to bound constraints is solved approximately by Powell’s dogleg method [NumOpt]. The required Gauss-Newton step can be computed exactly for dense Jacobians or approximately by scipy.sparse.linalg.lsmr for large sparse Jacobians. The algorithm is likely to exhibit slow convergence when the rank of Jacobian is less than the number of variables. The algorithm often outperforms ‘trf’ in bounded problems with a small number of variables.

Robust loss functions are implemented as described in [BA]. The idea is to modify a residual vector and a Jacobian matrix on each iteration such that computed gradient and Gauss-Newton Hessian approximation match the true gradient and Hessian approximation of the cost function. Then the algorithm proceeds in a normal way, i.e. robust loss functions are implemented as a simple wrapper over standard least-squares algorithms.

New in version 0.17.0.

References
[STIR], [NR], [Byrd], [Curtis], [JJMore], [Voglis], [NumOpt], [BA]

Examples
In this example we find a minimum of the Rosenbrock function without bounds on independent variables.
```python
>>> def fun_rosenbrock(x):
...     return np.array([10 * (x[1] - x[0])**2, (1 - x[0])])
```

Notice that we only provide the vector of the residuals. The algorithm constructs the cost function as a sum of squares of the residuals, which gives the Rosenbrock function. The exact minimum is at \( x = [1.0, 1.0] \).

```python
>>> from scipy.optimize import least_squares
>>> x0_rosenbrock = np.array([2, 2])
>>> res_1 = least_squares(fun_rosenbrock, x0_rosenbrock)
>>> res_1.x
array([ 1., 1.])
>>> res_1.cost
9.8669242910846867e-30
>>> res_1.optimality
8.8928864934219529e-14
```

We now constrain the variables, in such a way that the previous solution becomes infeasible. Specifically, we require that \( x[1] \geq 1.5 \), and \( x[0] \) left unconstrained. To this end, we specify the `bounds` parameter to `least_squares` in the form `bounds=([-np.inf, 1.5], np.inf)`.

We also provide the analytic Jacobian:

```python
>>> def jac_rosenbrock(x):
...     return np.array([[-20 * x[0], 10], [-1, 0]])
```

Putting this all together, we see that the new solution lies on the bound:

```python
>>> res_2 = least_squares(fun_rosenbrock, x0_rosenbrock, jac_rosenbrock,
...                        bounds=([-np.inf, 1.5], np.inf))
>>> res_2.x
array([ 1.22437075, 1.5       ])
>>> res_2.cost
0.025213093946805685
>>> res_2.optimality
1.5885401433157753e-07
```

Now we solve a system of equations (i.e., the cost function should be zero at a minimum) for a Broyden tridiagonal vector-valued function of 100000 variables:

```python
>>> def fun_broyden(x):
...     f = (3 - x) * x + 1
...     f[1:] -= x[:-1]
...     f[:-1] -= 2 * x[1:]
...     return f
```

The corresponding Jacobian matrix is sparse. We tell the algorithm to estimate it by finite differences and provide the sparsity structure of Jacobian to significantly speed up this process.

```python
>>> from scipy.sparse import lil_matrix
>>> def sparsity_broyden(n):
...     sparsity = lil_matrix((n, n), dtype=int)
```

(continues on next page)
Let’s also solve a curve fitting problem using robust loss function to take care of outliers in the data. Define the model function as \( y = a + b \cdot \exp(c \cdot t) \), where \( t \) is a predictor variable, \( y \) is an observation and \( a, b, c \) are parameters to estimate.

First, define the function which generates the data with noise and outliers, define the model parameters, and generate data:

```python
>>> def gen_data(t, a, b, c, noise=0, n_outliers=0, random_state=0):
...     y = a + b * np.exp(t * c)
...     ...
...     rnd = np.random.RandomState(random_state)
...     error = noise * rnd.randn(t.size)
...     outliers = rnd.randint(0, t.size, n_outliers)
...     error[outliers] *= 10
...     ...
...     return y + error
... >>> a = 0.5
... >>> b = 2.0
... >>> c = -1
... >>> t_min = 0
... >>> t_max = 10
... >>> n_points = 15
... >>> t_train = np.linspace(t_min, t_max, n_points)
... >>> y_train = gen_data(t_train, a, b, c, noise=0.1, n_outliers=3)
```

Define function for computing residuals and initial estimate of parameters.

```python
>>> def fun(x, t, y):
...     return x[0] + x[1] * np.exp(x[2] * t) - y
... >>> x0 = np.array([1.0, 1.0, 0.0])
```

Compute a standard least-squares solution:

```python
>>> res_3 = least_squares(fun_broyden, x0_broyden, jac_sparsity=sparsity_broyden(n))
```
Now compute two solutions with two different robust loss functions. The parameter \( f\_scale \) is set to 0.1, meaning that inlier residuals should not significantly exceed 0.1 (the noise level used).

```python
>>> res_soft_l1 = least_squares(fun, x0, loss='soft_l1', f_scale=0.1, ...
   args=(t_train, y_train))
>>> res_log = least_squares(fun, x0, loss='cauchy', f_scale=0.1, ...
   args=(t_train, y_train))
```

And finally plot all the curves. We see that by selecting an appropriate \texttt{loss} we can get estimates close to optimal even in the presence of strong outliers. But keep in mind that generally it is recommended to try `soft_l1` or `huber` losses first (if at all necessary) as the other two options may cause difficulties in optimization process.

```python
>>> t_test = np.linspace(t_min, t_max, n_points * 10)
>>> y_true = gen_data(t_test, a, b, c)
>>> y_lsq = gen_data(t_test, *res_lsq.x)
>>> y_soft_l1 = gen_data(t_test, *res_soft_l1.x)
>>> y_log = gen_data(t_test, *res_log.x)
...)
>>> import matplotlib.pyplot as plt
>>> plt.plot(t_train, y_train, 'o')
>>> plt.plot(t_test, y_true, 'k', linewidth=2, label='true')
>>> plt.plot(t_test, y_lsq, label='linear loss')
>>> plt.plot(t_test, y_soft_l1, label='soft_l1 loss')
>>> plt.plot(t_test, y_log, label='cauchy loss')
>>> plt.xlabel("t")
>>> plt.ylabel("y")
>>> plt.legend()
>>> plt.show()
```

In the next example, we show how complex-valued residual functions of complex variables can be optimized with \texttt{least_squares()}. Consider the following function:

```
```
>>> def f(z):
...     return z - (0.5 + 0.5j)

We wrap it into a function of real variables that returns real residuals by simply handling the real and imaginary parts as independent variables:

```python
>>> def f_wrap(x):
...     fx = f(x[0] + 1j*x[1])
...     return np.array([fx.real, fx.imag])
```

Thus, instead of the original m-dimensional complex function of n complex variables we optimize a 2m-dimensional real function of 2n real variables:

```python
>>> from scipy.optimize import least_squares
>>> res_wrapped = least_squares(f_wrap, (0.1, 0.1), bounds=([0, 0], [1, 1]))
>>> z = res_wrapped.x[0] + res_wrapped.x[1]*j
>>> z
(0.49999999999925893+0.49999999999925893j)
```

### Linear Least-Squares

<table>
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**scipy.optimize.nnls**

Solve $\arg\min_x \|Ax - b\|_2$ for $x \geq 0$. This is a wrapper for a FORTRAN non-negative least squares solver.

**Parameters**

- **A** [ndarray] Matrix A as shown above.
- **b** [ndarray] Right-hand side vector.
- **maxiter**: int, optional
  - Maximum number of iterations, optional. Default is $3 \times A.shape[1]$.

**Returns**

- **x** [ndarray] Solution vector.
- **rnorm** [float] The residual, $\|Ax-b\|_2$.

**Notes**

The FORTRAN code was published in the book below. The algorithm is an active set method. It solves the KKT (Karush-Kuhn-Tucker) conditions for the non-negative least squares problem.

**References**


**scipy.optimize.lsq_linear**

Solve a linear least-squares problem with bounds on the variables.

Given a m-by-n design matrix A and a target vector b with m elements, `lsq_linear` solves the following optimization problem:
This optimization problem is convex, hence a found minimum (if iterations have converged) is guaranteed to be global.

**Parameters**

- **A**
  - [array_like, sparse matrix of LinearOperator, shape (m, n)] Design matrix. Can be `scipy.sparse.linalg.LinearOperator`.
- **b**
  - [array_like, shape (m,)] Target vector.
- **bounds**
  - [2-tuple of array_like, optional] Lower and upper bounds on independent variables. Defaults to no bounds. Each array must have shape (n,) or be a scalar, in the latter case a bound will be the same for all variables. Use `np.inf` with an appropriate sign to disable bounds on all or some variables.
- **method**
  - ['trf' or 'bvls', optional] Method to perform minimization.
    - 'trf': Trust Region Reflective algorithm adapted for a linear least-squares problem. This is an interior-point-like method and the required number of iterations is weakly correlated with the number of variables.
    - 'bvls': Bounded-Variable Least-Squares algorithm. This is an active set method, which requires the number of iterations comparable to the number of variables. Can’t be used when A is sparse or LinearOperator.
      - Default is 'trf'.
- **tol**
  - [float, optional] Tolerance parameter. The algorithm terminates if a relative change of the cost function is less than `tol` on the last iteration. Additionally the first-order optimality measure is considered:
    - method='trf' terminates if the uniform norm of the gradient, scaled to account for the presence of the bounds, is less than `tol`.
    - method='bvls' terminates if Karush-Kuhn-Tucker conditions are satisfied within `tol` tolerance.
- **lsq_solver**
  - [{None, 'exact', 'lsmr'}, optional] Method of solving unbounded least-squares problems throughout iterations:
    - 'exact': Use dense QR or SVD decomposition approach. Can’t be used when A is sparse or LinearOperator.
    - 'lsmr': Use `scipy.sparse.linalg.lsmr` iterative procedure which requires only matrix-vector product evaluations. Can’t be used with method='bvls'.
      - If None (default) the solver is chosen based on type of A.
- **lsmr_tol**
  - [None, float or 'auto', optional] Tolerance parameters 'atol' and 'btol' for scipy.sparse.linalg.lsmr. If None (default), it is set to 1e-2 * tol. If 'auto', the tolerance will be adjusted based on the optimality of the current iterate, which can speed up the optimization process, but is not always reliable.
- **max_iter**
  - [None or int, optional] Maximum number of iterations before termination. If None (default), it is set to 100 for method='trf' or to the number of variables for method='bvls' (not counting iterations for 'bvls' initialization).
- **verbose**
  - [{0, 1, 2}, optional] Level of algorithm’s verbosity:
    - 0: work silently (default).
    - 1: display a termination report.
    - 2: display progress during iterations.

**Returns**

- `OptimizeResult` with the following fields defined:

  - **x**
    - [ndarray, shape (n,)] Solution found.
cost  [float] Value of the cost function at the solution.
fun  [ndarray, shape (m,)] Vector of residuals at the solution.
optimality  [float] First-order optimality measure. The exact meaning depends on method, refer to the description of tol parameter.
active_mask  [ndarray of int, shape (n,)] Each component shows whether a corresponding constraint is active (that is, whether a variable is at the bound):
- 0 : a constraint is not active.
- -1 : a lower bound is active.
- 1 : an upper bound is active.
Might be somewhat arbitrary for the trf method as it generates a sequence of strictly feasible iterates and active_mask is determined within a tolerance threshold.
nit  [int] Number of iterations. Zero if the unconstrained solution is optimal.
status  [int] Reason for algorithm termination:
- -1 : the algorithm was not able to make progress on the last iteration.
- 0 : the maximum number of iterations is exceeded.
- 1 : the first-order optimality measure is less than tol.
- 2 : the relative change of the cost function is less than tol.
- 3 : the unconstrained solution is optimal.
message  [str] Verbal description of the termination reason.
success  [bool] True if one of the convergence criteria is satisfied (status > 0).

See also:
nlsls
Linear least squares with non-negativity constraint.
least_squares
Nonlinear least squares with bounds on the variables.

Notes
The algorithm first computes the unconstrained least-squares solution by numpy.linalg.lstsq or scipy.sparse.linalg.lsmr depending on lsq_solver. This solution is returned as optimal if it lies within the bounds.

Method ‘trf’ runs the adaptation of the algorithm described in [STIR] for a linear least-squares problem. The iterations are essentially the same as in the nonlinear least-squares algorithm, but as the quadratic function model is always accurate, we don’t need to track or modify the radius of a trust region. The line search (backtracking) is used as a safety net when a selected step does not decrease the cost function. Read more detailed description of the algorithm in scipy.optimize.least_squares.

Method ‘bvls’ runs a Python implementation of the algorithm described in [BVLS]. The algorithm maintains active and free sets of variables, on each iteration chooses a new variable to move from the active set to the free set and then solves the unconstrained least-squares problem on free variables. This algorithm is guaranteed to give an accurate solution eventually, but may require up to n iterations for a problem with n variables. Additionally, an ad-hoc initialization procedure is implemented, that determines which variables to set free or active initially. It takes some number of iterations before actual BVLS starts, but can significantly reduce the number of further iterations.

References
[STIR], [BVLS]
Examples
In this example a problem with a large sparse matrix and bounds on the variables is solved.

```python
from scipy.sparse import rand
from scipy.optimize import lsq_linear

np.random.seed(0)

m = 20000
n = 10000

A = rand(m, n, density=1e-4)
b = np.random.randn(m)

lb = np.random.randn(n)
ub = lb + 1

res = lsq_linear(A, b, bounds=(lb, ub), lsmr_tol='auto', verbose=1)
# may vary
The relative change of the cost function is less than `tol`.
Number of iterations 16, initial cost 1.5039e+04, final cost 1.1112e+04,
first-order optimality 4.66e-08.
```

Curve Fitting

```python
curve_fit(f, xdata, ydata[, p0, sigma, ...])
```
Use non-linear least squares to fit a function, f, to data.

Assumes $ydata = f(xdata, *params) + \text{eps}$

Parameters

- **f**: [callable] The model function, $f(x, ...)$. It must take the independent variable as the first argument and the parameters to fit as separate remaining arguments.
- **xdata**: [An M-length sequence or an (k,M)-shaped array for functions with k predictors] The independent variable where the data is measured.
- **ydata**: [M-length sequence] The dependent data — nominally $f(xdata, ...)$
- **p0**: [None, scalar, or N-length sequence, optional] Initial guess for the parameters. If None, then the initial values will all be 1 (if the number of parameters for the function can be determined using introspection, otherwise a ValueError is raised).
- **sigma**: [None or M-length sequence or MxM array, optional] Determines the uncertainty in $ydata$. If we define residuals as $r = ydata - f(xdata, *popt)$, then the interpretation of $sigma$ depends on its number of dimensions:
  - A 1-d $sigma$ should contain values of standard deviations of errors in $ydata$. In this case, the optimized function is $\text{chisq} = \text{sum}((r / sigma)^2)$.
  - A 2-d $sigma$ should contain the covariance matrix of errors in $ydata$. In this case, the optimized function is $\text{chisq} = r.T @ \text{inv}(sigma) @ r$.

New in version 0.19.
None (default) is equivalent of 1-d \textit{sigma} filled with ones.

**absolute\_sigma**

[bool, optional] If True, \textit{sigma} is used in an absolute sense and the estimated parameter covariance \textit{pcov} reflects these absolute values. If False, only the relative magnitudes of the \textit{sigma} values matter. The returned parameter covariance matrix \textit{pcov} is based on scaling \textit{sigma} by a constant factor. This constant is set by demanding that the reduced \textit{chisq} for the optimal parameters \textit{popt} when using the \textit{scaled sigma} equals unity. In other words, \textit{sigma} is scaled to match the sample variance of the residuals after the fit. Mathematically, \textit{pcov(absolute\_sigma=False)} = \textit{pcov(absolute\_sigma=True)} * \textit{chisq(popt)/(M-N)}

**check\_finite**

[bool, optional] If True, check that the input arrays do not contain nans or infs, and raise a ValueError if they do. Setting this parameter to False may silently produce nonsensical results if the input arrays do contain nans. Default is True.

**bounds**

[2-tuple of array_like, optional] Lower and upper bounds on parameters. Defaults to no bounds. Each element of the tuple must be either an array with the length equal to the number of parameters, or a scalar (in which case the bound is taken to be the same for all parameters.) Use np.inf with an appropriate sign to disable bounds on all or some parameters.

New in version 0.17.

**method**

[\{'lm', 'trf', 'dogbox'\}, optional] Method to use for optimization. See \textit{least\_squares} for more details. Default is ‘lm’ for unconstrained problems and ‘trf’ if \textit{bounds} are provided. The method ‘lm’ won’t work when the number of observations is less than the number of variables, use ‘trf’ or ‘dogbox’ in this case.

New in version 0.17.

**jac**

[callback, string or None, optional] Function with signature \texttt{jac(x, ...)} which computes the Jacobian matrix of the model function with respect to parameters as a dense array_like structure. It will be scaled according to provided \textit{sigma}. If None (default), the Jacobian will be estimated numerically. String keywords for ‘trf’ and ‘dogbox’ methods can be used to select a finite difference scheme, see \textit{least\_squares}.

New in version 0.18.

**kwargs**

Keyword arguments passed to \texttt{leastsq} for method=’lm’ or \textit{least\_squares} otherwise.

Returns

- \textit{popt} [array] Optimal values for the parameters so that the sum of the squared residuals of \texttt{f(xdata, *popt) - ydata} is minimized
- \textit{pcov} [2d array] The estimated covariance of \textit{popt}. The diagonals provide the variance of the parameter estimate. To compute one standard deviation errors on the parameters use \texttt{perr = np.sqrt(np.diag(pcov))}.

How the \textit{sigma} parameter affects the estimated covariance depends on \textit{absolute\_sigma} argument, as described above.

If the Jacobian matrix at the solution doesn’t have a full rank, then ‘lm’ method returns a matrix filled with \texttt{np.inf}, on the other hand ‘trf’ and ‘dogbox’ methods use Moore-Penrose pseudoinverse to compute the covariance matrix.

Raises

- \texttt{ValueError}
  - if either \textit{ydata} or \textit{xdata} contain NaNs, or if incompatible options are used.
- \texttt{RuntimeError}
  - if the least-squares minimization fails.
OptimizeWarning
if covariance of the parameters can not be estimated.

See also:

least_squares
Minimize the sum of squares of nonlinear functions.

scipy.stats.linregress
Calculate a linear least squares regression for two sets of measurements.

Notes
With method='lm', the algorithm uses the Levenberg-Marquardt algorithm through leastsq. Note that this algorithm can only deal with unconstrained problems.

Box constraints can be handled by methods ‘trf’ and ‘dogbox’. Refer to the docstring of least_squares for more information.

Examples

```python
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> from scipy.optimize import curve_fit

>>> def func(x, a, b, c):
...     return a * np.exp(-b * x) + c

Define the data to be fit with some noise:

```python
>>> xdata = np.linspace(0, 4, 50)
>>> y = func(xdata, 2.5, 1.3, 0.5)
>>> np.random.seed(1729)
>>> y_noise = 0.2 * np.random.normal(size=xdata.size)
>>> ydata = y + y_noise
>>> plt.plot(xdata, ydata, 'b-', label='data')
```

Fit for the parameters a, b, c of the function func:

```python
>>> popt, pcov = curve_fit(func, xdata, ydata)
>>> popt
array([ 2.55423706, 1.35190947, 0.47450618])
>>> plt.plot(xdata, func(xdata, *popt), 'r-',
...           label='fit: a=%5.3f, b=%5.3f, c=%5.3f' % tuple(popt))
```

Constrain the optimization to the region of $0 \leq a \leq 3$, $0 \leq b \leq 1$ and $0 \leq c \leq 0.5$:

```python
>>> popt, pcov = curve_fit(func, xdata, ydata, bounds=(0, [3., 1., 0.5]))
>>> popt
array([ 2.43708906, 1. , 0.35015434])
>>> plt.plot(xdata, func(xdata, *popt), 'g-',
...           label='fit: a=%5.3f, b=%5.3f, c=%5.3f' % tuple(popt))
```

```python
>>> plt.xlabel('x')
>>> plt.ylabel('y')
>>> plt.legend()
>>> plt.show()
```
6.18.6 Root finding

Scalar functions

- `root_scalar(f[, args, method, bracket, ...])`: Find a root of a scalar function.
- `brentq(f, a, b[, args, xtol, rtol, maxiter, ...])`: Find a root of a function in a bracketing interval using Brent’s method.
- `brenth(f, a, b[, args, xtol, rtol, maxiter, ...])`: Find a root of a function in a bracketing interval using Brent’s method with hyperbolic extrapolation.
- `ridder(f, a, b[, args, xtol, rtol, maxiter, ...])`: Find a root of a function in an interval using Ridder’s method.
- `bisect(f, a, b[, args, xtol, rtol, maxiter, ...])`: Find root of a function within an interval using bisection.
- `newton(func, x0[, fprime, args, tol, ...])`: Find a zero of a real or complex function using the Newton-Raphson (or secant or Halley’s) method.

- `toms748(f, a, b[, args, k, xtol, rtol, ...])`: Find a zero using TOMS Algorithm 748 method.

- `RootResults(root, iterations, ...)`: Represents the root finding result.

---

**scipy.optimize.root_scalar**

`scipy.optimize.root_scalar(f, args=(), method=None, bracket=None, fprime=None, fprime2=None, x0=None, x1=None, xtol=None, rtol=None, maxiter=None, options=None)`

Find a root of a scalar function.

**Parameters**

- `f` [callable] A function to find a root of.
- `args` [tuple, optional] Extra arguments passed to the objective function and its derivative(s).
- `method` [str, optional] Type of solver. Should be one of
  - ‘bisect’ *(see here)*
  - ‘brentq’ *(see here)*
  - ‘brenth’ *(see here)*
  - ‘ridder’ *(see here)*
  - ‘toms748’ *(see here)*
  - ‘newton’ *(see here)*
  - ‘secant’ *(see here)*

- `bracket` [sequence of 2 floats, optional] An interval bracketing a root. \( f(x, *args) \) must have different signs at the two endpoints.
- `x0` [float, optional] Initial guess.
options [dict, optional] A dictionary of solver options. E.g. k, see show_options() for details.

Returns

sol [RootResults] The solution represented as a RootResults object. Important attributes are: root the solution, converged a boolean flag indicating if the algorithm exited successfully and flag which describes the cause of the termination. See RootResults for a description of other attributes.

See also:

show_options

Additional options accepted by the solvers

root

Find a root of a vector function.

Notes

This section describes the available solvers that can be selected by the ‘method’ parameter.

The default is to use the best method available for the situation presented. If a bracket is provided, it may use one of the bracketing methods. If a derivative and an initial value are specified, it may select one of the derivative-based methods. If no method is judged applicable, it will raise an Exception.

Examples

Find the root of a simple cubic

```python
>>> from scipy import optimize
>>> def f(x):
...     return (x**3 - 1)  # only one real root at x = 1
...  
>>> def fprime(x):
...     return 3*x**2

The brentq method takes as input a bracket

```python
>>> sol = optimize.root_scalar(f, bracket=[0, 3], method='brentq')
>>> sol.root, sol.iterations, sol.function_calls
(1.0, 10, 11)
``` 

The newton method takes as input a single point and uses the derivative(s)

```python
>>> sol = optimize.root_scalar(f, x0=0.2, fprime=fprime, method='newton')
>>> sol.root, sol.iterations, sol.function_calls
(1.0, 11, 22)
``` 

The function can provide the value and derivative(s) in a single call.

```python
>>> def f_p_pp(x):
...     return (x**3 - 1), 3*x**2, 6*x

```python
```python
>>> sol = optimize.root_scalar(f_p_pp, x0=0.2, fprime=True, method='newton')
>>> sol.root, sol.iterations, sol.function_calls
(1.0, 11, 11)
```
>>> sol = optimize.root_scalar(f_p_pp, x0=0.2, fprime=True, fprime2=True, method='halley')
>>> sol.root, sol.iterations, sol.function_calls
(1.0, 7, 8)

scipy.optimize.brentq

Find a root of a function in a bracketing interval using Brent’s method.

Uses the classic Brent’s method to find a zero of the function \( f \) on the sign changing interval \([a, b]\). Generally considered the best of the rootfinding routines here. It is a safe version of the secant method that uses inverse quadratic extrapolation. Brent’s method combines root bracketing, interval bisection, and inverse quadratic interpolation. It is sometimes known as the van Wijngaarden-Dekker-Brent method. Brent (1973) claims convergence is guaranteed for functions computable within \([a,b]\).

[Brent1973] provides the classic description of the algorithm. Another description can be found in a recent edition of Numerical Recipes, including [PressEtal1992]. Another description is at http://mathworld.wolfram.com/BrentsMethod.html. It should be easy to understand the algorithm just by reading our code. Our code diverges a bit from standard presentations: we choose a different formula for the extrapolation step.

**Parameters**

- **f** [function] Python function returning a number. The function \( f \) must be continuous, and \( f(a) \) and \( f(b) \) must have opposite signs.
- **a** [scalar] One end of the bracketing interval \([a, b]\).
- **b** [scalar] The other end of the bracketing interval \([a, b]\).
- **xtol** [number, optional] The computed root \( x_0 \) will satisfy \( \text{np.allclose}(x, x_0, atol=xtol, rtol=rtol) \), where \( x \) is the exact root. The parameter must be non-negative. For nice functions, Brent’s method will often satisfy the above condition with \( x_{\text{tol}}/2 \) and \( x_{\text{rtol}}/2 \). [Brent1973]
- **rtol** [number, optional] The computed root \( x_0 \) will satisfy \( \text{np.allclose}(x, x_0, atol=xtol, rtol=rtol) \), where \( x \) is the exact root. The parameter cannot be smaller than its default value of \( 4\times\text{np.finfo(float).eps} \). For nice functions, Brent’s method will often satisfy the above condition with \( x_{\text{tol}}/2 \) and \( x_{\text{rtol}}/2 \). [Brent1973]
- **maxiter** [int, optional] if convergence is not achieved in \( \text{maxiter} \) iterations, an error is raised. Must be \( \geq 0 \).
- **args** [tuple, optional] containing extra arguments for the function \( f \). \( f \) is called by \( \text{apply}(f, (x)+\text{args}) \).
- **full_output** [bool, optional] If \( \text{full_output} \) is False, the root is returned. If \( \text{full_output} \) is True, the return value is \( (x, r) \), where \( x \) is the root, and \( r \) is a \text{RootResults} object.
- **disp** [bool, optional] If True, raise RuntimeError if the algorithm didn’t converge. Otherwise the convergence status is recorded in any \text{RootResults} return object.

**Returns**

- **x0** [float] Zero of \( f \) between \( a \) and \( b \).
- **r** [\text{RootResults} (present if \( \text{full_output} = \text{True} \))] Object containing information about the convergence. In particular, \( r.\text{converged} \) is True if the routine converged.

See also:

- multivariate

  - \text{fmin}, \text{fmin_powell}, \text{fmin_cg}, \text{fmin_bfgs}, \text{fmin_ncg}
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nonlinear
   leastsq

constrained
   fmin_l_bfgs_b, fmin_tnc, fmin_cobyla

global
   basinhopping, brute, differential_evolution

local
   fminbound, brent, golden, bracket

n-dimensional
   fsolve

one-dimensional
   brent, ridder, bisect, newton

scalar
   fixed_point

Notes
f must be continuous. f(a) and f(b) must have opposite signs.

References
[Brent1973], [PressEtal1992]

Examples
>>> def f(x):
...   return (x**2 - 1)

>>> from scipy import optimize

>>> root = optimize.brentq(f, -2, 0)
>>> root
-1.0

>>> root = optimize.brentq(f, 0, 2)
>>> root
1.0

scipy.optimize.brent

Parameters
   f [function] Python function returning a number. f must be continuous, and f(a) and
   f(b) must have opposite signs.
SciPy Reference Guide, Release 1.2.0

a  [scalar] One end of the bracketing interval [a, b].
b  [scalar] The other end of the bracketing interval [a, b].
xtol [number, optional] The computed root $x_0$ will satisfy $\text{np.allclose}(x, x_0, atol=\text{xtol}, rtol=\text{rtol})$, where $x$ is the exact root. The parameter must be non-negative. As with `brentq`, for nice functions the method will often satisfy the above condition with $\text{xtol}/2$ and $\text{rtol}/2$.
rtol [number, optional] The computed root $x_0$ will satisfy $\text{np.allclose}(x, x_0, atol=\text{xtol}, rtol=\text{rtol})$, where $x$ is the exact root. The parameter cannot be smaller than its default value of $4*\text{np.finfo(float).eps}$. As with `brentq`, for nice functions the method will often satisfy the above condition with $\text{xtol}/2$ and $\text{rtol}/2$.
maxiter [int, optional] if convergence is not achieved in `maxiter` iterations, an error is raised. Must be $\geq 0$.
args [tuple, optional] containing extra arguments for the function $f$. $f$ is called by $\text{apply}(f, (x)+\text{args})$.
full_output [bool, optional] If `full_output` is False, the root is returned. If `full_output` is True, the return value is $(x, r)$, where $x$ is the root, and $r$ is a `RootResults` object.
disp [bool, optional] If True, raise `RuntimeError` if the algorithm didn’t converge. Otherwise the convergence status is recorded in any `RootResults` return object.

Returns

$x_0$ [float] Zero of $f$ between $a$ and $b$.
$r$ [RootResults (present if `full_output` = True)] Object containing information about the convergence. In particular, $r$.\text{converged} is True if the routine converged.

See also:

fmin, fmin_powell, fmin_cg
leastsq
     nonlinear least squares minimizer
fmin_l_bfgs_b, fmin_tnc, fmin_cobyla, basinhopping, differential_evolution, brute, fminbound, brent, golden, bracket
fsolve
     n-dimensional root-finding
brentq, brent, ridder, bisect, newton
fixed_point
     scalar fixed-point finder

Examples

```python
>>> def f(x):
...     return (x**2 - 1)
```

```python
>>> from scipy import optimize
```

```python
>>> root = optimize.brentq(f, -2, 0)
>>> root
-1.0
```
```python
>>> root = optimize.brenth(f, 0, 2)
>>> root
1.0
```

```python
scipy.optimize.ridder
scipy.optimize.ridder(f, a, b, args=(), xtol=2e-12, rtol=8.881784197001252e-16, maxiter=100, full_output=False, disp=True)
```

Find a root of a function in an interval using Ridder’s method.

**Parameters**

- **f** [function] Python function returning a number. f must be continuous, and f(a) and f(b) must have opposite signs.
- **a** [scalar] One end of the bracketing interval [a,b].
- **b** [scalar] The other end of the bracketing interval [a,b].
- **xtol** [number, optional] The computed root x0 will satisfy np.allclose(x, x0, atol=xtol, rtol=rtol), where x is the exact root. The parameter must be non-negative.
- **rtol** [number, optional] The computed root x0 will satisfy np.allclose(x, x0, atol=xtol, rtol=rtol), where x is the exact root. The parameter cannot be smaller than its default value of 4*np.finfo(float).eps.
- **maxiter** [int, optional] if convergence is not achieved in maxiter iterations, an error is raised. Must be >= 0.
- **args** [tuple, optional] containing extra arguments for the function f. f is called by apply(f, (x)+args).
- **full_output** [bool, optional] If full_output is False, the root is returned. If full_output is True, the return value is (x, r), where x is the root, and r is a RootResults object.
- **disp** [bool, optional] If True, raise RuntimeError if the algorithm didn’t converge. Otherwise the convergence status is recorded in any RootResults return object.

**Returns**

- **x0** [float] Zero of f between a and b.
- **r** [RootResults (present if full_output = True)] Object containing information about the convergence. In particular, r.converged is True if the routine converged.

**See also:**

- brentq, brenth, bisect, newton
- fixed_point

- scalar fixed-point finder

**Notes**

Uses [Ridders1979] method to find a zero of the function f between the arguments a and b. Ridders' method is faster than bisection, but not generally as fast as the Brent routines. [Ridders1979] provides the classic description and source of the algorithm. A description can also be found in any recent edition of Numerical Recipes.

The routine used here diverges slightly from standard presentations in order to be a bit more careful of tolerance.

**References**

[Ridders1979]
Examples

```python
>>> def f(x):
...     return (x**2 - 1)

>>> from scipy import optimize

>>> root = optimize.ridder(f, 0, 2)
>>> root
1.0

>>> root = optimize.ridder(f, -2, 0)
>>> root
-1.0
```

`scipy.optimize.bisect`

Find root of a function within an interval using bisection.

Basic bisection routine to find a zero of the function \( f \) between the arguments \( a \) and \( b \). \( f(a) \) and \( f(b) \) cannot have the same signs. Slow but sure.

**Parameters**

- `f` [function] Python function returning a number. \( f \) must be continuous, and \( f(a) \) and \( f(b) \) must have opposite signs.
- `a` [scalar] One end of the bracketing interval \([a, b]\).
- `b` [scalar] The other end of the bracketing interval \([a, b]\).
- `xtol` [number, optional] The computed root \( x_0 \) will satisfy \( np.allclose(x, x_0, atol=xtol, rtol=rtol) \), where \( x \) is the exact root. The parameter must be non-negative.
- `rtol` [number, optional] The computed root \( x_0 \) will satisfy \( np.allclose(x, x_0, atol=xtol, rtol=rtol) \), where \( x \) is the exact root. The parameter cannot be smaller than its default value of \( 4*\text{np.finfo(float).eps} \).
- `maxiter` [int, optional] if convergence is not achieved in \( \text{maxiter} \) iterations, an error is raised. Must be \( \geq 0 \).
- `args` [tuple, optional] containing extra arguments for the function \( f \). \( f \) is called by \( \text{apply}(f, (x)+\text{args}) \).
- `full_output` [bool, optional] If \( \text{full_output} = \text{False} \), the root is returned. If \( \text{full_output} = \text{True} \), the return value is \( (x, r) \), where \( x \) is the root, and \( r \) is a \( \text{RootResults} \) object.
- `disp` [bool, optional] If \( \text{True} \), raise `RuntimeError` if the algorithm didn’t converge. Otherwise the convergence status is recorded in a \( \text{RootResults} \) return object.

**Returns**

- `x0` [float] Zero of \( f \) between \( a \) and \( b \).
- `r` [\( \text{RootResults} \) (present if \( \text{full_output} = \text{True} \))] Object containing information about the convergence. In particular, \( r.\text{converged} \) is True if the routine converged.

See also:

- `brentq`, `brent`, `bisect`, `newton`
- `fixed_point`
  scalar fixed-point finder
fsolve
	n-dimensional root-finding

Examples

```python
def f(x):
    return (x**2 - 1)
```

```python
from scipy import optimize

root = optimize.bisect(f, 0, 2)
root 1.0

root = optimize.bisect(f, -2, 0)
root -1.0
```

`scipy.optimize.newton`

`scipy.optimize.newton(func, x0, fprime=None, args=(), tol=1.48e-08, maxiter=50, fprime2=None, x1=None, rtol=0.0, full_output=False, disp=True)`

Find a zero of a real or complex function using the Newton-Raphson (or secant or Halley’s) method.

Find a zero of the function `func` given a nearby starting point `x0`. The Newton-Raphson method is used if the derivative `fprime` of `func` is provided, otherwise the secant method is used. If the second order derivative `fprime2` of `func` is also provided, then Halley’s method is used.

If `x0` is a sequence, then `newton` returns an array, and `func` must be vectorized and return a sequence or array of the same shape as its first argument.

Parameters

- `func` [callable] The function whose zero is wanted. It must be a function of a single variable of the form `f(x,a,b,c...)`, where `a,b,c...` are extra arguments that can be passed in the `args` parameter.
- `x0` [float, sequence, or ndarray] An initial estimate of the zero that should be somewhere near the actual zero. If not scalar, then `func` must be vectorized and return a sequence or array of the same shape as its first argument.
- `fprime` [callable, optional] The derivative of the function when available and convenient. If it is None (default), then the secant method is used.
- `args` [tuple, optional] Extra arguments to be used in the function call.
- `tol` [float] The allowable error of the zero value. If `func` is complex-valued, a larger `tol` is recommended as both the real and imaginary parts of `x` contribute to `|x - x0|`.
- `maxiter` [int] Maximum number of iterations.
- `fprime2` [callable, optional] The second order derivative of the function when available and convenient. If it is None (default), then the normal Newton-Raphson or the secant method is used. If it is not None, then Halley’s method is used.
- `x1` [float, optional] Another estimate of the zero that should be somewhere near the actual zero. Used if `fprime` is not provided.
- `rtol` [float, optional] Tolerance (relative) for termination.
- `full_output` [bool, optional] If `full_output` is False (default), the root is returned. If True and `x0` is scalar, the return value is `(x, r)`, where `x` is the root and `r` is a `RootResults` object. If True and `x0` is non-scalar, the return value is `(x, converged, zero_der)` (see Returns section for details).
disp  [bool, optional] If True, raise a RuntimeError if the algorithm didn’t converge, with the error message containing the number of iterations and current function value. Otherwise the convergence status is recorded in a RootResults return object. Ignored if x0 is not scalar. Note: this has little to do with displaying, however the ‘disp’ keyword cannot be renamed for backwards compatibility.

Returns

root  [float, sequence, or ndarray] Estimated location where function is zero.

r    [RootResults, optional] Present if full_output=True and x0 is scalar. Object containing information about the convergence. In particular, r.converged is True if the routine converged.

converged  [ndarray of bool, optional] Present if full_output=True and x0 is non-scalar. For vector functions, indicates which elements converged successfully.

zero_der  [ndarray of bool, optional] Present if full_output=True and x0 is non-scalar. For vector functions, indicates which elements had a zero derivative.

See also:
brentq, brent, ridder, bisect

fsolve

find zeros in n dimensions.

Notes

The convergence rate of the Newton-Raphson method is quadratic, the Halley method is cubic, and the secant method is sub-quadratic. This means that if the function is well behaved the actual error in the estimated zero after the n-th iteration is approximately the square (cube for Halley) of the error after the (n-1)-th step. However, the stopping criterion used here is the step size and there is no guarantee that a zero has been found. Consequently the result should be verified. Safer algorithms are brentq, brent, ridder, and bisect, but they all require that the root first be bracketed in an interval where the function changes sign. The brentq algorithm is recommended for general use in one dimensional problems when such an interval has been found.

When newton is used with arrays, it is best suited for the following types of problems:

- The initial guesses, x0, are all relatively the same distance from the roots.
- Some or all of the extra arguments, args, are also arrays so that a class of similar problems can be solved together.
- The size of the initial guesses, x0, is larger than O(100) elements. Otherwise, a naive loop may perform as well or better than a vector.

Examples

```python
>>> from scipy import optimize
>>> import matplotlib.pyplot as plt

>>> def f(x):
...   return (x**3 - 1)  # only one real root at x = 1

fprime is not provided, use the secant method:

>>> root = optimize.newton(f, 1.5)
>>> root
1.0000000000000016
```

(continues on next page)


```python
>>> root = optimize.newton(f, 1.5, fprime=lambda x: 6 * x)
>>> root
1.0000000000000016
```

Only `fprime` is provided, use the Newton-Raphson method:

```python
>>> root = optimize.newton(f, 1.5, fprime=lambda x: 3 * x**2)
>>> root
1.0
```

Both `fprime2` and `fprime` are provided, use Halley’s method:

```python
>>> root = optimize.newton(f, 1.5, fprime=lambda x: 3 * x**2, ...
                           fprime2=lambda x: 6 * x)
>>> root
1.0
```

When we want to find zeros for a set of related starting values and/or function parameters, we can provide both of those as an array of inputs:

```python
>>> f = lambda x, a: x**3 - a
>>> fder = lambda x, a: 3 * x**2
>>> x = np.random.randn(100)
>>> a = np.arange(-50, 50)
>>> vec_res = optimize.newton(f, x, fprime=fder, args=(a, ))
```

The above is the equivalent of solving for each value in \((x, a)\) separately in a for-loop, just faster:

```python
>>> loop_res = [optimize.newton(f, x0, fprime=fder, args=(a0,)) ...
              for x0, a0 in zip(x, a)]
>>> np.allclose(vec_res, loop_res)
True
```

Plot the results found for all values of \(a\):

```python
>>> analytical_result = np.sign(a) * np.abs(a)**(1/3)
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(a, analytical_result, 'o')
>>> ax.plot(a, vec_res, ',')
>>> ax.set_xlabel('\$a\$')
>>> ax.set_ylabel('\$x$ where \$f(x, a)=0\$')
>>> plt.show()
```

`scipy.optimize.toms748`

Implement the Algorithm 748 method of Alefeld, Potro and Shi to find a zero of the function \(f\) on the interval \([a, b]\), where \(f(a)\) and \(f(b)\) must have opposite signs.

It uses a mixture of inverse cubic interpolation and “Newton-quadratic” steps. [APS1995].

**Parameters**
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40
 20
 0 20 40
a
4
2
0
2
4
x where f(x, a) = 0

f  [function] Python function returning a scalar. The function f must be continuous, and f(a) and f(b) have opposite signs.

a  [scalar,] lower boundary of the search interval

b  [scalar,] upper boundary of the search interval

args  [tuple, optional] containing extra arguments for the function f. f is called by f(x, *args).

k  [int, optional] The number of Newton quadratic steps to perform each iteration. k>=1.

xtol  [scalar, optional] The computed root x0 will satisfy np.allclose(x, x0, atol=xtol, rtol=rtol), where x is the exact root. The parameter must be non-negative.

rtol  [scalar, optional] The computed root x0 will satisfy np.allclose(x, x0, atol=xtol, rtol=rtol), where x is the exact root.

maxiter  [int, optional] if convergence is not achieved in maxiter iterations, an error is raised. Must be >= 0.

full_output  [bool, optional] If full_output is False, the root is returned. If full_output is True, the return value is (x, r), where x is the root, and r is a RootResults object.

disp  [bool, optional] If True, raise RuntimeError if the algorithm didn’t converge. Otherwise the convergence status is recorded in the RootResults return object.

Returns

x0  [float] Approximate Zero of f

r  [RootResults (present if full_output = True)] Object containing information about the convergence. In particular, r.converged is True if the routine converged.

See also:
brentq, brent, ridder, bisect, newton

fsolve

find zeroes in n dimensions.

Notes

f must be continuous. Algorithm 748 with k=2 is asymptotically the most efficient algorithm known for finding roots of a four times continuously differentiable function. In contrast with Brent’s algorithm,
which may only decrease the length of the enclosing bracket on the last step, Algorithm 748 decreases it each iteration with the same asymptotic efficiency as it finds the root.

For easy statement of efficiency indices, assume that $f$ has 4 continuous derivatives. For $k=1$, the convergence order is at least 2.7, and with about asymptotically 2 function evaluations per iteration, the efficiency index is approximately 1.65. For $k=2$, the order is about 4.6 with asymptotically 3 function evaluations per iteration, and the efficiency index 1.66. For higher values of $k$, the efficiency index approaches the $k$-th root of $(3k-2)$, hence $k=1$ or $k=2$ are usually appropriate.

References

[APS1995]

Examples

```python
>>> def f(x):
...     return (x**3 - 1) # only one real root at x = 1

>>> from scipy import optimize
>>> root, results = optimize.toms748(f, 0, 2, full_output=True)
>>> root
1.0
>>> results
    converged: True
    flag: 'converged'
    function_calls: 11
    iterations: 5
    root: 1.0
```

scipy.optimize.RootResults

class scipy.optimize.RootResults(root, iterations, function_calls, flag)

Represented the root finding result.

Attributes

- root: float Estimated root location.
- iterations: int Number of iterations needed to find the root.
- function_calls: int Number of times the function was called.
- converged: int Number of times the function was called.
- flag: str Description of the cause of termination.

The `root_scalar` function supports the following methods:

```python
scipy.optimize.root_scalar(method='brentq')
```

See also:

For documentation for the rest of the parameters, see `scipy.optimize.root_scalar`

Options

- args: tuple, optional Extra arguments passed to the objective function.
- xtol: float, optional Tolerance (absolute) for termination.
- rtol: float, optional Tolerance (relative) for termination.
- maxiter: int, optional Maximum number of iterations.
options: dict, optional

Specifies any method-specific options not covered above

```python
root_scalar(method='brenth')
scipy.optimize.root_scalar(args=(), method='brenth', x0=None, options={})
```

See also:
For documentation for the rest of the parameters, see `scipy.optimize.root_scalar`

**Options**

- **args** [tuple, optional] Extra arguments passed to the objective function.
- **xtol** [float, optional] Tolerance (absolute) for termination.
- **rtol** [float, optional] Tolerance (relative) for termination.
- **maxiter** [int, optional] Maximum number of iterations.
- **options**: dict, optional

Specifies any method-specific options not covered above

```python
root_scalar(method='bisect')
scipy.optimize.root_scalar(args=(), method='bisect', x0=None, options={})
```

See also:
For documentation for the rest of the parameters, see `scipy.optimize.root_scalar`

**Options**

- **args** [tuple, optional] Extra arguments passed to the objective function.
- **xtol** [float, optional] Tolerance (absolute) for termination.
- **rtol** [float, optional] Tolerance (relative) for termination.
- **maxiter** [int, optional] Maximum number of iterations.
- **options**: dict, optional

Specifies any method-specific options not covered above

```python
root_scalar(method='ridder')
scipy.optimize.root_scalar(args=(), method='ridder', x0=None, options={})
```

See also:
For documentation for the rest of the parameters, see `scipy.optimize.root_scalar`

**Options**

- **args** [tuple, optional] Extra arguments passed to the objective function.
- **xtol** [float, optional] Tolerance (absolute) for termination.
- **rtol** [float, optional] Tolerance (relative) for termination.
- **maxiter** [int, optional] Maximum number of iterations.
- **options**: dict, optional

Specifies any method-specific options not covered above
root_scalar(method='newton')
scipy.optimize.root_scalar(args=(), method='newton', x0=None, options={})

See also:
For documentation for the rest of the parameters, see scipy.optimize.root_scalar

Options
args [tuple, optional] Extra arguments passed to the objective function and its derivative.
xtol [float, optional] Tolerance (absolute) for termination.
rtol [float, optional] Tolerance (relative) for termination.
maxiter [int, optional] Maximum number of iterations.
x0 [float, required] Initial guess.
fprime [bool or callable, optional] If fprime is a boolean and is True, f is assumed to return the value of derivative along with the objective function. fprime can also be a callable returning the derivative of f. In this case, it must accept the same arguments as f.
options: dict, optional
  Specifies any method-specific options not covered above

root_scalar(method='toms748')
scipy.optimize.root_scalar(args=(), method='toms748', x0=None, options={})

See also:
For documentation for the rest of the parameters, see scipy.optimize.root_scalar

Options
args [tuple, optional] Extra arguments passed to the objective function.
xtol [float, optional] Tolerance (absolute) for termination.
rtol [float, optional] Tolerance (relative) for termination.
maxiter [int, optional] Maximum number of iterations.
options: dict, optional
  Specifies any method-specific options not covered above

root_scalar(method='secant')
scipy.optimize.root_scalar(args=(), method='secant', x0=None, options={})

See also:
For documentation for the rest of the parameters, see scipy.optimize.root_scalar

Options
args [tuple, optional] Extra arguments passed to the objective function.
xtol [float, optional] Tolerance (absolute) for termination.
rtol [float, optional] Tolerance (relative) for termination.
maxiter [int, optional] Maximum number of iterations.
x0 [float, required] Initial guess.
x1 [float, required] A second guess.
options: dict, optional
  Specifies any method-specific options not covered above
root_scalar(method=’halley’)
scipy.optimize.root_scalar(args=(), method=’halley’, x0=None, options={})

See also:
For documentation for the rest of the parameters, see scipy.optimize.root_scalar

Options

**args**
tuple, optional
Extra arguments passed to the objective function and its derivatives.

**xtol**
float, optional
Tolerance (absolute) for termination.

**rtol**
float, optional
Tolerance (relative) for termination.

**maxiter**
int, optional
Maximum number of iterations.

**x0**
float, required
Initial guess.

**fprime**
bool or callable, required
If fprime is a boolean and is True, f is assumed to return the value of derivative along with the objective function. fprime can also be a callable returning the derivative of f. In this case, it must accept the same arguments as f.

**fprime2**
bool or callable, required
If fprime2 is a boolean and is True, f is assumed to return the value of 1st and 2nd derivatives along with the objective function. fprime2 can also be a callable returning the 2nd derivative of f. In this case, it must accept the same arguments as f.

**options**
dict, optional
Specifies any method-specific options not covered above

The table below lists situations and appropriate methods, along with asymptotic convergence rates per iteration (and per function evaluation) for successful convergence to a simple root(*). Bisection is the slowest of them all, adding one bit of accuracy for each function evaluation, but is guaranteed to converge. The other bracketing methods all (eventually) increase the number of accurate bits by about 50% for every function evaluation. The derivative-based methods, all built on newton, can converge quite quickly if the initial value is close to the root. They can also be applied to functions defined on (a subset of) the complex plane.

<table>
<thead>
<tr>
<th>Domain of f</th>
<th>Bracket?</th>
<th>Derivatives?</th>
<th>Solvers</th>
<th>Convergence</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>fprime</td>
<td>fprime2</td>
<td>Guaranteed?</td>
</tr>
<tr>
<td>R</td>
<td>Yes</td>
<td>N/A</td>
<td>N/A</td>
<td>Yes</td>
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<td></td>
</tr>
<tr>
<td>R or C</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td>secant</td>
</tr>
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<td></td>
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<td></td>
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</tr>
<tr>
<td>R or C</td>
<td>No</td>
<td>Yes</td>
<td>No</td>
<td>newton</td>
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<td></td>
</tr>
<tr>
<td>R or C</td>
<td>No</td>
<td>Yes</td>
<td>Yes</td>
<td>halley</td>
</tr>
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<td></td>
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<td></td>
<td></td>
</tr>
</tbody>
</table>
Fixed point finding:

```python
fixed_point(func, x0[, args, xtol, maxiter, ...]) Find a fixed point of the function.
```

Given a function of one or more variables and a starting point, find a fixed-point of the function: i.e. where \( \text{func}(x_0) = x_0 \).

**Parameters**

- `func` [function] Function to evaluate.
- `x0` [array_like] Fixed point of function.
- `args` [tuple, optional] Extra arguments to `func`.
- `xtol` [float, optional] Convergence tolerance, defaults to 1e-08.
- `maxiter` [int, optional] Maximum number of iterations, defaults to 500.
- `method` [{"del2", "iteration"}, optional] Method of finding the fixed-point, defaults to "del2" which uses Steffensen’s Method with Aitken’s Del^2 convergence acceleration [1]. The “iteration” method simply iterates the function until convergence is detected, without attempting to accelerate the convergence.

**References**

[1]

**Examples**

```python
>>> from scipy import optimize
>>> def func(x, c1, c2):
...     return np.sqrt(c1/(x+c2))
>>> c1 = np.array([10, 12.])
>>> c2 = np.array([3, 5.])
>>> optimize.fixed_point(func, [1.2, 1.3], args=(c1,c2))
array([1.4920333 , 1.37228132])
```

Multidimensional

```python
root(fun, x0, args, method, jac, tol, ...)) Find a root of a vector function.
```

Given a function of multiple variables and a starting point, find a root of the function: i.e. where \( \text{fun} (x_0) = 0 \).

**Parameters**

- `fun` [callable] A vector function to find a root of.
- `x0` [ndarray] Initial guess.
- `args` [tuple, optional] Extra arguments passed to the objective function and its Jacobian.
- `method` [str, optional] Type of solver. Should be one of
  - ‘hybr’ (see here)
  - ‘lm’ (see here)
  - ‘broyden1’ (see here)
  - ‘broyden2’ (see here)
  - ‘anderson’ (see here)
  - ‘linearmixing’ (see here)
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- 'diagbroyden' (see here)
- 'excitingmixing' (see here)
- 'krylov' (see here)
- 'df-sane' (see here)

jac [bool or callable, optional] If jac is a Boolean and is True, fun is assumed to return the value of Jacobian along with the objective function. If False, the Jacobian will be estimated numerically. jac can also be a callable returning the Jacobian of fun. In this case, it must accept the same arguments as fun.

tol [float, optional] Tolerance for termination. For detailed control, use solver-specific options.

callback [function, optional] Optional callback function. It is called on every iteration as callback(x, f) where x is the current solution and f the corresponding residual. For all methods but 'hybr' and 'lm'.

options [dict, optional] A dictionary of solver options. E.g. xtol or maxiter, see show_options() for details.

Returns

sol [OptimizeResult] The solution represented as a OptimizeResult object. Important attributes are: x the solution array, success a Boolean flag indicating if the algorithm exited successfully and message which describes the cause of the termination. See OptimizeResult for a description of other attributes.

See also:

show_options

Additional options accepted by the solvers

Notes

This section describes the available solvers that can be selected by the 'method' parameter. The default method is hybr.

Method hybr uses a modification of the Powell hybrid method as implemented in MINPACK [1].

Method ln solves the system of nonlinear equations in a least squares sense using a modification of the Levenberg-Marquardt algorithm as implemented in MINPACK [1].

Method df-sane is a derivative-free spectral method. [3]

Methods broyden1, broyden2, anderson, linearmixing, diagbroyden, excitingmixing, krylov are inexact Newton methods, with backtracking or full line searches [2]. Each method corresponds to a particular Jacobian approximations. See nonlin for details.

- Method broyden1 uses Broyden’s first Jacobian approximation, it is known as Broyden’s good method.
- Method broyden2 uses Broyden’s second Jacobian approximation, it is known as Broyden’s bad method.
- Method anderson uses (extended) Anderson mixing.
- Method Krylov uses Krylov approximation for inverse Jacobian. It is suitable for large-scale problem.
- Method diagbroyden uses diagonal Broyden Jacobian approximation.
- Method linearmixing uses a scalar Jacobian approximation.
- Method excitingmixing uses a tuned diagonal Jacobian approximation.
**Warning:** The algorithms implemented for methods `diagbroyden`, `linearmixing` and `excitingmixing` may be useful for specific problems, but whether they will work may depend strongly on the problem.

New in version 0.11.0.

**References**

[1], [2], [3]

**Examples**

The following functions define a system of nonlinear equations and its jacobian.

```python
>>> def fun(x):
...     return [x[0] + 0.5 * (x[0] - x[1])**3 - 1.0,
...            0.5 * (x[1] - x[0])**3 + x[1]]
```

```python
>>> def jac(x):
...     return np.array([[1 + 1.5 * (x[0] - x[1])**2,
...                       -1.5 * (x[0] - x[1])**2],
...                      [-1.5 * (x[1] - x[0])**2,
...                       1 + 1.5 * (x[1] - x[0])**2]])
```

A solution can be obtained as follows.

```python
>>> from scipy import optimize
>>> sol = optimize.root(fun, [0, 0], jac=jac, method='hybr')
>>> sol.x
array([ 0.8411639, 0.1588361])
```

The `root` function supports the following methods:

`root(method='hybr')`

`scipy.optimize.root(fun, x0, args=(), method='hybr', jac=None, tol=None, callback=None, options={})`

Find the roots of a multivariate function using MINPACK's hybrd and hybrj routines (modified Powell method).

**See also:**

For documentation for the rest of the parameters, see `scipy.optimize.root`
factor : [float] A parameter determining the initial step bound (factor * || diag * x||). Should be in the interval (0.1, 100).

diag : [sequence] N positive entries that serve as a scale factors for the variables.

**root(method='lm')**

```python
scipy.optimize.root(fun, x0, args=(), method='lm', jac=None, tol=None, callback=None, options={'func': None, 'col_deriv': 0, 'xtol': 1.49012e-08, 'ftol': 1.49012e-08, 'gtol': 0.0, 'maxiter': 0, 'eps': 0.0, 'factor': 100, 'diag': None})
```

Solve for least squares with Levenberg-Marquardt

See also:

For documentation for the rest of the parameters, see `scipy.optimize.root`

**Options**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>col_deriv</td>
<td>[bool]</td>
<td>non-zero to specify that the Jacobian function computes derivatives down the columns (faster, because there is no transpose operation).</td>
</tr>
<tr>
<td>ftol</td>
<td>[float]</td>
<td>Relative error desired in the sum of squares.</td>
</tr>
<tr>
<td>xtol</td>
<td>[float]</td>
<td>Relative error desired in the approximate solution.</td>
</tr>
<tr>
<td>gtol</td>
<td>[float]</td>
<td>Orthogonality desired between the function vector and the columns of the Jacobian.</td>
</tr>
<tr>
<td>maxiter</td>
<td>[int]</td>
<td>The maximum number of calls to the function. If zero, then 100*(N+1) is the maximum where N is the number of elements in x0.</td>
</tr>
<tr>
<td>epsfcn</td>
<td>[float]</td>
<td>A suitable step length for the forward-difference approximation of the Jacobian (for Dfun= None). If epsfcn is less than the machine precision, it is assumed that the relative errors in the functions are of the order of the machine precision.</td>
</tr>
<tr>
<td>factor</td>
<td>[float]</td>
<td>A parameter determining the initial step bound (factor *</td>
</tr>
<tr>
<td>diag</td>
<td>[sequence]</td>
<td>N positive entries that serve as a scale factors for the variables.</td>
</tr>
</tbody>
</table>

**root(method='broyden1')**

```python
scipy.optimize.root(fun, x0, args=(), method='broyden1', tol=None, callback=None, options={})
```

See also:

For documentation for the rest of the parameters, see `scipy.optimize.root`

**Options**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>nit</td>
<td>[int, optional]</td>
<td>Number of iterations to make. If omitted (default), make as many as required to meet tolerances.</td>
</tr>
<tr>
<td>disp</td>
<td>[bool, optional]</td>
<td>Print status to stdout on every iteration.</td>
</tr>
<tr>
<td>maxiter</td>
<td>[int, optional]</td>
<td>Maximum number of iterations to make. If more are needed to meet convergence, NoConvergence is raised.</td>
</tr>
<tr>
<td>ftol</td>
<td>[float, optional]</td>
<td>Relative tolerance for the residual. If omitted, not used.</td>
</tr>
<tr>
<td>fatol</td>
<td>[float, optional]</td>
<td>Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.</td>
</tr>
<tr>
<td>xtol</td>
<td>[float, optional]</td>
<td>Relative minimum step size. If omitted, not used.</td>
</tr>
<tr>
<td>xatol</td>
<td>[float, optional]</td>
<td>Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.</td>
</tr>
<tr>
<td>tol_norm</td>
<td>[function(vector) -&gt; scalar, optional]</td>
<td>Norm to use in convergence check. Default is the maximum norm.</td>
</tr>
</tbody>
</table>
line_search

[{None, 'armijo' (default), 'wolfe'}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

jac_options

[dict, optional]

Options for the respective Jacobian approximation.

alpha [float, optional] Initial guess for the Jacobian is (-1/alpha).

reduction_method

[str or tuple, optional] Method used in ensuring that the rank of the Broyden matrix stays low. Can either be a string giving the name of the method, or a tuple of the form (method, param1, param2, ...) that gives the name of the method and values for additional parameters. Methods available:

- **restart**: drop all matrix columns. Has no extra parameters.
- **simple**: drop oldest matrix column. Has no extra parameters.
- **svd**: keep only the most significant SVD components.

Extra parameters:

- **to_retain**: number of SVD components to retain when rank reduction is done. Default is \( \text{max\_rank} - 2 \).

max_rank [int, optional] Maximum rank for the Broyden matrix. Default is infinity (ie., no rank reduction).

root(method='broyden2')

`scipy.optimize.root(fun, x0, args=(), method='broyden2', tol=None, callback=None, options={})`

See also:

For documentation for the rest of the parameters, see `scipy.optimize.root`

Options

nit [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

disp [bool, optional] Print status to stdout on every iteration.

maxiter [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, `NoConvergence` is raised.

ftol [float, optional] Relative tolerance for the residual. If omitted, not used.

fatol [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

xtol [float, optional] Relative minimum step size. If omitted, not used.
xatol  [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

tol_norm  [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.

line_search  [{'None', 'armijo' (default), 'wolfe'}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to ‘armijo’.

jac_options  [dict, optional] Options for the respective Jacobian approximation.

alpha  [float, optional] Initial guess for the Jacobian is (-1/alpha).

reduction_method  [str or tuple, optional] Method used in ensuring that the rank of the Broyden matrix stays low. Can either be a string giving the name of the method, or a tuple of the form (method, param1, param2, ...) that gives the name of the method and values for additional parameters.

Methods available:

- **restart**: drop all matrix columns. Has no extra parameters.
- **simple**: drop oldest matrix column. Has no extra parameters.
- **svd**: keep only the most significant SVD components.

Extra parameters:

- to_retain: number of SVD components to retain when rank reduction is done. Default is max_rank - 2.

max_rank  [int, optional] Maximum rank for the Broyden matrix. Default is infinity (i.e., no rank reduction).

root(method='anderson')

scipy.optimize.root(fun, x0, args=(), method='anderson', tol=None, callback=None, options={})

See also:

For documentation for the rest of the parameters, see scipy.optimize.root

Options

- nit  [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.
- disp  [bool, optional] Print status to stdout on every iteration.
- maxiter  [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, NoConvergence is raised.
- ftol  [float, optional] Relative tolerance for the residual. If omitted, not used.
- fatol  [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.
- xtol  [float, optional] Relative minimum step size. If omitted, not used.
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\texttt{xatol} \  [\texttt{float}, \text{optional}]  Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

\texttt{tol\_norm} \  [\text{function(vector) -> scalar, optional}]  Norm to use in convergence check. Default is the maximum norm.

\texttt{line\_search} \  [(\text{None, ‘armijo’ (default), ‘wolfe’}, optional)]  Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to ‘armijo’.

\texttt{jac\_options} \  [\text{dict, optional}]  Options for the respective Jacobian approximation.

\texttt{alpha} \  [\texttt{float, optional}]  Initial guess for the Jacobian is \((-1/\text{alpha})\).

\texttt{M} \  [\texttt{float, optional}]  Number of previous vectors to retain. Defaults to 5.

\texttt{w0} \  [\texttt{float, optional}]  Regularization parameter for numerical stability. Compared to unity, good values of the order of 0.01.

\texttt{root(method='linearmixing')}  
\texttt{scipy.optimize.root(fun, x0, args=(), method='linearmixing', tol=None, callback=None, options={})}

See also:

For documentation for the rest of the parameters, see \texttt{scipy.optimize.root}

\textbf{Options}

\texttt{nit} \  [\texttt{int, optional}]  Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

\texttt{disp} \  [\texttt{bool, optional}]  Print status to stdout on every iteration.

\texttt{maxiter} \  [\texttt{int, optional}]  Maximum number of iterations to make. If more are needed to meet convergence, \texttt{NoConvergence} is raised.

\texttt{ftol} \  [\texttt{float, optional}]  Relative tolerance for the residual. If omitted, not used.

\texttt{fatol} \  [\texttt{float, optional}]  Absolute tolerance (in max-norm) for the residual. If omitted, default is \texttt{6e-6}.

\texttt{xtol} \  [\texttt{float, optional}]  Relative minimum step size. If omitted, not used.

\texttt{xatol} \  [\texttt{float, optional}]  Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

\texttt{tol\_norm} \  [\text{function(vector) -> scalar, optional}]  Norm to use in convergence check. Default is the maximum norm.

\texttt{line\_search} \  [(\text{None, ‘armijo’ (default), ‘wolfe’}, optional)]  Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to ‘armijo’.

\texttt{jac\_options} \  [\text{dict, optional}]  Options for the respective Jacobian approximation.

\texttt{alpha} \  [\texttt{float, optional}]  Initial guess for the Jacobian is \((-1/\text{alpha})\).

\texttt{root(method='diagbroyden')}  
\texttt{scipy.optimize.root(fun, x0, args=(), method='diagbroyden', tol=None, callback=None, options={})}

See also:
For documentation for the rest of the parameters, see `scipy.optimize.root`

**Options**

- **nit**  
  int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

- **disp**  
  bool, optional] Print status to stdout on every iteration.

- **maxiter**  
  int, optional] Maximum number of iterations to make. If more are needed to meet convergence, `NoConvergence` is raised.

- **ftol**  
  float, optional] Relative tolerance for the residual. If omitted, not used.

- **fatol**  
  float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

- **xtol**  
  float, optional] Relative minimum step size. If omitted, not used.

- **xatol**  
  float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

- **tol_norm**  
  [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.

- **line_search**  
  [{None, ‘armijo’ (default), ‘wolfe’}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to ‘armijo’.

- **jac_options**  
  [dict, optional] Options for the respective Jacobian approximation.

- **alpha**  
  float, optional] initial guess for the jacobian is (-1/alpha).

```
root(method='excitingmixing')
scipy.optimize.root(fun, x0, args=(), method='excitingmixing', tol=None, callback=None, options={})
```

See also:

For documentation for the rest of the parameters, see `scipy.optimize.root`

**Options**

- **nit**  
  int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

- **disp**  
  bool, optional] Print status to stdout on every iteration.

- **maxiter**  
  int, optional] Maximum number of iterations to make. If more are needed to meet convergence, `NoConvergence` is raised.

- **ftol**  
  float, optional] Relative tolerance for the residual. If omitted, not used.

- **fatol**  
  float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

- **xtol**  
  float, optional] Relative minimum step size. If omitted, not used.

- **xatol**  
  float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

- **tol_norm**  
  [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.

- **line_search**  
  [{None, ‘armijo’ (default), ‘wolfe’}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to ‘armijo’.

6.18. Optimization and Root Finding (scipy.optimize)
jac_options
    [dict, optional] Options for the respective Jacobian approximation.
alpha    [float, optional] Initial Jacobian approximation is (-1/alpha).
alphamax [float, optional] The entries of the diagonal Jacobian are kept in the
            range [alpha, alphamax].

root(method='krylov')
scipy.optimize.root(fun, x0, args=(), method='krylov', tol=None, callback=None, options={})

See also:
For documentation for the rest of the parameters, see scipy.optimize.root

Options
    nit    [int, optional] Number of iterations to make. If omitted (default), make as many
            as required to meet tolerances.
disp   [bool, optional] Print status to stdout on every iteration.
maxiter [int, optional] Maximum number of iterations to make. If more are needed to meet
            convergence, NoConvergence is raised.
ftol    [float, optional] Relative tolerance for the residual. If omitted, not used.
fatol   [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted,
            default is 6e-6.
xtol    [float, optional] Relative minimum step size. If omitted, not used.
xatol   [float, optional] Absolute minimum step size, as determined from the Jacobian
            approximation. If the step size is smaller than this, optimization is terminated as
            successful. If omitted, not used.
tol_norm [function(vector) -> scalar, optional] Norm to use in convergence check. Default
            is the maximum norm.

line_search
    [{None, ‘armijo’ (default), ‘wolfe’}, optional] Which type of a line search to use
            to determine the step size in the direction given by the Jacobian approximation.
            Defaults to ‘armijo’.

jac_options
    [dict, optional] Options for the respective Jacobian approximation.
rdiff   [float, optional] Relative step size to use in numerical differentiation.
            method to use to approximate the Jacobian. Can be a string, or a
            function implementing the same interface as the iterative solvers in
            scipy.sparse.linalg.
            The default is scipy.sparse.linalg.lgmres.

inner_M  [LinearOperator or InverseJacobian] Preconditioner for the inner
            Krylov iteration. Note that you can use also inverse Jacobians as (adapt-
            ive) preconditioners. For example,

            >>> jac = BroydenFirst()
            >>> kjac = KrylovJacobian(inner_M=jac.inverse).

If the preconditioner has a method named ‘update’, it will be called
as update(x, f) after each nonlinear step, with x giving the current
point, and f the current function value.
inner_tol, inner_maxiter, ...

Parameters to pass on to the “inner” Krylov solver. See scipy.sparse.linalg.gmres for details.

outer_k [int, optional] Size of the subspace kept across LGMRES nonlinear iterations.

See scipy.sparse.linalg.lgmres for details.

root(method='df-sane')

scipy.optimize.root(fun, x0, args=(), method='df-sane', tol=None, callback=None, options={'func': None, 'ftol': 1e-08, 'fatol': 1e-300, 'maxfev': 1000, 'fnorm': None, 'disp': False, 'M': 10, 'eta_strategy': None, 'sigma_eps': 1e-10, 'sigma_0': 1.0, 'line_search': 'cruz'})

Solve nonlinear equation with the DF-SANE method

See also:

For documentation for the rest of the parameters, see scipy.optimize.root

Options

ftol [float, optional] Relative norm tolerance.
fatol [float, optional] Absolute norm tolerance. Algorithm terminates when \|\|func(x)\|\| < fatol + ftol \|\|func(x_0)\|\|.

fnorm [callable, optional] Norm to use in the convergence check. If None, 2-norm is used.

maxfev [int, optional] Maximum number of function evaluations.

disp [bool, optional] Whether to print convergence process to stdout.

eta_strategy [callable, optional] Choice of the eta_k parameter, which gives slack for growth of \|\|F\|\|^2. Called as eta_k = eta_strategy(k, x, F) with k the iteration number, x the current iterate and F the current residual. Should satisfy eta_k > 0 and sum(eta, k=0..inf) < inf. Default: \|\|F\|\|^2 / (1 + k)**2.

sigma_eps [float, optional] The spectral coefficient is constrained to sigma_eps < sigma < 1/sigma_eps. Default: 1e-10

sigma_0 [float, optional] Initial spectral coefficient. Default: 1.0

M [int, optional] Number of iterates to include in the nonmonotonic line search. Default: 10

line_search [{'cruz', 'cheng'}] Type of line search to employ. ‘cruz’ is the original one defined in [Martinez & Raydan. Math. Comp. 75, 1429 (2006)], ‘cheng’ is a modified search defined in [Cheng & Li. IMA J. Numer. Anal. 29, 814 (2009)]. Default: ‘cruz’

References
[1], [2], [3]

6.18.7 Linear Programming

linprog(c[, A_ub, b_ub, A_eq, b_eq, bounds, ...]) Minimize a linear objective function subject to linear equality and inequality constraints.

scipy.optimize.linprog

scipy.optimize.linprog(c, A_ub=None, b_ub=None, A_eq=None, b_eq=None, bounds=None, method='simplex', callback=None, options=None)

Minimize a linear objective function subject to linear equality and inequality constraints. Linear
Programming is intended to solve the following problem form:

Minimize:

\[ c \odot x \]

Subject to:

\[
\begin{align*}
A_{\text{ub}} \odot x & \leq b_{\text{ub}} \\
A_{\text{eq}} \odot x & = b_{\text{eq}} \\
1b & \leq x \leq ub
\end{align*}
\]

where \( lb = 0 \) and \( ub = \text{None} \) unless set in \text{bounds}.

**Parameters**

- **c** [1D array] Coefficients of the linear objective function to be minimized.
- **A_ub** [2D array, optional] 2D array such that \( A_{\text{ub}} \odot x \) gives the values of the upper-bound inequality constraints at \( x \).
- **b_ub** [1D array, optional] 1D array of values representing the upper-bound of each inequality constraint (row) in \( A_{\text{ub}} \).
- **A_eq** [2D, optional] 2D array such that \( A_{\text{eq}} \odot x \) gives the values of the equality constraints at \( x \).
- **b_eq** [1D array, optional] 1D array of values representing the RHS of each equality constraint (row) in \( A_{\text{eq}} \).
- **bounds** [sequence, optional] \((\text{min}, \text{max})\) pairs for each element in \( x \), defining the bounds on that parameter. Use None for one of \text{min} or \text{max} when there is no bound in that direction. By default bounds are \((0, \text{None})\) (non-negative). If a sequence containing a single tuple is provided, then \text{min} and \text{max} will be applied to all variables in the problem.
- **method** [str, optional] Type of solver. ‘simplex’ and ‘interior-point’ are supported.
- **callback** [callable, optional (simplex only)] If a callback function is provided, it will be called within each iteration of the simplex algorithm. The callback must require a `scipy.optimize.OptimizeResult` consisting of the following fields:
  - **x** [1D array] The independent variable vector which optimizes the linear programming problem.
  - **fun** [float] Value of the objective function.
  - **success** [bool] True if the algorithm succeeded in finding an optimal solution.
  - **slack** [1D array] The values of the slack variables. Each slack variable corresponds to an inequality constraint. If the slack is zero, the corresponding constraint is active.
  - **con** [1D array] The (nominally zero) residuals of the equality constraints that is, \( b - A_{\text{eq}} \odot x \)
  - **phase** [int] The phase of the optimization being executed. In phase 1 a basic feasible solution is sought and the \( T \) has an additional row representing an alternate objective function.
  - **status** [int] An integer representing the exit status of the optimization:
    - 0: Optimization terminated successfully
    - 1: Iteration limit reached
    - 2: Problem appears to be infeasible
    - 3: Problem appears to be unbounded
    - 4: Serious numerical difficulties encountered
  - **nit** [int] The number of iterations performed.
  - **message** [str] A string descriptor of the exit status of the optimization.
options [dict, optional] A dictionary of solver options. All methods accept the following generic options:

- maxiter [int] Maximum number of iterations to perform.
- disp [bool] Set to True to print convergence messages.

For method-specific options, see show_options('linprog').

Returns

res [OptimizeResult] A scipy.optimize.OptimizeResult consisting of the fields:

- x [1D array] The independent variable vector which optimizes the linear programming problem.
- fun [float] Value of the objective function.
- slack [1D array] The values of the slack variables. Each slack variable corresponds to an inequality constraint. If the slack is zero, then the corresponding constraint is active.
- con [1D array] The (nominally zero) residuals of the equality constraints, that is, $b - A_{eq} @ x$
- success [bool] Returns True if the algorithm succeeded in finding an optimal solution.
- status [int] An integer representing the exit status of the optimization:

<table>
<thead>
<tr>
<th>Status Code</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Optimization terminated successfully</td>
</tr>
<tr>
<td>1</td>
<td>Iteration limit reached</td>
</tr>
<tr>
<td>2</td>
<td>Problem appears to be infeasible</td>
</tr>
<tr>
<td>3</td>
<td>Problem appears to be unbounded</td>
</tr>
<tr>
<td>4</td>
<td>Serious numerical difficulties encountered</td>
</tr>
</tbody>
</table>

- nit [int] The number of iterations performed.

See also:

- show_options

Additional options accepted by the solvers

Notes

This section describes the available solvers that can be selected by the ‘method’ parameter. The default method is Simplex. Interior point is also available.

Method simplex uses the simplex algorithm (as it relates to linear programming, NOT the Nelder-Mead simplex) [1], [2]. This algorithm should be reasonably reliable and fast for small problems.

New in version 0.15.0.

Method interior-point uses the primal-dual path following algorithm as outlined in [4]. This algorithm is intended to provide a faster and more reliable alternative to simplex, especially for large, sparse problems. Note, however, that the solution returned may be slightly less accurate than that of the simplex method and may not correspond with a vertex of the polytope defined by the constraints.

Before applying either method a presolve procedure based on [8] attempts to identify trivial infeasibilities, trivial unboundedness, and potential problem simplifications. Specifically, it checks for:

- rows of zeros in $A_{eq}$ or $A_{ub}$, representing trivial constraints;
- columns of zeros in $A_{eq}$ and $A_{ub}$, representing unconstrained variables;
- column singletons in $A_{eq}$, representing fixed variables; and
- column singletons in $A_{ub}$, representing simple bounds.
If presolve reveals that the problem is unbounded (e.g. an unconstrained and unbounded variable has negative cost) or infeasible (e.g. a row of zeros in \( A_{eq} \) corresponds with a nonzero in \( b_{eq} \)), the solver terminates with the appropriate status code. Note that presolve terminates as soon as any sign of unboundedness is detected; consequently, a problem may be reported as unbounded when in reality the problem is infeasible (but infeasibility has not been detected yet). Therefore, if the output message states that unboundedness is detected in presolve and it is necessary to know whether the problem is actually infeasible, set option \( \text{presolve} = \text{False} \).

If neither infeasibility nor unboundedness are detected in a single pass of the presolve check, bounds are tightened where possible and fixed variables are removed from the problem. Then, linearly dependent rows of the \( A_{eq} \) matrix are removed, (unless they represent an infeasibility) to avoid numerical difficulties in the primary solve routine. Note that rows that are nearly linearly dependent (within a prescribed tolerance) may also be removed, which can change the optimal solution in rare cases. If this is a concern, eliminate redundancy from your problem formulation and run with option \( \text{rr} = \text{False} \) or \( \text{presolve} = \text{False} \).

Several potential improvements can be made here: additional presolve checks outlined in [8] should be implemented, the presolve routine should be run multiple times (until no further simplifications can be made), and more of the efficiency improvements from [5] should be implemented in the redundancy removal routines.

After presolve, the problem is transformed to standard form by converting the (tightened) simple bounds to upper bound constraints, introducing non-negative slack variables for inequality constraints, and expressing unbounded variables as the difference between two non-negative variables.

**References**

[1], [2], [3], [4], [5], [6], [7], [8], [9], [10]

**Examples**

Consider the following problem:

**Minimize:**

\[
\begin{align*}
    f &= -1x[0] + 4x[1] \\
\end{align*}
\]

**Subject to:**

\[
\begin{align*}
    -3x[0] + 1x[1] & \leq 6 \\
    1x[0] + 2x[1] & \leq 4 \\
    x[1] & \geq -3 \\
    -\infty & \leq x[0] \leq \infty
\end{align*}
\]

This problem deviates from the standard linear programming problem. In standard form, linear programming problems assume the variables \( x \) are non-negative. Since the problem variables don't have the standard bounds of \((0, \infty)\), the variable bounds must be set using \( \text{bounds} \) explicitly.

There are two upper-bound constraints, which can be expressed as

\[
\text{dot}(A_{ub}, x) \leq b_{ub}
\]

The input for this problem is as follows:

```python
>>> c = [-1, 4]
>>> A = [[-3, 1], [1, 2]]
>>> b = [6, 4]
>>> x0_bounds = (None, None)
>>> x1_bounds = (-3, None)
>>> from scipy.optimize import linprog
```
The `linprog` function supports the following methods:

```
linprog(method=’simplex’)
```

```
scipy.optimize.linprog(c, method=’simplex’, callback=None, options={’c0’: None, ’A’: None, ’b’: None, ’maxiter’: 1000, ’disp’: False, ’tol’: 1e-12, ’bland’: False, ’_T_o’: None})
```

Minimize a linear objective function subject to linear equality and non-negativity constraints using the two phase simplex method. Linear programming is intended to solve problems of the following form:

Minimize:

```
c @ x
```

Subject to:

```
A @ x == b
x >= 0
```

**Parameters**

- `c` [1D array] Coefficients of the linear objective function to be minimized.
- `c0` [float] Constant term in objective function due to fixed (and eliminated) variables. (Purely for display.)
- `A` [2D array] 2D array such that `A @ x`, gives the values of the equality constraints at `x`.
- `b` [1D array] 1D array of values representing the right hand side of each equality constraint (row) in `A`.
- `callback` [callable, optional (simplex only)] If a callback function is provided, it will be called within each iteration of the simplex algorithm. The callback must require a `scipy.optimize.OptimizeResult` consisting of the following fields:
  - `x` [1D array] The independent variable vector which optimizes the linear programming problem.
  - `fun` [float] Value of the objective function.
  - `success` [bool] True if the algorithm succeeded in finding an optimal solution.
  - `slack` [1D array] The values of the slack variables. Each slack variable corresponds to an inequality constraint. If the slack is zero, the corresponding constraint is active.
con [1D array] The (nominally zero) residuals of the equality constraints, that is, $b - A_{eq} @ x$

phase [int] The phase of the optimization being executed. In phase 1 a basic feasible solution is sought and the $T$ has an additional row representing an alternate objective function.

status [int] An integer representing the exit status of the optimization:

<table>
<thead>
<tr>
<th>Value</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Optimization terminated successfully</td>
</tr>
<tr>
<td>1</td>
<td>Iteration limit reached</td>
</tr>
<tr>
<td>2</td>
<td>Problem appears to be infeasible</td>
</tr>
<tr>
<td>3</td>
<td>Problem appears to be unbounded</td>
</tr>
<tr>
<td>4</td>
<td>Serious numerical difficulties encountered</td>
</tr>
</tbody>
</table>

nit [int] The number of iterations performed.

message [str] A string descriptor of the exit status of the optimization.

Other Parameters

maxiter [int] The maximum number of iterations to perform.
disp [bool] If True, print exit status message to sys.stdout
tol [float] The tolerance which determines when a solution is “close enough” to zero in Phase 1 to be considered a basic feasible solution or close enough to positive to serve as an optimal solution.
bland [bool] If True, use Bland’s anti-cycling rule [3] to choose pivots to prevent cycling. If False, choose pivots which should lead to a converged solution more quickly. The latter method is subject to cycling (non-convergence) in rare instances.

Returns

x [1D array] Solution vector.

status [int] An integer representing the exit status of the optimization:

<table>
<thead>
<tr>
<th>Value</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Optimization terminated successfully</td>
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<tr>
<td>1</td>
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<tr>
<td>2</td>
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</tr>
<tr>
<td>3</td>
<td>Problem appears to be unbounded</td>
</tr>
<tr>
<td>4</td>
<td>Serious numerical difficulties encountered</td>
</tr>
</tbody>
</table>

message [str] A string descriptor of the exit status of the optimization.

iteration [int] The number of iterations taken to solve the problem.

Notes

The expected problem formulation differs between the top level linprog module and the method specific solvers. The method specific solvers expect a problem in standard form:

Minimize:

$$c @ x$$

Subject to:

$$A @ x == b$$
$$x >= 0$$

Whereas the top level linprog module expects a problem of form:

Minimize:
Subject to:

\[
\begin{align*}
A_{ub} @ x & \leq b_{ub} \\
A_{eq} @ x & = b_{eq} \\
1b & \leq x \leq ub
\end{align*}
\]

where \(1b = 0\) and \(ub = \text{None}\) unless set in `bounds`.

The original problem contains equality, upper-bound and variable constraints whereas the method specific solver requires equality constraints and variable non-negativity.

`linprog` module converts the original problem to standard form by converting the simple bounds to upper bound constraints, introducing non-negative slack variables for inequality constraints, and expressing unbounded variables as the difference between two non-negative variables.

**References**

[1], [2], [3]

**linprog**(method=`'interior-point'`)  

```python
scipy.optimize.linprog(c, method='interior-point', callback=None, options={'c0': 0, 'A': None, 'b': None, 'alpha0': 0.99995, 'beta': 0.1, 'maxiter': 1000, 'disp': False, 'tol': 1e-08, 'sparse': False, 'lstsq': False, 'sym_pos': True, 'cholesky': None, 'pc': True, 'ip': False, 'permc_spec': 'MMD_AT_PLUS_A'})
```

Minimize a linear objective function subject to linear equality and non-negativity constraints using the interior point method of [4]. Linear programming is intended to solve problems of the following form:

Minimize:

\[
c @ x
\]

Subject to:

\[
A @ x = b \\
x \geq 0
\]

**Parameters**

- **c** [1D array] Coefficients of the linear objective function to be minimized.
- **c0** [float] Constant term in objective function due to fixed (and eliminated) variables. (Purely for display.)
- **A** [2D array] 2D array such that \(A @ x\), gives the values of the equality constraints at \(x\).
- **b** [1D array] 1D array of values representing the right hand side of each equality constraint (row) in \(A\).

**Returns**

- **x** [1D array] Solution vector.
- **status** [int] An integer representing the exit status of the optimization:

\[
\begin{align*}
0 & : \text{Optimization terminated successfully} \\
1 & : \text{Iteration limit reached} \\
2 & : \text{Problem appears to be infeasible}
\end{align*}
\]

(continues on next page)
Problem appears to be unbounded
Serious numerical difficulties encountered

message [str] A string descriptor of the exit status of the optimization.
iteration [int] The number of iterations taken to solve the problem.

See also:
For documentation for the rest of the parameters, see `scipy.optimize.linprog`

Options

maxiter [int (default = 1000)] The maximum number of iterations of the algorithm.
disp [bool (default = False)] Set to True if indicators of optimization status are to be printed to the console each iteration.
tol [float (default = 1e-8)] Termination tolerance to be used for all termination criteria; see [4] Section 4.5.
alpha0 [float (default = 0.99995)] The maximal step size for Mehrota's predictor-corrector search direction; see $\beta_3$ of [4] Table 8.1.
beta [float (default = 0.1)] The desired reduction of the path parameter $\mu$ (see [6]) when Mehrota's predictor-corrector is not in use (uncommon).
sparse [bool (default = False)] Set to True if the problem is to be treated as sparse after presolve. If either $A_{eq}$ or $A_{ub}$ is a sparse matrix, this option will automatically be set True, and the problem will be treated as sparse even during presolve. If your constraint matrices contain mostly zeros and the problem is not very small (less than about 100 constraints or variables), consider setting True or providing $A_{eq}$ and $A_{ub}$ as sparse matrices.
lstsq [bool (default = False)] Set to True if the problem is expected to be very poorly conditioned. This should always be left False unless severe numerical difficulties are encountered. Leave this at the default unless you receive a warning message suggesting otherwise.
symmetric [bool (default = True)] Leave True if the problem is expected to yield a well conditioned symmetric positive definite normal equation matrix (almost always). Leave this at the default unless you receive a warning message suggesting otherwise.
cholesky [bool (default = True)] Set to True if the normal equations are to be solved by explicit Cholesky decomposition followed by explicit forward/backward substitution. This is typically faster for moderate, dense problems that are numerically well-behaved.
pc [bool (default = True)] Leave True if the predictor-corrector method of Mehrota is to be used. This is almost always (if not always) beneficial.
ip [bool (default = False)] Set to True if the improved initial point suggestion due to [4] Section 4.3 is desired. Whether this is beneficial or not depends on the problem.
perm_spec [str (default = ‘MMD_AT_PLUS_A’)] (Has effect only with sparse = True, lstsq = False, sym_pos = True.) A matrix is factorized in each iteration of the algorithm. This option specifies how to permute the columns of the matrix for sparsity preservation. Acceptable values are:
- NATURAL: natural ordering.
- MMD_ATA: minimum degree ordering on the structure of $A^T A$.
- MMD_AT_PLUS_A: minimum degree ordering on the structure of $A^T + A$.
- COLAMD: approximate minimum degree column ordering.
This option can impact the convergence of the interior point algorithm; test different values to determine which performs best for your problem. For more information, refer to scipy.sparse.linalg.splu.

Notes

This method implements the algorithm outlined in [4] with ideas from [8] and a structure inspired by the simpler methods of [6] and [4].

The primal-dual path following method begins with initial ‘guesses’ of the primal and dual variables of the standard form problem and iteratively attempts to solve the (nonlinear) Karush-Kuhn-Tucker conditions for the problem with a gradually reduced logarithmic barrier term added to the objective. This particular implementation uses a homogeneous self-dual formulation, which provides certificates of infeasibility or unboundedness where applicable.

The default initial point for the primal and dual variables is that defined in [4] Section 4.4 Equation 8.22. Optionally (by setting initial point option ip=True), an alternate (potentially improved) starting point can be calculated according to the additional recommendations of [4] Section 4.4.

A search direction is calculated using the predictor-corrector method (single correction) proposed by Mehrota and detailed in [4] Section 4.1. (A potential improvement would be to implement the method of multiple corrections described in [4] Section 4.2.) In practice, this is accomplished by solving the normal equations, [4] Section 5.1 Equations 8.31 and 8.32, derived from the Newton equations [4] Section 5 Equations 8.25 (compare to [4] Section 4 Equations 8.6-8.8). The advantage of solving the normal equations rather than 8.25 directly is that the matrices involved are symmetric positive definite, so Cholesky decomposition can be used rather than the more expensive LU factorization.

With the default cholesky=True, this is accomplished using scipy.linalg.cho_factor followed by forward/backward substitutions via scipy.linalg.cho_solve. With cholesky=False and sym_pos=True, Cholesky decomposition is performed instead by scipy.linalg.solve. Based on speed tests, this also appears to retain the Cholesky decomposition of the matrix for later use, which is beneficial as the same system is solved four times with different right hand sides in each iteration of the algorithm.

In problems with redundancy (e.g. if presolve is turned off with option presolve=False) or if the matrices become ill-conditioned (e.g. as the solution is approached and some decision variables approach zero), Cholesky decomposition can fail. Should this occur, successively more robust solvers (scipy.linalg.solve with sym_pos=False then scipy.linalg.lstsq) are tried, at the cost of computational efficiency. These solvers can be used from the outset by setting the options sym_pos=False and lstsq=True, respectively.

Note that with the option sparse=True, the normal equations are solved using scipy.sparse.linalg.spsolve. Unfortunately, this uses the more expensive LU decomposition from the outset, but for large, sparse problems, the use of sparse linear algebra techniques improves the solve speed despite the use of LU rather than Cholesky decomposition. A simple improvement would be to use the sparse Cholesky decomposition of CHOLMOD via scikit-sparse when available.

Other potential improvements for combatting issues associated with dense columns in otherwise sparse problems are outlined in [4] Section 5.3 and [10] Section 4.1-4.2; the latter also discusses the alleviation of accuracy issues associated with the substitution approach to free variables.

After calculating the search direction, the maximum possible step size that does not activate the non-negativity constraints is calculated, and the smaller of this step size and unity is applied (as in [4] Section 4.1.) [4] Section 4.3 suggests improvements for choosing the step size.

The new point is tested according to the termination conditions of [4] Section 4.5. The same tolerance, which can be set using the tol option, is used for all checks. (A potential improvement would be to expose the different tolerances to be set independently.) If optimality, unboundedness, or infeasibility is detected, the solve procedure terminates; otherwise it repeats.
The expected problem formulation differs between the top level `linprog` module and the method specific solvers. The method specific solvers expect a problem in standard form:

Minimize:

\[ \mathbf{c} \mathbf{x} \]

Subject to:

\[ \mathbf{A} \mathbf{x} = \mathbf{b} \]
\[ \mathbf{x} \geq 0 \]

Whereas the top level `linprog` module expects a problem of form:

Minimize:

\[ \mathbf{c} \mathbf{x} \]

Subject to:

\[ \mathbf{A}_{\text{ub}} \mathbf{x} \leq \mathbf{b}_{\text{ub}} \]
\[ \mathbf{A}_{\text{eq}} \mathbf{x} = \mathbf{b}_{\text{eq}} \]
\[ \mathbf{lb} \leq \mathbf{x} \leq \mathbf{ub} \]

where \( \mathbf{lb} = 0 \) and \( \mathbf{ub} = \text{None} \) unless set in `bounds`.

The original problem contains equality, upper-bound and variable constraints whereas the method specific solver requires equality constraints and variable non-negativity.

`linprog` module converts the original problem to standard form by converting the simple bounds to upper bound constraints, introducing non-negative slack variables for inequality constraints, and expressing unbounded variables as the difference between two non-negative variables.

**References**

[4], [6], [8], [9], [10]

The simplex method supports callback functions, such as:

```python
scipy.optimize.linprog_verbose_callback(res)
```

A sample callback function demonstrating the `linprog` callback interface. This callback produces detailed output to `sys.stdout` before each iteration and after the final iteration of the simplex algorithm.

**Parameters**

- `res` ([A `scipy.optimize.OptimizeResult` consisting of the following fields:]
  - `x` [1D array] The independent variable vector which optimizes the linear programming problem.
  - `fun` [float] Value of the objective function.
  - `success` [bool] True if the algorithm succeeded in finding an optimal solution.
  - `slack` [1D array] The values of the slack variables. Each slack variable corresponds to an inequality constraint. If the slack is zero, then the corresponding constraint is active.)
Assignment problems:

```python
linear_sum_assignment(cost_matrix)
```

Solve the linear sum assignment problem.

**scipy.optimize.linear_sum_assignment**

Solve the linear sum assignment problem.

The linear sum assignment problem is also known as minimum weight matching in bipartite graphs. A problem instance is described by a matrix C, where each C[i,j] is the cost of matching vertex i of the first partite set (a “worker”) and vertex j of the second set (a “job”). The goal is to find a complete assignment of workers to jobs of minimal cost.

Formally, let X be a boolean matrix where X[i,j] = 1 iff row i is assigned to column j. Then the optimal assignment has cost

\[
\min \sum_i \sum_j C_{i,j} X_{i,j}
\]

s.t. each row is assignment to at most one column, and each column to at most one row.

This function can also solve a generalization of the classic assignment problem where the cost matrix is rectangular. If it has more rows than columns, then not every row needs to be assigned to a column, and vice versa.

The method used is the Hungarian algorithm, also known as the Munkres or Kuhn-Munkres algorithm.

**Parameters**

- `cost_matrix` [array] The cost matrix of the bipartite graph.

**Returns**

- `row_ind, col_ind` [array] An array of row indices and one of corresponding column indices giving the optimal assignment. The cost of the assignment can be computed as `cost_matrix[row_ind, col_ind].sum()`. The row indices will be sorted; in the case of a square cost matrix they will be equal to `numpy.arange(cost_matrix.shape[0])`.

**Notes**

New in version 0.17.0.
References


Examples

```python
>>> cost = np.array([[4, 1, 3], [2, 0, 5], [3, 2, 2]])
>>> from scipy.optimize import linear_sum_assignment
>>> row_ind, col_ind = linear_sum_assignment(cost)
>>> col_ind
array([1, 0, 2])
>>> cost[row_ind, col_ind].sum()
5
```

6.18.8 Utilities

Finite-Difference Approximation

approx_fprime(xk, f, epsilon, *args)

Finite-difference approximation of the gradient of a scalar function.

Parameters

- `xk` [array_like] The coordinate vector at which to determine the gradient of `f`.
- `f` [callable] The function of which to determine the gradient (partial derivatives). Should take `xk` as first argument, other arguments to `f` can be supplied in *args. Should return a scalar, the value of the function at `xk`.
- `epsilon` [array_like] Increment to `xk` to use for determining the function gradient. If a scalar, uses the same finite difference delta for all partial derivatives. If an array, should contain one value per element of `xk`.
- `*args` [args, optional] Any other arguments that are to be passed to `f`.

Returns


See also:

check_grad

Check correctness of gradient function against approx_fprime.
Notes
The function gradient is determined by the forward finite difference formula:

\[
\frac{f(x_k[i] + \epsilon[i]) - f(x_k[i])}{\epsilon[i]}
\]

The main use of `approx_fprime` is in scalar function optimizers like `fmin_bfgs`, to determine numerically the Jacobian of a function.

Examples

```python
>>> from scipy import optimize
>>> def func(x, c0, c1):
...     "Coordinate vector \`x` should be an array of size two."
...     return c0 * x[0]**2 + c1*x[1]**2

>>> x = np.ones(2)
>>> c0, c1 = (1, 200)
>>> eps = np.sqrt(np.finfo(float).eps)
>>> optimize.approx_fprime(x, func, [eps, np.sqrt(200) * eps], c0, c1)
array([ 2. , 400.00004198])
```

`scipy.optimize.check_grad`

`scipy.optimize.check_grad(func, grad, x0, *args, **kwargs)`

Check the correctness of a gradient function by comparing it against a (forward) finite-difference approximation of the gradient.

Parameters

- `func`: [callable `func(x0, *args)`] Function whose derivative is to be checked.
- `grad`: [callable `grad(x0, *args)`] Gradient of `func`.
- `x0`: [ndarray] Points to check `grad` against forward difference approximation of `grad` using `func`.
- `args`: [\*args, optional] Extra arguments passed to `func` and `grad`.
- `epsilon`: [float, optional] Step size used for the finite difference approximation. It defaults to `sqrt(numpy.finfo(float).eps)`, which is approximately 1.49e-08.

Returns

- `err`: [float] The square root of the sum of squares (i.e. the 2-norm) of the difference between `grad(x0, *args)` and the finite difference approximation of `grad` using `func` at the points `x0`.

See also:

`approx_fprime`

Examples

```python
>>> def func(x):
...     return x[0]**2 - 0.5 * x[1]**3

>>> def grad(x):
...     return [2 * x[0], -1.5 * x[1]**2]

>>> from scipy.optimize import check_grad

>>> check_grad(func, grad, [1.5, -1.5])
2.9802322387695312e-08
```
**Line Search**

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>bracket(func[, xa, xb, args, grow_limit, ...])</code></td>
<td>Bracket the minimum of the function.</td>
</tr>
<tr>
<td><code>line_search(f, myfprime, xk, pk[, gfk, ...])</code></td>
<td>Find alpha that satisfies strong Wolfe conditions.</td>
</tr>
</tbody>
</table>

**scipy.optimize.bracket**

Bracket the minimum of the function.

Given a function and distinct initial points, search in the downhill direction (as defined by the initial points) and return new points xa, xb, xc that bracket the minimum of the function f(xa) > f(xb) < f(xc). It doesn’t always mean that obtained solution will satisfy xa<=x<=xb

**Parameters**

- **func**: [callable f(x,*args)] Objective function to minimize.
- **xa, xb**: [float, optional] Bracketing interval. Defaults xa to 0.0, and xb to 1.0.
- **args**: [tuple, optional] Additional arguments (if present), passed to func.
- **grow_limit**: [float, optional] Maximum grow limit. Defaults to 110.0
- **maxiter**: [int, optional] Maximum number of iterations to perform. Defaults to 1000.

**Returns**

- **xa, xb, xc**: [float] Bracket.
- **fa, fb, fc**: [float] Objective function values in bracket.
- **funcalls**: [int] Number of function evaluations made.

**scipy.optimize.line_search**

Find alpha that satisfies strong Wolfe conditions.

**Parameters**

- **f**: [callable f(x,*args)] Objective function.
- **myfprime**: [callable f'(x,*args)] Objective function gradient.
- **xk**: [ndarray] Starting point.
- **pk**: [ndarray] Search direction.
- **gfk**: [ndarray, optional] Gradient value for x=xk (xk being the current parameter estimate). Will be recomputed if omitted.
- **old_fval**: [float, optional] Function value for x=xk. Will be recomputed if omitted.
- **old_old_fval**: [float, optional] Function value for the point preceding x=xk
- **args**: [tuple, optional] Additional arguments passed to objective function.
- **c1**: [float, optional] Parameter for Armijo condition rule.
- **c2**: [float, optional] Parameter for curvature condition rule.
- **amax**: [float, optional] Maximum step size
- **extra_condition**: [callable, optional] A callable of the form extra_condition(alpha, x, f, g) returning a boolean. Arguments are the proposed step alpha and the corresponding x, f and g values. The line search accepts the value of alpha only if this callable returns True. If the callable returns False for the step length, the algorithm will continue with new iterates. The callable is only called for iterates satisfying the strong Wolfe conditions.
maxiter  [int, optional] Maximum number of iterations to perform

Returns

alpha  [float or None] Alpha for which \(x_{\text{new}} = x_0 + \alpha \cdot p_k\), or None if the line search algorithm did not converge.

fc  [int] Number of function evaluations made.

gc  [int] Number of gradient evaluations made.

new_fval  [float or None] New function value \(f(x_{\text{new}})\) = \(f(x_0 + \alpha \cdot p_k)\), or None if the line search algorithm did not converge.

old_fval  [float] Old function value \(f(x_0)\).

new_slope  [float or None] The local slope along the search direction at the new value \(\langle myfprime(x_{\text{new}}), p_k \rangle\), or None if the line search algorithm did not converge.

Notes

Uses the line search algorithm to enforce strong Wolfe conditions. See Wright and Nocedal, ‘Numerical Optimization’, 1999, pg. 59-60.

For the zoom phase it uses an algorithm by [...].

Hessian Approximation

<table>
<thead>
<tr>
<th>LbfgsInvHessProduct((sk, yk))</th>
<th>Linear operator for the L-BFGS approximate inverse Hessian.</th>
</tr>
</thead>
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scipy.optimize.LbfgsInvHessProduct
class scipy.optimize.LbfgsInvHessProduct\((sk, yk)\)

Linear operator for the L-BFGS approximate inverse Hessian.

This operator computes the product of a vector with the approximate inverse of the Hessian of the objective function, using the L-BFGS limited memory approximation to the inverse Hessian, accumulated during the optimization.

Objects of this class implement the scipy.sparse.linalg.LinearOperator interface.

Parameters

- \(sk\)  [array_like, shape=(n_corr, n)] Array of \(n\_corr\) most recent updates to the solution vector. (See [1]).
- \(yk\)  [array_like, shape=(n_corr, n)] Array of \(n\_corr\) most recent updates to the gradient. (See [1]).

References

[1]

Attributes

- \(H\)  Hermitian adjoint.
- \(T\)  Transpose this linear operator.

Methods

- \(_{\text{call}}\_\(x\)\)  Call self as a function.
- \(adjoint()\)  Hermitian adjoint.
- \(dot(x)\)  Matrix-matrix or matrix-vector multiplication.
Table 134 – continued from previous page

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
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<tbody>
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<td><code>matmat(X)</code></td>
<td>Matrix-matrix multiplication.</td>
</tr>
<tr>
<td><code>matvec(x)</code></td>
<td>Matrix-vector multiplication.</td>
</tr>
<tr>
<td><code>rmatvec(x)</code></td>
<td>Adjoint matrix-vector multiplication.</td>
</tr>
<tr>
<td><code>todense()</code></td>
<td>Return a dense array representation of this operator.</td>
</tr>
<tr>
<td><code>transpose()</code></td>
<td>Transpose this linear operator.</td>
</tr>
</tbody>
</table>

**scipy.optimize.LbfgsInvHessProduct.__call__**

LbfgsInvHessProduct.__call__(x)

Call self as a function.

**scipy.optimize.LbfgsInvHessProduct.adjoint**

LbfgsInvHessProduct.adjoint()

Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns


**scipy.optimize.LbfgsInvHessProduct.dot**

LbfgsInvHessProduct.dot(x)

Matrix-matrix or matrix-vector multiplication.

Parameters

x [array_like] 1-d or 2-d array, representing a vector or matrix.

Returns

Ax [array] 1-d or 2-d array (depending on the shape of x) that represents the result of applying this linear operator on x.

**scipy.optimize.LbfgsInvHessProduct.matmat**

LbfgsInvHessProduct.matmat(X)

Matrix-matrix multiplication.

Performs the operation y=A*X where A is an MxN linear operator and X dense N*K matrix or ndarray.

Parameters

X [{matrix, ndarray}] An array with shape (N,K).

Returns

Y [{matrix, ndarray}] A matrix or ndarray with shape (M,K) depending on the type of the X argument.

Notes

This matmat wraps any user-specified matmat routine or overridden _matmat method to ensure that y has the correct type.
scipy.optimize.LbfgsInvHessProduct.matvec

LbfgsInvHessProduct.matvec(x)
Matrix-vector multiplication.
Performs the operation $y = A^T x$ where $A$ is an MxN linear operator and $x$ is a column vector or 1-d array.

**Parameters**

- **x** [{matrix, ndarray}] An array with shape (N,) or (N,1).

**Returns**

- **y** [{matrix, ndarray}] A matrix or ndarray with shape (M,) or (M,1) depending on the type and shape of the x argument.

**Notes**

This matvec wraps the user-specified matvec routine or overridden _matvec method to ensure that y has the correct shape and type.

scipy.optimize.LbfgsInvHessProduct.rmatvec

LbfgsInvHessProduct.rmatvec(x)
Adjoint matrix-vector multiplication.
Performs the operation $y = A^T x$ where $A$ is an MxN linear operator and $x$ is a column vector or 1-d array.

**Parameters**

- **x** [{matrix, ndarray}] An array with shape (M,) or (M,1).

**Returns**

- **y** [{matrix, ndarray}] A matrix or ndarray with shape (N,) or (N,1) depending on the type and shape of the x argument.

**Notes**

This rmatvec wraps the user-specified rmatvec routine or overridden _rmatvec method to ensure that y has the correct shape and type.

scipy.optimize.LbfgsInvHessProduct.todense

LbfgsInvHessProduct.todense()
Return a dense array representation of this operator.

**Returns**

- **arr** [ndarray, shape=(n, n)] An array with the same shape and containing the same data represented by this LinearOperator.

scipy.optimize.LbfgsInvHessProduct.transpose

LbfgsInvHessProduct.transpose()
Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().
**scipy.optimize.HessianUpdateStrategy**

Class `scipy.optimize.HessianUpdateStrategy`

Interface for implementing Hessian update strategies.

Many optimization methods make use of Hessian (or inverse Hessian) approximations, such as the quasi-Newton methods BFGS, SR1, L-BFGS. Some of these approximations, however, do not actually need to store the entire matrix or can compute the internal matrix product with a given vector in a very efficiently manner. This class serves as an abstract interface between the optimization algorithm and the quasi-Newton update strategies, giving freedom of implementation to store and update the internal matrix as efficiently as possible. Different choices of initialization and update procedure will result in different quasi-Newton strategies.

Four methods should be implemented in derived classes: `initialize`, `update`, `dot` and `get_matrix`.

**Notes**

Any instance of a class that implements this interface, can be accepted by the method `minimize` and used by the compatible solvers to approximate the Hessian (or inverse Hessian) used by the optimization algorithms.

**Methods**

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
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<tbody>
<tr>
<td><code>dot(p)</code></td>
<td>Compute the product of the internal matrix with the given vector.</td>
</tr>
<tr>
<td><code>get_matrix()</code></td>
<td>Return current internal matrix.</td>
</tr>
<tr>
<td><code>initialize(n, approx_type)</code></td>
<td>Initialize internal matrix.</td>
</tr>
<tr>
<td><code>update(delta_x, delta_grad)</code></td>
<td>Update internal matrix.</td>
</tr>
</tbody>
</table>

---

### `scipy.optimize.HessianUpdateStrategy.dot`

**HessianUpdateStrategy.dot(p)**

Compute the product of the internal matrix with the given vector.

**Parameters**

- `p` [array_like] 1-d array representing a vector.

**Returns**

- `Hp` [array] 1-d represents the result of multiplying the approximation matrix by vector `p`.

### `scipy.optimize.HessianUpdateStrategy.get_matrix`

**HessianUpdateStrategy.get_matrix()**

Return current internal matrix.

**Returns**

- `H` [ndarray, shape (n, n)] Dense matrix containing either the Hessian or its inverse (depending on how ‘approx_type’ is defined).

### `scipy.optimize.HessianUpdateStrategy.initialize`

**HessianUpdateStrategy.initialize(n, approx_type)**

Initialize internal matrix.

Allocate internal memory for storing and updating the Hessian or its inverse.

**Parameters**

- `n` [int] Problem dimension.
approx_type
[{'hess', 'inv_hess'}] Selects either the Hessian or the inverse Hessian. When set to ‘hess’ the Hessian will be stored and updated. When set to ‘inv_hess’ its inverse will be used instead.

scipy.optimize.HessianUpdateStrategy.update

HessianUpdateStrategy.update(delta_x, delta_grad)
Update internal matrix.
Update Hessian matrix or its inverse (depending on how ‘approx_type’ is defined) using information about the last evaluated points.

Parameters

delta_x [ndarray] The difference between two points the gradient function have been evaluated at: delta_x = x2 - x1.
delta_grad [ndarray] The difference between the gradients: delta_grad = grad(x2) - grad(x1).

Benchmark Problems

| rosen(x)                                        | The Rosenbrock function. |
| rosen_der(x)                                    | The derivative (i.e.     |
| rosen_hess(x)                                   | The Hessian matrix of the Rosenbrock function. |
| rosen_hess_prod(x, p)                           | Product of the Hessian matrix of the Rosenbrock function with a vector. |

scipy.optimize.rosen
scipy.optimize.rosen(x)
The Rosenbrock function.
The function computed is:

\[
\text{sum}(100.0 * (x[1:] - x[:-1]**2.0)**2.0 + (1 - x[:-1])**2.0)
\]

Parameters

x [array_like] 1-D array of points at which the Rosenbrock function is to be computed.

Returns

f [float] The value of the Rosenbrock function.

See also:

rosen_der, rosen_hess, rosen_hess_prod

Examples

```python
>>> from scipy.optimize import rosen
>>> X = 0.1 * np.arange(10)
>>> rosen(X)
76.56
```
scipy.optimize.rosen_der

scipy.optimize.rosen_der(x)

The derivative (i.e. gradient) of the Rosenbrock function.

**Parameters**

- `x` [array_like] 1-D array of points at which the derivative is to be computed.

**Returns**

- `rosen_der` [(N,) ndarray] The gradient of the Rosenbrock function at x.

**See also:**

rosen, rosen_hess, rosen_hess_prod

scipy.optimize.rosen_hess

scipy.optimize.rosen_hess(x)

The Hessian matrix of the Rosenbrock function.

**Parameters**

- `x` [array_like] 1-D array of points at which the Hessian matrix is to be computed.

**Returns**

- `rosen_hess` [ndarray] The Hessian matrix of the Rosenbrock function at x.

**See also:**

rosen, rosen_der, rosen_hess_prod

scipy.optimize.rosen_hess_prod

scipy.optimize.rosen_hess_prod(x, p)

Product of the Hessian matrix of the Rosenbrock function with a vector.

**Parameters**

- `x` [array_like] 1-D array of points at which the Hessian matrix is to be computed.
- `p` [array_like] 1-D array, the vector to be multiplied by the Hessian matrix.

**Returns**


**See also:**

rosen, rosen_der, rosen_hess

### 6.18.9 Legacy Functions

The functions below are not recommended for use in new scripts; all of these methods are accessible via a newer, more consistent interfaces, provided by the interfaces above.

**Optimization**

General-purpose multivariate methods:
Minimize a function using the downhill simplex algorithm.

Minimize a function using modified Powell’s method.

Minimize a function using a nonlinear conjugate gradient algorithm.

Minimize a function using the BFGS algorithm.

Unconstrained minimization of a function using the Newton-CG method.

Minimize a function using the downhill simplex algorithm. This algorithm only uses function values, not derivatives or second derivatives.

**Parameters**

- **func**
  - [callable func(x,*args)] The objective function to be minimized.
- **x0**
  - [ndarray] Initial guess.
- **args**
  - [tuple, optional] Extra arguments passed to func, i.e. f(x,*args).
- **xtol**
  - [float, optional] Absolute error in xopt between iterations that is acceptable for convergence.
- **ftol**
  - [number, optional] Absolute error in func(xopt) between iterations that is acceptable for convergence.
- **maxiter**
  - [int, optional] Maximum number of iterations to perform.
- **maxfun**
  - [number, optional] Maximum number of function evaluations to make.
- **full_output**
  - [bool, optional] Set to True if fopt and warnflag outputs are desired.
- **disp**
  - [bool, optional] Set to True to print convergence messages.
- **retall**
  - [bool, optional] Set to True to return list of solutions at each iteration.
- **callback**
  - [callable, optional] Called after each iteration, as callback(xk), where xk is the current parameter vector.
- **initial_simplex**
  - [array_like of shape (N + 1, N), optional] Initial simplex. If given, overrides x0. initial_simplex[j,:] should contain the coordinates of the j-th vertex of the N+1 vertices in the simplex, where N is the dimension.

**Returns**

- **xopt**
  - [ndarray] Parameter that minimizes function.
- **fopt**
  - [float] Value of function at minimum: fopt = func(xopt).
- **iter**
  - [int] Number of iterations performed.
- **funcalls**
  - [int] Number of function calls made.
- **warnflag**
  - [int] 1 : Maximum number of function evaluations made. 2 : Maximum number of iterations reached.
- **allvecs**
  - [list] Solution at each iteration.

**See also:**

- minimize
  - Interface to minimization algorithms for multivariate functions. See the ‘Nelder-Mead’ method in particular.
Notes
Uses a Nelder-Mead simplex algorithm to find the minimum of function of one or more variables.

This algorithm has a long history of successful use in applications. But it will usually be slower than
an algorithm that uses first or second derivative information. In practice it can have poor performance
in high-dimensional problems and is not robust to minimizing complicated functions. Additionally,
there currently is no complete theory describing when the algorithm will successfully converge to the
minimum, or how fast it will if it does. Both the ftol and xtol criteria must be met for convergence.

References
[1], [2]

Examples

```python
>>> def f(x):
...     return x**2
```

```python
>>> from scipy import optimize
```

```python
>>> minimum = optimize.fmin(f, 1)
Optimization terminated successfully.
Current function value: 0.000000
Iterations: 17
Function evaluations: 34
>>> minimum[0]
-8.8817841970012523e-16
```

```
scipy.optimize.fmin_powell
```

Minimize a function using modified Powell’s method. This method only uses function values, not
derivatives.

**Parameters**

- `func` [callable f(x,*args)] Objective function to be minimized.
- `x0` [ndarray] Initial guess.
- `args` [tuple, optional] Extra arguments passed to func.
- `callback` [callable, optional] An optional user-supplied function, called after each iteration.
  Called as `callback(xk)`, where `xk` is the current parameter vector.
- `direc` [ndarray, optional] Initial direction set.
- `xtol` [float, optional] Line-search error tolerance.
- `ftol` [float, optional] Relative error in `func(xopt)` acceptable for convergence.
- `maxiter` [int, optional] Maximum number of iterations to perform.
- `maxfun` [int, optional] Maximum number of function evaluations to make.
- `full_output` [bool, optional] If True, fopt, xi, direc, iter, funcalls, and warnflag are returned.
- `disp` [bool, optional] If True, print convergence messages.
- `retall` [bool, optional] If True, return a list of the solution at each iteration.

**Returns**

- `xopt` [ndarray] Parameter which minimizes `func`.
- `fopt` [number] Value of function at minimum: `fopt = func(xopt)`.
- `iter` [int] Number of iterations.
- `funcalls` [int] Number of function calls made.
warnflag [int]

Integer warning flag:

1 : Maximum number of function evaluations. 2 : Maximum number of iterations.

allvecs [list] List of solutions at each iteration.

See also:

minimize

Interface to unconstrained minimization algorithms for multivariate functions. See the ‘Powell’ method in particular.

Notes
Uses a modification of Powell’s method to find the minimum of a function of N variables. Powell’s method is a conjugate direction method.

The algorithm has two loops. The outer loop merely iterates over the inner loop. The inner loop minimizes over each current direction in the direction set. At the end of the inner loop, if certain conditions are met, the direction that gave the largest decrease is dropped and replaced with the difference between the current estimated x and the estimated x from the beginning of the inner-loop.

The technical conditions for replacing the direction of greatest increase amount to checking that

1. No further gain can be made along the direction of greatest increase from that iteration.

2. The direction of greatest increase accounted for a large sufficient fraction of the decrease in the function value from that iteration of the inner loop.

References


Examples

```python
>>> def f(x):
...     return x**2

>>> from scipy import optimize

>>> minimum = optimize.fmin_powell(f, -1)
Optimization terminated successfully.
    Current function value: 0.000000
    Iterations: 2
    Function evaluations: 18

>>> minimum
array(0.0)
```

scipy.optimize.fmin_cg

Minimize a function using a nonlinear conjugate gradient algorithm.

Parameters

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**f** [callable, f(x, *args)] Objective function to be minimized. Here x must be a 1-D array of the variables that are to be changed in the search for a minimum, and args are the other (fixed) parameters of f.

**x0** [ndarray] A user-supplied initial estimate of xopt, the optimal value of x. It must be a 1-D array of values.

**fprime** [callable, fprime(x, *args), optional] A function that returns the gradient of f at x. Here x and args are as described above for f. The returned value must be a 1-D array. Defaults to None, in which case the gradient is approximated numerically (see epsilon, below).

**args** [tuple, optional] Parameter values passed to f and fprime. Must be supplied whenever additional fixed parameters are needed to completely specify the functions f and fprime.

**gtol** [float, optional] Stop when the norm of the gradient is less than gtol.

**norm** [float, optional] Order to use for the norm of the gradient (\(-\infty\) is min, \(+\infty\) is max).

**epsilon** [float or ndarray, optional] Step size(s) to use when fprime is approximated numerically. Can be a scalar or a 1-D array. Defaults to \(\sqrt{\text{eps}}\), with eps the floating point machine precision. Usually \(\sqrt{\text{eps}}\) is about 1.5e-8.

**maxiter** [int, optional] Maximum number of iterations to perform. Default is \(200 \times \text{len}(x0)\).

**full_output** [bool, optional] If True, return xopt, func_calls, grad_calls, and warnflag in addition to xopt. See the Returns section below for additional information on optional return values.

**disp** [bool, optional] If True, return a convergence message, followed by xopt.

**retall** [bool, optional] If True, add to the returned values the results of each iteration. Called as callback(xk), where xk is the current value of x0.

**callback** [callable, optional] An optional user-supplied function, called after each iteration.

**Returns**

**xopt** [ndarray] Parameters which minimize f, i.e. \(f(xopt) \approx fopt\).

**fopt** [float, optional] Minimum value found, f(xopt). Only returned if full_output is True.

**func_calls** [int, optional] The number of function_calls made. Only returned if full_output is True.

**grad_calls** [int, optional] The number of gradient calls made. Only returned if full_output is True.

**warnflag** [int, optional] Integer value with warning status, only returned if full_output is True. 0 : Success. 1 : The maximum number of iterations was exceeded. 2 [Gradient and/or function calls were not changing. May indicate] that precision was lost, i.e., the routine did not converge.

**allvecs** [list of ndarray, optional] List of arrays, containing the results at each iteration. Only returned if retall is True.

See also:

**minimize**

The common interface to all scipy.optimize algorithms for unconstrained and constrained minimization of multivariate functions. It provides an alternative way to call fmin_cg, by specifying method='CG'.

---

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Notes
This conjugate gradient algorithm is based on that of Polak and Ribiere [1].

Conjugate gradient methods tend to work better when:

1. \( f \) has a unique global minimizing point, and no local minima or other stationary points,
2. \( f \) is, at least locally, reasonably well approximated by a quadratic function of the variables,
3. \( f \) is continuous and has a continuous gradient,
4. \( f' \) is not too large, e.g., has a norm less than 1000,
5. The initial guess, \( x_0 \), is reasonably close to \( f \)'s global minimizing point, \( x_{opt} \).

References
[1]

Examples
Example 1: seek the minimum value of the expression \( a*u^2 + b*u*v + c*v^2 + d*u + e*v + f \) for given values of the parameters and an initial guess \((u, v) = (0, 0)\).

```python
>>> args = (2, 3, 7, 8, 9, 10)  # parameter values
>>> def f(x, *args):
...     u, v = x
...     a, b, c, d, e, f = args
...     return a*u**2 + b*u*v + c*v**2 + d*u + e*v + f
>>> def gradf(x, *args):
...     u, v = x
...     a, b, c, d, e, f = args
...     gu = 2*a*u + b*v + d  # u-component of the gradient
...     gv = b*u + 2*c*v + e  # v-component of the gradient
...     return np.asarray((gu, gv))
>>> x0 = np.asarray((0, 0))  # Initial guess.
>>> from scipy import optimize
>>> res1 = optimize.fmin_cg(f, x0, fprime=gradf, args=args)
Optimization terminated successfully.
Current function value: 1.617021
Iterations: 4
Function evaluations: 8
Gradient evaluations: 8
>>> res1
array([-1.80851064, -0.25531915])
```

Example 2: solve the same problem using the \texttt{minimize} function. (This \texttt{myopts} dictionary shows all of the available options, although in practice only non-default values would be needed. The returned value will be a dictionary.)

```python
>>> opts = {'maxiter': None,  # default value.
...         'disp': True,  # non-default value.
...         'gtol': 1e-5,  # default value.
...         'norm': np.inf,  # default value.
...         'eps': 1.4901161193847656e-08}  # default value.
>>> res2 = optimize.minimize(f, x0, jac=gradf, args=args,
...                           method='CG', options=opts)
Optimization terminated successfully.
Current function value: 1.617021
Iterations: 4
```

(continues on next page)
Function evaluations: 8
Gradient evaluations: 8

```
res2.x # minimum found
array([-1.80851064, -0.25531915])
```

**scipy.optimize.fmin_bfgs**

```python
scipy.optimize.fmin_bfgs(f, x0, fprime=None, args=(), gtol=1e-05, norm=np.inf,
epsilon=1.4901161193847656e-08, maxiter=None, full_output=0,
disp=1, retall=0, callback=None)
```

Minimize a function using the BFGS algorithm.

**Parameters**

- `f` [callable f(x,*args)] Objective function to be minimized.
- `x0` [ndarray] Initial guess.
- `fprime` [callable f'(x,*args), optional] Gradient of f.
- `args` [tuple, optional] Extra arguments passed to f and fprime.
- `gtol` [float, optional] Gradient norm must be less than gtol before successful termination.
- `norm` [float, optional] Order of norm (Inf is max, -Inf is min)
- `epsilon` [int or ndarray, optional] If fprime is approximated, use this value for the step size.
- `callback` [callable, optional] An optional user-supplied function to call after each iteration. Called as callback(xk), where xk is the current parameter vector.
- `maxiter` [int, optional] Maximum number of iterations to perform.
- `full_output` [bool, optional] If True, return fopt, func_calls, grad_calls, and warnflag in addition to xopt.
- `disp` [bool, optional] Print convergence message if True.
- `retall` [bool, optional] Return a list of results at each iteration if True.

**Returns**

- `xopt` [ndarray] Parameters which minimize f, i.e. f(xopt) == fopt.
- `gopt` [ndarray] Value of gradient at minimum, f'(xopt), which should be near 0.
- `Bopt` [ndarray] Value of 1/f''(xopt), i.e. the inverse hessian matrix.
- `func_calls` [int] Number of function calls made.
- `grad_calls` [int] Number of gradient calls made.
- `warnflag` [integer] 1: Maximum number of iterations exceeded. 2: Gradient and/or function calls not changing.
- `allvecs` [list] The value of xopt at each iteration. Only returned if retall is True.

See also:

**minimize**

Interface to minimization algorithms for multivariate functions. See the ‘BFGS’ method in particular.

**Notes**

Optimize the function, f, whose gradient is given by fprime using the quasi-Newton method of Broyden, Fletcher, Goldfarb, and Shanno (BFGS)

**References**

Unconstrained minimization of a function using the Newton-CG method.

Parameters

- **f**: [callable f(x, *args)] Objective function to be minimized.
- **x0**: [ndarray] Initial guess.
- **fprime**: [callable f'(x, *args)] Gradient of f.
- **fhess_p**: [callable fhess_p(x, p, *args), optional] Function which computes the Hessian of f times an arbitrary vector, p.
- **fhess**: [callable fhess(x, *args), optional] Function to compute the Hessian matrix of f.
- **args**: [tuple, optional] Extra arguments passed to f, fprime, fhess_p, and fhess (the same set of extra arguments is supplied to all of these functions).
- **epsilon**: [float or ndarray, optional] If fhess is approximated, use this value for the step size.
- **callback**: [callable, optional] An optional user-supplied function which is called after each iteration. Called as callback(xk), where xk is the current parameter vector.
- **avextol**: [float, optional] Convergence is assumed when the average relative error in the minimizer falls below this amount.
- **maxiter**: [int, optional] Maximum number of iterations to perform.
- **full_output**: [bool, optional] If True, return the optional outputs.
- **disp**: [bool, optional] If True, print convergence message.
- **retall**: [bool, optional] If True, return a list of results at each iteration.

Returns

- **xopt**: [ndarray] Parameters which minimize f, i.e. f(xopt) == fopt.
- **fopt**: [float] Value of the function at xopt, i.e. fopt = f(xopt).
- **fcalls**: [int] Number of function calls made.
- **gcalls**: [int] Number of gradient calls made.
- **hcalls**: [int] Number of hessian calls made.
- **warnflag**: [int] Warnings generated by the algorithm. 1: Maximum number of iterations exceeded.
- **allvecs**: [list] The result at each iteration, if retall is True (see below).

See also:

**minimize**

Interface to minimization algorithms for multivariate functions. See the ‘Newton-CG’ method in particular.

Notes

Only one of fhess_p or fhess need to be given. If fhess is provided, then fhess_p will be ignored. If neither fhess nor fhess_p is provided, then the hessian product will be approximated using finite differences on fprime. fhess_p must compute the hessian times an arbitrary vector. If it is not given, finite-differences on fprime are used to compute it.

Newton-CG methods are also called truncated Newton methods. This function differs from scipy.optimize.fmin_tnc because

1. **scipy.optimize.fmin_ncg is written purely in python using numpy** and scipy while scipy.optimize.fmin_tnc calls a C function.
2. **scipy.optimize.fmin_ncg is only for unconstrained minimization**

while scipy.optimize.fmin_tnc is for unconstrained minimization or box constrained minimization. (Box constraints give lower and upper bounds for each variable separately.)

**References**


Constrained multivariate methods:

- `fmin_l_bfgs_b(func, x0[, fprime, args, ...])` Minimize a function func using the L-BFGS-B algorithm.

- `fmin_tnc(func, x0[, fprime, args, ...])` Minimize a function with variables subject to bounds, using gradient information in a truncated Newton algorithm.

- `fmin_cobyla(func, x0, cons[, args, ...])` Minimize a function using the Constrained Optimization BY Linear Approximation (COBYLA) method.

- `fmin_slsqp(func, x0[, eqcons, f_eqcons, ...])` Minimize a function using Sequential Least SQUares Programming.

- `differential_evolution(func, bounds[, args, ...])` Finds the global minimum of a multivariate function.

**scipy.optimize.fmin_l_bfgs_b**

```python
scipy.optimize.fmin_l_bfgs_b(func, x0, fprime=None, args=(), approx_grad=0, bounds=None, m=10, factr=10000000.0, pgtol=1e-05, epsilon=1e-08, iprint=-1, maxfun=15000, maxiter=15000, disp=None, callback=None, maxls=20)
```

Minimize a function func using the L-BFGS-B algorithm.

**Parameters**

- `func` [callable f(x,*args)] Function to minimise.
- `x0` [ndarray] Initial guess.
- `fprime` [callable fprime(x,*args), optional] The gradient of `func`. If None, then `func` returns the function value and the gradient (f, g = func(x, *args)), unless `approx_grad` is True in which case `func` returns only `f`.
- `args` [sequence, optional] Arguments to pass to `func` and `fprime`.
- `approx_grad` [bool, optional] Whether to approximate the gradient numerically (in which case `func` returns only the function value).
- `bounds` [list, optional] `(min, max)` pairs for each element in `x`, defining the bounds on that parameter. Use None or `+inf` for one of `min` or `max` when there is no bound in that direction.
- `m` [int, optional] The maximum number of variable metric corrections used to define the limited memory matrix. (The limited memory BFGS method does not store the full hessian but uses this many terms in an approximation to it.)
- `factr` [float, optional] The iteration stops when `(f^k - f^{k+1})/max{|f^k|, |f^k-1|, 1} <= factr * eps`, where `eps` is the machine precision, which is automatically generated by the code. Typical values for `factr` are: 1e12 for low accuracy; 1e7 for moderate accuracy; 10.0 for extremely high accuracy. See Notes for relationship to `ftol`, which is exposed (instead of `factr`) by the `scipy.optimize.minimize` interface to L-BFGS-B.
- `pgtol` [float, optional] The iteration will stop when `max{|proj g_i | i = 1, ..., n} <= pgtol` where `pg_i` is the i-th component of the projected gradient.
epsilon [float, optional] Step size used when approx_grad is True, for numerically calculating the gradient

iprint [int, optional] Controls the frequency of output. iprint < 0 means no output; iprint = 0 print only one line at the last iteration; 0 < iprint < 99 print also f and [proj g] every iprint iterations; iprint = 99 print details of every iteration except n-vectors; iprint = 100 print also the changes of active set and final x; iprint > 100 print details of every iteration including x and g.

disp [int, optional] If zero, then no output. If a positive number, then this over-rides iprint (i.e., iprint gets the value of disp).

maxfun [int, optional] Maximum number of function evaluations.

maxiter [int, optional] Maximum number of iterations.

callback [callable, optional] Called after each iteration, as callback(xk), where xk is the current parameter vector.

maxls [int, optional] Maximum number of line search steps (per iteration). Default is 20.

Returns

x [array_like] Estimated position of the minimum.

f [float] Value of func at the minimum.

d [dict] Information dictionary.
- d['warnflag'] is
  - 0 if converged,
  - 1 if too many function evaluations or too many iterations,
  - 2 if stopped for another reason, given in d['task']
- d['grad'] is the gradient at the minimum (should be 0 ish)
- d['funcalls'] is the number of function calls made.
- d['nit'] is the number of iterations.

See also:

minimize

Interface to minimization algorithms for multivariate functions. See the ‘L-BFGS-B’ method in particular. Note that the ftol option is made available via that interface, while factr is provided via this interface, where factr is the factor multiplying the default machine floating-point precision to arrive at ftol: ftol = factr * numpy.finfo(float).eps.

Notes

License of L-BFGS-B (FORTRAN code):

The version included here (in fortran code) is 3.0 (released April 25, 2011). It was written by Ciyou Zhu, Richard Byrd, and Jorge Nocedal <nocedal@ece.nwu.edu>. It carries the following condition for use:

This software is freely available, but we expect that all publications describing work using this software, or all commercial products using it, quote at least one of the references given below. This software is released under the BSD License.

References

scipy.optimize.fmin_tnc

scipy.optimize.fmin_tnc(func, x0, fprime=None, args=(), approx_grad=0, bounds=None, epsilon=1e-08, scale=None, offset=None, messages=15, maxCGit=-1, maxfun=None, eta=-1, stepmx=0, accuracy=0, fmin=0, ftol=-1, xtol=-1, pgtol=-1, rescale=-1, disp=None, callback=None)

Minimize a function with variables subject to bounds, using gradient information in a truncated Newton algorithm. This method wraps a C implementation of the algorithm.

**Parameters**

- **func** ([callable func(x, *args)]) Function to minimize. Must do one of:
  1. Return f and g, where f is the value of the function and g its gradient (a list of floats).
  2. Return the function value but supply gradient function separately as fprime.
  3. Return the function value and set approx_grad=True.

- **x0** ([array_like]) Initial estimate of minimum.

- **fprime** ([callable fprime(x, *args)], optional) Gradient of func. If None, then either func must return the function value and the gradient (f, g = func(x, *args)) or approx_grad must be True.

- **args** ([tuple, optional]) Arguments to pass to function.

- **approx_grad** ([bool, optional]) If true, approximate the gradient numerically.

- **bounds** ([list, optional]) (min, max) pairs for each element in x0, defining the bounds on that parameter. Use None or +/-inf for one of min or max when there is no bound in that direction.

- **epsilon** ([float, optional]) Used if approx_grad is True. The stepsize in a finite difference approximation for fprime.

- **scale** ([array_like, optional]) Scaling factors to apply to each variable. If None, the factors are up-low for interval bounded variables and 1+|x| for the others. Defaults to None.

- **offset** ([array_like, optional]) Value to subtract from each variable. If None, the offsets are (up+low)/2 for interval bounded variables and x for the others.

- **messages** ([int, optional]) Bit mask used to select messages display during minimization values defined in the MSGS dict. Defaults to MGS_ALL.

- **disp** ([int, optional]) Integer interface to messages. 0 = no message, 5 = all messages

- **maxCGit** ([int, optional]) Maximum number of hessian*vector evaluations per main iteration. If maxCGit == 0, the direction chosen is -gradient if maxCGit < 0, maxCGit is set to max(1, min(50, n/2)). Defaults to -1.

- **maxfun** ([int, optional]) Maximum number of function evaluation. if None, maxfun is set to max(100, 10*len(x0)). Defaults to None.

- **eta** ([float, optional]) Severity of the line search. if < 0 or > 1, set to 0.25. Defaults to -1.

- **stepmx** ([float, optional]) Maximum step for the line search. May be increased during call. If too small, it will be set to 10.0. Defaults to 0.

- **accuracy** ([float, optional]) Relative precision for finite difference calculations. If <= machine_precision, set to sqrt(machine_precision). Defaults to 0.

- **fmin** ([float, optional]) Minimum function value estimate. Defaults to 0.

- **ftol** ([float, optional]) Precision goal for the value of f in the stopping criterion. If ftol < 0.0, ftol is set to 0.0 defaults to -1.

- **xtol** ([float, optional]) Precision goal for the value of x in the stopping criterion (after applying x scaling factors). If xtol < 0.0, xtol is set to sqrt(machine_precision). Defaults to -1.
pgtol  [float, optional] Precision goal for the value of the projected gradient in the stopping
        criterion (after applying x scaling factors). If pgtol < 0.0, pgtol is set to 1e-2 *
        sqrt(accuracy). Setting it to 0.0 is not recommended. Defaults to -1.
rescale  [float, optional] Scaling factor (in log10) used to trigger f value rescaling. If 0,
        rescale at each iteration. If a large value, never rescale. If < 0, rescale is set to 1.3.
callback  [callable, optional] Called after each iteration, as callback(xk), where xk is the
        current parameter vector.

Returns

x  [ndarray] The solution.
nfeval  [int] The number of function evaluations.
rc  [int] Return code, see below

See also:

minimize

Interface to minimization algorithms for multivariate functions. See the ‘TNC’ method in particular.

Notes

The underlying algorithm is truncated Newton, also called Newton Conjugate-Gradient. This method
differs from scipy.optimize.fmin_ncg in that

1. It wraps a C implementation of the algorithm
2. It allows each variable to be given an upper and lower bound.
The algorithm incorporates the bound constraints by determining the descent direction as in an uncon-
strained truncated Newton, but never taking a step-size large enough to leave the space of feasible x’s.
The algorithm keeps track of a set of currently active constraints, and ignores them when computing
the minimum allowable step size. (The x’s associated with the active constraint are kept fixed.) If the
maximum allowable step size is zero then a new constraint is added. At the end of each iteration one
of the constraints may be deemed no longer active and removed. A constraint is considered no longer
active is if it is currently active but the gradient for that variable points inward from the constraint.
The specific constraint removed is the one associated with the variable of largest index whose constraint
is no longer active.

Return codes are defined as follows:

-1 : Infeasible (lower bound > upper bound)
  0 : Local minimum reached (|pg| -= 0)
  1 : Converged (|f_n-f_(n-1)| -= 0)
  2 : Converged (|x_n-x_(n-1)| -= 0)
  3 : Max. number of function evaluations reached
  4 : Linear search failed
  5 : All lower bounds are equal to the upper bounds
  6 : Unable to progress
  7 : User requested end of minimization

References

Wright S., Nocedal J. (2006), ‘Numerical Optimization’

Analysis 21, pp. 770-778
**scipy.optimize.fmin_cobyla**

Minimize a function using the Constrained Optimization BY Linear Approximation (COBYLA) method. This method wraps a FORTRAN implementation of the algorithm.

**Parameters**

- **func** *(callable)* Function to minimize. In the form func(x, *args).
- **x0** *(ndarray)* Initial guess.
- **cons** *(sequence)* Constraint functions; must all be >=0 (a single function if only 1 constraint). Each function takes the parameters x as its first argument, and it can return either a single number or an array or list of numbers.
- **args** *(tuple, optional)* Extra arguments to pass to function.
- **consargs** *(tuple, optional)* Extra arguments to pass to constraint functions (default of None means use same extra arguments as those passed to func). Use () for no extra arguments.
- **rhobeg** *(float, optional)* Reasonable initial changes to the variables.
- **rhoend** *(float, optional)* Final accuracy in the optimization (not precisely guaranteed). This is a lower bound on the size of the trust region.
- **disp** *(0, 1, 2, 3, optional)* Controls the frequency of output; 0 implies no output.
- **maxfun** *(int, optional)* Maximum number of function evaluations.
- **catol** *(float, optional)* Absolute tolerance for constraint violations.

**Returns**

- **x** *(ndarray)* The argument that minimises f.

See also:

- **minimize**

  Interface to minimization algorithms for multivariate functions. See the ‘COBYLA’ method in particular.

**Notes**

This algorithm is based on linear approximations to the objective function and each constraint. We briefly describe the algorithm.

Suppose the function is being minimized over k variables. At the jth iteration the algorithm has k+1 points v_1, ..., v_(k+1), an approximate solution x_j, and a radius RHO_j. (i.e. linear plus a constant) approximations to the objective function and constraint functions such that their function values agree with the linear approximation on the k+1 points v_1,.., v_(k+1). This gives a linear program to solve (where the linear approximations of the constraint functions are constrained to be non-negative).

However the linear approximations are likely only good approximations near the current simplex, so the linear program is given the further requirement that the solution, which will become x_(j+1), must be within RHO_j from x_j. RHO_j only decreases, never increases. The initial RHO_j is rhobeg and the final RHO_j is rhoend. In this way COBYLA's iterations behave like a trust region algorithm.

Additionally, the linear program may be inconsistent, or the approximation may give poor improvement. For details about how these issues are resolved, as well as how the points v_j are updated, refer to the source code or the references below.

**References**


Examples

Minimize the objective function \( f(x,y) = x^*y \) subject to the constraints \( x^2 + y^2 < 1 \) and \( y > 0 \):

```python
>>> def objective(x):
...   return x[0]*x[1]
...
>>> def constr1(x):
...   return 1 - (x[0]**2 + x[1]**2)
...
>>> def constr2(x):
...   return x[1]
...
>>> from scipy.optimize import fmin_cobyla
>>> fmin_cobyla(objective, [0.0, 0.1], [constr1, constr2], rhoend=1e-7)
array([-0.70710685, 0.70710671])
```

The exact solution is \((-\sqrt{2})/2, \sqrt{2}/2\).

**scipy.optimize.fmin_slsqp**

Python interface function for the SLSQP Optimization subroutine originally implemented by Dieter Kraft.

**Parameters**

- `func` [callable f(x,*args)] Objective function. Must return a scalar.
- `x0` [1-D ndarray of float] Initial guess for the independent variable(s).
- `eqcons` [list, optional] A list of functions of length n such that eqcons[j](x,*args) == 0.0 in a successfully optimized problem.
- `f_eqcons` [callable f(x,*args), optional] Returns a 1-D array in which each element must equal 0.0 in a successfully optimized problem. If f_eqcons is specified, eqcons is ignored.
- `ieqcons` [list, optional] A list of functions of length n such that ieqcons[j](x,*args) >= 0.0 in a successfully optimized problem.
- `f_ieqcons` [callable f(x,*args), optional] Returns a 1-D ndarray in which each element must be greater or equal to 0.0 in a successfully optimized problem. If f_ieqcons is specified, ieqcons is ignored.
- `bounds` [list, optional] A list of tuples specifying the lower and upper bound for each independent variable [(x0l, xu0),(x1l, xu1),...]. Infinite values will be interpreted as large floating values.
- `fprime` [callable f(x,*args), optional] A function that evaluates the partial derivatives of func.
- `fprime_eqcons` [callable f(x,*args), optional] A function that returns the m by n array of equality constraint normals. If not provided, the normals will be ap-

6.18. Optimization and Root Finding (scipy.optimize)
proximated. The array returned by fprime_eqcons should be sized as \( \text{len(eqcons)}, \text{len(x0)} \).

**fprime_eqcons**

[callable \( f(x, *args) \), optional] A function of the form \( f(x, *args) \) that returns the \( m \) by \( n \) array of inequality constraint normals. If not provided, the normals will be approximated. The array returned by fprime_eqcons should be sized as \( \text{len(ieqcons)}, \text{len(x0)} \).

**args** [sequence, optional] Additional arguments passed to func and fprime.

**iter** [int, optional] The maximum number of iterations.

**acc** [float, optional] Requested accuracy.

**iprint** [int, optional] The verbosity of fmin_slsqp:
- \( \text{iprint} \leq 0 \): Silent operation
- \( \text{iprint} == 1 \): Print summary upon completion (default)
- \( \text{iprint} \geq 2 \): Print status of each iterate and summary

**disp** [int, optional] Over-rides the iprint interface (preferred).

**full_output** [bool, optional] If False, return only the minimizer of func (default). Otherwise, output final objective function and summary information.

**epsilon** [float, optional] The step size for finite-difference derivative estimates.

**callback** [callable, optional] Called after each iteration, as \( \text{callback}(x) \), where \( x \) is the current parameter vector.

### Returns

- **out** [ndarray of float] The final minimizer of func.
- **fx** [ndarray of float, if full_output is true] The final value of the objective function.
- **its** [int, if full_output is true] The number of iterations.
- **imode** [int, if full_output is true] The exit mode from the optimizer (see below).
- **smode** [string, if full_output is true] Message describing the exit mode from the optimizer.

### See also:

**minimize**

Interface to minimization algorithms for multivariate functions. See the ‘SLSQP’ method in particular.

### Notes

Exit modes are defined as follows:

- \(-1\): Gradient evaluation required \((g \& a)\)
- \(0\): Optimization terminated successfully.
- \(1\): Function evaluation required \((f \& c)\)
- \(2\): More equality constraints than independent variables
- \(3\): More than \(3*n\) iterations in LSQ subproblem
- \(4\): Inequality constraints incompatible
- \(5\): Singular matrix \(E\) in LSQ subproblem
- \(6\): Singular matrix \(C\) in LSQ subproblem
- \(7\): Rank-deficient equality constraint subproblem HFTI
- \(8\): Positive directional derivative for linesearch
- \(9\): Iteration limit exceeded

### Examples

Examples are given in the tutorial.

Univariate (scalar) minimization methods:
**fminbound** *(func, x1, x2[, args, xtol, ...])*

Bounded minimization for scalar functions.

**brent** *(func[, args, brack, tol, full_output, ...])*

Given a function of one-variable and a possible bracket, return the local minimum of the function isolated to a fractional precision of tol.

**golden** *(func[, args, brack, tol, ...])*

Return the minimum of a function of one variable using golden section method.

---

**scipy.optimize.fminbound**

**scipy.optimize.fminbound** *(func, x1, x2, args=(), xtol=1e-05, maxfun=500, full_output=0, disp=1)*

Bounded minimization for scalar functions.

**Parameters**

- **func** *(callable f(x,*args)*) Objective function to be minimized (must accept and return scalars).
- **x1, x2** *(float or array scalar)* The optimization bounds.
- **args** *(tuple, optional)* Extra arguments passed to function.
- **xtol** *(float, optional)* The convergence tolerance.
- **maxfun** *(int, optional)* Maximum number of function evaluations allowed.
- **full_output** *(bool, optional)* If True, return optional outputs.
- **disp** *(int, optional)*
  
  If non-zero, print messages.
  
  - 0: no message printing.
  - 1: non-convergence notification messages only.
  - 2: print a message on convergence too.
  - 3: print iteration results.

**Returns**

- **xopt** *(ndarray)* Parameters (over given interval) which minimize the objective function.
- **fval** *(number)* The function value at the minimum point.
- **ierr** *(int)* An error flag (0 if converged, 1 if maximum number of function calls reached).
- **numfunc** *(int)* The number of function calls made.

**See also:**

- **minimize_scalar**
  Interface to minimization algorithms for scalar univariate functions. See the ‘Bounded’ method in particular.

**Notes**

Finds a local minimizer of the scalar function *func* in the interval *x1 < xopt < x2* using Brent’s method. (See **brent** for auto-bracketing).

**Examples**

**fminbound** finds the minimum of the function in the given range. The following examples illustrate the same.

```python
>>> def f(x):
...   return x**2
```

```python
golden(f, -1, 2)
```

(continues on next page)
0.0

```python
>>> minimum = optimize.fminbound(f, 1, 2)
>>> minimum
1.0000059608609866
```

scipy.optimize.brent

`scipy.optimize.brent(func, args=(), brack=None, tol=1.48e-08, full_output=0, maxiter=500)`

Given a function of one-variable and a possible bracket, return the local minimum of the function isolated to a fractional precision of `tol`.

**Parameters**

- `func` [callable f(x,*args)] Objective function.
- `args` [tuple, optional] Additional arguments (if present).
- `brack` [tuple, optional] Either a triple (xa,xb,xc) where xa<xb<xc and func(xb) < func(xa), func(xc) or a pair (xa,xb) which are used as a starting interval for a downhill bracket search (see `bracket`). Providing the pair (xa,xb) does not always mean the obtained solution will satisfy xa<xe<=xb.
- `tol` [float, optional] Stop if between iteration change is less than `tol`.
- `full_output` [bool, optional] If True, return all output args (xmin, fval, iter, funcalls).
- `maxiter` [int, optional] Maximum number of iterations in solution.

**Returns**

- `xmin` [ndarray] Optimum point.
- `fval` [float] Optimum value.
- `iter` [int] Number of iterations.
- `funcalls` [int] Number of objective function evaluations made.

**See also:**

`minimize_scalar`

Interface to minimization algorithms for scalar univariate functions. See the ‘Brent’ method in particular.

**Notes**

Uses inverse parabolic interpolation when possible to speed up convergence of golden section method.

Does not ensure that the minimum lies in the range specified by `brack`. See `fminbound`.

**Examples**

We illustrate the behaviour of the function when `brack` is of size 2 and 3 respectively. In the case where `brack` is of the form (xa,xb), we can see for the given values, the output need not necessarily lie in the range (xa,xb).

```python
>>> def f(x):
...    return x**2

>>> from scipy import optimize

>>> minimum = optimize.brent(f,brack=(1,2))
>>> minimum
0.0
>>> minimum = optimize.brent(f,brack=(-1,0.5,2))
```

(continues on next page)
Return the minimum of a function of one variable using golden section method.

Given a function of one variable and a possible bracketing interval, return the minimum of the function isolated to a fractional precision of tol.

Parameters

- **func**: [callable func(x,*args)] Objective function to minimize.
- **args**: [tuple, optional] Additional arguments (if present), passed to func.
- **brack**: [tuple, optional] Triple (a,b,c), where (a<b<c) and func(b) < func(a),func(c). If bracket consists of two numbers (a, c), then they are assumed to be a starting interval for a downhill bracket search (see bracket); it doesn’t always mean that obtained solution will satisfy a<=x<=c.
- **tol**: [float, optional] x tolerance stop criterion
- **full_output**: [bool, optional] If True, return optional outputs.
- **maxiter**: [int] Maximum number of iterations to perform.

See also:

**minimize_scalar**

Interface to minimization algorithms for scalar univariate functions. See the ‘Golden’ method in particular.

Notes

Uses analog of bisection method to decrease the bracketed interval.

Examples

We illustrate the behaviour of the function when brack is of size 2 and 3 respectively. In the case where brack is of the form (xa,xb), we can see for the given values, the output need not necessarily lie in the range (xa, xb).

```python
>>> def f(x):
...     return x**2

>>> from scipy import optimize

>>> minimum = optimize.golden(f, brack=(1, 2))
>>> minimum
1.5712777884848732e-162
>>> minimum = optimize.golden(f, brack=(-1, 0.5, 2))
>>> minimum
-1.5712777884848732e-162
```

Least-Squares
**leastsq**(*func*, *x0*, *args*, *Dfun*, *full_output*, ...)  
Minimize the sum of squares of a set of equations.

**scipy.optimize.leastsq**

```
scipy.optimize.leastsq(func, x0, args=(), Dfun=None, full_output=0, col_deriv=0,
                        ftol=1.49012e-08, xtol=1.49012e-08, gtol=0.0, maxfev=0,
                        factor=100, diag=None)
```

Minimize the sum of squares of a set of equations.

```
x = arg min(sum(func(y)**2,axis=0))
y
```

**Parameters**

- **func**  
  [callable] should take at least one (possibly length N vector) argument and returns M floating point numbers. It must not return NaNs or fitting might fail.

- **x0**  
  [ndarray] The starting estimate for the minimization.

- **args**  
  [tuple, optional] Any extra arguments to func are placed in this tuple.

- **Dfun**  
  [callable, optional] A function or method to compute the Jacobian of func with derivatives across the rows. If this is None, the Jacobian will be estimated.

- **full_output**  
  [bool, optional] non-zero to return all optional outputs.

- **col_deriv**  
  [bool, optional] non-zero to specify that the Jacobian function computes derivatives down the columns (faster, because there is no transpose operation).

- **ftol**  
  [float, optional] Relative error desired in the sum of squares.

- **xtol**  
  [float, optional] Relative error desired in the approximate solution.

- **gtol**  
  [float, optional] Orthogonality desired between the function vector and the columns of the Jacobian.

- **maxfev**  
  [int, optional] The maximum number of calls to the function. If Dfun is provided then the default maxfev is 100*(N+1) where N is the number of elements in x0, otherwise the default maxfev is 200*(N+1).

- **epsfcn**  
  [float, optional] A variable used in determining a suitable step length for the forward difference approximation of the Jacobian (for Dfun=None). Normally the actual step length will be sqrt(epsfcn)*x If epsfcn is less than the machine precision, it is assumed that the relative errors are of the order of the machine precision.

- **factor**  
  [float, optional] A parameter determining the initial step bound (factor * || diag * x||). Should be in interval (0.1, 100).

- **diag**  
  [sequence, optional] N positive entries that serve as a scale factors for the variables.

**Returns**

- **x**  
  [ndarray] The solution (or the result of the last iteration for an unsuccessful call).

- **cov_x**  
  [ndarray] Uses the fjac and ipvt optional outputs to construct an estimate of the Jacobian around the solution. None if a singular matrix encountered (indicates very flat curvature in some direction). This matrix must be multiplied by the residual variance to get the covariance of the parameter estimates – see curve_fit.

- **infodict**  
  [dict] a dictionary of optional outputs with the key s:

  - **nf`ev**  
    The number of function calls

  - **f`vec**  
    The function evaluated at the output

  - **f`jac**  
    A permutation of the R matrix of a QR factorization of the final approximate Jacobian matrix, stored column wise. Together with ipvt, the covariance of the estimate can be approximated.
**Notes**

“leastsq” is a wrapper around MINPACK’s lmdif and lmder algorithms.

cov_x is a Jacobian approximation to the Hessian of the least squares objective function. This approximation assumes that the objective function is based on the difference between some observed target data (ydata) and a (non-linear) function of the parameters \( f(xdata, params) \)

\[
\text{func}(params) = ydata - f(xdata, params)
\]

so that the objective function is

\[
\min_{params} \sum ((ydata - f(xdata, params))**2, \text{axis}=0)
\]

The solution, \( x \), is always a 1D array, regardless of the shape of \( x0 \), or whether \( x0 \) is a scalar.

**Root Finding**

General nonlinear solvers:

- `fsolve(func, x0[, args, fprime, ...])`: Find the roots of a function.
- `broyden1(F, xin[, iter, alpha, ...])`: Find a root of a function, using Broyden's first Jacobian approximation.
- `broyden2(F, xin[, iter, alpha, ...])`: Find a root of a function, using Broyden's second Jacobian approximation.

`scipy.optimize.fsolve`

Find the roots of a function.

Return the roots of the (non-linear) equations defined by \( \text{func}(x) = 0 \) given a starting estimate.

**Parameters**

- `func` ([callable f(x, *args)]: A function that takes at least one (possibly vector) argument, and returns a value of the same length.
- `x0` ([ndarray]: The starting estimate for the roots of \( \text{func}(x) = 0 \).
- `args` ([tuple, optional]: Any extra arguments to \( \text{func} \).
- `fprime` ([callable f(x, *args), optional]: A function to compute the Jacobian of \( \text{func} \) with derivatives across the rows. By default, the Jacobian will be estimated.
- `full_output` ([bool, optional]: If True, return optional outputs.
- `col_deriv` ([bool, optional]: If True, return optional outputs.
SciPy Reference Guide, Release 1.2.0

[bool, optional] Specify whether the Jacobian function computes derivatives down the columns (faster, because there is no transpose operation).

**xtol** [float, optional] The calculation will terminate if the relative error between two consecutive iterates is at most \( xtol \).

**maxfev** [int, optional] The maximum number of calls to the function. If zero, then \( 100 \times (N+1) \) is the maximum where \( N \) is the number of elements in \( x0 \).

**band** [tuple, optional] If set to a two-sequence containing the number of sub- and super-diagonals within the band of the Jacobi matrix, the Jacobi matrix is considered banded (only for \( fprime=None \)).

**epsfcn** [float, optional] A suitable step length for the forward-difference approximation of the Jacobian (for \( fprime=None \)). If epsfcn is less than the machine precision, it is assumed that the relative errors in the functions are of the order of the machine precision.

**factor** [float, optional] A parameter determining the initial step bound (\( \text{factor} \times || \text{diag} \times x|| \)). Should be in the interval \((0.1, 100)\).

**diag** [sequence, optional] N positive entries that serve as a scale factors for the variables.

**Returns**

**x** [ndarray] The solution (or the result of the last iteration for an unsuccessful call).

**infodict** [dict] A dictionary of optional outputs with the keys:

- **nfev** number of function calls
- **njev** number of Jacobian calls
- **fvec** function evaluated at the output
- **fjac** the orthogonal matrix, \( q \), produced by the QR factorization of the final approximate Jacobian matrix, stored column wise
- **r** upper triangular matrix produced by QR factorization of the same matrix
- **qtf** the vector \((\text{transpose}(q) \times fvec)\)
- **ier** [int] An integer flag. Set to 1 if a solution was found, otherwise refer to **mesg** for more information.
- **mesg** [str] If no solution is found, mesg details the cause of failure.

See also:

**root**

Interface to root finding algorithms for multivariate functions.

Notes

\( \text{fsolve} \) is a wrapper around MINPACK’s hybrd and hybrj algorithms.

scipy.optimize.broyden1

(scipy.optimize.broyden1(F, xin, iter=None, alpha=None, reduction_method='restart',
max_rank=None, verbose=False, maxiter=None, f_tol=None, f_rtol=None, x_tol=None, x_rtol=None, tol_norm=None, line_search='armijo', callback=None, **kw))

Find a root of a function, using Broyden’s first Jacobian approximation.

This method is also known as “Broyden’s good method”.

**Parameters**

**F** [function(x) -> f] Function whose root to find; should take and return an array-like object.

**xin** [array_like] Initial guess for the solution

**alpha** [float, optional] Initial guess for the Jacobian is \((-1/\text{alpha})\).
reduction_method
[ str or tuple, optional] Method used in ensuring that the rank of the Broyden matrix stays low. Can either be a string giving the name of the method, or a tuple of the form (method, param1, param2, ...) that gives the name of the method and values for additional parameters.

Methods available:
- restart: drop all matrix columns. Has no extra parameters.
- simple: drop oldest matrix column. Has no extra parameters.
- svd: keep only the most significant SVD components. Takes an extra parameter, to_retain, which determines the number of SVD components to retain when rank reduction is done. Default is max_rank - 2.

max_rank
[int, optional] Maximum rank for the Broyden matrix. Default is infinity (ie., no rank reduction).

iter
[int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

verbose
[bool, optional] Print status to stdout on every iteration.

maxiter
[int, optional] Maximum number of iterations to make. If more are needed to meet convergence, NoConvergence is raised.

f_tol
[float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

f_rtol
[float, optional] Relative tolerance for the residual. If omitted, not used.

x_tol
[float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

x_rtol
[float, optional] Relative minimum step size. If omitted, not used.

tol_norm
[function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.

line_search
[{None, 'armijo' (default), 'wolfe'}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

callback
[function, optional] Optional callback function. It is called on every iteration as callback(x, f) where x is the current solution and f the corresponding residual.

Returns

sol
[ndarray] An array (of similar array type as x0) containing the final solution.

Raises

NoConvergence
When a solution was not found.

Notes
This algorithm implements the inverse Jacobian Quasi-Newton update

\[ H_+ = H + (dx - H df) dx^\dagger H / (dx^\dagger H df) \]

which corresponds to Broyden’s first Jacobian update

\[ J_+ = J + (df - J dx) dx^\dagger / dx^\dagger dx \]

References
[1]
scipy.optimize.broyden2

```
scipy.optimize.broyden2(F, xin, iter=None, alpha=None, reduction_method='restart',
                         max_rank=None, verbose=False, maxiter=None, f_tol=None,
                         f_rtol=None, x_tol=None, x_rtol=None, tol_norm=None,
                         line_search='armijo', callback=None, **kw)
```

Find a root of a function, using Broyden’s second Jacobian approximation.

This method is also known as “Broyden’s bad method”.

**Parameters**

- **F** ([function(x) -> f]) Function whose root to find; should take and return an array-like object.
- **xin** ([array_like]) Initial guess for the solution
- **alpha** ([float, optional]) Initial guess for the Jacobian is \((-1/\alpha)\).
- **reduction_method** ([str or tuple, optional]) Method used in ensuring that the rank of the Broyden matrix stays low. Can either be a string giving the name of the method, or a tuple of the form (method, param1, param2, ...) that gives the name of the method and values for additional parameters.
  - restart: drop all matrix columns. Has no extra parameters.
  - simple: drop oldest matrix column. Has no extra parameters.
  - svd: keep only the most significant SVD components. Takes an extra parameter, to_retain, which determines the number of SVD components to retain when rank reduction is done. Default is max_rank - 2.
- **max_rank** ([int, optional]) Maximum rank for the Broyden matrix. Default is infinity (ie., no rank reduction).
- **iter** ([int, optional]) Number of iterations to make. If omitted (default), make as many as required to meet tolerances.
- **verbose** ([bool, optional]) Print status to stdout on every iteration.
- **maxiter** ([int, optional]) Maximum number of iterations to make. If more are needed to meet convergence, `NoConvergence` is raised.
- **f_tol** ([float, optional]) Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.
- **f_rtol** ([float, optional]) Relative tolerance for the residual. If omitted, not used.
- **x_tol** ([float, optional]) Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.
- **x_rtol** ([float, optional]) Relative minimum step size. If omitted, not used.
- **tol_norm** ([function(vector) -> scalar, optional]) Norm to use in convergence check. Default is the maximum norm.
- **line_search** ([None, ‘armijo’ (default), ‘wolfe’], optional) Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to ‘armijo’.
- **callback** ([function, optional]) Optional callback function. It is called on every iteration as `callback(x, f)` where `x` is the current solution and `f` the corresponding residual.

**Returns**

- **sol** ([ndarray]) An array (of similar array type as x0) containing the final solution.

**Raises**
NoConvergence
When a solution was not found.

Notes
This algorithm implements the inverse Jacobian Quasi-Newton update

\[ H_+ = H + (dx - H df) df^\dagger / (df^\dagger df) \]

corresponding to Broyden's second method.

References
[1]
Large-scale nonlinear solvers:

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**scipy.optimize.newton_krylov**

Find a root of a function, using Krylov approximation for inverse Jacobian.

This method is suitable for solving large-scale problems.

**Parameters**

- **F**
  [function(x) -> f] Function whose root to find; should take and return an array-like object.

- **xin**
  [array_like] Initial guess for the solution

- **rdiff**
  [float, optional] Relative step size to use in numerical differentiation.

- **method**
  [{'lgmres', 'gmres', 'bicgstab', 'cgs', 'minres'} or function] Krylov method to use to approximate the Jacobian. Can be a string, or a function implementing the same interface as the iterative solvers in scipy.sparse.linalg. The default is scipy.sparse.linalg.lgmres.

- **inner_M**
  [LinearOperator or InverseJacobian] Preconditioner for the inner Krylov iteration. Note that you can use also inverse Jacobians as (adaptive) preconditioners. For example,

```python
>>> from scipy.optimize.nonlin import BroydenFirst, KrylovJacobian
>>> from scipy.optimize.nonlin import InverseJacobian
>>> jac = BroydenFirst()
>>> kjac = KrylovJacobian(inner_M=InverseJacobian(jac))
```

If the preconditioner has a method named ‘update’, it will be called as \(\text{update}(x, f)\) after each nonlinear step, with \(x\) giving the current point, and \(f\) the current function value.

- **inner_tol, inner_maxiter, ...**
  Parameters to pass on to the “inner” Krylov solver. See scipy.sparse.linalg.lgmres for details.

- **outer_k**
  [int, optional] Size of the subspace kept across LGMRES nonlinear iterations. See scipy.sparse.linalg.lgmres for details.
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iter [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

verbose [bool, optional] Print status to stdout on every iteration.

maxiter [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, NoConvergence is raised.

f_tol [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

f_rtol [float, optional] Relative tolerance for the residual. If omitted, not used.

x_tol [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

x_rtol [float, optional] Relative minimum step size. If omitted, not used.

tol_norm [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.

line_search [{None, 'armijo' (default), 'wolfe'}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

callback [function, optional] Optional callback function. It is called on every iteration as callback(x, f) where x is the current solution and f the corresponding residual.

Returns

sol [ndarray] An array (of similar array type as x0) containing the final solution.

Raises

NoConvergence
When a solution was not found.

See also:

scipy.sparse.linalg.gmres, scipy.sparse.linalg.lgmres

Notes

This function implements a Newton-Krylov solver. The basic idea is to compute the inverse of the Jacobian with an iterative Krylov method. These methods require only evaluating the Jacobian-vector products, which are conveniently approximated by a finite difference:

\[ Jv \approx \frac{(f(x + \omega * v/|v|) - f(x))}{\omega} \]

Due to the use of iterative matrix inverses, these methods can deal with large nonlinear problems.

Scipy’s scipy.sparse.linalg module offers a selection of Krylov solvers to choose from. The default here is lgmres, which is a variant of restarted GMRES iteration that reuses some of the information obtained in the previous Newton steps to invert Jacobians in subsequent steps.

For a review on Newton-Krylov methods, see for example [1], and for the LGMRES sparse inverse method, see [2].

References

[1], [2]

scipy.optimize.anderson

scipy.optimize.anderson(F, xin, iter=None, alpha=None, w0=0.01, M=5, verbose=False, maxiter=None, f_tol=None, f_rtol=None, x_tol=None, x_rtol=None, tol_norm=None, line_search='armijo', callback=None, **kw)

Find a root of a function, using (extended) Anderson mixing.
The Jacobian is formed by for a ‘best’ solution in the space spanned by last $M$ vectors. As a result, only a $M \times M$ matrix inversions and $M \times N$ multiplications are required. 

**Parameters**

- **F** [function(x) -> f] Function whose root to find; should take and return an array-like object.
- **xin** [array_like] Initial guess for the solution
- **alpha** [float, optional] Initial guess for the Jacobian is $(-1/\text{alpha})$.
- **M** [float, optional] Number of previous vectors to retain. Defaults to 5.
- **w0** [float, optional] Regularization parameter for numerical stability. Compared to unity, good values of the order of 0.01.
- **iter** [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.
- **verbose** [bool, optional] Print status to stdout on every iteration.
- **maxiter** [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, NoConvergence is raised.
- **f_tol** [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.
- **f_rtol** [float, optional] Relative tolerance for the residual. If omitted, not used.
- **x_tol** [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.
- **x_rtol** [float, optional] Relative minimum step size. If omitted, not used.
- **tol_norm** [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.
- **line_search** [{None, ‘armijo’ (default), ‘wolfe’}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to ‘armijo’.
- **callback** [function, optional] Optional callback function. It is called on every iteration as callback(x, f) where x is the current solution and f the corresponding residual.

**Returns**

- **sol** [ndarray] An array (of similar array type as x0) containing the final solution.

**Raises**

- **NoConvergence** When a solution was not found.

**References**

When a solution was not found.

Simple iteration solvers:

- **excitingmixing**([F, xin[, iter, alpha, ...]]) Find a root of a function, using a tuned diagonal Jacobian approximation.
- **linearmixing**([F, xin[, iter, alpha, verbose, ...]]) Find a root of a function, using a scalar Jacobian approximation.
- **diagbroyden**([F, xin[, iter, alpha, verbose, ...]]) Find a root of a function, using diagonal Broyden Jacobian approximation.
Find a root of a function, using a tuned diagonal Jacobian approximation.

The Jacobian matrix is diagonal and is tuned on each iteration.

**Warning:** This algorithm may be useful for specific problems, but whether it will work may depend strongly on the problem.

### Parameters

- **F**: [function(x) -> f] Function whose root to find; should take and return an array-like object.
- **xin**: [array_like] Initial guess for the solution
- **alpha**: [float, optional] Initial Jacobian approximation is (-1/alpha).
- **alphamax**: [float, optional] The entries of the diagonal Jacobian are kept in the range [alpha, alphamax].
- **iter**: [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.
- **verbose**: [bool, optional] Print status to stdout on every iteration.
- **maxiter**: [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, NoConvergence is raised.
- **f_tol**: [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.
- **f_rtol**: [float, optional] Relative tolerance for the residual. If omitted, not used.
- **x_tol**: [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.
- **x_rtol**: [float, optional] Relative minimum step size. If omitted, not used.
- **tol_norm**: [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.
- **line_search**: [{None, ‘armijo’ (default), ‘wolfe’}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to ‘armijo’.
- **callback**: [function, optional] Optional callback function. It is called on every iteration as callback(x, f) where x is the current solution and f the corresponding residual.

### Returns

- **sol**: [ndarray] An array (of similar array type as x0) containing the final solution.

### Raises

- **NoConvergence**
  When a solution was not found.
SciPy Reference Guide, Release 1.2.0

scipy.optimize.linearmixing

scipy.optimize.linearmixing(F, xin, iter=None, alpha=None, verbose=False, maxiter=None, f_tol=None, f_rtol=None, x_tol=None, x_rtol=None, tol_norm=None, line_search='armijo', callback=None, **kw)

Find a root of a function, using a scalar Jacobian approximation.

**Warning:** This algorithm may be useful for specific problems, but whether it will work may depend strongly on the problem.

**Parameters**

- **F** [function(x) -> f] Function whose root to find; should take and return an array-like object.
- **xin** [array_like] Initial guess for the solution
- **alpha** [float, optional] The Jacobian approximation is (-1/alpha).
- **iter** [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.
- **verbose** [bool, optional] Print status to stdout on every iteration.
- **maxiter** [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, `NoConvergence` is raised.
- **f_tol** [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.
- **f_rtol** [float, optional] Relative tolerance for the residual. If omitted, not used.
- **x_tol** [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.
- **x_rtol** [float, optional] Relative minimum step size. If omitted, not used.
- **tol_norm** [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.
- **line_search** [{None, ‘armijo’ (default), ‘wolfe’}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to ‘armijo’.
- **callback** [function, optional] Optional callback function. It is called on every iteration as `callback(x, f)` where `x` is the current solution and `f` the corresponding residual.

**Returns**

- **sol** [ndarray] An array (of similar array type as `x0`) containing the final solution.

**Raises**

- `NoConvergence` When a solution was not found.

scipy.optimize.diagbroyden

scipy.optimize.diagbroyden(F, xin, iter=None, alpha=None, verbose=False, maxiter=None, f_tol=None, f_rtol=None, x_tol=None, x_rtol=None, tol_norm=None, line_search='armijo', callback=None, **kw)

Find a root of a function, using diagonal Broyden Jacobian approximation.

The Jacobian approximation is derived from previous iterations, by retaining only the diagonal of Broyden matrices.
Warning: This algorithm may be useful for specific problems, but whether it will work may depend strongly on the problem.

Parameters

- **F** ([function(x) -> f]) Function whose root to find; should take and return an array-like object.
- **xin** ([array_like]) Initial guess for the solution
- **alpha** ([float, optional]) Initial guess for the Jacobian is (-1/alpha).
- **iter** ([int, optional]) Number of iterations to make. If omitted (default), make as many as required to meet tolerances.
- **verbose** ([bool, optional]) Print status to stdout on every iteration.
- **maxiter** ([int, optional]) Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.
- **f_tol** ([float, optional]) Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.
- **f_rtol** ([float, optional]) Relative tolerance for the residual. If omitted, not used.
- **x_tol** ([float, optional]) Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.
- **x_rtol** ([float, optional]) Relative minimum step size. If omitted, not used.
- **tol_norm** ([function(vector) -> scalar, optional]) Norm to use in convergence check. Default is the maximum norm.
- **line_search** ([{'None', 'armijo' (default), ‘wolfe’}, optional]) Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to ‘armijo’.
- **callback** ([function, optional]) Optional callback function. It is called on every iteration as *callback(x, f)* where *x* is the current solution and *f* the corresponding residual.

Returns

- **sol** ([ndarray]) An array (of similar array type as *x0*) containing the final solution.

Raises

- **NoConvergence** When a solution was not found.

*Additional information on the nonlinear solvers*

### 6.19 Nonlinear solvers

This is a collection of general-purpose nonlinear multidimensional solvers. These solvers find $x$ for which $F(x) = 0$. Both $x$ and $F$ can be multidimensional.

#### 6.19.1 Routines

Large-scale nonlinear solvers:

```python
newton_krylov(F, xin[, iter, rdiff, method, ...])
```
Find a root of a function, using Krylov approximation for inverse Jacobian.
Table 144 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>anderson(F, xin[, iter, alpha, w0, M, ...])</code></td>
<td>Find a root of a function, using (extended) Anderson mixing.</td>
</tr>
</tbody>
</table>

General nonlinear solvers:

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>broyden1(F, xin[, iter, alpha, ...])</code></td>
<td>Find a root of a function, using Broyden’s first Jacobian approximation.</td>
</tr>
<tr>
<td><code>broyden2(F, xin[, iter, alpha, ...])</code></td>
<td>Find a root of a function, using Broyden’s second Jacobian approximation.</td>
</tr>
</tbody>
</table>

Simple iterations:

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>excitingmixing(F, xin[, iter, alpha, ...])</code></td>
<td>Find a root of a function, using a tuned diagonal Jacobian approximation.</td>
</tr>
<tr>
<td><code>linearmixing(F, xin[, iter, alpha, verbose, ...])</code></td>
<td>Find a root of a function, using a scalar Jacobian approximation.</td>
</tr>
<tr>
<td><code>diagbroyden(F, xin[, iter, alpha, verbose, ...])</code></td>
<td>Find a root of a function, using diagonal Broyden Jacobian approximation.</td>
</tr>
</tbody>
</table>

6.19.2 Examples

Small problem

```python
>>> def F(x):
...     return np.cos(x) + x[::-1] - [1, 2, 3, 4]
>>> import scipy.optimize
>>> x = scipy.optimize.broyden1(F, [1,1,1,1], f_tol=1e-14)
>>> x
array([ 4.04674914, 3.91158389, 2.71791677, 1.61756251])
>>> np.cos(x) + x[::-1]
array([ 1.,  2.,  3.,  4.])
```

Large problem

Suppose that we needed to solve the following integrodifferential equation on the square \([0, 1] \times [0, 1]\):

\[
\nabla^2 P = 10 \left( \int_0^1 \int_0^1 \cosh(P) \, dx \, dy \right)^2
\]

with \(P(x, 1) = 1\) and \(P = 0\) elsewhere on the boundary of the square.

The solution can be found using the `newton_krylov` solver:

```python
import numpy as np
from scipy.optimize import newton_krylov
from numpy import cosh, zeros_like, mgrid, zeros

# parameters
nx, ny = 75, 75
hx, hy = 1./(nx-1), 1./(ny-1)

P_left, P_right = 0, 0
```
```python
P_top, P_bottom = 1, 0

def residual(P):
    d2x = zeros_like(P)
    d2y = zeros_like(P)

    d2x[1:-1] = (P[2:] - 2*P[1:-1] + P[:-2]) / hx/hx
    d2x[0] = (P[1] - 2*P[0] + P_left)/hx/hx
    d2x[-1] = (P_right - 2*P[-1] + P[-2])/hx/hx

    d2y[:,1:-1] = (P[:,2:] - 2*P[:,1:-1] + P[:,2:-2])/hy/hy
    d2y[:,0] = (P[:,1] - 2*P[:,0] + P_bottom)/hy/hy
    d2y[:,-1] = (P_top - 2*P[:,1] + P[:,0])/hy/hy

    return d2x + d2y - 10*cosh(P).mean()**2

# solve
guess = zeros((nx, ny), float)
sol = newton_krylov(residual, guess, method='lgmres', verbose=1)
print('Residual: %g' % abs(residual(sol)).max())

# visualize
import matplotlib.pyplot as plt
x, y = mgrid[0:1:(nx*1j), 0:1:(ny*1j)]
plt.pcolor(x, y, sol)
plt.colorbar()
plt.show()
```

---

The code calculates the residual function, sets the initial guess, solves the equation using Newton-Krylov method, prints the residual, and visualizes the solution using matplotlib.
6.20 Signal processing (scipy.signal)

6.20.1 Convolution

```python
cconvolve(in1, in2, [mode, method])
```
Convolve two N-dimensional arrays.

```python
correlate(in1, in2, [mode, method])
```
Cross-correlate two N-dimensional arrays.

```python
cfftconvolve(in1, in2, [mode, axes])
```
Convolve two N-dimensional arrays using FFT.

```python
cconvolve2d(in1, in2, [mode, boundary, fillvalue])
```
Convolve two 2-dimensional arrays.

```python
ccorrelate2d(in1, in2, [mode, boundary, ...])
```
Cross-correlate two 2-dimensional arrays.

```python
csepfir2d(input, hrow, hcol)
```
Description:

```python
cchoose_conv_method(in1, in2, [mode, measure])
```
Find the fastest convolution/correlation method.

**scipy.signal.convolve**

```python
cscipy.signal.convolve(in1, in2, mode='full', method='auto')
```
Convolve two N-dimensional arrays.

Convolve `in1` and `in2`, with the output size determined by the `mode` argument.

**Parameters**

- `in1` [array_like] First input.
- `in2` [array_like] Second input. Should have the same number of dimensions as `in1`.
- `mode` [str {'full', 'valid', 'same'}, optional] A string indicating the size of the output:
  - `full`: The output is the full discrete linear convolution of the inputs. (Default)
  - `valid`: The output consists only of those elements that do not rely on the zero-padding. In `valid` mode, either `in1` or `in2` must be at least as large as the other in every dimension.
  - `same`: The output is the same size as `in1`, centered with respect to the `full` output.
- `method` [str {'auto', 'direct', 'fft'}, optional] A string indicating which method to use to calculate the convolution:
  - `direct`: The convolution is determined directly from sums, the definition of convolution.
  - `fft`: The Fourier Transform is used to perform the convolution by calling `cfftconvolve`.
  - `auto`: Automatically chooses direct or Fourier method based on an estimate of which is faster (default). See Notes for more detail. New in version 0.19.0.

**Returns**

- `convolve` [array] An N-dimensional array containing a subset of the discrete linear convolution of `in1` with `in2`.

**See also:**

- `numpy.polymul`
  - performs polynomial multiplication (same operation, but also accepts poly1d objects)
- `cchoose_conv_method`
  - chooses the fastest appropriate convolution method
- `cfftconvolve`
Notes
By default, `convolve` and `correlate` use `method='auto'`, which calls `choose_conv_method` to choose the fastest method using pre-computed values (`choose_conv_method` can also measure real-world timing with a keyword argument). Because `fftconvolve` relies on floating point numbers, there are certain constraints that may force `method='direct'` (more detail in `choose_conv_method` docstring).

Examples
Smooth a square pulse using a Hann window:

```python
>>> from scipy import signal
correlate

scipy.signal.correlate
```

```python
scipy.signal.correlate(in1, in2, mode='full', method='auto')
cross-correlate two N-dimensional arrays.

Cross-correlate `in1` and `in2`, with the output size determined by the `mode` argument.

Parameters
```
in1  [array_like] First input.
in2  [array_like] Second input. Should have the same number of dimensions as in1.
mode  [str {'full', 'valid', 'same'}, optional] A string indicating the size of the output:
full  The output is the full discrete linear cross-correlation of the inputs. (Default)
valid  The output consists only of those elements that do not rely on the zero-padding. In ‘valid’ mode, either in1 or in2 must be at least as large as the other in every dimension.
same  The output is the same size as in1, centered with respect to the ‘full’ output.
method  [str {'auto', 'direct', 'fft'}, optional] A string indicating which method to use to calculate the correlation.
direct  The correlation is determined directly from sums, the definition of correlation.
fft  The Fast Fourier Transform is used to perform the correlation more quickly (only available for numerical arrays.)
auto  Automatically chooses direct or Fourier method based on an estimate of which is faster (default). See convolve Notes for more detail. New in version 0.19.0.

Returns

correlate  [array] An N-dimensional array containing a subset of the discrete linear cross-correlation of in1 with in2.

See also:

choose_conv_method
contains more documentation on method.

Notes
The correlation z of two d-dimensional arrays x and y is defined as:

\[ z[\ldots, k, \ldots] = \text{sum}[\ldots, i_1, \ldots] x[\ldots, i_1, \ldots] \ast \text{conj}(y[\ldots, i_1 - k, \ldots]) \]

This way, if x and y are 1-D arrays and \( z = \text{correlate}(x, y, 'full') \) then

\[ z[k] = (x \ast y)(k - N + 1) = \sum_{l=0}^{||x||-1} x_l y_{l-k+N-1} \]

for \( k = 0, 1, \ldots, ||x|| + ||y|| - 2 \)

where \( ||x|| \) is the length of x, \( N = \max(||x||, ||y||) \), and \( y_m \) is 0 when \( m \) is outside the range of y.

method='fft' only works for numerical arrays as it relies on fftconvolve. In certain cases (i.e., arrays of objects or when rounding integers can lose precision), method='direct' is always used.

Examples
Implement a matched filter using cross-correlation, to recover a signal that has passed through a noisy channel.

```python
>>> from scipy import signal
>>> sig = np.repeat([0., 1., 1., 0., 1., 0., 0., 1.], 128)
>>> sig_noise = sig + np.random.randn(len(sig))
>>> corr = signal.correlate(sig_noise, np.ones(128), mode='same') / 128
```
scipy.signal.fftconvolve

`scipy.signal.fftconvolve(in1, in2, mode='full', axes=None)`

Convolve two N-dimensional arrays using FFT.

Convolve `in1` and `in2` using the fast Fourier transform method, with the output size determined by the `mode` argument.

This is generally much faster than `convolve` for large arrays (n > ~500), but can be slower when only a few output values are needed, and can only output float arrays (int or object array inputs will be cast to float).

As of v0.19, `convolve` automatically chooses this method or the direct method based on an estimation of which is faster.

**Parameters**

- `in1` [array_like] First input.
- `in2` [array_like] Second input. Should have the same number of dimensions as `in1`.
- `mode` [str {'full', 'valid', 'same'}, optional] A string indicating the size of the output:
The output is the full discrete linear convolution of the inputs. (Default)

valid

The output consists only of those elements that do not rely on the zero-padding. In ‘valid’ mode, either \( \text{in1} \) or \( \text{in2} \) must be at least as large as the other in every dimension.

same

The output is the same size as \( \text{in1} \), centered with respect to the ‘full’ output.

axes

[int or array_like of ints or None, optional] Axes over which to compute the convolution. The default is over all axes.

Returns

correlogram [array] An N-dimensional array containing a subset of the discrete linear convolution of \( \text{in1} \) with \( \text{in2} \).

Examples

Autocorrelation of white noise is an impulse.

```python
>>> from scipy import signal
>>> sig = np.random.randn(1000)
>>> autocorr = signal.fftconvolve(sig, sig[::-1], mode='full')
```

Gaussian blur implemented using FFT convolution. Notice the dark borders around the image, due to the zero-padding beyond its boundaries. The `convolve2d` function allows for other types of image boundaries, but is far slower.

```python
>>> from scipy import misc
>>> face = misc.face(gray=True)
>>> kernel = np.outer(signal.gaussian(70, 8), signal.gaussian(70, 8))
>>> blurred = signal.fftconvolve(face, kernel, mode='same')
```

```python
>>> fig, (ax_orig, ax_kernel, ax_blurred) = plt.subplots(3, 1, ...
figsize=(6, 15))
>>> ax_orig.imshow(face, cmap='gray')
>>> ax_orig.set_title('Original')
>>> ax_orig.set_axis_off()
>>> ax_kernel.imshow(kernel, cmap='gray')
>>> ax_kernel.set_title('Gaussian kernel')
>>> ax_kernel.set_axis_off()
>>> ax_blurred.imshow(blurred, cmap='gray')
>>> ax_blurred.set_title('Blurred')
>>> ax_blurred.set_axis_off()
>>> fig.show()
```
scipy.signal.convolve2d

```
scipy.signal.convolve2d(in1, in2, mode='full', boundary='fill', fillvalue=0)
```

Convolves `in1` and `in2` with output size determined by `mode`, and boundary conditions determined by `boundary` and `fillvalue`.

**Parameters**

- **in1** [array_like] First input.
- **in2** [array_like] Second input. Should have the same number of dimensions as `in1`.
- **mode** [str {'full', 'valid', 'same'}, optional] A string indicating the size of the output:
  - `full` The output is the full discrete linear convolution of the inputs. (Default)
  - `valid` The output consists only of those elements that do not rely on the zero-padding. In `valid` mode, either `in1` or `in2` must be at least as large as the other in every dimension.
  - `same` The output is the same size as `in1`, centered with respect to the `full` output.
- **boundary** [str {'fill', 'wrap', 'symm'}, optional] A flag indicating how to handle boundaries:
  - `fill` pad input arrays with fillvalue. (default)
  - `wrap` circular boundary conditions.
  - `symm` symmetrical boundary conditions.
- **fillvalue** [scalar, optional] Value to fill pad input arrays with. Default is 0.

**Returns**

- **out** [ndarray] A 2-dimensional array containing a subset of the discrete linear convolution of `in1` with `in2`.

**Examples**

Compute the gradient of an image by 2D convolution with a complex Scharr operator. (Horizontal operator is real, vertical is imaginary.) Use symmetric boundary condition to avoid creating edges at the image boundaries.
6.20. Signal processing (`scipy.signal`)
```python
>>> from scipy import signal
>>> from scipy import misc

ascent = misc.ascent()
scharr = np.array([[-3-3j, 0-10j, +3-3j],
                  ...                  [-10+0j, +0j, +10+0j],
                  ...                  [-3+3j, +0j, +3+3j]])  # Gx + j*Gy

grad = signal.convolve2d(ascent, scharr, boundary='symm', mode='same')

import matplotlib.pyplot as plt

fig, (ax_orig, ax_mag, ax_ang) = plt.subplots(3, 1, figsize=(6, 15))

ax_orig.imshow(ascent, cmap='gray')
ax_orig.set_title('Original')
ax_orig.set_axis_off()

ax_mag.imshow(np.absolute(grad), cmap='gray')
ax_mag.set_title('Gradient magnitude')
ax_mag.set_axis_off()

ax_ang.imshow(np.angle(grad), cmap='hsv')  # hsv is cyclic, like angles
ax_ang.set_title('Gradient orientation')
ax_ang.set_axis_off()

fig.show()
```

scipy.signal.correlate2d

**scipy.signal.correlate2d(in1, in2, mode='full', boundary='fill', fillvalue=0)**

Cross-correlate two 2-dimensional arrays.

Cross correlate `in1` and `in2` with output size determined by `mode`, and boundary conditions determined by `boundary` and `fillvalue`.

**Parameters**

- **in1** [array_like] First input.
- **in2** [array_like] Second input. Should have the same number of dimensions as `in1`.
- **mode** [str {‘full’, ‘valid’, ‘same’}, optional] A string indicating the size of the output:
  - **full** The output is the full discrete linear cross-correlation of the inputs.
  - **valid** The output consists only of those elements that do not rely on the zero-padding. In ‘valid’ mode, either `in1` or `in2` must be at least as large as the other in every dimension.
  - **same** The output is the same size as `in1`, centered with respect to the ‘full’ output.
- **boundary** [str {‘fill’, ‘wrap’, ‘symm’}, optional] A flag indicating how to handle boundaries:
  - **fill** pad input arrays with fillvalue. (default)
  - **wrap** circular boundary conditions.
  - **symm** symmetrical boundary conditions.
- **fillvalue** [scalar, optional] Value to fill pad input arrays with. Default is 0.

**Returns**

- **correlate2d** [ndarray] A 2-dimensional array containing a subset of the discrete linear cross-correlation of `in1` with `in2`. 

Original

Gradient magnitude

Gradient orientation
Examples

Use 2D cross-correlation to find the location of a template in a noisy image:

```python
>>> from scipy import signal
>>> from scipy import misc
>>> face = misc.face(gray=True) - misc.face(gray=True).mean()
>>> template = np.copy(face[300:365, 670:750])  # right eye
>>> template -= template.mean()
>>> face = face + np.random.randn(*face.shape) * 50  # add noise
>>> corr = signal.correlate2d(face, template, boundary='symm', mode='same')
>>> y, x = np.unravel_index(np.argmax(corr), corr.shape)  # find the match
```

```python
>>> import matplotlib.pyplot as plt
>>> fig, (ax_orig, ax_template, ax_corr) = plt.subplots(3, 1, ...
... figsize=(6, 15))
>>> ax_orig.imshow(face, cmap='gray')
>>> ax_orig.set_title('Original')
>>> ax_orig.set_axis_off()
>>> ax_template.imshow(template, cmap='gray')
>>> ax_template.set_title('Template')
>>> ax_template.set_axis_off()
>>> ax_corr.imshow(corr, cmap='gray')
>>> ax_corr.set_title('Cross-correlation')
>>> ax_corr.set_axis_off()
>>> ax_orig.plot(x, y, 'ro')
>>> fig.show()
```

**scipy.signal.sepfir2d**

`scipy.signal.sepfir2d(input, hrow, hcol) → output`

Description:

Convolve the rank-2 input array with the separable filter defined by the rank-1 arrays hrow, and hcol. Mirror symmetric boundary conditions are assumed. This function can be used to find an image given its B-spline representation.

**scipy.signal.choose_conv_method**

`scipy.signal.choose_conv_method(in1, in2, mode='full', measure=False)`

Find the fastest convolution/correlation method.

This primarily exists to be called during the `method='auto'` option in `convolve` and `correlate`, but can also be used when performing many convolutions of the same input shapes and dtypes, determining which method to use for all of them, either to avoid the overhead of the ‘auto’ option or to use accurate real-world measurements.

**Parameters**

- **in1** [array_like] The first argument passed into the convolution function.
- **in2** [array_like] The second argument passed into the convolution function.
- **mode** [str {‘full’, ‘valid’, ‘same’}, optional] A string indicating the size of the output:
  - **full** The output is the full discrete linear convolution of the inputs. (Default)
  - **valid** The output consists only of those elements that do not rely on the zero-padding.
6.20. Signal processing (scipy.signal)
same The output is the same size as in1, centered with respect to the ‘full’ output.

measure [bool, optional] If True, run and time the convolution of in1 and in2 with both methods and return the fastest. If False (default), predict the fastest method using precomputed values.

Returns

method [str] A string indicating which convolution method is fastest, either ‘direct’ or ‘fft’
times [dict, optional] A dictionary containing the times (in seconds) needed for each method. This value is only returned if measure=True.

See also:
convolve, correlate

Notes
For large n, measure=False is accurate and can quickly determine the fastest method to perform the convolution. However, this is not as accurate for small n (when any dimension in the input or output is small).

In practice, we found that this function estimates the faster method up to a multiplicative factor of 5 (i.e., the estimated method is at most 5 times slower than the fastest method). The estimation values were tuned on an early 2015 MacBook Pro with 8GB RAM but we found that the prediction held fairly accurately across different machines.

If measure=True, time the convolutions. Because this function uses fftconvolve, an error will be thrown if it does not support the inputs. There are cases when fftconvolve supports the inputs but this function returns direct (e.g., to protect against floating point integer precision).

New in version 0.19.

Examples
Estimate the fastest method for a given input:

```python
>>> from scipy import signal
>>> a = np.random.randn(1000)
>>> b = np.random.randn(1000000)
>>> method = signal.choose_conv_method(a, b, mode='same')
>>> method
'fft'
```

This can then be applied to other arrays of the same dtype and shape:

```python
>>> c = np.random.randn(1000)
>>> d = np.random.randn(1000000)
>>> # 'method' works with correlate and convolve
>>> corr1 = signal.correlate(a, b, mode='same', method=method)
>>> corr2 = signal.correlate(c, d, mode='same', method=method)
>>> conv1 = signal.convolve(a, b, mode='same', method=method)
>>> conv2 = signal.convolve(c, d, mode='same', method=method)
```

6.20.2 B-splines

bspline(x, n) B-spline basis function of order n.
cubic(x) A cubic B-spline.
```
Table 148 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>gauss_spline(x, n)</code></td>
<td>Gaussian approximation to B-spline basis function of order n.</td>
</tr>
<tr>
<td><code>cspline1d(signal[, lamb])</code></td>
<td>Compute cubic spline coefficients for rank-1 array.</td>
</tr>
<tr>
<td><code>qspline1d(signal[, lamb])</code></td>
<td>Compute quadratic spline coefficients for rank-1 array.</td>
</tr>
<tr>
<td><code>cspline2d(input {, lambda, precision})</code></td>
<td>Description:</td>
</tr>
<tr>
<td><code>qspline2d(input {, lambda, precision})</code></td>
<td>Description:</td>
</tr>
<tr>
<td><code>cspline1d_eval(cj, newx[, dx, x0])</code></td>
<td>Evaluate a spline at the new set of points.</td>
</tr>
<tr>
<td><code>qspline1d_eval(cj, newx[, dx, x0])</code></td>
<td>Evaluate a quadratic spline at the new set of points.</td>
</tr>
<tr>
<td><code>spline_filter(Iin[, lmbda])</code></td>
<td>Smoothing spline (cubic) filtering of a rank-2 array.</td>
</tr>
</tbody>
</table>

**scipy.signal.bspline**

`scipy.signal.bspline(x, n)`  
B-spline basis function of order n.

**Notes**  
Uses numpy.piecewise and automatic function-generator.

**scipy.signal.cubic**

`scipy.signal.cubic(x)`  
A cubic B-spline.

This is a special case of `bspline`, and equivalent to `bspline(x, 3).

**scipy.signal.quadratic**

`scipy.signal.quadratic(x)`  
A quadratic B-spline.

This is a special case of `bspline`, and equivalent to `bspline(x, 2).

**scipy.signal.gauss_spline**

`scipy.signal.gauss_spline(x, n)`  
Gaussian approximation to B-spline basis function of order n.

**Parameters**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>n</td>
<td>[int] The order of the spline. Must be nonnegative, i.e. n &gt;= 0</td>
</tr>
</tbody>
</table>

**References**

[1]

**scipy.signal.cspline1d**

`scipy.signal.cspline1d(signal, lamb=0.0)`  
Compute cubic spline coefficients for rank-1 array.

Find the cubic spline coefficients for a 1-D signal assuming mirror-symmetric boundary conditions. To obtain the signal back from the spline representation mirror-symmetric-convolve these coefficients with a length 3 FIR window [1.0, 4.0, 1.0]/ 6.0 .

**Parameters**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>signal</td>
<td>[ndarray] A rank-1 array representing samples of a signal.</td>
</tr>
<tr>
<td>lamb</td>
<td>[float, optional] Smoothing coefficient, default is 0.0.</td>
</tr>
</tbody>
</table>
Returns

c  [ndarray] Cubic spline coefficients.

scipy.signal.qspline1d

scipy.signal.qspline1d(signal, lamb=0.0)

Compute quadratic spline coefficients for rank-1 array.

Find the quadratic spline coefficients for a 1-D signal assuming mirror-symmetric boundary conditions. To obtain the signal back from the spline representation mirror-symmetric-convolve these coefficients with a length 3 FIR window \([1.0, 6.0, 1.0]/8.0\).

Parameters

- **signal** [ndarray] A rank-1 array representing samples of a signal.
- **lamb** [float, optional] Smoothing coefficient (must be zero for now).

Returns

c  [ndarray] Cubic spline coefficients.

scipy.signal.cspline2d

scipy.signal.cspline2d(input {, lambda, precision}) \rightarrow ck

Description:

Return the third-order B-spline coefficients over a regularly spaced input grid for the two-dimensional input image. The lambda argument specifies the amount of smoothing. The precision argument allows specifying the precision used when computing the infinite sum needed to apply mirror-symmetric boundary conditions.

scipy.signal.qspline2d

scipy.signal.qspline2d(input {, lambda, precision}) \rightarrow qk

Description:

Return the second-order B-spline coefficients over a regularly spaced input grid for the two-dimensional input image. The lambda argument specifies the amount of smoothing. The precision argument allows specifying the precision used when computing the infinite sum needed to apply mirror-symmetric boundary conditions.

scipy.signal.cspline1d_eval

scipy.signal.cspline1d_eval(cj, newx, dx=1.0, x0=0)

Evaluate a spline at the new set of points.

- **dx** is the old sample-spacing while **x0** was the old origin. In other-words the old-sample points (knot-points) for which the **cj** represent spline coefficients were at equally-spaced points of:

  \[oldx = x0 + j*dx \text{ for } j=0...N-1, \text{ with } N=\text{len}(cj)\]

  Edges are handled using mirror-symmetric boundary conditions.

scipy.signal.qspline1d_eval

scipy.signal.qspline1d_eval(cj, newx, dx=1.0, x0=0)

Evaluate a quadratic spline at the new set of points.

- **dx** is the old sample-spacing while **x0** was the old origin. In other-words the old-sample points (knot-points) for which the **cj** represent spline coefficients were at equally-spaced points of:

  \[oldx = x0 + j*dx \text{ for } j=0...N-1, \text{ with } N=\text{len}(cj)\]
oldx = x0 + j*dx  j=0...N-1, with N=len(cj)

Edges are handled using mirror-symmetric boundary conditions.

scipy.signal.spline_filter

scipy.signal.spline_filter(Iin, lmbda=5.0)

Smoothing spline (cubic) filtering of a rank-2 array.

Filter an input data set, Iin, using a (cubic) smoothing spline of fall-off lmbda.

6.20.3 Filtering

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scipy.signal.order_filter

**scipy.signal.order_filter**(a, domain, rank)

Perform an order filter on an N-dimensional array.

Perform an order filter on the array in. The domain argument acts as a mask centered over each pixel. The non-zero elements of domain are used to select elements surrounding each input pixel which are placed in a list. The list is sorted, and the output for that pixel is the element corresponding to rank in the sorted list.

**Parameters**

- `a` : [ndarray] The N-dimensional input array.
- `domain` : [array_like] A mask array with the same number of dimensions as `a`. Each dimension should have an odd number of elements.
- `rank` : [int] A non-negative integer which selects the element from the sorted list (0 corresponds to the smallest element, 1 is the next smallest element, etc.).

**Returns**

- `out` : [ndarray] The results of the order filter in an array with the same shape as `a`.

**Examples**

```python
>>> from scipy import signal
>>> x = np.arange(25).reshape(5, 5)
>>> domain = np.identity(3)
>>> x
array([[ 0,  1,  2,  3,  4],
       [ 5,  6,  7,  8,  9],
       [10, 11, 12, 13, 14],
       [15, 16, 17, 18, 19],
       [20, 21, 22, 23, 24]])
>>> signal.order_filter(x, domain, 0)
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  2.,  0.],
       [ 0.,  5.,  6.,  7.,  0.],
       [ 0., 10., 11., 12.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
>>> signal.order_filter(x, domain, 2)
array([[ 6.,  7.,  8.,  9.,  4.],
       [16., 17., 18., 19., 14.],
       [21., 22., 23., 24., 19.],
       [20., 21., 22., 23., 24.]])
```

scipy.signal.medfilt

**scipy.signal.medfilt**(volume, kernel_size=None)

Perform a median filter on an N-dimensional array.

Apply a median filter to the input array using a local window-size given by `kernel_size`.

**Parameters**

- `volume` : [array_like] An N-dimensional input array.
- `kernel_size` : [array_like, optional] A scalar or an N-length list giving the size of the median filter window in each dimension. Elements of `kernel_size` should be odd. If `kernel_size`
is a scalar, then this scalar is used as the size in each dimension. Default size is 3
for each dimension.

**Returns**

- `out` [ndarray] An array the same size as input containing the median filtered result.

### scipy.signal.medfilt2d

**scipy.signal.medfilt2d**

**scipy.signal.medfilt2d(input, kernel_size=3)**

Median filter a 2-dimensional array.

Apply a median filter to the `input` array using a local window-size given by `kernel_size` (must be odd).

**Parameters**

- `input` [array_like] A 2-dimensional input array.
- `kernel_size` [array_like, optional] A scalar or a list of length 2, giving the size of the median filter window in each dimension. Elements of `kernel_size` should be odd. If `kernel_size` is a scalar, then this scalar is used as the size in each dimension. Default is a kernel of size (3, 3).

**Returns**

- `out` [ndarray] An array the same size as input containing the median filtered result.

### scipy.signal.wiener

**scipy.signal.wiener**

**scipy.signal.wiener(im, mysize=None, noise=None)**

Perform a Wiener filter on an N-dimensional array.

Apply a Wiener filter to the N-dimensional array `im`.

**Parameters**

- `mysize` [int or array_like, optional] A scalar or an N-length list giving the size of the Wiener filter window in each dimension. Elements of mysize should be odd. If mysize is a scalar, then this scalar is used as the size in each dimension.
- `noise` [float, optional] The noise-power to use. If None, then noise is estimated as the average of the local variance of the input.

**Returns**

- `out` [ndarray] Wiener filtered result with the same shape as `im`.

### scipy.signal.symiirorder1

**scipy.signal.symiirorder1**

**scipy.signal.symiirorder1(input, c0, z1, precision)**

Implement a smoothing IIR filter with mirror-symmetric boundary conditions using a cascade of first-order sections. The second section uses a reversed sequence. This implements a system with the following transfer function and mirror-symmetric boundary conditions:

\[
H(z) = \frac{c_0}{(1-z_1/z)(1 - z_1 z)}
\]

The resulting signal will have mirror symmetric boundary conditions as well.

**Parameters**
input  [ndarray] The input signal.
c0, z1  [scalar] Parameters in the transfer function.
precision :
    Specifies the precision for calculating initial conditions of the recursive filter based
    on mirror-symmetric input.

Returns
output  [ndarray] The filtered signal.

scipy.signal.symiirorder2

scipy.signal.symiirorder2(input, r, omega {, precision}) → output
Implement a smoothing IIR filter with mirror-symmetric boundary conditions using a cascade of second-
order sections. The second section uses a reversed sequence. This implements the following transfer
function:

\[
H(z) = \frac{cs^-2}{(1 - a2/z - a3/z^-2)(1 - a2 z - a3 z^-2)}
\]

where:

\[
\begin{align*}
a2 &= (2 r \cos \omega) \\
a3 &= -r^-2 \\
CS &= 1 - 2 r \cos \omega + r^-2
\end{align*}
\]

Parameters
input  [ndarray] The input signal.
r, omega  [scalar] Parameters in the transfer function.
precision :
    Specifies the precision for calculating initial conditions of the recursive filter based
    on mirror-symmetric input.

Returns
output  [ndarray] The filtered signal.

scipy.signal.lfilter

scipy.signal.lfilter(b, a, x, axis=-1, zi=None)
Filter data along one-dimension with an IIR or FIR filter.

Filter a data sequence, x, using a digital filter. This works for many fundamental data types (including
Object type). The filter is a direct form II transposed implementation of the standard difference
equation (see Notes).

Parameters
b  [array_like] The numerator coefficient vector in a 1-D sequence.
a  [array_like] The denominator coefficient vector in a 1-D sequence. If a[0] is not
    1, then both a and b are normalized by a[0].
x  [array_like] An N-dimensional input array.
axis  [int, optional] The axis of the input data array along which to apply the linear
    filter. The filter is applied to each subarray along this axis. Default is -1.
zi  [array_like, optional] Initial conditions for the filter delays. It is a vector (or array of vectors for an N-dimensional input) of length \( \max(\text{len}(a), \text{len}(b)) - 1 \). If zi is None or is not given then initial rest is assumed. See lfiltic for more information.

Returns

y  [array] The output of the digital filter.

zf  [array, optional] If zi is None, this is not returned, otherwise, zf holds the final filter delay values.

See also:

lfiltic

Construct initial conditions for lfilter.

lfilter_zi

Compute initial state (steady state of step response) for lfilter.

filtfilt

A forward-backward filter, to obtain a filter with linear phase.

savgol_filter

A Savitzky-Golay filter.

sosfilt

Filter data using cascaded second-order sections.

sosfiltfilt

A forward-backward filter using second-order sections.

Notes

The filter function is implemented as a direct II transposed structure. This means that the filter implements:

\[
\]

where \( M \) is the degree of the numerator, \( N \) is the degree of the denominator, and \( n \) is the sample number. It is implemented using the following difference equations (assuming \( M = N \)):

\[
\begin{align*}
a[0]y[n] &= b[0]x[n] + d[0]y[n-1] \\
\vdots \\
\end{align*}
\]

where \( d \) are the state variables.

The rational transfer function describing this filter in the z-transform domain is:

\[
Y(z) = \frac{-1}{b[0] + b[1]z + \ldots + b[M]z^{-M}} X(z)
\]

(continues on next page)
Examples

Generate a noisy signal to be filtered:

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> t = np.linspace(-1, 1, 201)
>>> x = (np.sin(2*np.pi*0.75*t*(1-t)) +
... 0.1*np.sin(2*np.pi*1.25*t + 1) +
... 0.18*np.cos(2*np.pi*3.85*t))
>>> xn = x + np.random.randn(len(t)) * 0.08
```

Create an order 3 lowpass butterworth filter:

```python
>>> b, a = signal.butter(3, 0.05)
```

Apply the filter to xn. Use `lfiltic` to choose the initial condition of the filter:

```python
>>> zi = signal.lfiltic(b, a, y)
>>> z, _ = signal.lfilter(b, a, xn, zi=zi*xn[0])
```

Apply the filter again, to have a result filtered at an order the same as `filtfilt`:

```python
>>> z2, _ = signal.lfilter(b, a, z, zi=zi*z[0])
```

Use `filtfilt` to apply the filter:

```python
>>> y = signal.filtfilt(b, a, xn)
```

Plot the original signal and the various filtered versions:

```python
>>> plt.figure
>>> plt.plot(t, xn, 'b', alpha=0.75)
>>> plt.plot(t, z, 'r--', t, z2, 'r', t, y, 'k')
>>> plt.legend(['noisy signal', 'lfilter, once', 'lfilter, twice',
... 'filtfilt'], loc='best')
>>> plt.grid(True)
>>> plt.show()
```

*scipy.signal.lfiltic*

**scipy.signal.lfiltic(b, a, y, x=None)**

Construct initial conditions for `lfilter` given input and output vectors.

Given a linear filter (b, a) and initial conditions on the output y and the input x, return the initial conditions on the state vector zi which is used by `lfilter` to generate the output given the input.

**Parameters**

- **b** : [array_like] Linear filter term.
- **a** : [array_like] Linear filter term.
- **y** : [array_like] Initial conditions.
  - If N = len(a) - 1, then y = {y[-1], y[-2], ..., y[-N]}. If y is too short, it is padded with zeros.
x  [array_like, optional] Initial conditions.
    If M = len(b) - 1, then x = {x[-1], x[-2], ..., x[-M]}.
    If x is not given, its initial conditions are assumed zero.
    If x is too short, it is padded with zeros.

Returns
zi  [ndarray] The state vector \( z_i = \{z_0[-1], z_1[-1], \ldots, z_{K-1}[{-1}]\} \), where
    \( K = \max(M, N) \).

See also:
lfilt, lfilter_zi

scipy.signal.lfilter_zi
scipy.signal.lfilter_zi(b, a)
    Construct initial conditions for lfilter for step response steady-state.

    Compute an initial state \( zi \) for the lfilter function that corresponds to the steady state of the step
    response. A typical use of this function is to set the initial state so that the output of the filter starts at the same
    value as the first element of the signal to be filtered.

Parameters
b, a  [array_like (1-D)] The IIR filter coefficients. See lfilter for more information.

Returns
zi  [1-D ndarray] The initial state for the filter.

See also:
lfilt, lfilter, filtfilt
**Notes**

A linear filter with order \( m \) has a state space representation \((A, B, C, D)\), for which the output \( y \) of the filter can be expressed as:

\[
\begin{align*}
    z(n+1) & = A \cdot z(n) + B \cdot x(n) \\
    y(n) & = C \cdot z(n) + D \cdot x(n)
\end{align*}
\]

where \( z(n) \) is a vector of length \( m \), \( A \) has shape \((m, m)\), \( B \) has shape \((m, 1)\), \( C \) has shape \((1, m)\) and \( D \) has shape \((1, 1)\) (assuming \( x(n) \) is a scalar). \texttt{lfilter\_zi} solves:

\[
\begin{align*}
    z_i & = A \cdot z_i + B
\end{align*}
\]

In other words, it finds the initial condition for which the response to an input of all ones is a constant.

Given the filter coefficients \( a \) and \( b \), the state space matrices for the transposed direct form II implementation of the linear filter, which is the implementation used by scipy.signal.lfilter, are:

\[
\begin{align*}
    A & = \texttt{scipy.linalg.companion}(a).T \\
    B & = b[1:] - a[1:] \cdot b[0]
\end{align*}
\]

assuming \( a[0] \) is 1.0; if \( a[0] \) is not 1, \( a \) and \( b \) are first divided by \( a[0] \).

**Examples**

The following code creates a lowpass Butterworth filter. Then it applies that filter to an array whose values are all 1.0; the output is also all 1.0, as expected for a lowpass filter. If the \( z_i \) argument of \texttt{lfilter} had not been given, the output would have shown the transient signal.

```python
>>> from numpy import array, ones
>>> from scipy.signal import lfilter, lfilter_zi, butter
>>> b, a = butter(5, 0.25)
>>> zi = lfilter_zi(b, a)
>>> y, zo = lfilter(b, a, ones(10), zi=zi)
>>> y
array([1., 1., 1., 1., 1., 1., 1., 1., 1., 1.])
```

Another example:

```python
>>> x = array([0.5, 0.5, 0.5, 0.0, 0.0, 0.0, 0.0])
>>> y, zf = lfilter(b, a, x, zi=zi*x[0])
>>> y
array([ 0.5 , 0.5 , 0.5 , 0.49836039, 0.48610528,
        0.44399389, 0.35505241])
```

Note that the \( z_i \) argument to \texttt{lfilter} was computed using \texttt{lfilter\_zi} and scaled by \( x[0] \). Then the output \( y \) has no transient until the input drops from 0.5 to 0.0.

**scipy.signal.filtfilt**

\[
\texttt{scipy.signal.filtfilt}(b, a, x, axis=-1, padtype='odd', padlen=None, method='pad', iirlen=None)
\]

Apply a digital filter forward and backward to a signal.

This function applies a linear digital filter twice, once forward and once backwards. The combined filter has zero phase and a filter order twice that of the original.

The function provides options for handling the edges of the signal.

**Parameters**
b  [(N,) array_like] The numerator coefficient vector of the filter.

a  [(N,) array_like] The denominator coefficient vector of the filter. If a[0] is not 1, then both a and b are normalized by a[0].

x  [array_like] The array of data to be filtered.

axis  [int, optional] The axis of x to which the filter is applied. Default is -1.

padtype  [str or None, optional] Must be ‘odd’, ‘even’, ‘constant’, or None. This determines the type of extension to use for the padded signal to which the filter is applied. If padtype is None, no padding is used. The default is ‘odd’.

padlen  [int or None, optional] The number of elements by which to extend x at both ends of axis before applying the filter. This value must be less than x.shape[axis] - 1. padlen=0 implies no padding. The default value is 3 * max(len(a), len(b)).

method  [str, optional] Determines the method for handling the edges of the signal, either “pad” or “gust”. When method is “pad”, the signal is padded; the type of padding is determined by padtype and padlen, and ilen is ignored. When method is “gust”, Gustafsson’s method is used, and padtype and padlen are ignored.

ilen  [int or None, optional] When method is “gust”, ilen specifies the length of the impulse response of the filter. If ilen is None, no part of the impulse response is ignored. For a long signal, specifying ilen can significantly improve the performance of the filter.

Returns

y  [ndarray] The filtered output with the same shape as x.

See also:

sosfiltfilt, lfilter_zi, lfilter, lfilteric, savgol_filter, sosfilt

Notes

When method is “pad”, the function pads the data along the given axis in one of three ways: odd, even or constant. The odd and even extensions have the corresponding symmetry about the end point of the data. The constant extension extends the data with the values at the end points. On both the forward and backward passes, the initial condition of the filter is found by using lfilter_zi and scaling it by the end point of the extended data.

When method is “gust”, Gustafsson’s method [1] is used. Initial conditions are chosen for the forward and backward passes so that the forward-backward filter gives the same result as the backward-forward filter.

The option to use Gustafsson’s method was added in scipy version 0.16.0.

References

[1]

Examples

The examples will use several functions from scipy.signal.

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

First we create a one second signal that is the sum of two pure sine waves, with frequencies 5 Hz and 250 Hz, sampled at 2000 Hz.

```python
>>> t = np.linspace(0, 1.0, 2001)
>>> xlow = np.sin(2 * np.pi * 5 * t)
>>> xhigh = np.sin(2 * np.pi * 250 * t)
>>> x = xlow + xhigh
```
Now create a lowpass Butterworth filter with a cutoff of 0.125 times the Nyquist frequency, or 125 Hz, and apply it to \( x \) with \texttt{filtfilt}. The result should be approximately \( x_{\text{low}} \), with no phase shift.

```python
>>> b, a = signal.butter(8, 0.125)
>>> y = signal.filtfilt(b, a, x, padlen=150)
>>> np.abs(y - xlow).max()
9.1086182074789912e-06
```

We get a fairly clean result for this artificial example because the odd extension is exact, and with the moderately long padding, the filter’s transients have dissipated by the time the actual data is reached. In general, transient effects at the edges are unavoidable.

The following example demonstrates the option \texttt{method=gust}.

First, create a filter.

```python
>>> b, a = signal.ellip(4, 0.01, 120, 0.125)  # Filter to be applied.
>>> np.random.seed(123456)
```

\( \text{sig} \) is a random input signal to be filtered.

```python
>>> n = 60
>>> sig = np.random.randn(n)**3 + 3*np.random.randn(n).cumsum()
```

Apply \texttt{filtfilt} to \( \text{sig} \), once using the Gustafsson method, and once using padding, and plot the results for comparison.

```python
>>> fgust = signal.filtfilt(b, a, sig, method="gust")
>>> fpad = signal.filtfilt(b, a, sig, padlen=50)
>>> plt.plot(sig, 'k-', label='input')
>>> plt.plot(fgust, 'b-', linewidth=4, label='gust')
>>> plt.plot(fpad, 'c-', linewidth=1.5, label='pad')
>>> plt.legend(loc='best')
>>> plt.show()
```

![Plot of input, Gustafsson method, and padding](image)

The \texttt{irlen} argument can be used to improve the performance of Gustafsson’s method.
Estimate the impulse response length of the filter.

```python
>>> z, p, k = signal.tf2zpk(b, a)
>>> eps = 1e-9
>>> r = np.max(np.abs(p))
>>> approx_impulse_len = int(np.ceil(np.log(eps) / np.log(r)))
>>> approx_impulse_len
137
```

Apply the filter to a longer signal, with and without the `irlen` argument. The difference between $y_1$ and $y_2$ is small. For long signals, using `irlen` gives a significant performance improvement.

```python
>>> x = np.random.randn(5000)
>>> y1 = signal.filtfilt(b, a, x, method='gust')
>>> y2 = signal.filtfilt(b, a, x, method='gust', irlen=approx_impulse_len)
>>> print(np.max(np.abs(y1 - y2)))
1.80056858312e-10
```

The function `scipy.signal.savgol_filter` is used to apply a Savitzky-Golay filter to an array.

This is a 1-d filter. If `x` has dimension greater than 1, `axis` determines the axis along which the filter is applied.

**Parameters**

- `x` ([array_like]) The data to be filtered. If `x` is not a single or double precision floating point array, it will be converted to type `numpy.float64` before filtering.
- `window_length` ([int]) The length of the filter window (i.e. the number of coefficients). `window_length` must be a positive odd integer. If `mode` is ‘interp’, `window_length` must be less than or equal to the size of `x`.
- `polyorder` ([int]) The order of the polynomial used to fit the samples. `polyorder` must be less than `window_length`.
- `deriv` ([int, optional]) The order of the derivative to compute. This must be a nonnegative integer. The default is 0, which means to filter the data without differentiating.
- `delta` ([float, optional]) The spacing of the samples to which the filter will be applied. This is only used if `deriv` > 0. Default is 1.0.
- `axis` ([int, optional]) The axis of the array `x` along which the filter is to be applied. Default is -1.
- `mode` ([str, optional]) Must be ‘mirror’, ‘constant’, ‘nearest’, ‘wrap’ or ‘interp’. This determines the type of extension to use for the padded signal to which the filter is applied. When `mode` is ‘constant’, the padding value is given by `cval`. See the Notes for more details on ‘mirror’, ‘constant’, ‘wrap’, and ‘nearest’. When the ‘interp’ mode is selected (the default), no extension is used. Instead, a degree `polyorder` polynomial is fit to the last `window_length` values of the edges, and this polynomial is used to evaluate the last `window_length // 2` output values.
- `cval` ([scalar, optional]) Value to fill past the edges of the input if `mode` is ‘constant’. Default is 0.0.

**Returns**

- `y` ([ndarray, same shape as `x`]) The filtered data.
See also:

savgol_coeffs

Notes
Details on the mode options:

'mirror':
Repeats the values at the edges in reverse order. The value closest to the edge is not included.

'nearest':
The extension contains the nearest input value.

'constant':
The extension contains the value given by the cval argument.

'wrap':
The extension contains the values from the other end of the array.

For example, if the input is [1, 2, 3, 4, 5, 6, 7, 8], and window_length is 7, the following shows the extended data for the various mode options (assuming cval is 0):

<table>
<thead>
<tr>
<th>mode</th>
<th>Ext</th>
<th>Input</th>
<th>Ext</th>
</tr>
</thead>
<tbody>
<tr>
<td>'mirror'</td>
<td>4 3 2</td>
<td>1 2 3 4 5 6 7 8</td>
<td>1 2 3 4 5 6 7 8</td>
</tr>
<tr>
<td>'nearest'</td>
<td>1 1 1</td>
<td>1 2 3 4 5 6 7 8</td>
<td>1 2 3 4 5 6 7 8</td>
</tr>
<tr>
<td>'constant'</td>
<td>0 0 0</td>
<td>1 2 3 4 5 6 7 8</td>
<td>0 0 0 1 2 3 4 5 6 7 8</td>
</tr>
<tr>
<td>'wrap'</td>
<td>6 7 8</td>
<td>1 2 3 4 5 6 7 8</td>
<td>1 2 3 4 5 6 7 8</td>
</tr>
</tbody>
</table>

New in version 0.14.0.

Examples

```python
>>> from scipy.signal import savgol_filter
>>> np.set_printoptions(precision=2)  # For compact display.
>>> x = np.array([2, 2, 5, 2, 1, 0, 1, 4, 9])
```

Filter with a window length of 5 and a degree 2 polynomial. Use the defaults for all other parameters.

```python
>>> savgol_filter(x, 5, 2)
array([ 1.66, 3.17, 3.54, 2.86, 0.66, 0.17, 1.0 , 4.0 , 9.0 ])
```

Note that the last five values in x are samples of a parabola, so when mode='interp' (the default) is used with polyorder=2, the last three values are unchanged. Compare that to, for example, mode='nearest':

```python
>>> savgol_filter(x, 5, 2, mode='nearest')
array([ 1.74, 3.03, 3.54, 2.86, 0.66, 0.17, 1.0 , 4.6 , 7.97])
```

scipy.signal.deconvolve

scipy.signal.deconvolve(signal, divisor)

Deconvolves divisor out of signal using inverse filtering.

Returns the quotient and remainder such that signal = convolve(divisor, quotient) + remainder

Parameters

- signal [array_like] Signal data, typically a recorded signal
- divisor [array_like] Divisor data, typically an impulse response or filter that was applied to the original signal

Returns
**quotient** [ndarray] Quotient, typically the recovered original signal

**remainder** [ndarray] Remainder

**See also:**

* numpy.polydiv
  
  performs polynomial division (same operation, but also accepts poly1d objects)

**Examples**

Deconvolve a signal that’s been filtered:

```python
>>> from scipy import signal
>>> original = [0, 1, 0, 0, 1, 1, 0, 0]
>>> impulse_response = [2, 1]
>>> recorded = signal.convolve(impulse_response, original)
>>> recorded
array([0, 2, 1, 0, 2, 3, 1, 0, 0])
>>> recovered, remainder = signal.deconvolve(recorded, impulse_response)
>>> recovered
array([ 0., 1., 0., 0., 1., 1., 0., 0.])
```

**scipy.signal.sosfilt**

**scipy.signal.sosfilt**(sos, x, axis=-1, zi=None)

Filter data along one dimension using cascaded second-order sections.

Filter a data sequence, x, using a digital IIR filter defined by sos. This is implemented by performing lfilter for each second-order section. See lfilter for details.

**Parameters**

- **sos** [array_like] Array of second-order filter coefficients, must have shape (n_sections, 6). Each row corresponds to a second-order section, with the first three columns providing the numerator coefficients and the last three providing the denominator coefficients.

- **x** [array_like] An N-dimensional input array.

- **axis** [int, optional] The axis of the input data array along which to apply the linear filter. The filter is applied to each subarray along this axis. Default is -1.

- **zi** [array_like, optional] Initial conditions for the cascaded filter delays. It is a (at least 2D) vector of shape (n_sections, ..., 2, ...), where ..., 2, ... denotes the shape of x, but with x.shape[axis] replaced by 2. If zi is None or is not given then initial rest (i.e. all zeros) is assumed. Note that these initial conditions are not the same as the initial conditions given by lfilter or lfilter_zi.

**Returns**

- **y** [ndarray] The output of the digital filter.

- **zf** [ndarray, optional] If zi is None, this is not returned, otherwise, zf holds the final filter delay values.

**See also:**

zpk2sos, sos2zpk, sosfilt_zi, sosfiltfilt, sosfreqz
Notes
The filter function is implemented as a series of second-order filters with direct-form II transposed structure. It is designed to minimize numerical precision errors for high-order filters.

New in version 0.16.0.

Examples
Plot a 13th-order filter’s impulse response using both \texttt{lfilter} and \texttt{sosfilt}, showing the instability that results from trying to do a 13th-order filter in a single stage (the numerical error pushes some poles outside of the unit circle):

```python
>>> import matplotlib.pyplot as plt
>>> from scipy import signal
>>> b, a = signal.ellip(13, 0.009, 80, 0.05, output='ba')
>>> sos = signal.ellip(13, 0.009, 80, 0.05, output='sos')
>>> x = signal.unit_impulse(700)
>>> y_tf = signal.lfilter(b, a, x)
>>> y_sos = signal.sosfilt(sos, x)
>>> plt.plot(y_tf, 'r', label='TF')
>>> plt.plot(y_sos, 'k', label='SOS')
>>> plt.legend(loc='best')
>>> plt.show()
```

![Plot of impulse response](image)

\texttt{scipy.signal.sosfilt\_zi}

\texttt{scipy.signal.sosfilt\_zi(sos)}

Construct initial conditions for \texttt{sosfilt} for step response steady-state.

Compute an initial state $z_i$ for the \texttt{sosfilt} function that corresponds to the steady state of the step response.

A typical use of this function is to set the initial state so that the output of the filter starts at the same value as the first element of the signal to be filtered.

**Parameters**

- \texttt{sos} [array\_like] Array of second-order filter coefficients, must have shape (n\_sections, 6). See \texttt{sosfilt} for the SOS filter format specification.
**Returns**

\( zi \) [ndarray] Initial conditions suitable for use with `sosfilt`, shape \((n \text{\_sections}, 2)\).

See also:

`sosfilt`, `zpk2sos`

**Notes**

New in version 0.16.0.

**Examples**

Filter a rectangular pulse that begins at time 0, with and without the use of the \( zi \) argument of `scipy.signal.sosfilt`.

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

>>> sos = signal.butter(9, 0.125, output='sos')
>>> zi = signal.sosfilt_zi(sos)
>>> x = (np.arange(250) < 100).astype(int)
>>> f1 = signal.sosfilt(sos, x)
>>> f2, zo = signal.sosfilt(sos, x, zi=zi)

>>> plt.plot(x, 'k--', label='x')
>>> plt.plot(f1, 'b', alpha=0.5, linewidth=2, label='filtered')
>>> plt.plot(f2, 'g', alpha=0.25, linewidth=4, label='filtered with zi')
>>> plt.legend(loc='best')
>>> plt.show()
```

`scipy.signal.sosfiltfilt`

`scipy.signal.sosfiltfilt(sos, x, axis=-1, padtype='odd', padlen=None)`

A forward-backward digital filter using cascaded second-order sections.

See `filtfilt` for more complete information about this method.
Parameters

sos  [array_like] Array of second-order filter coefficients, must have shape (n_sections, 6). Each row corresponds to a second-order section, with the first three columns providing the numerator coefficients and the last three providing the denominator coefficients.

x  [array_like] The array of data to be filtered.

axis  [int, optional] The axis of x to which the filter is applied. Default is -1.

padtype  [str or None, optional] Must be ‘odd’, ‘even’, ‘constant’, or None. This determines the type of extension to use for the padded signal to which the filter is applied. If padtype is None, no padding is used. The default is ‘odd’.

padlen  [int or None, optional] The number of elements by which to extend x at both ends of axis before applying the filter. This value must be less than x.shape[axis] - 1. padlen=0 implies no padding. The default value is:

\[
3 \times (2 \times \text{len(sos)} + 1 - \min((\text{sos}[:, 2] == 0).\text{sum()}, \\
(\text{sos}[:, 5] == 0).\text{sum()}))
\]

The extra subtraction at the end attempts to compensate for poles and zeros at the origin (e.g. for odd-order filters) to yield equivalent estimates of padlen to those of \text{filtfilt} for second-order section filters built with \text{scipy.signal} functions.

Returns

y  [ndarray] The filtered output with the same shape as x.

See also:

\text{filtfilt, sosfilt, sosfilt_zi, sosfreqz}

Notes

New in version 0.18.0.

Examples

```python
>>> from scipy.signal import sosfiltfilt, butter
>>> import matplotlib.pyplot as plt

Create an interesting signal to filter.

>>> n = 201
>>> t = np.linspace(0, 1, n)
>>> np.random.seed(123)
>>> x = 1 + (t < 0.5) - 0.25*t**2 + 0.05*np.random.randn(n)

Create a lowpass Butterworth filter, and use it to filter x.

```python
>>> sos = butter(4, 0.125, output='sos')
>>> y = sosfiltfilt(sos, x)
```  
For comparison, apply an 8th order filter using \text{sosfilt}. The filter is initialized using the mean of the first four values of x.

```python
>>> from scipy.signal import sosfilt, sosfilt_zi
>>> sos8 = butter(8, 0.125, output='sos')
>>> zi = x[:4].mean() * sosfilt_zi(sos8)
>>> y2, zo = sosfilt(sos8, x, zi=zi)
```  
Plot the results. Note that the phase of y matches the input, while y2 has a significant phase delay.
>>> plt.plot(t, x, alpha=0.5, label='x(t)')
>>> plt.plot(t, y, label='y(t)')
>>> plt.plot(t, y2, label='y2(t)')
>>> plt.legend(framealpha=1, shadow=True)
>>> plt.grid(alpha=0.25)
>>> plt.xlabel('t')
>>> plt.show()
In other words, the negative half of the frequency spectrum is zeroed out, turning the real-valued signal into a complex signal. The Hilbert transformed signal can be obtained from \( \text{np.imag(hilbert(x))} \), and the original signal from \( \text{np.real(hilbert(x))} \).

References
[1], [2], [3]

Examples
In this example we use the Hilbert transform to determine the amplitude envelope and instantaneous frequency of an amplitude-modulated signal.

```python
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> from scipy.signal import hilbert, chirp

>>> duration = 1.0
>>> fs = 400.0
>>> samples = int(fs*duration)
>>> t = np.arange(samples) / fs

We create a chirp of which the frequency increases from 20 Hz to 100 Hz and apply an amplitude modulation.

>>> signal = chirp(t, 20.0, t[-1], 100.0)
>>> signal *= (1.0 + 0.5 * np.sin(2.0*np.pi*3.0*t))

The amplitude envelope is given by magnitude of the analytic signal. The instantaneous frequency can be obtained by differentiating the instantaneous phase in respect to time. The instantaneous phase corresponds to the phase angle of the analytic signal.

```python
>>> analytic_signal = hilbert(signal)
>>> amplitude_envelope = np.abs(analytic_signal)
>>> instantaneous_phase = np.unwrap(np.angle(analytic_signal))
>>> instantaneous_frequency = (np.diff(instantaneous_phase) / (2.0*np.pi) * fs)
```
N [int or tuple of two ints, optional] Number of Fourier components. Default is x. shape

Returns

xa [ndarray] Analytic signal of x taken along axes (0,1).

References

[1]

scipy.signal.decimate

scipy.signal.decimate(x, q, n=None, ftype='iir', axis=-1, zero_phase=True)

Downsample the signal after applying an anti-aliasing filter.

By default, an order 8 Chebyshev type I filter is used. A 30 point FIR filter with Hamming window is
used if ftype is ‘fir’.

Parameters

x [array_like] The signal to be downsampled, as an N-dimensional array.
q [int] The downsampling factor. When using IIR downsampling, it is recommended
to call decimate multiple times for downsampling factors higher than 13.
n [int, optional] The order of the filter (1 less than the length for ‘fir’). Defaults to
8 for ‘iir’ and 20 times the downsampling factor for ‘fir’.
ftype [str {'iir', 'fir'} or dlti instance, optional] If ‘iir’ or ‘fir’, specifies the type of
lowpass filter. If an instance of an dlti object, uses that object to filter before
downsampling.
axis [int, optional] The axis along which to decimate.
zero_phase [bool, optional] Prevent phase shift by filtering with filtfilt instead of lfilter
when using an IIR filter, and shifting the outputs back by the filter’s group delay
when using an FIR filter. The default value of True is recommended, since a phase
shift is generally not desired.
New in version 0.18.0.

Returns

y [ndarray] The down-sampled signal.
See also:

resample

Resample up or down using the FFT method.

resample_poly

Resample using polyphase filtering and an FIR filter.

Notes

The zero_phase keyword was added in 0.18.0. The possibility to use instances of dlti as ftype was added in 0.18.0.

scipy.signal.detrend

scipy.signal.detrend(data, axis=-1, type='linear', bp=0)

Remove linear trend along axis from data.

Parameters

data [array_like] The input data.
axis [int, optional] The axis along which to detrend the data. By default this is the last axis (-1).
type [{‘linear’, ‘constant’}, optional] The type of detrending. If type == ‘linear’ (default), the result of a linear least-squares fit to data is subtracted from data. If type == ‘constant’, only the mean of data is subtracted.
bp [array_like of ints, optional] A sequence of break points. If given, an individual linear fit is performed for each part of data between two break points. Break points are specified as indices into data.

Returns

ret [ndarray] The detrended input data.

Examples

```python
>>> from scipy import signal
>>> randgen = np.random.RandomState(9)
>>> npoints = 1000
>>> noise = randgen.randn(npoints)
>>> x = 3 + 2*np.linspace(0, 1, npoints) + noise
>>> (signal.detrend(x) - noise).max() < 0.01
True
```

scipy.signal.resample

scipy.signal.resample(x, num, t=None, axis=0, window=None)

Resample x to num samples using Fourier method along the given axis.

The resampled signal starts at the same value as x but is sampled with a spacing of \( \text{len}(x) / \text{num} \) (spacing of x). Because a Fourier method is used, the signal is assumed to be periodic.

Parameters

x [array_like] The data to be resampled.
num [int] The number of samples in the resampled signal.
t [array_like, optional] If t is given, it is assumed to be the sample positions associated with the signal data in x.
axis [int, optional] The axis of x that is resampled. Default is 0.
window  [array_like, callable, string, float, or tuple, optional] Specifies the window applied to the signal in the Fourier domain. See below for details.

Returns

resampled_x or (resampled_x, resampled_t)

Either the resampled array, or, if t was given, a tuple containing the resampled array and the corresponding resampled positions.

See also:

decimate

Downsample the signal after applying an FIR or IIR filter.

resample_poly

Resample using polyphase filtering and an FIR filter.

Notes

The argument window controls a Fourier-domain window that tapers the Fourier spectrum before zero-padding to alleviate ringing in the resampled values for sampled signals you didn’t intend to be interpreted as band-limited.

If window is a function, then it is called with a vector of inputs indicating the frequency bins (i.e. fftfreq(x.shape[axis])).

If window is an array of the same length as x.shape[axis] it is assumed to be the window to be applied directly in the Fourier domain (with dc and low-frequency first).

For any other type of window, the function scipy.signal.get_window is called to generate the window.

The first sample of the returned vector is the same as the first sample of the input vector. The spacing between samples is changed from dx to dx * len(x) / num.

If t is not None, then it represents the old sample positions, and the new sample positions will be returned as well as the new samples.

As noted, resample uses FFT transformations, which can be very slow if the number of input or output samples is large and prime; see scipy.fftpack.fft.

Examples

Note that the end of the resampled data rises to meet the first sample of the next cycle:

```python
>>> from scipy import signal

>>> x = np.linspace(0, 10, 20, endpoint=False)
>>> y = np.cos(-x**2/6.0)
>>> f = signal.resample(y, 100)
>>> xnew = np.linspace(0, 10, 100, endpoint=False)

>>> import matplotlib.pyplot as plt
>>> plt.plot(x, y, 'go-', xnew, f, '.-', 10, y[0], 'ro')
>>> plt.legend([['data', 'resampled'], loc='best'])
>>> plt.show()
```

scipy.signal.resample_poly

scipy.signal.resample_poly(x, up, down, axis=0, window=('kaiser', 5.0))

Resample x along the given axis using polyphase filtering.
The signal $x$ is upsampled by the factor $up$, a zero-phase low-pass FIR filter is applied, and then it is downsampled by the factor $down$. The resulting sample rate is $up / down$ times the original sample rate. Values beyond the boundary of the signal are assumed to be zero during the filtering step.

**Parameters**

- `x` : [array_like] The data to be resampled.
- `up` : [int] The upsampling factor.
- `down` : [int] The downsampling factor.
- `axis` : [int, optional] The axis of $x$ that is resampled. Default is 0.
- `window` : [string, tuple, or array_like, optional] Desired window to use to design the low-pass filter, or the FIR filter coefficients to employ. See below for details.

**Returns**

- `resampled_x` : [array] The resampled array.

**See also:**

decimate

Downsample the signal after applying an FIR or IIR filter.

resample

Resample up or down using the FFT method.

**Notes**

This polyphase method will likely be faster than the Fourier method in *scipy.signal.resample* when the number of samples is large and prime, or when the number of samples is large and $up$ and $down$ share a large greatest common denominator. The length of the FIR filter used will depend on $\max(up, down) // \gcd(up, down)$, and the number of operations during polyphase filtering will depend on the filter length and $down$ (see *scipy.signal.upfirdn* for details).

The argument `window` specifies the FIR low-pass filter design.

If `window` is an array_like it is assumed to be the FIR filter coefficients. Note that the FIR filter is applied after the upsampling step, so it should be designed to operate on a signal at a sampling rate of $up$. 
frequency higher than the original by a factor of \( \frac{up}{\gcd(up, down)} \). This function’s output will be centered with respect to this array, so it is best to pass a symmetric filter with an odd number of samples if, as is usually the case, a zero-phase filter is desired.

For any other type of window, the functions \texttt{scipy.signal.get_window} and \texttt{scipy.signal.firwin} are called to generate the appropriate filter coefficients.

The first sample of the returned vector is the same as the first sample of the input vector. The spacing between samples is changed from \( dx \) to \( dx \times \frac{down}{float(up)} \).

**Examples**

Note that the end of the resampled data rises to meet the first sample of the next cycle for the FFT method, and gets closer to zero for the polyphase method:

```python
>>> from scipy import signal

>>> x = np.linspace(0, 10, 20, endpoint=False)
>>> y = np.cos(-x**2/6.0)
>>> f_fft = signal.resample(y, 100)
>>> f_poly = signal.resample_poly(y, 100, 20)
>>> xnew = np.linspace(0, 10, 100, endpoint=False)

>>> import matplotlib.pyplot as plt
>>> plt.plot(xnew, f_fft, 'b-', xnew, f_poly, 'r-')
>>> plt.plot(x, y, 'ko-')  # boundaries
>>> plt.legend([['resample', 'resamp_poly', 'data'], loc='best'])
>>> plt.show()
```

**scipy.signal.upfirdn**

\texttt{scipy.signal.upfirdn}(h, x, up=1, down=1, axis=-1)

Upsample, FIR filter, and downsample

**Parameters**

- \( h \)  
  
  [array_like] 1-dimensional FIR (finite-impulse response) filter coefficients.
x  [array_like] Input signal array.
up  [int, optional] Upsampling rate. Default is 1.
down [int, optional] Downsampling rate. Default is 1.
axis [int, optional] The axis of the input data array along which to apply the linear filter. The filter is applied to each subarray along this axis. Default is -1.

Returns

y  [ndarray] The output signal array. Dimensions will be the same as x except for along axis, which will change size according to the h, up, and down parameters.

Notes

The algorithm is an implementation of the block diagram shown on page 129 of the Vaidyanathan text [1] (Figure 4.3-8d).

The direct approach of upsampling by factor of P with zero insertion, FIR filtering of length N, and downsampling by factor of Q is O(N*Q) per output sample. The polyphase implementation used here is O(N/P).

New in version 0.18.

Examples

Simple operations:

```python
>>> from scipy.signal import upfirdn
>>> upfirdn([1, 1, 1], [1, 1, 1])  # FIR filter
array([1., 1., 1.])
>>> upfirdn([1], [1, 2, 3], 3)  # upsampling with zeros insertion
array([1., 0., 0., 2., 0., 0., 3., 0., 0.])
>>> upfirdn([1, 1, 1], [1, 2, 3], 3)  # upsampling with sample-and-hold
array([1., 1., 1., 2., 2., 2., 3., 3., 3.])
>>> upfirdn([.5, 1, .5], [1, 1, 1], 2)  # linear interpolation
array([0.5, 1.0, 1.0, 1.0, 1.0, 1.0, 0.5, 0.0])
>>> upfirdn([1], np.arange(10), 1, 3)  # decimation by 3
array([0., 3., 6., 9.])
>>> upfirdn([.5, 1, .5], np.arange(10), 2, 3)  # linear interp, rate 2/3
array([0.0, 1.0, 2.5, 4.0, 5.5, 7.0, 8.5, 0.0])
```

Apply a single filter to multiple signals:

```python
>>> x = np.reshape(np.arange(8), (4, 2))
>>> x
array([[0, 1],
       [2, 3],
       [4, 5],
       [6, 7]])
```

Apply along the last dimension of x:

```python
>>> h = [1, 1]
>>> upfirdn(h, x, 2)
array([[ 0.,  0.,  1.,  1.],
       [ 2.,  2.,  3.,  3.],
       [ 4.,  4.,  5.,  5.],
       [ 6.,  6.,  7.,  7.]])
```

Apply along the 0th dimension of x:

```python
>>> h = [1, 1]
>>> upfirdn(h, x, 2)
array([[ 0.,  0.,  1.,  1.],
       [ 2.,  2.,  3.,  3.],
       [ 4.,  4.,  5.,  5.],
       [ 6.,  6.,  7.,  7.]])
```
>> upfirdn(h, x, 2, axis=0)
array([[ 0., 1.],
   [ 0., 1.],
   [ 2., 3.],
   [ 2., 3.],
   [ 4., 5.],
   [ 4., 5.],
   [ 6., 7.],
   [ 6., 7.]])

6.20.4 Filter design

*bilinear*(b, a[, fs])

Return a digital filter from an analog one using a bilinear transform.

*bilinear_zpk*(z, p, k, fs)

Return a digital IIR filter from an analog one using a bilinear transform.

*findfreqs*(num, den, N[, kind])

Find array of frequencies for computing the response of an analog filter.

*firls*(numtaps, bands, desired[, weight, nyq, fs])

FIR filter design using least-squares error minimization.

*firwin*(numtaps, cutoff[, width, window, ...])

FIR filter design using the window method.

*firwin2*(numtaps, freq, gain[, nfreqs, ...])

FIR filter design using the window method.

*freqs*(b, a[, worN, plot])

Compute frequency response of analog filter.

*freqs_zpk*(z, p, k[, worN])

Compute frequency response of analog filter.

*freqz*(b[, a, worN, whole, plot, fs])

Compute the frequency response of a digital filter.

*freqz_zpk*(z, p, k[, worN, whole, fs])

Compute the frequency response of a digital filter in ZPK form.

*sosfreqz*(sos[, worN, whole, fs])

Compute the frequency response of a digital filter in SOS format.

*group_delay*(system[, w, whole, fs])

Compute the group delay of a digital filter.

*iirdesign*(wp, ws, gpass, gstop[, analog, ...])

Complete IIR digital and analog filter design.

*iirfilter*(N, Wn[, rp, rs, btype, analog, ...])

IIR digital and analog filter design given order and critical points.

*kaiser_atten*(numtaps, width)

Compute the attenuation of a Kaiser FIR filter.

*kaiser_beta*(a)

Compute the Kaiser parameter beta, given the attenuation a.

*kaiserord*(ripple, width)

Determine the filter window parameters for the Kaiser window method.

*minimum_phase*[h[, method, n_fft]]

Convert a linear-phase FIR filter to minimum phase.

*savgol_coeffs*(window_length, polyorder[, ...])

Compute the coefficients for a 1-d Savitzky-Golay FIR filter.

*remez*(numtaps, bands, desired[, weight, Hz, ...])

Calculate the minimax optimal filter using the Remez exchange algorithm.

*unique_roots*(p[, tol, rtype])

Determine unique roots and their multiplicities from a list of roots.

*residue*[b, a[, tol, rtype]]

Compute partial-fraction expansion of b(s) / a(s).

*residuez*[b, a[, tol, rtype]]

Compute partial-fraction expansion of b(z) / a(z).

*invres*[r, p, k[, tol, rtype]]

Compute b(s) and a(s) from partial fraction expansion.
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### scipy.signal.bilinear

**scipy.signal.bilinear**

\(\texttt{scipy.signal.bilinear}(b, a, fs=1.0)\)

Return a digital filter from an analog one using a bilinear transform.

The bilinear transform substitutes \((z-1) / (z+1)\) for \(s\).

See also:

\(\texttt{lp2lp}, \texttt{lp2hp}, \texttt{lp2bp}, \texttt{lp2bs}, \texttt{bilinear_zpk}\)

### scipy.signal.bilinear_zpk

**scipy.signal.bilinear_zpk**

\(\texttt{scipy.signal.bilinear_zpk}(z, p, k, fs)\)

Return a digital IIR filter from an analog one using a bilinear transform.

Transform a set of poles and zeros from the analog \(s\)-plane to the digital \(z\)-plane using Tustin’s method, which substitutes \((z-1) / (z+1)\) for \(s\), maintaining the shape of the frequency response.

**Parameters**

- \(z\) : [array_like] Zeros of the analog filter transfer function.
- \(p\) : [array_like] Poles of the analog filter transfer function.
- \(k\) : [float] System gain of the analog filter transfer function.
- \(fs\) : [float] Sample rate, as ordinary frequency (e.g. hertz). No prewarping is done in this function.

**Returns**

- \(z\) : [ndarray] Zeros of the transformed digital filter transfer function.
- \(p\) : [ndarray] Poles of the transformed digital filter transfer function.
- \(k\) : [float] System gain of the transformed digital filter.

See also:

\(\texttt{lp2lp_zpk}, \texttt{lp2hp_zpk}, \texttt{lp2bp_zpk}, \texttt{lp2bs_zpk}, \texttt{bilinear}\)

**Notes**

New in version 1.1.0.

### scipy.signal.findfreqs

**scipy.signal.findfreqs**

\(\texttt{scipy.signal.findfreqs}(num, den, N, kind='ba')\)

Find array of frequencies for computing the response of an analog filter.

**Parameters**

- \(num, den\) : [array_like, 1-D] The polynomial coefficients of the numerator and denominator of the transfer function of the filter or LTI system, where the coefficients are ordered from highest to lowest degree. Or, the roots of the transfer function numerator and denominator (i.e. zeroes and poles).
- \(N\) : [int] The length of the array to be computed.
- \(kind\) : [str {'ba', 'zp'}, optional] Specifies whether the numerator and denominator are specified by their polynomial coefficients ('ba'), or their roots ('zp').

**Returns**

Examples
Find a set of nine frequencies that span the “interesting part” of the frequency response for the filter
with the transfer function

\[ H(s) = \frac{s}{s^2 + 8s + 25} \]

```python
>>> from scipy import signal
>>> signal.findfreqs([1, 0], [1, 8, 25], N=9)
array([ 1.00000000e-02, 3.16227766e-02, 1.00000000e-01,
        3.16227766e-01, 1.00000000e+00, 3.16227766e+00,
        1.00000000e+01, 3.16227766e+01, 1.00000000e+02])
```

scipy.signal.firls

scipy.signal.firls(numtaps, bands, desired, weight=None, nyq=None, fs=None)

FIR filter design using least-squares error minimization.

Calculate the filter coefficients for the linear-phase finite impulse response (FIR) filter which has the
best approximation to the desired frequency response described by bands and desired in the least squares
sense (i.e., the integral of the weighted mean-squared error within the specified bands is minimized).

Parameters

- **numtaps** [int] The number of taps in the FIR filter. numtaps must be odd.
- **bands** [array_like] A monotonic nondecreasing sequence containing the band edges in Hz.
  All elements must be non-negative and less than or equal to the Nyquist frequency
given by nyq.
- **desired** [array_like] A sequence the same size as bands containing the desired gain at the
  start and end point of each band.
- **weight** [array_like, optional] A relative weighting to give to each band region when solving
  the least squares problem. weight has to be half the size of bands.
  in bands must be between 0 and nyq (inclusive). Default is 1.
- **fs** [float, optional] The sampling frequency of the signal. Each frequency in bands
  must be between 0 and fs/2 (inclusive). Default is 2.

Returns

- **coeffs** [ndarray] Coefficients of the optimal (in a least squares sense) FIR filter.

See also:

fird, fird2, minimum_phase, remez

Notes

This implementation follows the algorithm given in [1]. As noted there, least squares design has
multiple advantages:

1. Optimal in a least-squares sense.
2. Simple, non-iterative method.
3. The general solution can obtained by solving a linear system of equations.
4. Allows the use of a frequency dependent weighting function.

This function constructs a Type I linear phase FIR filter, which contains an odd number of coeffs
satisfying for \( n < \text{numtaps} \):

\[ \text{coeffs}(n) = \text{coeffs}(\text{numtaps} - 1 - n) \]
The odd number of coefficients and filter symmetry avoid boundary conditions that could otherwise occur at the Nyquist and 0 frequencies (e.g., for Type II, III, or IV variants).

New in version 0.18.

References
[1]

Examples

We want to construct a band-pass filter. Note that the behavior in the frequency ranges between our stop bands and pass bands is unspecified, and thus may overshoot depending on the parameters of our filter:

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> fig, axs = plt.subplots(2)
>>> fs = 10.0  # Hz
>>> desired = (0, 0, 1, 1, 0, 0)
>>> for bi, bands in enumerate(((0, 1, 2, 3, 4, 5), (0, 1, 2, 4, 4.5, 5))):
...    fir_firls = signal.firls(73, bands, desired, fs=fs)
...    fir_remez = signal.remez(73, bands, desired, fs=fs)
...    fir_firwin2 = signal.firwin2(73, bands, desired, fs=fs)
...    hs = list()
...    ax = axs[bi]
...    for fir in (fir_firls, fir_remez, fir_firwin2):
...        freq, response = signal.freqz(fir)
...        hs.append(ax.semilogy(0.5*fs*freq/np.pi, np.abs(response))[0])
...        for band, gains in zip(bands[::2], bands[1::2]),
...            zip(desired[::2], desired[1::2])):
...            ax.semilogy(band, np.maximum(gains, 1e-7), 'k--', linewidth=2)
...            if bi == 0:
...                ax.legend(hs, ('firls', 'remez', 'firwin2'),
...                    loc='lower center', frameon=False)
...            else:
...                ax.set_xlabel('Frequency (Hz)')
...                ax.grid(True)
...                ax.set(title='Band-pass %d-%d Hz' % bands[2:4], ylabel='Magnitude')
...                ax.set_xlabel('Frequency (Hz)')
...                ax.grid(True)
...                ax.set(title='Band-pass %d-%d Hz' % bands[2:4], ylabel='Magnitude')
>>> fig.tight_layout()
>>> plt.show()
```

`scipy.signal.firwin`

The function `scipy.signal.firwin` computes the coefficients of a finite impulse response filter. The filter will have linear phase; it will be Type I if `numtaps` is odd and Type II if `numtaps` is even.

Type II filters always have zero response at the Nyquist frequency, so a ValueError exception is raised if `firwin` is called with `numtaps` even and having a passband whose right end is at the Nyquist frequency.

**Parameters**

- `numtaps` [int] Length of the filter (number of coefficients, i.e. the filter order + 1). `numtaps` must be odd if a passband includes the Nyquist frequency.
cutoff  [float or 1D array_like] Cutoff frequency of filter (expressed in the same units as
fs) OR an array of cutoff frequencies (that is, band edges). In the latter case, the
frequencies in cutoff should be positive and monotonically increasing between 0
and fs/2. The values 0 and fs/2 must not be included in cutoff.

width  [float or None, optional] If width is not None, then assume it is the approximate
width of the transition region (expressed in the same units as fs) for use in Kaiser
FIR filter design. In this case, the window argument is ignored.

window  [string or tuple of string and parameter values, optional] Desired window to use.
See scipy.signal.get_window for a list of windows and required parameters.

pass_zero  [bool, optional] If True, the gain at the frequency 0 (i.e. the “DC gain”) is 1.
Otherwise the DC gain is 0.

scale  [bool, optional] Set to True to scale the coefficients so that the frequency response
is exactly unity at a certain frequency. That frequency is either:
• 0 (DC) if the first passband starts at 0 (i.e. pass_zero is True)
• fs/2 (the Nyquist frequency) if the first passband ends at fs/2 (i.e the filter is a
single band highpass filter); center of first passband otherwise

nyq  [float, optional] Deprecated. Use ‘fs’ instead. This is the Nyquist frequency. Each
frequency in cutoff must be between 0 and nyq. Default is 1.

fs  [float, optional] The sampling frequency of the signal. Each frequency in cutoff
must be between 0 and fs/2. Default is 2.

Returns

h  [(numtaps,) ndarray] Coefficients of length numtaps FIR filter.

Raises

ValueError

If any value in cutoff is less than or equal to 0 or greater than or equal to fs/2, if
the values in cutoff are not strictly monotonically increasing, or if numtaps is even
but a passband includes the Nyquist frequency.

See also:

firwin2, firls, minimum_phase, remez
Examples

Low-pass from 0 to f:

```python
>>> from scipy import signal
>>> numtaps = 3
>>> f = 0.1
>>> signal.firwin(numtaps, f)
array([ 0.06799017, 0.86401967, 0.06799017])
```

Use a specific window function:

```python
>>> signal.firwin(numtaps, f, window='nuttall')
array([ 3.56607041e-04, 9.99286786e-01, 3.56607041e-04])
```

High-pass ('stop' from 0 to f):

```python
>>> signal.firwin(numtaps, f, pass_zero=False)
array([-0.00859313, 0.98281375, -0.00859313])
```

Band-pass:

```python
>>> f1, f2 = 0.1, 0.2
>>> signal.firwin(numtaps, [f1, f2], pass_zero=False)
array([ 0.06301614, 0.88770441, 0.06301614])
```

Band-stop:

```python
>>> signal.firwin(numtaps, [f1, f2])
array([-0.00801395, 1.0160279 , -0.00801395])
```

Multi-band (passbands are [0, f1], [f2, f3] and [f4, 1]):

```python
>>> f3, f4 = 0.3, 0.4
>>> signal.firwin(numtaps, [f1, f2, f3, f4])
array([-0.01376344, 1.02752689, -0.01376344])
```

Multi-band (passbands are [f1, f2] and [f3,f4]):

```python
>>> signal.firwin(numtaps, [f1, f2, f3, f4], pass_zero=False)
array([ 0.04890915, 0.91284326, 0.04890915])
```

**scipy.signal.firwin2**

`scipy.signal.firwin2(numtaps, freq, gain, nfreqs=None, window='hamming', nyq=None, antisymmetric=False, fs=None)`

FIR filter design using the window method.

From the given frequencies `freq` and corresponding gains `gain`, this function constructs an FIR filter with linear phase and (approximately) the given frequency response.

**Parameters**

- `numtaps` [int] The number of taps in the FIR filter. `numtaps` must be less than `nfreqs`.
- `freq` [array_like, 1D] The frequency sampling points. Typically 0.0 to 1.0 with 1.0 being Nyquist. The Nyquist frequency is half `fs`. The values in `freq` must be nondecreasing. A value can be repeated once to implement a discontinuity. The first value in `freq` must be 0, and the last value must be `fs/2`. 
gain  [array_like] The filter gains at the frequency sampling points. Certain constraints
to gain values, depending on the filter type, are applied, see Notes for details.

nfreqs  [int, optional] The size of the interpolation mesh used to construct the filter. For
most efficient behavior, this should be a power of 2 plus 1 (e.g, 129, 257, etc). The
default is one more than the smallest power of 2 that is not less than numtaps.
nfreqs must be greater than numtaps.

window  [string or (string, float) or float, or None, optional] Window function
to use. Default is “hamming”. See scipy.signal.get_window for the complete list of possible
values. If None, no window function is applied.

nyq  [float, optional] Deprecated. Use ‘fs’ instead. This is the Nyquist frequency. Each
frequency in freq must be between 0 and nyq. Default is 1.

antisymmetric  [bool, optional] Whether resulting impulse response is symmetric/antisymmetric.
See Notes for more details.

fs  [float, optional] The sampling frequency of the signal. Each frequency in cutoff
must be between 0 and fs/2. Default is 2.

Returns
taps  [ndarray] The filter coefficients of the FIR filter, as a 1-D array of length numtaps.

See also: fircls, firwin, minimum_phase, remez

Notes
From the given set of frequencies and gains, the desired response is constructed in the frequency domain.
The inverse FFT is applied to the desired response to create the associated convolution kernel, and
the first numtaps coefficients of this kernel, scaled by window, are returned.

The FIR filter will have linear phase. The type of filter is determined by the value of ‘numtaps’ and
antisymmetric flag. There are four possible combinations:

- odd numtaps, antisymmetric is False, type I filter is produced
- even numtaps, antisymmetric is False, type II filter is produced
- odd numtaps, antisymmetric is True, type III filter is produced
- even numtaps, antisymmetric is True, type IV filter is produced

Magnitude response of all but type I filters are subjects to following constraints:

- type II – zero at the Nyquist frequency
- type III – zero at zero and Nyquist frequencies
- type IV – zero at zero frequency

New in version 0.9.0.

References
[1], [2]

Examples
A lowpass FIR filter with a response that is 1 on [0.0, 0.5], and that decreases linearly on [0.5, 1.0]
from 1 to 0:

>>> from scipy import signal
>>> taps = signal.firwin2(150, [0.0, 0.5, 1.0], [1.0, 1.0, 0.0])
>>> print(taps[72:78])
[-0.02286961 -0.06362756 0.57310236 0.57310236 -0.06362756 -0.02286961]
**scipy.signal.freqs**

`scipy.signal.freqs(b, a, worN=200, plot=None)`

Compute frequency response of analog filter.

Given the M-order numerator \(b\) and N-order denominator \(a\) of an analog filter, compute its frequency response:

\[
H(\omega) = \frac{b[0] + j\omega b[1] + \cdots + \omega^{M-1} b[M]}{a[0] + j\omega a[1] + \cdots + \omega^{N-1} a[N]}
\]

**Parameters**

- **b** [array_like] Numerator of a linear filter.
- **a** [array_like] Denominator of a linear filter.
- **worN** [{None, int, array_like}, optional] If None, then compute at 200 frequencies around the interesting parts of the response curve (determined by pole-zero locations). If a single integer, then compute at that many frequencies. Otherwise, compute the response at the angular frequencies (e.g. rad/s) given in `worN`.
- **plot** [callable, optional] A callable that takes two arguments. If given, the return parameters \(w\) and \(h\) are passed to `plot`. Useful for plotting the frequency response inside `freqs`.

**Returns**

- **w** [ndarray] The angular frequencies at which \(h\) was computed.
- **h** [ndarray] The frequency response.

**See also:**

`freqz`

Compute the frequency response of a digital filter.

**Notes**

Using Matplotlib’s “plot” function as the callable for `plot` produces unexpected results, this plots the real part of the complex transfer function, not the magnitude. Try `lambda w, h: plot(w, abs(h))`.

**Examples**

```python
>>> from scipy.signal import freqs, iirfilter

>>> b, a = iirfilter(4, [1, 10], 1, 60, analog=True, ftype='cheby1')

>>> w, h = freqs(b, a, worN=np.logspace(-1, 2, 1000))

>>> import matplotlib.pyplot as plt
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.xlabel('Frequency')
>>> plt.ylabel('Amplitude response [dB]')
>>> plt.grid()
>>> plt.show()
```
scipy.signal.freqs_zpk

**scipy.signal.freqs_zpk(z, p, k, worN=200)**

Compute frequency response of analog filter.

Given the zeros \( z \), poles \( p \), and gain \( k \) of a filter, compute its frequency response:

\[
H(\omega) = k \frac{(j\omega - z[0]) \cdot (j\omega - z[1]) \cdot \ldots \cdot (j\omega - z[-1])}{(j\omega - p[0]) \cdot (j\omega - p[1]) \cdot \ldots \cdot (j\omega - p[-1])}
\]

**Parameters**

- \( z \) [array_like] Zeros of a linear filter
- \( p \) [array_like] Poles of a linear filter
- \( k \) [scalar] Gain of a linear filter
- \( worN \) [{None, int, array_like}, optional] If None, then compute at 200 frequencies around the interesting parts of the response curve (determined by pole-zero locations). If a single integer, then compute at that many frequencies. Otherwise, compute the response at the angular frequencies (e.g. rad/s) given in \( worN \).

**Returns**

- \( w \) [ndarray] The angular frequencies at which \( h \) was computed.
- \( h \) [ndarray] The frequency response.

**See also:**

- freqs
  - Compute the frequency response of an analog filter in TF form
- freqz
  - Compute the frequency response of a digital filter in TF form
- freqz_zpk
  - Compute the frequency response of a digital filter in ZPK form
Notes
New in version 0.19.0.

Examples

```python
>>> from scipy.signal import freqs_zpk, iirfilter

>>> z, p, k = iirfilter(4, [1, 10], 1, 60, analog=True, ftype='cheby1',
                      output='zpk')

>>> w, h = freqs_zpk(z, p, k, worN=np.logspace(-1, 2, 1000))

>>> import matplotlib.pyplot as plt
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.xlabel('Frequency')
>>> plt.ylabel('Amplitude response [dB]')
>>> plt.grid()
>>> plt.show()
```

SciPy Reference Guide, Release 1.2.0

scipy.signal.freqz

**scipy.signal.freqz**(*b*, *a=1*, *worN=512*, *whole=False*, *plot=None*, *fs=6.283185307179586*)

Compute the frequency response of a digital filter.

Given the M-order numerator \(b\) and N-order denominator \(a\) of a digital filter, compute its frequency response:

\[
H(e^{j\omega}) = \frac{\sum_{n=0}^{M} b[n]e^{-jn\omega}}{\sum_{n=0}^{N} a[n]e^{-jn\omega}}
\]

**Parameters**
b  [array_like] Numerator of a linear filter. If \( b \) has dimension greater than 1, it is assumed that the coefficients are stored in the first dimension, and \( b.shape[1:] \), \( a.shape[1:] \), and the shape of the frequencies array must be compatible for broadcasting.

a  [array_like] Denominator of a linear filter. If \( b \) has dimension greater than 1, it is assumed that the coefficients are stored in the first dimension, and \( b.shape[1:] \), \( a.shape[1:] \), and the shape of the frequencies array must be compatible for broadcasting.

worN  [(None, int, array_like), optional] If a single integer, then compute at that many frequencies (default is \( N=512 \)). This is a convenient alternative to:

\[
\text{np.linspace}(0, fs \text{ if whole else } fs/2, N, \text{endpoint=False})
\]

Using a number that is fast for FFT computations can result in faster computations (see Notes).

If an array_like, compute the response at the frequencies given. These are in the same units as \( fs \).

whole  [bool, optional] Normally, frequencies are computed from 0 to the Nyquist frequency, \( fs/2 \) (upper-half of unit-circle). If \( \text{whole} \) is True, compute frequencies from 0 to \( fs \). Ignored if \( w \) is array_like.

plot  [callable] A callable that takes two arguments. If given, the return parameters \( w \) and \( h \) are passed to plot. Useful for plotting the frequency response inside \( \text{freqz} \).

fs  [float, optional] The sampling frequency of the digital system. Defaults to \( 2\pi \) radians/sample (so \( w \) is from 0 to \( \pi \)). New in version 1.2.0.

Returns

\( w \)  [ndarray] The frequencies at which \( h \) was computed, in the same units as \( fs \). By default, \( w \) is normalized to the range \( [0, \pi) \) (radians/sample).

\( h \)  [ndarray] The frequency response, as complex numbers.

See also:

freqz_zpk, sosfreqz

Notes

Using Matplotlib's \text{matplotlib.pyplot.plot} function as the callable for \( \text{plot} \) produces unexpected results, as this plots the real part of the complex transfer function, not the magnitude. Try \text{lambda} \( w, h: \text{plot}(w, \text{np.abs}(h)) \).

A direct computation via (R)FFT is used to compute the frequency response when the following conditions are met:

1. An integer value is given for \( \text{worN} \).
2. \( \text{worN} \) is fast to compute via FFT (i.e., \text{next_fast_len(worN)} equals \( \text{worN} \)).
3. The denominator coefficients are a single value (\( a.shape[0] == 1 \)).
4. \( \text{worN} \) is at least as long as the numerator coefficients (\( \text{worN} >= b.shape[0] \)).
5. If \( b.ndim > 1 \), then \( b.shape[-1] == 1 \).

For long FIR filters, the FFT approach can have lower error and be much faster than the equivalent direct polynomial calculation.

Examples
>>> from scipy import signal
>>> b = signal.firwin(80, 0.5, window=('kaiser', 8))
>>> w, h = signal.freqz(b)

>>> import matplotlib.pyplot as plt
>>> fig, ax1 = plt.subplots()
>>> ax1.set_title('Digital filter frequency response')

>>> ax1.plot(w, 20 * np.log10(abs(h)), 'b')
>>> ax1.set_ylabel('Amplitude [dB]', color='b')
>>> ax1.set_xlabel('Frequency [rad/sample]')

>>> ax2 = ax1.twinx()
>>> angles = np.unwrap(np.angle(h))
>>> ax2.plot(w, angles, 'g')
>>> ax2.set_ylabel('Angle (radians)', color='g')
>>> ax2.grid()
>>> ax2.axis('tight')
>>> plt.show()

Broadcasting Examples

Suppose we have two FIR filters whose coefficients are stored in the rows of an array with shape (2, 25). For this demonstration we’ll use random data:

>>> np.random.seed(42)
>>> b = np.random.rand(2, 25)

To compute the frequency response for these two filters with one call to `freqz`, we must pass in `b.T`, because `freqz` expects the first axis to hold the coefficients. We must then extend the shape with a trivial dimension of length 1 to allow broadcasting with the array of frequencies. That is, we pass in `b.T[..., np.newaxis]`, which has shape (25, 2, 1):
Now suppose we have two transfer functions, with the same numerator coefficients \(b = [0.5, 0.5]\). The coefficients for the two denominators are stored in the first dimension of the two-dimensional array \(a\):

\[
\begin{bmatrix}
1 & 1 \\
-0.25 & -0.5
\end{bmatrix}
\]

```python
>>> b = np.array([0.5, 0.5])
>>> a = np.array([[1, 1], [-0.25, -0.5]])
```

Only \(a\) is more than one-dimensional. To make it compatible for broadcasting with the frequencies, we extend it with a trivial dimension in the call to `freqz`:

```python
>>> w, h = signal.freqz(b, a[:, np.newaxis], worN=1024)
```

```
scipy.signal.freqz_zpk
```

**scipy.signal.freqz_zpk**

`scipy.signal.freqz_zpk(z, p, k, worN=512, whole=False, fs=6.283185307179586)`

Compute the frequency response of a digital filter in ZPK form.

Given the Zeros, Poles and Gain of a digital filter, compute its frequency response:

\[
H(z) = k \prod_i (z - Z[i]) / \prod_j (z - P[j])
\]

where \(k\) is the gain, \(Z\) are the zeros and \(P\) are the poles.

**Parameters**

- \(z\) : [array_like] Zeros of a linear filter
- \(p\) : [array_like] Poles of a linear filter
- \(k\) : [scalar] Gain of a linear filter
- \(worN\) : [{None, int, array_like}, optional] If a single integer, then compute at that many frequencies (default is \(N=512\)). If an array_like, compute the response at the frequencies given. These are in the same units as \(fs\).
- \(whole\) : [bool, optional] Normally, frequencies are computed from 0 to the Nyquist frequency, \(fs/2\) (upper-half of unit-circle). If \(whole\) is True, compute frequencies from 0 to \(fs\). Ignored if \(w\) is array_like.
- \(fs\) : [float, optional] The sampling frequency of the digital system. Defaults to \(2*\pi\) radians/sample (so \(w\) is from 0 to \(\pi\)).

**Returns**

- \(w\) : [ndarray] The frequencies at which \(h\) was computed, in the same units as \(fs\). By default, \(w\) is normalized to the range \([0, \pi]\) (radians/sample).
- \(h\) : [ndarray] The frequency response, as complex numbers.

6.20. Signal processing (scipy.signal)
See also:

`freqs`
Compute the frequency response of an analog filter in TF form

`freqs_zpk`
Compute the frequency response of an analog filter in ZPK form

`freqz`
Compute the frequency response of a digital filter in TF form

**Notes**
New in version 0.19.0.

**Examples**
Design a 4th-order digital Butterworth filter with cut-off of 100 Hz in a system with sample rate of 1000 Hz, and plot the frequency response:

```python
>>> from scipy import signal
>>> z, p, k = signal.butter(4, 100, output='zpk', fs=1000)
>>> w, h = signal.freqz_zpk(z, p, k, fs=1000)
```

```python
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(1, 1, 1)
>>> ax1.set_title('Digital filter frequency response')
>>> ax1.plot(w, 20 * np.log10(abs(h)), 'b')
>>> ax1.set_ylabel('Amplitude [dB]', color='b')
>>> ax1.set_xlabel('Frequency [Hz]')
>>> ax1.grid()
```

```python
>>> ax2 = ax1.twinx()
>>> angles = np.unwrap(np.angle(h))
>>> ax2.plot(w, angles, 'g')
>>> ax2.set_ylabel('Angle [radians]', color='g')
```

```python
>>> plt.axis('tight')
>>> plt.show()
```

`scipy.signal.sosfreqz`

`scipy.signal.sosfreqz(sos, worN=512, whole=False, fs=6.283185307179586)`

Compute the frequency response of a digital filter in SOS format.

Given `sos`, an array with shape (n, 6) of second order sections of a digital filter, compute the frequency response of the system function:

\[
H(z) = \frac{B_0(z) \cdot B_1(z) \cdot \ldots \cdot B_{n-1}(z)}{A_0(z) \cdot A_1(z) \cdot \ldots \cdot A_{n-1}(z)}
\]

for \( z = \exp(\omega \cdot 1j) \), where \( B_k(z) \) and \( A_k(z) \) are numerator and denominator of the transfer function of the k-th second order section.
Parameters

- **sos**: [array_like] Array of second-order filter coefficients, must have shape (n_sections, 6). Each row corresponds to a second-order section, with the first three columns providing the numerator coefficients and the last three providing the denominator coefficients.
- **worN**: [{None, int, array_like}, optional] If a single integer, then compute at that many frequencies (default is N=512). Using a number that is fast for FFT computations can result in faster computations (see Notes of freqz). If an array_like, compute the response at the frequencies given (must be 1D). These are in the same units as fs.
- **whole**: [bool, optional] Normally, frequencies are computed from 0 to the Nyquist frequency, fs/2 (upper-half of unit-circle). If whole is True, compute frequencies from 0 to fs.
- **fs**: [float, optional] The sampling frequency of the digital system. Defaults to $2\pi$ radians/sample (so w is from 0 to pi).

Returns

- **w**: [ndarray] The frequencies at which $h$ was computed, in the same units as fs. By default, w is normalized to the range [0, pi) (radians/sample).
- **h**: [ndarray] The frequency response, as complex numbers.

See also:

- freqz, sosfilt

Notes

New in version 0.19.0.

Examples

Design a 15th-order bandpass filter in SOS format.

```python
>>> from scipy import signal
>>> sos = signal.ellip(15, 0.5, 60, (0.2, 0.4), btype='bandpass', output='sos')
```
Compute the frequency response at 1500 points from DC to Nyquist.

```python
>>> w, h = signal.sosfreqz(sos, worN=1500)
```

Plot the response.

```python
>>> import matplotlib.pyplot as plt
>>> plt.subplot(2, 1, 1)
>>> db = 20*np.log10(np.abs(h))
>>> plt.plot(w/np.pi, db)
>>> plt.ylim(-75, 5)
>>> plt.grid(True)
>>> plt.yticks([-np.pi, -0.5*np.pi, 0, 0.5*np.pi, np.pi],
...            [r'$-\pi$', r'$-\pi/2$', '0', r'$\pi/2$', r'$\pi$'])
>>> plt.ylabel('Gain [dB]

Frequency Response
```

If the same filter is implemented as a single transfer function, numerical error corrupts the frequency response:

```python
>>> b, a = signal.ellip(15, 0.5, 60, (0.2, 0.4), btype='bandpass',
...                      output='ba')
>>> w, h = signal.freqz(b, a, worN=1500)
>>> plt.subplot(2, 1, 1)
>>> db = 20*np.log10(np.abs(h))
>>> plt.plot(w/np.pi, db)
>>> plt.ylim(-75, 5)
```

(continues on next page)
```python
>>> plt.grid(True)
>>> plt.yticks([0, -20, -40, -60])
>>> plt.ylabel('Gain [dB]')
>>> plt.title('Frequency Response')
>>> plt.subplot(2, 1, 2)
>>> plt.plot(w/np.pi, np.angle(h))
>>> plt.grid(True)
>>> plt.xticks([-np.pi, -0.5*np.pi, 0, 0.5*np.pi, np.pi],
>>>             [r'$-\pi$', r'$-\pi/2$', '0', r'$\pi/2$', r'$\pi$'])
>>> plt.ylabel('Phase [rad]')
>>> plt.xlabel('Normalized frequency (1.0 = Nyquist)')
>>> plt.show()
```

**scipy.signal.group_delay**

`scipy.signal.group_delay(system, w=512, whole=False, fs=6.283185307179586)`

Compute the group delay of a digital filter.

The group delay measures by how many samples amplitude envelopes of various spectral components of a signal are delayed by a filter. It is formally defined as the derivative of continuous (unwrapped) phase:

\[
D(\omega) = - \frac{d}{d\omega} \arg H(e^{j\omega})
\]

**Parameters**

- `system` : [tuple of array_like (b, a)] Numerator and denominator coefficients of a filter transfer function.
- `w` : [{None, int, array_like}, optional] If a single integer, then compute at that many frequencies (default is N=512). If an array_like, compute the delay at the frequencies given. These are in the same units as `fs`.

---

*6.20. Signal processing (scipy.signal)*
whole [bool, optional] Normally, frequencies are computed from 0 to the Nyquist frequency, \(fs/2\) (upper-half of unit-circle). If `whole` is True, compute frequencies from 0 to \(fs\). Ignored if \(w\) is array-like.

fs [float, optional] The sampling frequency of the digital system. Defaults to \(2\pi\) radians/sample (so \(w\) is from 0 to \(\pi\)). New in version 1.2.0.

Returns

\(w\) [ndarray] The frequencies at which group delay was computed, in the same units as \(fs\). By default, \(w\) is normalized to the range \([0, \pi)\) (radians/sample).

gd [ndarray] The group delay.

See also:

freqz

Frequency response of a digital filter

Notes

The similar function in MATLAB is called `grpdelay`.

If the transfer function \(H(z)\) has zeros or poles on the unit circle, the group delay at corresponding frequencies is undefined. When such a case arises the warning is raised and the group delay is set to 0 at those frequencies.

For the details of numerical computation of the group delay refer to [1].

New in version 0.16.0.

References

[1]

Examples

```python
>>> from scipy import signal
>>> b, a = signal.iirdesign(0.1, 0.3, 5, 50, ftype='cheby1')
>>> w, gd = signal.group_delay((b, a))
```

```python
>>> import matplotlib.pyplot as plt
>>> plt.title('Digital filter group delay')
>>> plt.plot(w, gd)
>>> plt.ylabel('Group delay [samples]')
>>> plt.xlabel('Frequency [rad/sample]')
>>> plt.show()
```

scipy.signal.iirdesign

**scipy.signal.iirdesign**\((wp, ws, gpass, gstop, analog=False, ftype='ellip', output='ba', fs=None)\)

Complete IIR digital and analog filter design.

Given passband and stopband frequencies and gains, construct an analog or digital IIR filter of minimum order for a given basic type. Return the output in numerator, denominator (`'ba'`), pole-zero (`'zpk'`) or second order sections (`'sos'`) form.

Parameters

\(wp, ws\) [float] Passband and stopband edge frequencies. For digital filters, these are in the same units as \(fs\). By default, \(fs\) is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. For example:
Digital filter group delay

- Lowpass: \( wp = 0.2, ws = 0.3 \)
- Highpass: \( wp = 0.3, ws = 0.2 \)
- Bandpass: \( wp = [0.2, 0.5], ws = [0.1, 0.6] \)
- Bandstop: \( wp = [0.1, 0.6], ws = [0.2, 0.5] \)

For analog filters, \( wp \) and \( ws \) are angular frequencies (e.g. rad/s).

\[ \text{gpass} \text{ [float]} \text{ The maximum loss in the passband (dB).} \]
\[ \text{gstop} \text{ [float]} \text{ The minimum attenuation in the stopband (dB).} \]
\[ \text{analog} \text{ [bool, optional] When True, return an analog filter, otherwise a digital filter is returned.} \]
\[ \text{ftype} \text{ [str, optional] The type of IIR filter to design:} \]
  - Butterworth : ‘butter’
  - Chebyshev I : ‘cheby1’
  - Chebyshev II : ‘cheby2’
  - Cauer/elliptic: ‘ellip’
  - Bessel/Thomson: ‘bessel’
\[ \text{output} \text{ [{‘ba’, ‘zpk’, ‘sos’}, optional] Type of output: numerator/denominator (‘ba’), pole-zero (‘zpk’), or second-order sections (‘sos’). Default is ‘ba’.} \]
\[ \text{fs} \text{ [float, optional] The sampling frequency of the digital system.} \]

\[ \text{Returns} \]
\[ \text{b, a \ [ndarray, ndarray] Numerator (b) and denominator (a) polynomials of the IIR filter.} \]  
Only returned if \text{output}='ba'.'
\[ \text{z, p, k \ [ndarray, ndarray, float] Zeros, poles, and system gain of the IIR filter transfer function.} \]  
Only returned if \text{output}='zpk'.'
\[ \text{sos \ [ndarray] Second-order sections representation of the IIR filter.} \]  
Only returned if \text{output}='sos'.

\[ \text{See also:} \]
\[ \text{butter} \]
Filter design using order and critical points

\[ \text{cheby1, cheby2, ellip, bessel} \]
buttord

Find order and critical points from passband and stopband spec.

cheb1ord, cheb2ord, ellipord

iirfilter

General filter design using order and critical frequencies.

Notes
The ‘sos’ output parameter was added in 0.16.0.

scipy.signal.iirfilter

scipy.signal.iirfilter(N, Wn, rp=None, rs=None, btype='band', analog=False, ftype='butter', output='ba', fs=None)

IIR digital and analog filter design given order and critical points.

Design an Nth-order digital or analog filter and return the filter coefficients.

Parameters

N [int] The order of the filter.
Wn [array_like] A scalar or length-2 sequence giving the critical frequencies.
    For digital filters, Wn are in the same units as fs. By default, fs is 2 half-
    cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist fre-
    quency. (Wn is thus in half-cycles / sample.)
    For analog filters, Wn is an angular frequency (e.g. rad/s).
rp [float, optional] For Chebyshev and elliptic filters, provides the maximum ripple in
    the passband. (dB)
rs [float, optional] For Chebyshev and elliptic filters, provides the minimum attenuation
    in the stop band. (dB)
    fault is ‘bandpass’.
analog [bool, optional] When True, return an analog filter, otherwise a digital filter is
    returned.
ftype [str, optional] The type of IIR filter to design:
    • Butterworth : ‘butter’
    • Chebyshev I : ‘cheby1’
    • Chebyshev II : ‘cheby2’
    • Cauer/elliptic: ‘ellip’
    • Bessel/Thomson: ‘bessel’
output [{‘ba’, ‘zpk’, ‘sos’}, optional] Type of output: numerator/denominator (‘ba’), pole-
    zero (‘zpk’), or second-order sections (‘sos’). Default is ‘ba’.
fs [float, optional] The sampling frequency of the digital system.
    New in version 1.2.0.

Returns

b, a [ndarray, ndarray] Numerator (b) and denominator (a) polynomials of the IIR filter. Only
    returned if output=’ba’.
z, p, k [ndarray, ndarray, float] Zeros, poles, and system gain of the IIR filter transfer
    function. Only returned if output=’zpk’.
sos [ndarray] Second-order sections representation of the IIR filter. Only returned if
    output=’sos’.

See also:
butter

Filter design using order and critical points

double

double

double

double

double

double

double

double

double

double

cheby1, cheby2, ellip, bessel

buttord

Find order and critical points from passband and stopband spec

double

double

double

double

double

cheb1ord, cheb2ord, ellipord

iirdesign

General filter design using passband and stopband spec

Notes
The 'sos' output parameter was added in 0.16.0.

Examples
Generate a 17th-order Chebyshev II analog bandpass filter from 50 Hz to 200 Hz and plot the frequency response:

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

>>> b, a = signal.iirfilter(17, [2*np.pi*50, 2*np.pi*200], rs=60,
...     btype='band', analog=True, ftype='cheby2')

>>> w, h = signal.freqs(b, a, 1000)
>>> fig = plt.figure()
>>> ax = fig.add_subplot(1, 1, 1)
>>> ax.semilogx(w / (2*np.pi), 20 * np.log10(abs(h))

Chebyshev Type II bandpass frequency response

```

Chebyshev Type II bandpass frequency response

Amplitude [dB]

Frequency [Hz]
Create a digital filter with the same properties, in a system with sampling rate of 2000 Hz, and plot the frequency response. (Second-order sections implementation is required to ensure stability of a filter of this order):

```python
>>> sos = signal.iirfilter(17, [50, 200], rs=60, btype='band',
                          analog=False, ftype='cheby2', fs=2000,
                          output='sos')
>>> w, h = signal.sosfreqz(sos, 2000, fs=2000)
>>> fig = plt.figure()
>>> ax = fig.add_subplot(1, 1, 1)
>>> ax.semilogx(w, 20 * np.log10(abs(h)))
>>> ax.set_title('Chebyshev Type II bandpass frequency response')
>>> ax.set_xlabel('Frequency [Hz]')
>>> ax.set_ylabel('Amplitude [dB]')
>>> ax.axis((10, 1000, -100, 10))
>>> ax.grid(which='both', axis='both')
>>> plt.show()
```

`scipy.signal.kaiser_atten`

**scipy.signal.kaiser_atten(numtaps, width)**

Compute the attenuation of a Kaiser FIR filter.

Given the number of taps \( N \) and the transition width \( width \), compute the attenuation \( a \) in dB, given by Kaiser’s formula:

\[
a = 2.285 \times (N - 1) \times \pi \times width + 7.95
\]

**Parameters**

- **numtaps** [int] The number of taps in the FIR filter.
- **width** [float] The desired width of the transition region between passband and stopband (or, in general, at any discontinuity) for the filter, expressed as a fraction of the Nyquist frequency.

**Returns**
a [float] The attenuation of the ripple, in dB.

See also:

kaiserord, kaiser_beta

Examples

Suppose we want to design a FIR filter using the Kaiser window method that will have 211 taps and a transition width of 9 Hz for a signal that is sampled at 480 Hz. Expressed as a fraction of the Nyquist frequency, the width is $9/(0.5\times480) = 0.0375$. The approximate attenuation (in dB) is computed as follows:

```python
>>> from scipy.signal import kaiser_atten
>>> kaiser_atten(211, 0.0375)
64.48099630593983
```

scipy.signal.kaiser_beta

scipy.signal.kaiser_beta(a)

Compute the Kaiser parameter $\beta$, given the attenuation $a$.

Parameters

- a [float] The desired attenuation in the stopband and maximum ripple in the passband, in dB. This should be a positive number.

Returns

- beta [float] The $\beta$ parameter to be used in the formula for a Kaiser window.

References


Examples

Suppose we want to design a lowpass filter, with 65 dB attenuation in the stop band. The Kaiser window parameter to be used in the window method is computed by kaiser_beta(65):

```python
>>> from scipy.signal import kaiser_beta
>>> kaiser_beta(65)
6.20426
```

scipy.signal.kaiserord

scipy.signal.kaiserord(ripple, width)

Determine the filter window parameters for the Kaiser window method.

The parameters returned by this function are generally used to create a finite impulse response filter using the window method, with either firwin or firwin2.

Parameters

- ripple [float] Upper bound for the deviation (in dB) of the magnitude of the filter’s frequency response from that of the desired filter (not including frequencies in any transition intervals). That is, if $w$ is the frequency expressed as a fraction of the Nyquist frequency, $A(w)$ is the actual frequency response of the filter and $D(w)$ is the desired frequency response, the design requirement is that:

$$\text{abs}(A(w) - D(w)) < 10^{\frac{-\text{ripple}}{20}}$$

for $0 \leq w \leq 1$ and $w$ not in a transition interval.
width  [float] Width of transition region, normalized so that 1 corresponds to pi radians / sample. That is, the frequency is expressed as a fraction of the Nyquist frequency.

**Returns**

numtaps  [int] The length of the Kaiser window.
beta   [float] The beta parameter for the Kaiser window.

See also:
kaiser_beta, kaiser_atten

Notes
There are several ways to obtain the Kaiser window:

- signal.kaiser(numtaps, beta, sym=True)
- signal.get_window(beta, numtaps)
- signal.get_window(('kaiser', beta), numtaps)

The empirical equations discovered by Kaiser are used.

References

Examples
We will use the Kaiser window method to design a lowpass FIR filter for a signal that is sampled at 1000 Hz.

We want at least 65 dB rejection in the stop band, and in the pass band the gain should vary no more than 0.5%.

We want a cutoff frequency of 175 Hz, with a transition between the pass band and the stop band of 24 Hz. That is, in the band [0, 163], the gain varies no more than 0.5%, and in the band [187, 500], the signal is attenuated by at least 65 dB.

```python
>>> from scipy.signal import kaiserord, firwin, freqz
>>> import matplotlib.pyplot as plt
>>> fs = 1000.0
>>> cutoff = 175
>>> width = 24
```

The Kaiser method accepts just a single parameter to control the pass band ripple and the stop band rejection, so we use the more restrictive of the two. In this case, the pass band ripple is 0.005, or 46.02 dB, so we will use 65 dB as the design parameter.

Use kaiserord to determine the length of the filter and the parameter for the Kaiser window.

```python
>>> numtaps, beta = kaiserord(65, width/(0.5*fs))
>>> numtaps
167
>>> beta
6.20426
```

Use firwin to create the FIR filter.

```python
>>> taps = firwin(numtaps, cutoff, window=('kaiser', beta),
...                scale=False, nyq=0.5*fs)
```

Compute the frequency response of the filter. w is the array of frequencies, and h is the corresponding complex array of frequency responses.
Compute the deviation of the magnitude of the filter’s response from that of the ideal lowpass filter. Values in the transition region are set to nan, so they won’t appear in the plot.

```python
>>> ideal = w < cutoff  # The "ideal" frequency response.
>>> deviation = np.abs(np.abs(h) - ideal)
>>> deviation[(w > cutoff - 0.5*width) & (w < cutoff + 0.5*width)] = np.nan
```

Plot the deviation. A close look at the left end of the stop band shows that the requirement for 65 dB attenuation is violated in the first lobe by about 0.125 dB. This is not unusual for the Kaiser window method.

```python
>>> plt.plot(w, 20*np.log10(np.abs(deviation)))
>>> plt.xlim(0, 0.5*fs)
>>> plt.ylim(-90, -60)
>>> plt.grid(alpha=0.25)
>>> plt.axhline(-65, color='r', ls='--', alpha=0.3)
>>> plt.xlabel('Frequency (Hz)')
>>> plt.ylabel('Deviation from ideal (dB)')
>>> plt.title('Lowpass Filter Frequency Response')
>>> plt.show()
```

**scipy.signal.minimum_phase**

**scipy.signal.minimum_phase**(h, method='homomorphic', n_fft=None)

Convert a linear-phase FIR filter to minimum phase

**Parameters**

- **h** [array] Linear-phase FIR filter coefficients.
- **method** [{'hilbert', 'homomorphic'}] The method to use: ‘homomorphic’ (default)

6.20. Signal processing (**scipy.signal**)
This method [4] [5] works best with filters with an odd number of taps, and the resulting minimum phase filter will have a magnitude response that approximates the square root of the original filter’s magnitude response.

`hilbert` This method [1] is designed to be used with equiripple filters (e.g., from `remez`) with unity or zero gain regions.

`n_fft` [int] The number of points to use for the FFT. Should be at least a few times larger than the signal length (see Notes).

**Returns**

`h_minimum` [array] The minimum-phase version of the filter, with length \((\text{length}(h) + 1) \div 2\).

See also:

`firwin`, `firwin2`, `remez`

**Notes**


In the case of the Hilbert method, the deviation from the ideal spectrum \(\text{epsilon}\) is related to the number of stopband zeros \(n_{stop}\) and FFT length \(n_{fft}\) as:

\[
\text{epsilon} = 2. * \frac{n_{stop}}{n_{fft}}
\]

For example, with 100 stopband zeros and a FFT length of 2048, \(\text{epsilon} = 0.0976\). If we conservatively assume that the number of stopband zeros is one less than the filter length, we can take the FFT length to be the next power of 2 that satisfies \(\text{epsilon}=0.01\) as:

\[
\text{n_fft} = 2 ** \text{int}(\text{np.ceil}(\text{np.log2}(2 * (\text{len}(h) - 1) / 0.01)))
\]

This gives reasonable results for both the Hilbert and homomorphic methods, and gives the value used when \(\text{n_fft=None}\).

Alternative implementations exist for creating minimum-phase filters, including zero inversion [2] and spectral factorization [3] [4]. For more information, see:

http://dspguru.com/dsp/howtos/how-to-design-minimum-phase-fir-filters

**References**

[1], [2], [3], [4], [5]

**Examples**

Create an optimal linear-phase filter, then convert it to minimum phase:

```python
>>> from scipy.signal import remez, minimum_phase, freqz, group_delay
>>> import matplotlib.pyplot as plt
>>> freq = [0, 0.2, 0.3, 1.0]
>>> desired = [1, 0]
>>> h_linear = remez(151, freq, desired, Hz=2.)
```

Convert it to minimum phase:

```python
>>> h_min_hom = minimum_phase(h_linear, method='homomorphic')
>>> h_min_hil = minimum_phase(h_linear, method='hilbert')
```

Compare the three filters:
```python
>>> fig, axs = plt.subplots(4, figsize=(4, 8))
>>> for h, style, color in zip((h_linear, h_min_hom, h_min_hil),
    (('-', '+', '--'), ('k', 'r', 'c'))):
...    w, H = freqz(h)
...    w, gd = group_delay((h, 1))
...    w /= np.pi
...    axs[0].plot(h, color=color, linestyle=style)
...    axs[1].plot(w, np.abs(H), color=color, linestyle=style)
...    axs[2].plot(w, 20 * np.log10(np.abs(H)), color=color, linestyle=style)
...    axs[3].plot(w, gd, color=color, linestyle=style)
```
References

Examples

```python
>>> from scipy.signal import savgol_coeffs
>>> savgol_coeffs(5, 2)
array([-0.08571429, 0.34285714, 0.48571429, 0.34285714, -0.08571429])
>>> savgol_coeffs(5, 2, deriv=1)
array([ 2.00000000e-01, 1.00000000e-01, 2.0607895e-16, -1.00000000e-01, -2.00000000e-01])
```

Note that use='dot' simply reverses the coefficients.

```python
>>> savgol_coeffs(5, 2, pos=3)
array([ 0.25714286, 0.37142857, 0.34285714, 0.17142857, -0.14285714])
>>> savgol_coeffs(5, 2, pos=3, use='dot')
array([-0.14285714, 0.17142857, 0.34285714, 0.37142857, 0.25714286])
```

$x$ contains data from the parabola $x = t^2$, sampled at $t = -1, 0, 1, 2, 3$. $c$ holds the coefficients that will compute the derivative at the last position. When dotted with $x$ the result should be 6.

```python
>>> x = np.array([1, 0, 1, 4, 9])
>>> c = savgol_coeffs(5, 2, pos=4, deriv=1, use='dot')
>>> c.dot(x)
6.0000000000000018
```

`scipy.signal.remez`

`scipy.signal.remez(numtaps, bands, desired, weight=None, Hz=None, type='bandpass', maxiter=25, grid_density=16, fs=None)`

Calculate the minimax optimal filter using the Remez exchange algorithm.

Calculate the filter-coefficients for the finite impulse response (FIR) filter whose transfer function minimizes the maximum error between the desired gain and the realized gain in the specified frequency bands using the Remez exchange algorithm.

**Parameters**

- **numtaps** [int] The desired number of taps in the filter. The number of taps is the number of terms in the filter, or the filter order plus one.
- **bands** [array_like] A monotonic sequence containing the band edges. All elements must be non-negative and less than half the sampling frequency as given by `fs`.
- **desired** [array_like] A sequence half the size of bands containing the desired gain in each of the specified bands.
- **weight** [array_like, optional] A relative weighting to give to each band region. The length of `weight` has to be half the length of `bands`.
- **Hz** [scalar, optional] *Deprecated.* Use `fs` instead. The sampling frequency in Hz. Default is 1.
- **type** [{‘bandpass’, ‘differentiator’, ‘hilbert’}, optional] The type of filter:
  - ‘bandpass’ : flat response in bands. This is the default.
  - ‘differentiator’ : frequency proportional response in bands.
  - ‘hilbert’ [filter with odd symmetry, that is, type III] (for even order) or type IV (for odd order) linear phase filters.
- **maxiter** [int, optional] Maximum number of iterations of the algorithm. Default is 25.
grid_density

[int, optional] Grid density. The dense grid used in remez is of size (numtaps + 1) * grid_density. Default is 16.

fs

[float, optional] The sampling frequency of the signal. Default is 1.

Returns

out [ndarray] A rank-1 array containing the coefficients of the optimal (in a minimax sense) filter.

See also:

firls, firwin, firwin2, minimum_phase

References

[1], [2]

Examples

For a signal sampled at 100 Hz, we want to construct a filter with a passband at 20-40 Hz, and stop bands at 0-10 Hz and 45-50 Hz. Note that this means that the behavior in the frequency ranges between those bands is unspecified and may overshoot.

```python
>>> from scipy import signal
>>> fs = 100
>>> bpass = signal.remez(72, [0, 10, 20, 40, 45, 50], [0, 1, 0], fs=fs)
>>> freq, response = signal.freqz(bpass)
```

```python
>>> import matplotlib.pyplot as plt
>>> plt.semilogy(0.5*fs*freq/np.pi, np.abs(response), 'b-')
>>> plt.grid(alpha=0.25)
>>> plt.xlabel('Frequency (Hz)')
>>> plt.ylabel('Gain')
>>> plt.show()
```

scipy.signal.unique_roots

scipy.signal.unique_roots(p, tol=0.001, rtype='min')

Determine unique roots and their multiplicities from a list of roots.
Parameters

\[ \text{p} \quad \text{array_like} \] The list of roots.
\[ \text{tol} \quad \text{float, optional} \] The tolerance for two roots to be considered equal. Default is 1e-3.
\[ \text{rtype} \quad \{\text{max}, \text{min}, \text{avg}\}, \text{optional} \] How to determine the returned root if multiple roots are within \( \text{tol} \) of each other.
  - `max`: pick the maximum of those roots.
  - `min`: pick the minimum of those roots.
  - `avg`: take the average of those roots.

Returns

\[ \text{pout} \quad \text{ndarray} \] The list of unique roots, sorted from low to high.
\[ \text{mult} \quad \text{ndarray} \] The multiplicity of each root.

Notes

This utility function is not specific to roots but can be used for any sequence of values for which uniqueness and multiplicity has to be determined. For a more general routine, see \texttt{numpy.unique}.

Examples

```python
>>> from scipy import signal
>>> vals = [0, 1.3, 1.31, 2.8, 2.2, 10.3]
>>> uniq, mult = signal.unique_roots(vals, tol=2e-2, rtype='avg')
```

Check which roots have multiplicity larger than 1:

```python
>>> uniq[mult > 1]
array([ 1.305])
```

\texttt{scipy.signal.residue}

\texttt{scipy.signal.residue}(b, a, tol=0.001, rtype='avg')

Compute partial-fraction expansion of \( b(s) / a(s) \).

If \( M \) is the degree of numerator \( b \) and \( N \) the degree of denominator \( a \):

\[
\begin{align*}
 b(s) & = b[0] s^M + b[1] s^{M-1} + \ldots + b[M] \\
 a(s) & = a[0] s^N + a[1] s^{N-1} + \ldots + a[N]
\end{align*}
\]

then the partial-fraction expansion \( H(s) \) is defined as:

\[
\begin{align*}
 r[0] & \quad r[1] & \quad r[-1] \\
 (s-p[0]) & (s-p[1]) & (s-p[-1])
\end{align*}
\]

\[
\begin{align*}
 r[0] & \quad r[1] & \quad r[i+1] & \quad r[i+n-1] \\
 (s-p[i]) & (s-p[i])**2 & (s-p[i])**n
\end{align*}
\]

If there are any repeated roots (closer together than \( \text{tol} \)), then \( H(s) \) has terms like:

This function is used for polynomials in positive powers of \( s \) or \( z \), such as analog filters or digital filters in controls engineering. For negative powers of \( z \) (typical for digital filters in DSP), use \texttt{residuez}.

Parameters

\[ \text{b} \quad \text{array_like} \] Numerator polynomial coefficients.
a  [array_like] Denominator polynomial coefficients.

Returns:

r  [ndarray] Residues.
p  [ndarray] Poles.
k  [ndarray] Coefficients of the direct polynomial term.

See also:

invres, residuez, numpy.poly, unique_roots

scipy.signal.residuez

scipy.signal.residuez(b, a, tol=0.001, rtype='avg')

Compute partial-fraction expansion of b(z) / a(z).

If $M$ is the degree of numerator $b$ and $N$ the degree of denominator $a$:

\[
\frac{b(z)}{a(z)} = \frac{b[0] + b[1] z^{-1} + \ldots + b[M] z^{-M}}{a[0] + a[1] z^{-1} + \ldots + a[N] z^{-N}}
\]

then the partial-fraction expansion $H(z)$ is defined as:

\[
\frac{r[0]}{(1-p[0]z^{-1})} + \frac{r[-1]}{(1-p[-1]z^{-1})} + \ldots + \frac{k[0] + k[1]z^{-N}}{(1-p[0]z^{-1})(1-p[1]z^{-1})} + \ldots
\]

If there are any repeated roots (closer than $tol$), then the partial fraction expansion has terms like:

\[
\frac{r[i]}{(1-p[i]z^{-1})(1-p[i]z^{-1})} + \frac{r[i+1]}{(1-p[i]z^{-1})(1-p[i]z^{-1})^2} + \ldots + \frac{r[i+n]}{(1-p[i]z^{-1})(1-p[i]z^{-1})^n}
\]

This function is used for polynomials in negative powers of $z$, such as digital filters in DSP. For positive powers, use residue.

Parameters:

b  [array_like] Numerator polynomial coefficients.
a  [array_like] Denominator polynomial coefficients.

Returns:

r  [ndarray] Residues.
p  [ndarray] Poles.
k  [ndarray] Coefficients of the direct polynomial term.

See also:

invresz, residue, unique_roots

scipy.signal.invres

scipy.signal.invres(r, p, k, tol=0.001, rtype='avg')

Compute $b(s)$ and $a(s)$ from partial fraction expansion.

If $M$ is the degree of numerator $b$ and $N$ the degree of denominator $a$:
then the partial-fraction expansion $H(s)$ is defined as:

\[
\begin{align*}
\frac{r_0}{s-p[0]} &+ \frac{r_1}{s-p[1]} + \cdots + \frac{r[-1]}{s-p[-1]} + k(s)
\end{align*}
\]

If there are any repeated roots (closer together than $tol$), then $H(s)$ has terms like:

\[
\begin{align*}
\frac{r[i]}{(s-p[i])^2} &+ \frac{r[i+1]}{(s-p[i])^3} + \cdots + \frac{r[i+n-1]}{(s-p[i])^n}
\end{align*}
\]

This function is used for polynomials in positive powers of $s$ or $z$, such as analog filters or digital filters in controls engineering. For negative powers of $z$ (typical for digital filters in DSP), use `invresz`.

**Parameters**

- `r` [array_like] Residues.
- `p` [array_like] Poles.
- `k` [array_like] Coefficients of the direct polynomial term.
- `tol` [float, optional] The tolerance for two roots to be considered equal. Default is $1e-3$.
- `rtype` [{‘max’, ‘min’, ‘avg’}, optional] How to determine the returned root if multiple roots are within $tol$ of each other.
  - ‘max’: pick the maximum of those roots.
  - ‘min’: pick the minimum of those roots.
  - ‘avg’: take the average of those roots.

**Returns**

- `b` [ndarray] Numerator polynomial coefficients.
- `a` [ndarray] Denominator polynomial coefficients.

**See also:**

- `residue`, `invresz`, `unique_roots`

scipy.signal.invresz

**scipy.signal.invresz**($r$, $p$, $k$, $tol=0.001$, $rtype=’avg’$)

Compute $b(z)$ and $a(z)$ from partial fraction expansion.

If $M$ is the degree of numerator $b$ and $N$ the degree of denominator $a$:

\[
\begin{align*}
H(z) = \frac{b[0]}{z^M} + \frac{b[1]}{z^{M-1}} + \cdots + \frac{b[M]}{z^0} + k[0] + k[1]z^{N-1} + \cdots + a[N]z^{-N}
\end{align*}
\]

then the partial-fraction expansion $H(z)$ is defined as:

\[
\begin{align*}
\frac{r[0]}{(1-p[0]z^{-1})} &+ \frac{r[-1]}{(1-p[-1]z^{-1})} + \frac{r[i]}{(s-p[i])^2} + \frac{r[i+1]}{(s-p[i])^3} + \cdots + \frac{r[i+n-1]}{(s-p[i])^n}
\end{align*}
\]

If there are any repeated roots (closer than $tol$), then the partial fraction expansion has terms like:
This function is used for polynomials in negative powers of \( z \), such as digital filters in DSP. For positive powers, use \( \text{invres} \).

**Parameters**

- \( r \) [array_like] Residues.
- \( p \) [array_like] Poles.
- \( k \) [array_like] Coefficients of the direct polynomial term.
- \( \text{tol} \) [float, optional] The tolerance for two roots to be considered equal. Default is 1e-3.
- \( \text{rtype} \) [{'max', 'min', 'avg'}, optional] How to determine the returned root if multiple roots are within \( \text{tol} \) of each other.
  - 'max': pick the maximum of those roots.
  - 'min': pick the minimum of those roots.
  - 'avg': take the average of those roots.

**Returns**

- \( b \) [ndarray] Numerator polynomial coefficients.
- \( a \) [ndarray] Denominator polynomial coefficients.

See also:

- residuez, unique_roots, invres

scipy.signal.BadCoefficients

**exception scipy.signal.BadCoefficients**

Warning about badly conditioned filter coefficients

Lower-level filter design functions:

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<tr>
<th>Function</th>
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<tr>
<td><code>lp2bs_zpk(z, p, k[, wo, bw])</code></td>
<td>Transform a lowpass filter prototype to a bandstop filter.</td>
</tr>
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<td>Transform a lowpass filter prototype to a highpass filter.</td>
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</tr>
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<td><code>normalize(b, a)</code></td>
<td>Normalize numerator/denominator of a continuous-time transfer function.</td>
</tr>
</tbody>
</table>

**scipy.signal.abcd_normalize**

```python
scipy.signal.abcd_normalize(A=None, B=None, C=None, D=None)
```

Check state-space matrices and ensure they are two-dimensional.

If enough information on the system is provided, that is, enough properly-shaped arrays are passed to the function, the missing ones are built from this information, ensuring the correct number of rows and columns. Otherwise a ValueError is raised.

**Parameters**

A, B, C, D  
[array_like, optional] State-space matrices. All of them are None (missing) by default. See `ss2tf` for format.

**Returns**

A, B, C, D  
[array] Properly shaped state-space matrices.

**Raises**

ValueError  
If not enough information on the system was provided.

**scipy.signal.band_stop_obj**

```python
scipy.signal.band_stop_obj(wp, ind, passb, stopb, gpass, gstop, type)
```

Band Stop Objective Function for order minimization.

Returns the non-integer order for an analog band stop filter.

**Parameters**

wp  
[scalar] Edge of passband `passb`.

ind  
[int, {0, 1}] Index specifying which `passb` edge to vary (0 or 1).

passb  
[ndarray] Two element sequence of fixed passband edges.

stopb  
[ndarray] Two element sequence of fixed stopband edges.

gstop  
[float] Amount of attenuation in stopband in dB.

gpass  
[float] Amount of ripple in the passband in dB.

type  
[{'butter', 'cheby', 'ellip'}] Type of filter.

**Returns**

n  
[scalar] Filter order (possibly non-integer).
scipy.signal.besselap

scipy.signal.besselap(N, norm='phase')
Return (z,p,k) for analog prototype of an Nth-order Bessel filter.

Parameters
- **N** [int] The order of the filter.
- **norm** [{‘phase’, ‘delay’, ‘mag’}, optional] Frequency normalization:
  - **phase** The filter is normalized such that the phase response reaches its mid-point at an angular (e.g. rad/s) cutoff frequency of 1. This happens for both low-pass and high-pass filters, so this is the “phase-matched” case. [6]
    - The magnitude response asymptotes are the same as a Butterworth filter of the same order with a cutoff of $W_n$.
    - This is the default, and matches MATLAB’s implementation.
  - **delay** The filter is normalized such that the group delay in the passband is 1 (e.g. 1 second). This is the “natural” type obtained by solving Bessel polynomials
  - **mag** The filter is normalized such that the gain magnitude is -3 dB at angular frequency 1. This is called “frequency normalization” by Bond. [1]
    - New in version 0.18.0.

Returns
- **z** [ndarray] Zeros of the transfer function. Is always an empty array.
- **p** [ndarray] Poles of the transfer function.
- **k** [scalar] Gain of the transfer function. For phase-normalized, this is always 1.

See also:
- bessel
  - Filter design function using this prototype

Notes
To find the pole locations, approximate starting points are generated [2] for the zeros of the ordinary Bessel polynomial [3], then the Aberth-Ehrlich method [4] [5] is used on the $K_v(x)$ Bessel function to calculate more accurate zeros, and these locations are then inverted about the unit circle.

References
[1], [2], [3], [4], [5], [6]

scipy.signal.buttap

scipy.signal.buttap(N)
Return (z,p,k) for analog prototype of Nth-order Butterworth filter.
The filter will have an angular (e.g. rad/s) cutoff frequency of 1.

See also:
- butter
  - Filter design function using this prototype
scipy.signal.cheb1ap

scipy.signal.cheb1ap(N, rp)
Return (z,p,k) for Nth-order Chebyshev type I analog lowpass filter.
The returned filter prototype has \( rp \) decibels of ripple in the passband.
The filter’s angular (e.g. rad/s) cutoff frequency is normalized to 1, defined as the point at which the
gain first drops below \(-rp\).

See also:

cheby1
Filter design function using this prototype

scipy.signal.cheb2ap

scipy.signal.cheb2ap(N, rs)
Return (z,p,k) for Nth-order Chebyshev type I analog lowpass filter.
The returned filter prototype has \( rs \) decibels of ripple in the stopband.
The filter’s angular (e.g. rad/s) cutoff frequency is normalized to 1, defined as the point at which the
gain first reaches \(-rs\).

See also:

cheby2
Filter design function using this prototype

scipy.signal.cmplx_sort

scipy.signal.cmplx_sort(p)
Sort roots based on magnitude.

Parameters

p [array_like] The roots to sort, as a 1-D array.

Returns

indx [ndarray] Array of indices needed to sort the input \( p \).

Examples

```python
>>> from scipy import signal
>>> vals = [1, 4, 1+1.j, 3]
>>> p_sorted, indx = signal.cmplx_sort(vals)
>>> p_sorted
array([1.+0.j, 1.+1.j, 3.+0.j, 4.+0.j])
>>> indx
array([0, 2, 3, 1])
```

scipy.signal.ellipap

scipy.signal.ellipap(N, rp, rs)
Return (z,p,k) of Nth-order elliptic analog lowpass filter.
The filter is a normalized prototype that has \( r_p \) decibels of ripple in the passband and a stopband \( r_s \) decibels down.

The filter’s angular (e.g. rad/s) cutoff frequency is normalized to 1, defined as the point at which the gain first drops below \(-r_p\).

**See also:**

- `ellip`

  Filter design function using this prototype

**References**

[1]

**scipy.signal.lp2bp**

`scipy.signal.lp2bp(b, a, wo=1.0, bw=1.0)`

Transform a lowpass filter prototype to a bandpass filter.

Return an analog band-pass filter with center frequency \( wo \) and bandwidth \( bw \) from an analog low-pass filter prototype with unity cutoff frequency, in transfer function (`'ba'`) representation.

**See also:**

- `lp2lp`, `lp2hp`, `lp2bs`, `bilinear`, `lp2bp_zpk`

**scipy.signal.lp2bp_zpk**

`scipy.signal.lp2bp_zpk(z, p, k, wo=1.0, bw=1.0)`

Transform a lowpass filter prototype to a bandpass filter.

Return an analog band-pass filter with center frequency \( wo \) and bandwidth \( bw \) from an analog low-pass filter prototype with unity cutoff frequency, using zeros, poles, and gain (`'zpk'`) representation.

**Parameters**

- `z` [array_like] Zeros of the analog filter transfer function.
- `p` [array_like] Poles of the analog filter transfer function.
- `k` [float] System gain of the analog filter transfer function.
- `wo` [float] Desired passband center, as angular frequency (e.g. rad/s). Defaults to no change.
- `bw` [float] Desired passband width, as angular frequency (e.g. rad/s). Defaults to 1.

**Returns**

- `z` [ndarray] Zeros of the transformed band-pass filter transfer function.
- `p` [ndarray] Poles of the transformed band-pass filter transfer function.
- `k` [float] System gain of the transformed band-pass filter.

**See also:**

- `lp2lp_zpk`, `lp2hp_zpk`, `lp2bs_zpk`, `bilinear`, `lp2bp`

**Notes**

This is derived from the \( s \)-plane substitution

\[
s \rightarrow \frac{s^2 + \omega_0^2}{s \cdot BW}
\]

This is the “wideband” transformation, producing a passband with geometric (log frequency) symmetry about \( wo \).

New in version 1.1.0.
scipy.signal.lp2bs

scipy.signal.lp2bs(b, a, wo=1.0, bw=1.0)

Transform a lowpass filter prototype to a bandstop filter.

Return an analog band-stop filter with center frequency \( wo \) and bandwidth \( bw \) from an analog low-pass filter prototype with unity cutoff frequency, in transfer function (‘ba’) representation.

See also:
lp2lp, lp2hp, lp2bp, bilinear, lp2bs_zpk

scipy.signal.lp2bs_zpk

scipy.signal.lp2bs_zpk(z, p, k, wo=1.0, bw=1.0)

Transform a lowpass filter prototype to a bandstop filter.

Return an analog band-stop filter with center frequency \( wo \) and stopband width \( bw \) from an analog low-pass filter prototype with unity cutoff frequency, using zeros, poles, and gain (‘zpk’) representation.

Parameters

- \( z \) [array_like] Zeros of the analog filter transfer function.
- \( p \) [array_like] Poles of the analog filter transfer function.
- \( k \) [float] System gain of the analog filter transfer function.
- \( wo \) [float] Desired stopband center, as angular frequency (e.g. rad/s). Defaults to no change.
- \( bw \) [float] Desired stopband width, as angular frequency (e.g. rad/s). Defaults to 1.

Returns

- \( z \) [ndarray] Zeros of the transformed band-stop filter transfer function.
- \( p \) [ndarray] Poles of the transformed band-stop filter transfer function.
- \( k \) [float] System gain of the transformed band-stop filter.

See also:
lp2lp_zpk, lp2hp_zpk, lp2bp_zpk, bilinear, lp2bs

Notes

This is derived from the \( s \)-plane substitution

\[
s \rightarrow \frac{s \cdot BW}{s^2 + \omega_0^2}
\]

This is the “wideband” transformation, producing a stopband with geometric (log frequency) symmetry about \( wo \).

New in version 1.1.0.

scipy.signal.lp2hp

scipy.signal.lp2hp(b, a, wo=1.0)

Transform a lowpass filter prototype to a highpass filter.

Return an analog high-pass filter with cutoff frequency \( wo \) from an analog low-pass filter prototype with unity cutoff frequency, in transfer function (‘ba’) representation.

See also:
lp2lp, lp2hp, lp2bs, bilinear, lp2hp_zpk
scipy.signal.lp2hp_zpk

`scipy.signal.lp2hp_zpk(z, p, k, wo=1.0)`

Transform a lowpass filter prototype to a highpass filter.

Return an analog high-pass filter with cutoff frequency $wo$ from an analog low-pass filter prototype with unity cutoff frequency, using zeros, poles, and gain (‘zpk’) representation.

**Parameters**

- `z` : [array_like] Zeros of the analog filter transfer function.
- `p` : [array_like] Poles of the analog filter transfer function.
- `k` : [float] System gain of the analog filter transfer function.
- `wo` : [float] Desired cutoff, as angular frequency (e.g. rad/s). Defaults to no change.

**Returns**

- `z` : [ndarray] Zeros of the transformed high-pass filter transfer function.
- `p` : [ndarray] Poles of the transformed high-pass filter transfer function.
- `k` : [float] System gain of the transformed high-pass filter.

See also:

`lp2lp_zpk, lp2bp_zpk, lp2bs_zpk, bilinear, lp2hp`

**Notes**

This is derived from the s-plane substitution

\[ s \rightarrow \frac{\omega_0}{s} \]

This maintains symmetry of the lowpass and highpass responses on a logarithmic scale.

New in version 1.1.0.

scipy.signal.lp2lp

`scipy.signal.lp2lp(b, a, wo=1.0)`

Transform a lowpass filter prototype to a different frequency.

Return an analog low-pass filter with cutoff frequency $wo$ from an analog low-pass filter prototype with unity cutoff frequency, in transfer function (‘ba’) representation.

See also:

`lp2hp, lp2bp, lp2bs, bilinear, lp2lp_zpk`

scipy.signal.lp2lp_zpk

`scipy.signal.lp2lp_zpk(z, p, k, wo=1.0)`

Transform a lowpass filter prototype to a different frequency.

Return an analog low-pass filter with cutoff frequency $wo$ from an analog low-pass filter prototype with unity cutoff frequency, using zeros, poles, and gain (‘zpk’) representation.

**Parameters**

- `z` : [array_like] Zeros of the analog filter transfer function.
- `p` : [array_like] Poles of the analog filter transfer function.
- `k` : [float] System gain of the analog filter transfer function.
- `wo` : [float] Desired cutoff, as angular frequency (e.g. rad/s). Defaults to no change.

**Returns**

- `z` : [ndarray] Zeros of the transformed low-pass filter transfer function.
[ndarray] Poles of the transformed low-pass filter transfer function.

k [float] System gain of the transformed low-pass filter.

See also:
lp2hp_zpk, lp2bp_zpk, lp2bs_zpk, bilinear, lp2lp

Notes
This is derived from the s-plane substitution

\[ s \rightarrow \frac{s}{\omega_0} \]

New in version 1.1.0.

scipy.signal.normalize

scipy.signal.normalize(b, a)

Normalize numerator/denominator of a continuous-time transfer function.

If values of b are too close to 0, they are removed. In that case, a BadCoefficients warning is emitted.

Parameters
- b: array_like
  Numerator of the transfer function. Can be a 2d array to normalize multiple transfer functions.
- a: array_like
  Denominator of the transfer function. At most 1d.

Returns
- num: array
  The numerator of the normalized transfer function. At least a 1d array. A 2d-array if the input num is a 2d array.
- den: 1d-array
  The denominator of the normalized transfer function.

Notes
Coefficients for both the numerator and denominator should be specified in descending exponent order (e.g., \( s^2 + 3s + 5 \) would be represented as [1, 3, 5]).

6.20.5 Matlab-style IIR filter design

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scipy.signal.butter

scipy.signal.butter(N, Wn, btype='low', analog=False, output='ba', fs=None)

Butterworth digital and analog filter design.

Design an Nth-order digital or analog Butterworth filter and return the filter coefficients.

Parameters

- N [int] The order of the filter.
- Wn [array_like] A scalar or length-2 sequence giving the critical frequencies. For a Butterworth filter, this is the point at which the gain drops to 1/sqrt(2) that of the passband (the “-3 dB point”).
  - For digital filters, Wn are in the same units as fs. By default, fs is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. (Wn is thus in half-cycles/sample.)
  - For analog filters, Wn is an angular frequency (e.g. rad/s).
- btype [{'lowpass', 'highpass', 'bandpass', 'bandstop'}, optional] The type of filter. Default is 'lowpass'.
- analog [bool, optional] When True, return an analog filter, otherwise a digital filter is returned.
- output [{'ba', 'zpk', 'sos'}, optional] Type of output: numerator/denominator (‘ba’), pole-zero (‘zpk’), or second-order sections (‘sos’). Default is ‘ba’.

Returns

- b, a [ndarray, ndarray] Numerator (b) and denominator (a) polynomials of the IIR filter. Only returned if output='ba'.
- z, p, k [ndarray, ndarray, float] Zeros, poles, and system gain of the IIR filter transfer function. Only returned if output='zpk'.
- sos [ndarray] Second-order sections representation of the IIR filter. Only returned if output='sos'.

See also:

buttord, buttap

Notes

The Butterworth filter has maximally flat frequency response in the passband.

The ‘sos’ output parameter was added in 0.16.0.

Examples

Design an analog filter and plot its frequency response, showing the critical points:

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

>>> b, a = signal.butter(4, 100, 'low', analog=True)
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.title('Butterworth filter frequency response')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
```
>>> plt.axvline(100, color='green') # cutoff frequency
>>> plt.show()

Butterworth filter frequency response

Generate a signal made up of 10 Hz and 20 Hz, sampled at 1 kHz

```python
>>> t = np.linspace(0, 1, 1000, False) # 1 second
>>> sig = np.sin(2*np.pi*10*t) + np.sin(2*np.pi*20*t)
>>> fig, (ax1, ax2) = plt.subplots(2, 1, sharex=True)
>>> ax1.plot(t, sig)
>>> ax1.set_title('10 Hz and 20 Hz sinusoids')
>>> ax1.axis([0, 1, -2, 2])

Design a digital high-pass filter at 15 Hz to remove the 10 Hz tone, and apply it to the signal. (It's recommended to use second-order sections format when filtering, to avoid numerical error with transfer function (ba) format):

```python
>>> sos = signal.butter(10, 15, 'hp', fs=1000, output='sos')
>>> filtered = signal.sosfilt(sos, sig)
>>> ax2.plot(t, filtered)
>>> ax2.set_title('After 15 Hz high-pass filter')
>>> ax2.axis([0, 1, -2, 2])
>>> ax2.set_xlabel('Time [seconds]')
>>> plt.tight_layout()
>>> plt.show()
```

**scipy.signal.buttord**

**scipy.signal.buttord(wp, ws, gpass, gstop, analog=False, fs=None)**

Butterworth filter order selection.

Return the order of the lowest order digital or analog Butterworth filter that loses no more than \( gpass \) dB in the passband and has at least \( gstop \) dB attenuation in the stopband.

**Parameters**
wp, ws  [float] Passband and stopband edge frequencies.
For digital filters, these are in the same units as fs. By default, fs is 2 half-
cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist fre-
quency. (wp and ws are thus in half-cycles / sample.) For example:
- Lowpass: wp = 0.2, ws = 0.3
- Highpass: wp = 0.3, ws = 0.2
- Bandpass: wp = [0.2, 0.5], ws = [0.1, 0.6]
- Bandstop: wp = [0.1, 0.6], ws = [0.2, 0.5]
For analog filters, wp and ws are angular frequencies (e.g. rad/s).
gpass  [float] The maximum loss in the passband (dB).
gstop  [float] The minimum attenuation in the stopband (dB).
analog  [bool, optional] When True, return an analog filter, otherwise a digital filter is
returned.
fs  [float, optional] The sampling frequency of the digital system.
New in version 1.2.0.

Returns
- ord  [int] The lowest order for a Butterworth filter which meets specs.
- wn  [ndarray or float] The Butterworth natural frequency (i.e. the “3dB frequency”).
    Should be used with butter to give filter results. If fs is specified, this is in the
    same units, and fs must also be passed to butter.

See also:
- butter
  Filter design using order and critical points
- cheb1ord
  Find order and critical points from passband and stopband spec
- cheb2ord, ellipord
- iirfilter
  General filter design using order and critical frequencies
iirdesign

General filter design using passband and stopband spec

Examples

Design an analog bandpass filter with passband within 3 dB from 20 to 50 rad/s, while rejecting at least -40 dB below 14 and above 60 rad/s. Plot its frequency response, showing the passband and stopband constraints in gray.

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

>>> N, Wn = signal.buttord([20, 50], [14, 60], 3, 40, True)
>>> b, a = signal.butter(N, Wn, 'band', True)
>>> w, h = signal.freqs(b, a, np.logspace(1, 2, 500))
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.title('Butterworth bandpass filter fit to constraints')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.grid(which='both', axis='both')
>>> plt.fill([1, 14, 14, 1], [-40, -40, 99, 99], '0.9', lw=0)  # stop
>>> plt.fill([20, 20, 50, 50], [-99, -3, -3, -99], '0.9', lw=0)  # pass
>>> plt.fill([60, 60, 1e9, 1e9], [99, -40, -40, 99], '0.9', lw=0)  # stop
>>> plt.axis([10, 100, -60, 3])
>>> plt.show()
```

`scipy.signal.cheby1`

`scipy.signal.cheby1(N, rp, Wn, btype='low', analog=False, output='ba', fs=None)`

Chebyshev type I digital and analog filter design.

Design an Nth-order digital or analog Chebyshev type I filter and return the filter coefficients.

**Parameters**

- **N**  
  [int] The order of the filter.
**Parameters**

- **rp** [float]: The maximum ripple allowed below unity gain in the passband. Specified in decibels, as a positive number.
- **Wn** [array_like]: A scalar or length-2 sequence giving the critical frequencies. For Type I filters, this is the point in the transition band at which the gain first drops below -\(rp\).
  
  For digital filters, \(Wn\) are in the same units as \(fs\). By default, \(fs\) is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. (\(Wn\) is thus in half-cycles / sample.)
  
  For analog filters, \(Wn\) is an angular frequency (e.g. rad/s).
- **analog** [bool, optional]: When True, return an analog filter, otherwise a digital filter is returned.
- **output** [{‘ba’, ‘zpk’, ‘sos’}, optional]: Type of output: numerator/denominator (‘ba’), pole-zero (‘zpk’), or second-order sections (‘sos’). Default is ‘ba’.
- **fs** [float, optional]: The sampling frequency of the digital system.

**Returns**

- **b**, **a** [ndarray, ndarray]: Numerator \((b)\) and denominator \((a)\) polynomials of the IIR filter. Only returned if \(output=’ba’\).
- **z**, **p**, **k** [ndarray, ndarray, float]: Zeros, poles, and system gain of the IIR filter transfer function. Only returned if \(output=’zpk’\).
- **sos** [ndarray]: Second-order sections representation of the IIR filter. Only returned if \(output=’sos’\).

**See also:**

*cheb1ord*, *cheb1ap*

**Notes**

The Chebyshev type I filter maximizes the rate of cutoff between the frequency response’s passband and stopband, at the expense of ripple in the passband and increased ringing in the step response.

Type I filters roll off faster than Type II (*cheby2*), but Type II filters do not have any ripple in the passband.

The equiripple passband has \(N\) maxima or minima (for example, a 5th-order filter has 3 maxima and 2 minima). Consequently, the DC gain is unity for odd-order filters, or -\(rp\) dB for even-order filters.

The ‘sos’ output parameter was added in 0.16.0.

**Examples**

Design an analog filter and plot its frequency response, showing the critical points:

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

>>> b, a = signal.cheby1(4, 5, 100, ‘low’, analog=True)
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.title(‘Chebyshev Type I frequency response (rp=5)’)  
>>> plt.xlabel(‘Frequency [radians / second]’)  
>>> plt.ylabel(‘Amplitude [dB]’)  
>>> plt.margins(0, 0.1)  
>>> plt.grid(which=’both’, axis=’both’)  
>>> plt.axvline(100, color=’green’)  # cutoff frequency
```

(continues on next page)
 Generate a signal made up of 10 Hz and 20 Hz, sampled at 1 kHz

```
>>> t = np.linspace(0, 1, 1000, False)  # 1 second
>>> sig = np.sin(2*np.pi*10*t) + np.sin(2*np.pi*20*t)
>>> fig, (ax1, ax2) = plt.subplots(2, 1, sharex=True)
>>> ax1.plot(t, sig)
>>> ax1.set_title('10 Hz and 20 Hz sinusoids')
>>> ax1.axis([0, 1, -2, 2])
```

Design a digital high-pass filter at 15 Hz to remove the 10 Hz tone, and apply it to the signal. (It’s recommended to use second-order sections format when filtering, to avoid numerical error with transfer function (ba) format):

```
>>> sos = signal.cheby1(10, 1, 15, 'hp', fs=1000, output='sos')
>>> filtered = signal.sosfilt(sos, sig)
>>> ax2.plot(t, filtered)
>>> ax2.set_title('After 15 Hz high-pass filter')
>>> ax2.axis([0, 1, -2, 2])
>>> ax2.set_xlabel('Time [seconds]')
>>> plt.tight_layout()
>>> plt.show()
```

**scipy.signal.cheby1ord**

`scipy.signal.cheby1ord(wp, ws, gpass, gstop, analog=False, fs=None)`

Chebyshev type I filter order selection.

Return the order of the lowest order digital or analog Chebyshev Type I filter that loses no more than `gpass` dB in the passband and has at least `gstop` dB attenuation in the stopband.

**Parameters**
Passband and stopband edge frequencies.

For digital filters, these are in the same units as $fs$. By default, $fs$ is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. ($wp$ and $ws$ are thus in half-cycles / sample.) For example:

- Lowpass: $wp = 0.2$, $ws = 0.3$
- Highpass: $wp = 0.3$, $ws = 0.2$
- Bandpass: $wp = [0.2, 0.5]$, $ws = [0.1, 0.6]$
- Bandstop: $wp = [0.1, 0.6]$, $ws = [0.2, 0.5]$

For analog filters, $wp$ and $ws$ are angular frequencies (e.g. rad/s).

gpass [float] The maximum loss in the passband (dB).

gstop [float] The minimum attenuation in the stopband (dB).

analog [bool, optional] When True, return an analog filter, otherwise a digital filter is returned.

fs [float, optional] The sampling frequency of the digital system.

New in version 1.2.0.

Returns

ord [int] The lowest order for a Chebyshev type I filter that meets specs.

wn [ndarray or float] The Chebyshev natural frequency (the “3dB frequency”) for use with `cheby1` to give filter results. If $fs$ is specified, this is in the same units, and $fs$ must also be passed to `cheby1`.

See also:

- `cheby1`
  Filter design using order and critical points
- `buttord`
  Find order and critical points from passband and stopband spec
- `cheb2ord`, `ellipord`
- `iirfilter`
  General filter design using order and critical frequencies
iirdesign

General filter design using passband and stopband spec

Examples
Design a digital lowpass filter such that the passband is within 3 dB up to 0.2*(fs/2), while rejecting at least -40 dB above 0.3*(fs/2). Plot its frequency response, showing the passband and stopband constraints in gray.

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

>>> N, Wn = signal.cheby1ord(0.2, 0.3, 3, 40)
>>> b, a = signal.cheby1(N, 3, Wn, 'low')
>>> w, h = signal.freqz(b, a)
>>> plt.semilogx(w / np.pi, 20 * np.log10(abs(h)))
>>> plt.title('Chebyshev I lowpass filter fit to constraints')
>>> plt.xlabel('Normalized frequency')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.grid(which='both', axis='both')
>>> plt.fill([0.01, 0.2, 0.2, 0.01], [-3, -3, -99, -99], '0.9', lw=0)  # stop
>>> plt.fill([0.3, 0.3, 2, 2], [9, -40, -40, 9], '0.9', lw=0)  # pass
>>> plt.axis([0.08, 1, -60, 3])
>>> plt.show()
```

scipy.signal.cheby2

Design an Nth-order digital or analog Chebyshev type II filter and return the filter coefficients.

**Parameters**

- `N` : int The order of the filter.
- `rs` : float The minimum attenuation required in the stop band. Specified in decibels, as a positive number.
SciPy Reference Guide, Release 1.2.0

Wn

[array_like] A scalar or length-2 sequence giving the critical frequencies. For Type II filters, this is the point in the transition band at which the gain first reaches \(-rs\). For digital filters, Wn are in the same units as fs. By default, fs is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. (Wn is thus in half-cycles / sample.) For analog filters, Wn is an angular frequency (e.g. rad/s).

btype

[{'lowpass', 'highpass', 'bandpass', 'bandstop'}, optional] The type of filter. Default is 'lowpass'.

analog

[bool, optional] When True, return an analog filter, otherwise a digital filter is returned.

output

[{'ba', 'zpk', 'sos'}, optional] Type of output: numerator/denominator ('ba'), pole-zero ('zpk'), or second-order sections ('sos'). Default is 'ba'.

fs

[float, optional] The sampling frequency of the digital system. New in version 1.2.0.

Returns

b, a

[ndarray, ndarray] Numerator (b) and denominator (a) polynomials of the IIR filter. Only returned if output='ba'.

z, p, k

[ndarray, ndarray, float] Zeros, poles, and system gain of the IIR filter transfer function. Only returned if output='zpk'.

sos

[ndarray] Second-order sections representation of the IIR filter. Only returned if output=='sos'.

See also:

cheb2ord, cheb2ap

Notes

The Chebyshev type II filter maximizes the rate of cutoff between the frequency response’s passband and stopband, at the expense of ripple in the stopband and increased ringing in the step response.

Type II filters do not roll off as fast as Type I (cheby1).

The 'sos' output parameter was added in 0.16.0.

Examples

Design an analog filter and plot its frequency response, showing the critical points:

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

>>> b, a = signal.cheby2(4, 40, 100, 'low', analog=True)
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.title('Chebyshev Type II frequency response (rs=40)')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.axvline(100, color='green')  # cutoff frequency
>>> plt.axhline(-40, color='green')  # rs
>>> plt.show()
```

Generate a signal made up of 10 Hz and 20 Hz, sampled at 1 kHz
Design a digital high-pass filter at 17 Hz to remove the 10 Hz tone, and apply it to the signal. (It’s recommended to use second-order sections format when filtering, to avoid numerical error with transfer function (ba) format):

```python
>>> t = np.linspace(0, 1, 1000, False)  # 1 second
>>> sig = np.sin(2*np.pi*10*t) + np.sin(2*np.pi*20*t)
>>> fig, (ax1, ax2) = plt.subplots(2, 1, sharex=True)
>>> ax1.plot(t, sig)
>>> ax1.set_title('10 Hz and 20 Hz sinusoids')
>>> ax1.axis([0, 1, -2, 2])
```

```python
>>> sos = signal.cheby2(12, 20, 17, 'hp', fs=1000, output='sos')
>>> filtered = signal.sosfilt(sos, sig)
>>> ax2.plot(t, filtered)
>>> ax2.set_title('After 17 Hz high-pass filter')
>>> ax2.axis([0, 1, -2, 2])
>>> ax2.set_xlabel('Time [seconds]')
>>> plt.show()
```

### scipy.signal.cheb2ord

**scipy.signal.cheb2ord(wp, ws, gpass, gstop, analog=False, fs=None)**

Chebyshev type II filter order selection.

Return the order of the lowest order digital or analog Chebyshev Type II filter that loses no more than *gpass* dB in the passband and has at least *gstop* dB attenuation in the stopband.

**Parameters**

- **wp, ws** [float] Passband and stopband edge frequencies. For digital filters, these are in the same units as *fs*. By default, *fs* is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. (*wp* and *ws* are thus in half-cycles / sample.) For example:
  - Lowpass: *wp = 0.2, ws = 0.3*
  - Highpass: *wp = 0.3, ws = 0.2*
Bandpass: \( wp = [0.2, 0.5], ws = [0.1, 0.6] \)

Bandstop: \( wp = [0.1, 0.6], ws = [0.2, 0.5] \)

For analog filters, \( wp \) and \( ws \) are angular frequencies (e.g. rad/s).

- `gpass` [float] The maximum loss in the passband (dB).
- `gstop` [float] The minimum attenuation in the stopband (dB).
- `analog` [bool, optional] When True, return an analog filter, otherwise a digital filter is returned.
- `fs` [float, optional] The sampling frequency of the digital system.

New in version 1.2.0.

Returns

- `ord` [int] The lowest order for a Chebyshev type II filter that meets specs.
- `wn` [ndarray or float] The Chebyshev natural frequency (the “3dB frequency”) for use with `cheby2` to give filter results. If `fs` is specified, this is in the same units, and `fs` must also be passed to `cheby2`.

See also:

- `cheby2`
  Filter design using order and critical points
- `buttord`
  Find order and critical points from passband and stopband spec
- `cheb1ord, ellipord`
- `iirfilter`
  General filter design using order and critical frequencies
- `iirdesign`
  General filter design using passband and stopband spec
Examples
Design a digital bandstop filter which rejects \(-60\) dB from \(0.2*(fs/2)\) to \(0.5*(fs/2)\), while staying within 3 dB below \(0.1*(fs/2)\) or above \(0.6*(fs/2)\). Plot its frequency response, showing the passband and stopband constraints in gray.

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

>>> N, Wn = signal.cheb2ord([0.1, 0.6], [0.2, 0.5], 3, 60)
>>> b, a = signal.cheby2(N, 60, Wn, 'stop')
>>> w, h = signal.freqz(b, a)
>>> plt.semilogx(w / np.pi, 20 * np.log10(abs(h)))
>>> plt.title('Chebyshev II bandstop filter fit to constraints')
>>> plt.xlabel('Normalized frequency')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.grid(which='both', axis='both')
>>> plt.fill([.01, .1, .1, .01], [-3, -3, -99, -99], '0.9', lw=0) # stop
>>> plt.fill([.2, .2, .5, .5], [9, -60, -60, 9], '0.9', lw=0) # pass
>>> plt.fill([.6, .6, 2, 2], [-99, -3, -3, -99], '0.9', lw=0) # stop
>>> plt.axis([0.06, 1, -80, 3])
>>> plt.show()
```

scipy.signal.ellip

`scipy.signal.ellip(N, rp, rs, Wn, btype='low', analog=False, output='ba', fs=None)`

Elliptic (Cauer) digital and analog filter design.

Design an Nth-order digital or analog elliptic filter and return the filter coefficients.

**Parameters**

- **N** [int] The order of the filter.
- **rp** [float] The maximum ripple allowed below unity gain in the passband. Specified in decibels, as a positive number.
- **rs** [float] The minimum attenuation required in the stop band. Specified in decibels, as a positive number.
SciPy Reference Guide, Release 1.2.0

Wn [array_like] A scalar or length-2 sequence giving the critical frequencies. For elliptic filters, this is the point in the transition band at which the gain first drops below \( -rp \).

For digital filters, \( Wn \) are in the same units as \( fs \). By default, \( fs \) is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. (\( Wn \) is thus in half-cycles / sample.)

For analog filters, \( Wn \) is an angular frequency (e.g. rad/s).


analog [bool, optional] When True, return an analog filter, otherwise a digital filter is returned.

output [{‘ba’, ‘zpk’, ‘sos’}, optional] Type of output: numerator/denominator (‘ba’), pole-zero (‘zpk’), or second-order sections (‘sos’). Default is ‘ba’.

fs [float, optional] The sampling frequency of the digital system.

New in version 1.2.0.

Returns

\( b, a \) [ndarray, ndarray] Numerator (\( b \)) and denominator (\( a \)) polynomials of the IIR filter. Only returned if \( output='ba' \).

\( z, p, k \) [ndarray, ndarray, float] Zeros, poles, and system gain of the IIR filter transfer function. Only returned if \( output='zpk' \).

\( sos \) [ndarray] Second-order sections representation of the IIR filter. Only returned if \( output='sos' \).

See also:

ellipord, ellipap

Notes

Also known as Cauer or Zolotarev filters, the elliptical filter maximizes the rate of transition between the frequency response’s passband and stopband, at the expense of ripple in both, and increased ringing in the step response.

As \( rp \) approaches 0, the elliptical filter becomes a Chebyshev type II filter (\( \text{cheby2} \)). As \( rs \) approaches 0, it becomes a Chebyshev type I filter (\( \text{cheby1} \)). As both approach 0, it becomes a Butterworth filter (\( \text{butter} \)).

The equiripple passband has \( N \) maxima or minima (for example, a 5th-order filter has 3 maxima and 2 minima). Consequently, the DC gain is unity for odd-order filters, or \( -rp \) dB for even-order filters.

The ‘sos’ output parameter was added in 0.16.0.

Examples

Design an analog filter and plot its frequency response, showing the critical points:

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

>>> b, a = signal.ellip(4, 5, 40, 100, 'low', analog=True)
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.title('Elliptic filter frequency response (rp=5, rs=40)')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.grid(which='both', axis='both')
>>> plt.axvline(100, color='green') # cutoff frequency
```

(continues on next page)
Generate a signal made up of 10 Hz and 20 Hz, sampled at 1 kHz

```python
>>> t = np.linspace(0, 1, 1000, False)  # 1 second
>>> sig = np.sin(2*np.pi*10*t) + np.sin(2*np.pi*20*t)
>>> fig, (ax1, ax2) = plt.subplots(2, 1, sharex=True)
>>> ax1.plot(t, sig)
>>> ax1.set_title('10 Hz and 20 Hz sinusoids')
>>> ax1.axis([0, 1, -2, 2])
```

Design a digital high-pass filter at 17 Hz to remove the 10 Hz tone, and apply it to the signal. (It's recommended to use second-order sections format when filtering, to avoid numerical error with transfer function (ba) format):

```python
>>> sos = signal.ellip(8, 1, 100, 17, 'hp', fs=1000, output='sos')
>>> filtered = signal.sosfilt(sos, sig)
>>> ax2.plot(t, filtered)
>>> ax2.set_title('After 17 Hz high-pass filter')
>>> ax2.axis([0, 1, -2, 2])
>>> ax2.set_xlabel('Time [seconds]')
>>> plt.tight_layout()
>>> plt.show()
```

```python
scipy.signal.elliporder
```

scipy.signal.ellipord(wp, ws, gpass, gstop, analog=False, fs=None)
Elliptic (Cauer) filter order selection.

Return the order of the lowest order digital or analog elliptic filter that loses no more than \textit{gpass} dB in the passband and has at least \textit{gstop} dB attenuation in the stopband.

**Parameters**
wp, ws  [float] Passband and stopband edge frequencies. For digital filters, these are in the same units as fs. By default, fs is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. (wp and ws are thus in half-cycles/sample.) For example:

- Lowpass: wp = 0.2, ws = 0.3
- Highpass: wp = 0.3, ws = 0.2
- Bandpass: wp = [0.2, 0.5], ws = [0.1, 0.6]
- Bandstop: wp = [0.1, 0.6], ws = [0.2, 0.5]

For analog filters, wp and ws are angular frequencies (e.g. rad/s).

gpass  [float] The maximum loss in the passband (dB).
gstop  [float] The minimum attenuation in the stopband (dB).
analog  [bool, optional] When True, return an analog filter, otherwise a digital filter is returned.

fs  [float, optional] The sampling frequency of the digital system.

New in version 1.2.0.

Returns

ord  [int] The lowest order for an Elliptic (Cauer) filter that meets specs.

wn  [ndarray or float] The Chebyshev natural frequency (the “3dB frequency”) for use with ellip to give filter results. If fs is specified, this is in the same units, and fs must also be passed to ellip.

See also:

ellip
Filter design using order and critical points

buttord
Find order and critical points from passband and stopband spec

cheb1ord, cheb2ord

iirfilter
General filter design using order and critical frequencies
**iirdesign**

General filter design using passband and stopband spec

**Examples**

Design an analog highpass filter such that the passband is within 3 dB above 30 rad/s, while rejecting -60 dB at 10 rad/s. Plot its frequency response, showing the passband and stopband constraints in gray.

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

>>> N, Wn = signal.ellipord(30, 10, 3, 60, True)
>>> b, a = signal.ellip(N, 3, 60, Wn, 'high', True)
>>> w, h = signal.freqs(b, a, np.logspace(0, 3, 500))
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.title('Elliptical highpass filter fit to constraints')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.grid(which='both', axis='both')
>>> plt.fill([.1, 10, 10, .1], [1e4, 1e4, -60, -60], '0.9', lw=0)  # stop
>>> plt.fill([30, 30, 1e9, 1e9], [-99, -3, -3, -99], '0.9', lw=0)  # pass
>>> plt.axis([1, 300, -80, 3])
>>> plt.show()
```

**scipy.signal.bessel**

**scipy.signal.bessel**(*N, Wn*, **btype='low', analog=False, output='ba', norm='phase', fs=None*)

Bessel/Thomson digital and analog filter design.

Design an Nth-order digital or analog Bessel filter and return the filter coefficients.

**Parameters**

- **N** : int The order of the filter.
- **Wn** : array_like A scalar or length-2 sequence giving the critical frequencies (defined by the `norm` parameter). For analog filters, `Wn` is an angular frequency (e.g. rad/s).
For digital filters, \(W_n\) are in the same units as \(fs\). By default, \(fs\) is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. (\(W_n\) is thus in half-cycles / sample.)

**btype**
[\{'lowpass', 'highpass', 'bandpass', 'bandstop'}, optional] The type of filter. Default is 'lowpass'.

**analog**
[bool, optional] When True, return an analog filter, otherwise a digital filter is returned. (See Notes.)

**output**
[\{'ba', 'zpk', 'sos'}, optional] Type of output: numerator/denominator ('ba'), pole-zero ('zpk'), or second-order sections ('sos'). Default is 'ba'.

**norm**
[\{'phase', 'delay', 'mag'}, optional] Critical frequency normalization:

- **phase** The filter is normalized such that the phase response reaches its midpoint at angular (e.g. rad/s) frequency \(W_n\). This happens for both low-pass and high-pass filters, so this is the “phase-matched” case. The magnitude response asymptotes are the same as a Butterworth filter of the same order with a cutoff of \(W_n\). This is the default, and matches MATLAB’s implementation.

- **delay** The filter is normalized such that the group delay in the passband is \(1/W_n\) (e.g. seconds). This is the “natural” type obtained by solving Bessel polynomials.

- **mag** The filter is normalized such that the gain magnitude is -3 dB at angular frequency \(W_n\).

    New in version 0.18.0.

**fs**
[float, optional] The sampling frequency of the digital system.

    New in version 1.2.0.

**Returns**

- **b, a** [ndarray, ndarray] Numerator (\(b\)) and denominator (\(a\)) polynomials of the IIR filter. Only returned if output='ba'.

- **z, p, k** [ndarray, ndarray, float] Zeros, poles, and system gain of the IIR filter transfer function. Only returned if output='zpk'.

- **sos** [ndarray] Second-order sections representation of the IIR filter. Only returned if output='sos'.

**Notes**

Also known as a Thomson filter, the analog Bessel filter has maximally flat group delay and maximally linear phase response, with very little ringing in the step response. [1]

The Bessel is inherently an analog filter. This function generates digital Bessel filters using the bilinear transform, which does not preserve the phase response of the analog filter. As such, it is only approximately correct at frequencies below about \(fs/4\). To get maximally-flat group delay at higher frequencies, the analog Bessel filter must be transformed using phase-preserving techniques.

See besselap for implementation details and references.

The ‘sos’ output parameter was added in 0.16.0.

**References**

[1]

**Examples**

Plot the phase-normalized frequency response, showing the relationship to the Butterworth’s cutoff frequency (green):

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> import matplotlib.pyplot as plt
```
```python
>>> b, a = signal.butter(4, 100, 'low', analog=True)
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(np.abs(h)), color='silver', ls='dashed')
>>> b, a = signal.bessel(4, 100, 'low', analog=True, norm='phase')
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(np.abs(h)))
>>> plt.title('Bessel filter magnitude response (with Butterworth)')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.axvline(100, color='green') # cutoff frequency
>>> plt.show()
```

and the phase midpoint:

```python
>>> plt.figure()
>>> plt.semilogx(w, np.unwrap(np.angle(h)))
>>> plt.axvline(100, color='green') # cutoff frequency
>>> plt.axhline(-np.pi, color='red') # phase midpoint
>>> plt.title('Bessel filter phase response')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Phase [radians]')
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.show()
```

Plot the magnitude-normalized frequency response, showing the -3 dB cutoff:

```python
>>> b, a = signal.bessel(3, 10, 'low', analog=True, norm='mag')
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(np.abs(h)))
>>> plt.axhline(-3, color='red') # -3 dB magnitude
>>> plt.axvline(10, color='green') # cutoff frequency
```

(continues on next page)
Plot the delay-normalized filter, showing the maximally-flat group delay at 0.1 seconds:

```python
>>> b, a = signal.bessel(S, 1/0.1, 'low', analog=True, norm='delay')
>>> w, h = signal.freqs(b, a)
>>> plt.figure()
>>> plt.semilogx(w[1:], -np.diff(np.unwrap(np.angle(h)))/np.diff(w))
```

(continues on next page)
scipy.signal.iirnotch

scipy.signal.iirnotch(w0, Q, fs=2.0)

Design second-order IIR notch digital filter.

A notch filter is a band-stop filter with a narrow bandwidth (high quality factor). It rejects a narrow frequency band and leaves the rest of the spectrum little changed.

**Parameters**

- **w0** [float] Frequency to remove from a signal. If `fs` is specified, this is in the same units as `fs`. By default, it is a normalized scalar that must satisfy 0 < w0 < 1, with w0 = 1 corresponding to half of the sampling frequency.
- **Q** [float] Quality factor. Dimensionless parameter that characterizes notch filter -3 dB bandwidth bw relative to its center frequency, Q = w0/bw.
- **fs** [float, optional] The sampling frequency of the digital system. New in version 1.2.0.

**Returns**

- **b, a** [ndarray, ndarray] Numerator (b) and denominator (a) polynomials of the IIR filter.

**See also:**

- iirpeak

**Notes**

New in version 0.19.0.
References

[1]

Examples

Design and plot filter to remove the 60 Hz component from a signal sampled at 200 Hz, using a quality factor $Q = 30$

```python
>>> from scipy import signal
>>> import numpy as np
>>> import matplotlib.pyplot as plt

>>> fs = 200.0  # Sample frequency (Hz)
>>> f0 = 60.0   # Frequency to be removed from signal (Hz)
>>> Q = 30.0   # Quality factor

# Design notch filter
>>> b, a = signal.iirnotch(f0, Q, fs)

# Frequency response
>>> freq, h = signal.freqz(b, a, fs=fs)

# Plot
>>> fig, ax = plt.subplots(2, 1, figsize=(8, 6))
>>> ax[0].plot(freq, 20*np.log10(abs(h)), color='blue')
>>> ax[0].set_title("Frequency Response")
>>> ax[0].set_ylabel("Amplitude (dB)", color='blue')
>>> ax[0].set_xlim([0, 100])
>>> ax[0].set_ylim([-25, 10])
>>> ax[0].grid()
>>> ax[1].plot(freq, np.unwrap(np.angle(h))*180/np.pi, color='green')
>>> ax[1].set_ylabel("Angle (degrees)", color='green')
>>> ax[1].set_xlabel("Frequency (Hz)"
>>> ax[1].set_xlim([0, 100])
>>> ax[1].set_yticks([-90, -60, -30, 0, 30, 60, 90])
>>> ax[1].set_ylim([-90, 90])
>>> ax[1].grid()
>>> plt.show()
```

`scipy.signal.iirpeak`

`scipy.signal.iirpeak(w0, Q, fs=2.0)`

Design second-order IIR peak (resonant) digital filter.

A peak filter is a band-pass filter with a narrow bandwidth (high quality factor). It rejects components outside a narrow frequency band.

**Parameters**

- **w0**: [float] Frequency to be retained in a signal. If $fs$ is specified, this is in the same units as $fs$. By default, it is a normalized scalar that must satisfy $0 < w0 < 1$, with $w0 = 1$ corresponding to half of the sampling frequency.

- **Q**: [float] Quality factor. Dimensionless parameter that characterizes peak filter -3 dB bandwidth $bw$ relative to its center frequency, $Q = w0/bw$.

- **fs**: [float, optional] The sampling frequency of the digital system. New in version 1.2.0.

**Returns**
6.20. Signal processing (scipy.signal)
b, a [ndarray, ndarray] Numerator (b) and denominator (a) polynomials of the IIR filter.

See also:

iirnotch

Notes

New in version 0.19.0.

References

[1]

Examples

Design and plot filter to remove the frequencies other than the 300 Hz component from a signal sampled at 1000 Hz, using a quality factor Q = 30

```python
>>> from scipy import signal
>>> import numpy as np
>>> import matplotlib.pyplot as plt

>>> fs = 1000.0  # Sample frequency (Hz)
>>> f0 = 300.0   # Frequency to be retained (Hz)
>>> Q = 30.0    # Quality factor

>>> # Design peak filter
>>> b, a = signal.iirpeak(f0, Q, fs)

>>> # Frequency response
>>> freq, h = signal.freqz(b, a, fs=fs)

>>> # Plot
>>> fig, ax = plt.subplots(2, 1, figsize=(8, 6))
>>> ax[0].plot(freq, 20*np.log10(abs(h)), color='blue')
>>> ax[0].set_title("Frequency Response")
>>> ax[0].set_ylabel("Amplitude (dB)", color='blue')
>>> ax[0].set_xlim([0, 500])
>>> ax[0].set_ylim([-50, 10])
>>> ax[0].grid()

>>> ax[1].plot(freq, np.unwrap(np.angle(h))*180/np.pi, color='green')
>>> ax[1].set_ylabel("Angle (degrees)", color='green')
>>> ax[1].set_xlabel("Frequency (Hz)")
>>> ax[1].set_xlim([0, 500])
>>> ax[1].set_yticks([-90, -60, -30, 0, 30, 60, 90])
>>> ax[1].set_ylim([-90, 90])
>>> ax[1].grid()
>>> plt.show()
```

6.20.6 Continuous-Time Linear Systems

| lti(*system) | Continuous-time linear time invariant system base class. |
| StateSpace(*system, **kwargs) | Linear Time Invariant system in state-space form. |
| TransferFunction(*system, **kwargs) | Linear Time Invariant system class in transfer function form. |

Continued on next page
scipy.signal.lti

class scipy.signal.lti(*system)

Continuous-time linear time invariant system base class.

Parameters

*system [arguments] The lti class can be instantiated with either 2, 3 or 4 arguments. The following gives the number of arguments and the corresponding continuous-time subclass that is created:

- 2: TransferFunction: (numerator, denominator)
- 3: ZerosPolesGain: (zeros, poles, gain)
- 4: StateSpace: (A, B, C, D)

Each argument can be an array or a sequence.

See also:

ZerosPolesGain, StateSpace, TransferFunction, dlti

Notes

lti instances do not exist directly. Instead, lti creates an instance of one of its subclasses: StateSpace, TransferFunction or ZerosPolesGain.

If (numerator, denominator) is passed in for *system, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g., \(s^2 + 3s + 5\) would be represented as \([1, 3, 5]\)).

Changing the value of properties that are not directly part of the current system representation (such as the zeros of a StateSpace system) is very inefficient and may lead to numerical inaccuracies. It is better to convert to the specific system representation first. For example, call sys = sys.to_zpk() before accessing/changing the zeros, poles or gain.

Examples

```python
>>> from scipy import signal

>>> signal.lti(1, 2, 3, 4)
StateSpaceContinuous(
array([[1]]),
array([[2]]),
array([[3]]),
(continues on next page)
```
Attributes

- `dt` : Return the sampling time of the system, `None` for `lti` systems.
- `poles` : Poles of the system.
- `zeros` : Zeros of the system.

Methods

- `bode([w, n])` : Calculate Bode magnitude and phase data of a continuous-time system.
- `freqresp([w, n])` : Calculate the frequency response of a continuous-time system.
- `impulse([X0, T, N])` : Return the impulse response of a continuous-time system.
- `output(U, T[, X0])` : Return the response of a continuous-time system to input `U`.
- `step([X0, T, N])` : Return the step response of a continuous-time system.
- `to_discrete(dt[, method, alpha])` : Return a discretized version of the current system.

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array([[4]]),
dt: None
)

```python
>>> signal.lti([1, 2], [3, 4], 5)
ZerosPolesGainContinuous(
array([1, 2]),
array([3, 4]),
5,
dt: None
)
```

```python
>>> signal.lti([3, 4], [1, 2])
TransferFunctionContinuous(
array([3., 4.]),
array([1., 2.]),
dt: None
)
```

```python
Attributes

dt Return the sampling time of the system, None for lti systems.
poles Poles of the system.
zeros Zeros of the system.
```

Methods

```
bode([w, n]) Calculate Bode magnitude and phase data of a continuous-time system.

freqresp([w, n]) Calculate the frequency response of a continuous-time system.

impulse([X0, T, N]) Return the impulse response of a continuous-time system.

output(U, T[, X0]) Return the response of a continuous-time system to input U.

step([X0, T, N]) Return the step response of a continuous-time system.

to_discrete(dt[, method, alpha]) Return a discretized version of the current system.
```

```
scipy.signal.lti.bode

lti.bode(w=None, n=100)
Calculate Bode magnitude and phase data of a continuous-time system.

Returns a 3-tuple containing arrays of frequencies [rad/s], magnitude [dB] and phase [deg]. See bode for details.

Examples

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```
```python
>>> sys = signal.TransferFunction([[1], [1, 1]])
>>> w, mag, phase = sys.bode()
```

```python
>>> plt.figure()
>>> plt.semilogx(w, mag)  # Bode magnitude plot
>>> plt.figure()
>>> plt.semilogx(w, phase)  # Bode phase plot
>>> plt.show()
```

**scipy.signal.lti.freqresp**

`lti.freqresp(w=None, n=10000)`

Calculate the frequency response of a continuous-time system.

Returns a 2-tuple containing arrays of frequencies [rad/s] and complex magnitude. See `freqresp` for details.
scipy.signal.lti.impulse
lti.impulse(X0=None, T=None, N=None)

Return the impulse response of a continuous-time system. See `impulse` for details.

scipy.signal.lti.output
lti.output(U, T, X0=None)

Return the response of a continuous-time system to input U. See `lsim` for details.

scipy.signal.lti.step
lti.step(X0=None, T=None, N=None)

Return the step response of a continuous-time system. See `step` for details.

scipy.signal.lti.to_discrete
lti.to_discrete(dt, method='zoh', alpha=None)

Return a discretized version of the current system.

Parameters: See `cont2discrete` for details.

Returns
sys: instance of ‘dlti’

scipy.signal.StateSpace
class scipy.signal.StateSpace(*system, **kwargs)

Linear Time Invariant system in state-space form.

Repsents the system as the continuous-time, first order differential equation \( \dot{x} = Ax + Bu \) or the discrete-time difference equation \( x[k+1] = Ax[k] + Bu[k] \). `StateSpace` systems inherit additional functionality from the `lti`, respectively the `dlti` classes, depending on which system representation is used.

Parameters
- *system: arguments
  The `StateSpace` class can be instantiated with 1 or 3 arguments. The following gives the number of input arguments and their interpretation:
  - 1: `lti` or `dlti` system: (`StateSpace`, `TransferFunction` or `ZerosPolesGain`)
  - 4: array_like: (A, B, C, D)

- dt: float, optional
  Sampling time [s] of the discrete-time systems. Defaults to `None` (continuous-time). Must be specified as a keyword argument, for example, `dt=0.1`.

See also:
`TransferFunction`, `ZerosPolesGain`, `lti`, `dlti`, `ss2zpk`, `ss2tf`, `zpk2sos`

Notes
Changing the value of properties that are not part of the `StateSpace` system representation (such as `zeros` or `poles`) is very inefficient and may lead to numerical inaccuracies. It is better to convert to the specific system representation first. For example, call `sys = sys.to_zpk()` before accessing/changing the zeros, poles or gain.

Examples
```
>>> from scipy import signal

>>> a = np.array([[0, 1], [0, 0]])
>>> b = np.array([[0], [1]])
>>> c = np.array([[1, 0]])
>>> d = np.array([[0]])
```
```python
>>> sys = signal.StateSpace(a, b, c, d)
>>> print(sys)
StateSpaceContinuous(
    array([[0, 1],
           [0, 0]]),
    array([[0],
           [1]]),
    array([[1, 0]]),
    array([0]),
    dt: None)

>>> sys.to_discrete(0.1)
StateSpaceDiscrete(
    array([[1., 0.1],
           [0., 1.]im
    array([[0.005],
           [0.1  ]]),
    array([[1, 0]]),
    array([0]),
    dt: 0.1)

>>> a = np.array([[1, 0.1], [0, 1]])
>>> b = np.array([[0.005], [0.1]])
>>> signal.StateSpace(a, b, c, d, dt=0.1)
StateSpaceDiscrete(
    array([[1., 0.1],
           [0., 1.]im
    array([[0.005],
           [0.1  ]]),
    array([[1, 0]]),
    array([0]),
    dt: 0.1)
```

**Attributes**

- **A**: State matrix of the `StateSpace` system.
- **B**: Input matrix of the `StateSpace` system.
- **C**: Output matrix of the `StateSpace` system.
- **D**: Feedthrough matrix of the `StateSpace` system.
- **dt**: Return the sampling time of the system, `None` for `lti` systems.
- **poles**: Poles of the system.
- **zeros**: Zeros of the system.

**Methods**

- **to_ss()**: Return a copy of the current `StateSpace` system.

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**scipy.signal.StateSpace.to_ss**

state_space.to_ss()

Return a copy of the current StateSpace system.

**Returns**

- `sys` [instance of StateSpace] The current system (copy)

**scipy.signal.StateSpace.to_tf**

state_space.to_tf(kwargs)

Convert system representation to TransferFunction.

**Parameters**

- `kwargs` [dict, optional] Additional keywords passed to ss2zpk

**Returns**

- `sys` [instance of TransferFunction] Transfer function of the current system

**scipy.signal.StateSpace.to_zpk**

state_space.to_zpk(kwargs)

Convert system representation to ZerosPolesGain.

**Parameters**

- `kwargs` [dict, optional] Additional keywords passed to ss2zpk

**Returns**

- `sys` [instance of ZerosPolesGain] Zeros, poles, gain representation of the current system

**scipy.signal.TransferFunction**

class scipy.signal.TransferFunction(*system, **kwargs)

Linear Time Invariant system class in transfer function form.

Represents the system as the continuous-time transfer function \( H(s) = \sum_{i=0}^{N} b[N - i]s^i / \sum_{j=0}^{M} a[M - j]s^j \) or the discrete-time transfer function \( H(z) = \sum_{i=0}^{N} b[N - i]z^i / \sum_{j=0}^{M} a[M - j]z^j \), where \( b \) are elements of the numerator \( \text{num} \), \( a \) are elements of the denominator \( \text{den} \), and \( N == \text{len}(b) - 1, M == \text{len}(a) - 1 \). TransferFunction systems inherit additional functionality from the lti, respectively the dliti classes, depending on which system representation is used.

**Parameters**

- `*system`: arguments
  - The TransferFunction class can be instantiated with 1 or 2 arguments. The following gives the number of input arguments and their interpretation:
    - 1: lti or dliti system: (StateSpace, TransferFunction or ZerosPolesGain)
    - 2: array_like: (numerator, denominator)
  - `dt`: float, optional
    - Sampling time [s] of the discrete-time systems. Defaults to None (continuous-time). Must be specified as a keyword argument, for example, `dt=0.1`.
See also:

ZerosPolesGain, StateSpace, lti, dlti, tf2ss, tf2zpk, tf2sos

Notes
Changing the value of properties that are not part of the TransferFunction system representation (such as the A, B, C, D state-space matrices) is very inefficient and may lead to numerical inaccuracies. It is better to convert to the specific system representation first. For example, call `sys = sys.to_ss()` before accessing/changing the A, B, C, D system matrices.

If (numerator, denominator) is passed in for *system, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. $s^2 + 3s + 5$ or $z^{-2} + 3z + 5$ would be represented as `[1, 3, 5]`)

Examples
Construct the transfer function:

$$H(s) = \frac{s^2 + 3s + 3}{s^2 + 2s + 1}$$

```python
>>> from scipy import signal
```

```python
>>> num = [1, 3, 3]
>>> den = [1, 2, 1]
```

```python
>>> signal.TransferFunction(num, den)
TransferFunctionContinuous(  
    array([1., 3., 3.]),
    array([1., 2., 1.]),
    dt: None
)
```

Construct the transfer function with a sampling time of 0.1 seconds:

$$H(z) = \frac{z^2 + 3z + 3}{z^2 + 2z + 1}$$

```python
>>> signal.TransferFunction(num, den, dt=0.1)
TransferFunctionDiscrete(  
    array([1., 3., 3.]),
    array([1., 2., 1.]),
    dt: 0.1
)
```

Attributes
---

den : Denominator of the TransferFunction system.
dt : Return the sampling time of the system, None for lti systems.
um : Numerator of the TransferFunction system.
poles : Poles of the system.
zeros : Zeros of the system.

Methods
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### `scipy.signal.TransferFunction.to_ss` TransferFunction.to_ss()
Convert system representation to `StateSpace`.

**Returns**
- `sys`: [instance of `StateSpace`] State space model of the current system

### `scipy.signal.TransferFunction.to_tf` TransferFunction.to_tf()
Return a copy of the current `TransferFunction` system.

**Returns**
- `sys`: [instance of `TransferFunction`] The current system (copy)

### `scipy.signal.TransferFunction.to_zpk` TransferFunction.to_zpk()
Convert system representation to `ZerosPolesGain`.

**Returns**
- `sys`: [instance of `ZerosPolesGain`] Zeros, poles, gain representation of the current system

### `scipy.signal.ZerosPolesGain`

**class scipy.signal.ZerosPolesGain(*system, **kwargs)**

Linear Time Invariant system class in zeros, poles, gain form.

Represents the system as the continuous- or discrete-time transfer function \( H(s) = k \prod_i (s - z[i]) / \prod_j (s - p[j]) \), where \( k \) is the gain, \( z \) are the zeros and \( p \) are the poles. `ZerosPolesGain` systems inherit additional functionality from the `lti`, respectively the `dlti` classes, depending on which system representation is used.

**Parameters**
- `*system`: [arguments] The `ZerosPolesGain` class can be instantiated with 1 or 3 arguments. The following gives the number of input arguments and their interpretation:
  - 1: `lti` or `dlti` system: (`StateSpace`, `TransferFunction` or `ZerosPolesGain`)
  - 3: array-like: (zeros, poles, gain)
- `dt`: float, optional
  - Sampling time [s] of the discrete-time systems. Defaults to `None` (continuous-time). Must be specified as a keyword argument, for example, `dt=0.1`.

**See also:**
- `TransferFunction`, `StateSpace`, `lti`, `dlti`, `zpk2ss`, `zpk2tf`, `zpk2sos`

**Notes**
Changing the value of properties that are not part of the `ZerosPolesGain` system representation (such as the `A`, `B`, `C`, `D` state-space matrices) is very inefficient and may lead to numerical inaccuracies. It is better to convert to the specific system representation first. For example, call `sys = sys.to_ss()` before accessing/changing the `A`, `B`, `C`, `D` system matrices.
Examples

```python
>>> from scipy import signal
```

Transfer function: \( H(s) = \frac{5(s - 1)(s - 2)}{(s - 3)(s - 4)} \)

```python
>>> signal.ZerosPolesGain([1, 2], [3, 4], 5)
ZerosPolesGainContinuous(
    array([1, 2]),
    array([3, 4]),
    5,
    dt: None
)
```

Transfer function: \( H(z) = \frac{5(z - 1)(z - 2)}{(z - 3)(z - 4)} \)

```python
>>> signal.ZerosPolesGain([1, 2], [3, 4], 5, dt=0.1)
ZerosPolesGainDiscrete(
    array([1, 2]),
    array([3, 4]),
    5,
    dt: 0.1
)
```

**Attributes**

- `dt`  
  Return the sampling time of the system, `None` for `lti` systems.
- `gain`  
  Gain of the `ZerosPolesGain` system.
- `poles`  
  Poles of the `ZerosPolesGain` system.
- `zeros`  
  Zeros of the `ZerosPolesGain` system.

**Methods**

- `to_ss()`  
  Convert system representation to `StateSpace`.
- `to_tf()`  
  Convert system representation to `TransferFunction`.
- `to_zpk()`  
  Return a copy of the current ‘ZerosPolesGain’ system.

```python
scipy.signal.ZerosPolesGain.to_ss
ZerosPolesGain.to_ss()

    Convert system representation to StateSpace.

    Returns
    Predict
    sys  [instance of StateSpace] State space model of the current system

scipy.signal.ZerosPolesGain.to_tf
ZerosPolesGain.to_tf()

    Convert system representation to TransferFunction.

    Returns
    Predict
    sys  [instance of TransferFunction] Transfer function of the current system

scipy.signal.ZerosPolesGain.to_zpk
ZerosPolesGain.to_zpk()

    Return a copy of the current ‘ZerosPolesGain’ system.
```
Returns

sys       [instance of ZerosPolesGain] The current system (copy)

scipy.signal.lsim

scipy.signal.lsim(system, U, T, X0=None, interp=True)
Simulate output of a continuous-time linear system.

Parameters

system     [an instance of the LTI class or a tuple describing the system.] The following gives the number of elements in the tuple and the interpretation:
• 1: (instance of lti)
• 2: (num, den)
• 3: (zeros, poles, gain)
• 4: (A, B, C, D)
U         [array_like] An input array describing the input at each time T (interpolation is assumed between given times). If there are multiple inputs, then each column of the rank-2 array represents an input. If U = 0 or None, a zero input is used.
T         [array_like] The time steps at which the input is defined and at which the output is desired. Must be nonnegative, increasing, and equally spaced.
X0        [array_like, optional] The initial conditions on the state vector (zero by default).
interp    [bool, optional] Whether to use linear (True, the default) or zero-order-hold (False) interpolation for the input array.

Returns

T     [1D ndarray] Time values for the output.
yout [1D ndarray] System response.

Notes
If (num, den) is passed in for system, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. $s^2 + 3s + 5$ would be represented as [1, 3, 5]).

Examples
Simulate a double integrator $y'' = u$, with a constant input $u = 1$

```python
>>> from scipy import signal
>>> system = signal.lti([[0., 1.], [0., 0.]], [[0.], [1.]], [[1., 0.]], 0.)
>>> t = np.linspace(0, 5)
>>> u = np.ones_like(t)
>>> tout, y, x = signal.lsim(system, u, t)
>>> import matplotlib.pyplot as plt
>>> plt.plot(t, y)
```

scipy.signal.lsim2

scipy.signal.lsim2(system, U=None, T=None, X0=None, **kwargs)
Simulate output of a continuous-time linear system, by using the ODE solver scipy.integrate.odeint.

Parameters

system     [an instance of the lti class or a tuple describing the system.] The following gives the number of elements in the tuple and the interpretation:
• 1: (instance of lti)
• 2: (num, den)
lsim2(system, U, T, X0=None, N=101, Epsilon=1e-05, **kwargs)

**Parameters**
- **system**: An instance of the LTI class or a tuple of array_like describing the system. The following gives the number of elements in the tuple and the interpretation:
  - 1 (instance of lti)
  - 3: (zeros, poles, gain)
  - 4: (A, B, C, D)
- **U**: [array_like (1D or 2D), optional] An input array describing the input at each time T. Linear interpolation is used between given times. If there are multiple inputs, then each column of the rank-2 array represents an input. If U is not given, the input is assumed to be zero.
- **T**: [array_like (1D or 2D), optional] The time steps at which the input is defined and at which the output is desired. The default is 101 evenly spaced points on the interval [0,10.0].
- **X0**: [array_like (1D), optional] The initial condition of the state vector. If X0 is not given, the initial conditions are assumed to be 0.
- **kwargs**: [dict] Additional keyword arguments are passed on to the function odeint. See the notes below for more details.

**Returns**
- **T**: [1D ndarray] The time values for the output.
- **yout**: [ndarray] The response of the system.

**Notes**
This function uses scipy.integrate.odeint to solve the system’s differential equations. Additional keyword arguments given to lsim2 are passed on to odeint. See the documentation for scipy.integrate.odeint for the full list of arguments.

If (num, den) is passed in for system, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. \( s^2 + 3s + 5 \) would be represented as \([1, 3, 5]\)).

**scipy.signal.impulse**

scipy.signal.impulse(system, X0=None, T=None, N=None)

Impulse response of continuous-time system.

**Parameters**
- **system**: [an instance of the LTI class or a tuple of array_like] describing the system. The following gives the number of elements in the tuple and the interpretation:
  - 1 (instance of lti)
scipy.signal.impulse2

scipy.signal.impulse2(system, X0=None, T=None, N=None, **kwargs)

Impulse response of a single-input, continuous-time linear system.

Parameters

system [an instance of the LTI class or a tuple of array_like] describing the system. The following gives the number of elements in the tuple and the interpretation:

• 1 (instance of lti)
• 2 (num, den)
• 3 (zeros, poles, gain)
• 4 (A, B, C, D)

X0 [1-D array_like, optional] The initial condition of the state vector. Default: 0 (the zero vector).

T [1-D array_like, optional] The time steps at which the input is defined and at which the output is desired. If T is not given, the function will generate a set of time samples automatically.

N [int, optional] Number of time points to compute. Default: 100.

kwargs [various types] Additional keyword arguments are passed on to the function scipy.signal.lsim2, which in turn passes them on to scipy.integrate.odeint; see the latter’s documentation for information about these arguments.

Returns


yout [ndarray] A 1-D array containing the impulse response of the system (except for singularities at zero).

Notes

If (num, den) is passed in for system, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. \( s^2 + 3s + 5 \) would be represented as \([1, 3, 5]\)).
Examples
Second order system with a repeated root: \( x''(t) + 2x(t) + x(t) = u(t) \)

```python
from scipy import signal

system = ([1.0], [1.0, 2.0, 1.0])
t, y = signal.impulse2(system)

import matplotlib.pyplot as plt
plt.plot(t, y)
```

![Graph showing the step response of the system]

**scipy.signal.step**

`scipy.signal.step(system, X0=None, T=None, N=None)`

Step response of continuous-time system.

**Parameters**

- `system` [an instance of the LTI class or a tuple of array_like] describing the system. The following gives the number of elements in the tuple and the interpretation:
  - 1 (instance of `lti`)
  - 2 (num, den)
  - 3 (zeros, poles, gain)
  - 4 (A, B, C, D)
- `X0` [array_like, optional] Initial state-vector (default is zero).
- `T` [array_like, optional] Time points (computed if not given).
- `N` [int, optional] Number of time points to compute if `T` is not given.

**Returns**

- `T` [1D ndarray] Output time points.
- `yout` [1D ndarray] Step response of system.

**See also:**

`scipy.signal.step2`

**Notes**
If (num, den) is passed in for `system`, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. \( s^2 + 3s + 5 \) would be represented as [1, 3, 5]).
scipy.signal.step2

scipy.signal.step2(system, X0=None, T=None, N=None, **kwargs)

Step response of continuous-time system.

This function is functionally the same as scipy.signal.step, but it uses the function scipy.signal. lsim2 to compute the step response.

Parameters

- system [an instance of the LTI class or a tuple of array_like] describing the system. The following gives the number of elements in the tuple and the interpretation:
  - 1 (instance of lti)
  - 2 (num, den)
  - 3 (zeros, poles, gain)
  - 4 (A, B, C, D)

- X0 [array_like, optional] Initial state-vector (default is zero).

- T [array_like, optional] Time points (computed if not given).

- N [int, optional] Number of time points to compute if T is not given.

- kwargs [various types] Additional keyword arguments are passed on the function scipy.signal.lsim2, which in turn passes them on to scipy.integrate.odeint. See the documentation for scipy.integrate.odeint for information about these arguments.

Returns

- T [1D ndarray] Output time points.

- yout [1D ndarray] Step response of system.

See also:

scipy.signal.step

Notes

If (num, den) is passed in for system, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. $s^2 + 3s + 5$ would be represented as [1, 3, 5]).

New in version 0.8.0.

scipy.signal.freqresp

scipy.signal.freqresp(system, w=None, n=10000)

Calculate the frequency response of a continuous-time system.

Parameters

- system [an instance of the lti class or a tuple describing the system.] The following gives the number of elements in the tuple and the interpretation:
  - 1 (instance of lti)
  - 2 (num, den)
  - 3 (zeros, poles, gain)
  - 4 (A, B, C, D)

- w [array_like, optional] Array of frequencies (in rad/s). Magnitude and phase data is calculated for every value in this array. If not given, a reasonable set will be calculated.

- n [int, optional] Number of frequency points to compute if w is not given. The n frequencies are logarithmically spaced in an interval chosen to include the influence of the poles and zeros of the system.

Returns

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w  [1D ndarray] Frequency array [rad/s]
H  [1D ndarray] Array of complex magnitude values

**Notes**
If (num, den) is passed in for `system`, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. \( s^2 + 3s + 5 \) would be represented as \([1, 3, 5]\)).

**Examples**
Generating the Nyquist plot of a transfer function

```python
>>> from scipy import signal
def example_plot():
    import matplotlib.pyplot as plt
    # Transfer function: \( H(s) = \frac{5}{(s-1)^3} \)
    s1 = signal.ZerosPolesGain([], [1, 1, 1], [5])
    w, H = signal.freqresp(s1)
    plt.figure()
    plt.plot(H.real, H.imag, 'b')
    plt.plot(H.real, -H.imag, 'r')
    plt.show()
```

*scipy.signal.bode*

`scipy.signal.bode(system, w=None, n=100)`

Calculate Bode magnitude and phase data of a continuous-time system.

**Parameters**
- `system` [an instance of the LTI class or a tuple describing the system.]
The following gives the number of elements in the tuple and the interpretation:
  - 1 (instance of `lti`)
  - 2 (num, den)
  - 3 (zeros, poles, gain)
• 4 (A, B, C, D)

w
[array_like, optional] Array of frequencies (in rad/s). Magnitude and phase data is calculated for every value in this array. If not given a reasonable set will be calculated.

n
[int, optional] Number of frequency points to compute if \( w \) is not given. The \( n \) frequencies are logarithmically spaced in an interval chosen to include the influence of the poles and zeros of the system.

Returns

- w [1D ndarray] Frequency array [rad/s]
- mag [1D ndarray] Magnitude array [dB]
- phase [1D ndarray] Phase array [deg]

Notes

If (num, den) is passed in for system, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. \( s^2 + 3s + 5 \) would be represented as [1, 3, 5]).

New in version 0.11.0.

Examples

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

>>> sys = signal.TransferFunction([1], [1, 1])
>>> w, mag, phase = signal.bode(sys)

>>> plt.figure()
>>> plt.semilogx(w, mag)  # Bode magnitude plot
>>> plt.figure()
>>> plt.semilogx(w, phase)  # Bode phase plot
>>> plt.show()
```

6.20.7 Discrete-Time Linear Systems
dlti(*system, **kwargs)

Discrete-time linear time invariant system base class.

StateSpace(*system, **kwargs)
Linear Time Invariant system in state-space form.

TransferFunction(*system, **kwargs)
Linear Time Invariant system class in transfer function form.

ZerosPolesGain(*system, **kwargs)
Linear Time Invariant system class in zeros, poles, gain form.

dlsim(system, u[, t, x0])
Simulate output of a discrete-time linear system.

dimpulse(system[, x0, t, n])
Impulse response of discrete-time system.

dstep(system[, x0, t, n])
Step response of discrete-time system.

dfreqresp(system[, w, n, whole])
Calculate the frequency response of a discrete-time system.

dbode(system[, w, n])
Calculate Bode magnitude and phase data of a discrete-time system.

scipy.signal.dlti

class scipy.signal.dlti(*system, **kwargs)
Discrete-time linear time invariant system base class.

Parameters

*system: arguments
The dlti class can be instantiated with either 2, 3 or 4 arguments. The following gives the number of arguments and the corresponding discrete-time subclass that is created:
• 2: TransferFunction: (numerator, denominator)
• 3: ZerosPolesGain: (zeros, poles, gain)
• 4: StateSpace: (A, B, C, D)
Each argument can be an array or a sequence.

dt: float, optional
Sampling time [s] of the discrete-time systems. Defaults to True (unspecified sampling time). Must be specified as a keyword argument, for example, dt=0.1.

See also:
ZerosPolesGain, StateSpace, TransferFunction, lti

Notes

dlti instances do not exist directly. Instead, dlti creates an instance of one of its subclasses: StateSpace, TransferFunction or ZerosPolesGain.

Changing the value of properties that are not directly part of the current system representation (such as the zeros of a StateSpace system) is very inefficient and may lead to numerical inaccuracies. It is better to convert to the specific system representation first. For example, call sys = sys.to_zpk() before accessing/changing the zeros, poles or gain.
>>> signal.dlti(1, 2, 3, 4)
StateSpaceDiscrete(
    array([[1]]),
    array([[2]]),
    array([[3]]),
    array([[4]]),
    dt: True
)

>>> signal.dlti(1, 2, 3, 4, dt=0.1)
StateSpaceDiscrete(
    array([[1]]),
    array([[2]]),
    array([[3]]),
    array([[4]]),
    dt: 0.1
)

>>> signal.dlti([1, 2], [3, 4], 5, dt=0.1)
ZerosPolesGainDiscrete(
    array([1, 2]),
    array([3, 4]),
    5,
    dt: 0.1
)

>>> signal.dlti([3, 4], [1, 2], dt=0.1)
TransferFunctionDiscrete(
    array([3., 4.]),
    array([1., 2.]),
    dt: 0.1
)

Attributes

dtReturn the sampling time of the system.
polesPoles of the system.
zeros Zeros of the system.

Methods

bode([w, n]) Calculate Bode magnitude and phase data of a
discrete-time system.

freqresp([w, n, whole]) Calculate the frequency response of a discrete-
time system.

impulse([x0, t, n]) Return the impulse response of the discrete-time
dlti system.

output(u, t[, x0]) Return the response of the discrete-time system
to input u.

step([x0, t]) Return the step response of the discrete-time
dlti system.
**scipy.signal.dlti.bode**

dlti.bode(w=None, n=100)

Calculate Bode magnitude and phase data of a discrete-time system.

Returns a 3-tuple containing arrays of frequencies [rad/s], magnitude [dB] and phase [deg]. See `dbode` for details.

**Examples**

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

Transfer function: \( H(z) = \frac{1}{z^2 + 2z + 3} \) with sampling time 0.5s

```n

```python
>>> sys = signal.TransferFunction([1], [1, 2, 3], dt=0.5)

Equivalent: signal.dbode(sys)

```n

```python
>>> w, mag, phase = sys.bode()

```n

```python
>>> plt.figure()
>>> plt.semilogx(w, mag)  # Bode magnitude plot
>>> plt.figure()
>>> plt.semilogx(w, phase)  # Bode phase plot
>>> plt.show()
```

---

**scipy.signal.dlti.freqresp**

dlti.freqresp(w=None, n=10000, whole=False)

Calculate the frequency response of a discrete-time system.

Returns a 2-tuple containing arrays of frequencies [rad/s] and complex magnitude. See `dfreqresp` for details.

**scipy.signal.dlti.impulse**

dlti.impulse(x0=None, t=None, n=None)

Return the impulse response of the discrete-time `dlti` system. See `dimpulse` for details.
scipy.signal.dlti.output
dlti.output(u, t, x0=None)

Return the response of the discrete-time system to input u. See dlsim for details.

scipy.signal.dlti.step
dlti.step(x0=None, t=None, n=None)

Return the step response of the discrete-time dlti system. See dstep for details.

scipy.signal.dlsim

scipy.signal.dlsim(system, u, t=None, x0=None)

Simulate output of a discrete-time linear system.

Parameters

system [tuple of array_like or instance of dlti] A tuple describing the system. The following gives the number of elements in the tuple and the interpretation:
• 1: (instance of dlti)
• 3: (num, den, dt)
• 4: (zeros, poles, gain, dt)
• 5: (A, B, C, D, dt)

u [array_like] An input array describing the input at each time t (interpolation is assumed between given times). If there are multiple inputs, then each column of the rank-2 array represents an input.

t [array_like, optional] The time steps at which the input is defined. If t is given, it must be the same length as u, and the final value in t determines the number of steps returned in the output.

x0 [array_like, optional] The initial conditions on the state vector (zero by default).

Returns

tout [ndarray] Time values for the output, as a 1-D array.
yout [ndarray] System response, as a 1-D array.
xout [ndarray, optional] Time-evolution of the state-vector. Only generated if the input is a StateSpace system.

See also:
`lsim, dstep, dimpulse, cont2discrete`

**Examples**

A simple integrator transfer function with a discrete time step of 1.0 could be implemented as:

```python
>>> from scipy import signal
>>> tf = ([1.0], [1.0, -1.0], 1.0)
>>> t_in = [0.0, 1.0, 2.0, 3.0]
>>> u = np.asarray([0.0, 0.0, 1.0, 1.0])
>>> t_out, y = signal.dlsim(tf, u, t=t_in)
>>> y.T
array([[ 0.,  0.,  0.,  1.]])
```

`scipy.signal.dimpulse`

- **scipy.signal.dimpulse**(system, x0=None, t=None, n=None)
  - Impulse response of discrete-time system.

  **Parameters**
  - system [tuple of array_like or instance of `dlti`] A tuple describing the system. The following gives the number of elements in the tuple and the interpretation:
    - 1: (instance of `dlti`)
    - 3: (num, den, dt)
    - 4: (zeros, poles, gain, dt)
    - 5: (A, B, C, D, dt)
  - x0 [array_like, optional] Initial state-vector. Defaults to zero.
  - n [int, optional] The number of time points to compute (if `t` is not given).

  **Returns**
  - tout [ndarray] Time values for the output, as a 1-D array.
  - yout [tuple of ndarray] Impulse response of system. Each element of the tuple represents the output of the system based on an impulse in each input.

  **See also:**
  - `impulse, dstep, dlsim, cont2discrete`

`scipy.signal.dstep`

- **scipy.signal.dstep**(system, x0=None, t=None, n=None)
  - Step response of discrete-time system.

  **Parameters**
  - system [tuple of array_like] A tuple describing the system. The following gives the number of elements in the tuple and the interpretation:
    - 1: (instance of `dlti`)
    - 3: (num, den, dt)
    - 4: (zeros, poles, gain, dt)
    - 5: (A, B, C, D, dt)
  - x0 [array_like, optional] Initial state-vector. Defaults to zero.
  - n [int, optional] The number of time points to compute (if `t` is not given).

  **Returns**
  - tout [ndarray] Output time points, as a 1-D array.
yout  [tuple of ndarray] Step response of system. Each element of the tuple represents
the output of the system based on a step response to each input.

See also:
  step, dimpulse, dlsim, cont2discrete

scipy.signal.dfreqresp

scipy.signal.dfreqresp(system, w=None, n=10000, whole=False)
Calculate the frequency response of a discrete-time system.

Parameters
  system  [an instance of the dlti class or a tuple describing the system.] The following gives
           the number of elements in the tuple and the interpretation:
           • 1 (instance of dlti)
           • 2 (numerator, denominator, dt)
           • 3 (zeros, poles, gain, dt)
           • 4 (A, B, C, D, dt)
  w  [array_like, optional] Array of frequencies (in radians/sample). Magnitude and
      phase data is calculated for every value in this array. If not given a reasonable set
      will be calculated.
  n  [int, optional] Number of frequency points to compute if w is not given. The n
      frequencies are logarithmically spaced in an interval chosen to include the influence
      of the poles and zeros of the system.
  whole  [bool, optional] Normally, if ‘w’ is not given, frequencies are computed from 0 to
          the Nyquist frequency, pi radians/sample (upper-half of unit-circle). If whole is
          True, compute frequencies from 0 to 2*pi radians/sample.

Returns
  w  [1D ndarray] Frequency array [radians/sample]
  H  [1D ndarray] Array of complex magnitude values

Notes
If (num, den) is passed in for system, coefficients for both the numerator and denominator should be
specified in descending exponent order (e.g. z^2 + 3z + 5 would be represented as [1, 3, 5]).

New in version 0.18.0.

Examples
Generating the Nyquist plot of a transfer function

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

Transfer function: H(z) = 1 / (z^2 + 2z + 3)

>>> sys = signal.TransferFunction([1], [1, 2, 3], dt=0.05)

>>> w, H = signal.dfreqresp(sys)

>>> plt.figure()
>>> plt.plot(H.real, H.imag, "b")
>>> plt.plot(H.real, -H.imag, "r")
>>> plt.show()
```
scipy.signal.dbode

scipy.signal.dbode(system, w=None, n=100)

Calculate Bode magnitude and phase data of a discrete-time system.

Parameters

- **system** [an instance of the LTI class or a tuple describing the system.] The following gives the number of elements in the tuple and the interpretation:
  - 1 (instance of dti)
  - 2 (num, den, dt)
  - 3 (zeros, poles, gain, dt)
  - 4 (A, B, C, D, dt)

- **w** [array_like, optional] Array of frequencies (in radians/sample). Magnitude and phase data is calculated for every value in this array. If not given a reasonable set will be calculated.

- **n** [int, optional] Number of frequency points to compute if w is not given. The n frequencies are logarithmically spaced in an interval chosen to include the influence of the poles and zeros of the system.

Returns

- **w** [1D ndarray] Frequency array [rad/time_unit]
- **mag** [1D ndarray] Magnitude array [dB]
- **phase** [1D ndarray] Phase array [deg]

Notes

If (num, den) is passed in for system, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. \( z^2 + 3z + 5 \) would be represented as \([1, 3, 5]\)).

New in version 0.18.0.

Examples

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

Transfer function: H(z) = 1 / (z^2 + 2z + 3)
```
```python
>>> sys = signal.TransferFunction([1], [1, 2, 3], dt=0.05)

Equivalent: sys.bode()

>>> w, mag, phase = signal.dbode(sys)

>>> plt.figure()
>>> plt.semilogx(w, mag)  # Bode magnitude plot
>>> plt.figure()
>>> plt.semilogx(w, phase)  # Bode phase plot
>>> plt.show()
```

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**scipy.signal.tf2zpk**

Return zero, pole, gain (z, p, k) representation from a numerator, denominator representation of a linear filter.

**Parameters**
- `b` [array_like] Numerator polynomial coefficients.
- `a` [array_like] Denominator polynomial coefficients.

**Returns**
- `z` [ndarray] Zeros of the transfer function.
- `p` [ndarray] Poles of the transfer function.
- `k` [float] System gain.

**Notes**
If some values of `b` are too close to 0, they are removed. In that case, a BadCoefficients warning is emitted.

The `b` and `a` arrays are interpreted as coefficients for positive, descending powers of the transfer function variable. So the inputs `b = [b_0, b_1, ..., b_M]` and `a = [a_0, a_1, ..., a_N]` can represent an analog filter of the form:

\[ H(s) = \frac{b_0 s^M + b_1 s^{(M-1)} + \cdots + b_M}{a_0 s^N + a_1 s^{(N-1)} + \cdots + a_N} \]

or a discrete-time filter of the form:

\[ H(z) = \frac{b_0 z^M + b_1 z^{(M-1)} + \cdots + b_M}{a_0 z^N + a_1 z^{(N-1)} + \cdots + a_N} \]
This “positive powers” form is found more commonly in controls engineering. If $M$ and $N$ are equal (which is true for all filters generated by the bilinear transform), then this happens to be equivalent to the “negative powers” discrete-time form preferred in DSP:

$$H(z) = \frac{b_0 + b_1 z^{-1} + \cdots + b_M z^{-M}}{a_0 + a_1 z^{-1} + \cdots + a_N z^{-N}}$$

Although this is true for common filters, remember that this is not true in the general case. If $M$ and $N$ are not equal, the discrete-time transfer function coefficients must first be converted to the “positive powers” form before finding the poles and zeros.

**scipy.signal.tf2sos**

`scipy.signal.tf2sos(b, a, pairing='nearest')`

Return second-order sections from transfer function representation

**Parameters**

- `b` [array_like] Numerator polynomial coefficients.
- `a` [array_like] Denominator polynomial coefficients.
- `pairing` [{'nearest', 'keep_odd'}, optional] The method to use to combine pairs of poles and zeros into sections. See `zpk2sos`.

**Returns**

- `sos` [ndarray] Array of second-order filter coefficients, with shape `(n_sections, 6)`. See `sosfilt` for the SOS filter format specification.

**See also:**

`zpk2sos`, `sosfilt`

**Notes**

It is generally discouraged to convert from TF to SOS format, since doing so usually will not improve numerical precision errors. Instead, consider designing filters in ZPK format and converting directly to SOS. TF is converted to SOS by first converting to ZPK format, then converting ZPK to SOS.

New in version 0.16.0.

**scipy.signal.tf2ss**

`scipy.signal.tf2ss(num, den)`

Transfer function to state-space representation.

**Parameters**

- `num`, `den` [array_like] Sequences representing the coefficients of the numerator and denominator polynomials, in order of descending degree. The denominator needs to be at least as long as the numerator.

**Returns**

- `A`, `B`, `C`, `D` [ndarray] State space representation of the system, in controller canonical form.

**Examples**

Convert the transfer function:

$$H(s) = \frac{s^2 + 3s + 3}{s^2 + 2s + 1}$$
```python
>>> num = [1, 3, 3]
>>> den = [1, 2, 1]
```
to the state-space representation:

\[
\begin{bmatrix}
-2 & -1 \\
1 & 0
\end{bmatrix} \begin{bmatrix} x(t) \end{bmatrix} + \begin{bmatrix} 1 \\
0
\end{bmatrix} u(t)
\]

\[
y(t) = \begin{bmatrix} 1 & 2 \end{bmatrix} \begin{bmatrix} x(t) \end{bmatrix} + \begin{bmatrix} 1 \end{bmatrix} u(t)
\]

```python
>>> from scipy.signal import tf2ss
>>> A, B, C, D = tf2ss(num, den)
>>> A
array([[-2., -1.],
       [ 1.,  0.]])
>>> B
array([[ 1.],
       [ 0.]])
>>> C
array([[ 1.,  2.]])
>>> D
array([[ 1.]])
```

**scipy.signal.zpk2tf**

`scipy.signal.zpk2tf(z, p, k)`

Return polynomial transfer function representation from zeros and poles

**Parameters**

- `z` : [array_like] Zeros of the transfer function.
- `p` : [array_like] Poles of the transfer function.
- `k` : [float] System gain.

**Returns**

- `b` : [ndarray] Numerator polynomial coefficients.
- `a` : [ndarray] Denominator polynomial coefficients.

**scipy.signal.zpk2sos**

`scipy.signal.zpk2sos(z, p, k, pairing='nearest')`

Return second-order sections from zeros, poles, and gain of a system

**Parameters**

- `z` : [array_like] Zeros of the transfer function.
- `p` : [array_like] Poles of the transfer function.
- `k` : [float] System gain.
- `pairing` : [‘nearest’, ‘keep_odd’], optional The method to use to combine pairs of poles and zeros into sections. See Notes below.

**Returns**

- `sos` : [ndarray] Array of second-order filter coefficients, with shape (n_sections, 6). See `sosfilt` for the SOS filter format specification.
See also:
sosfilt

Notes
The algorithm used to convert ZPK to SOS format is designed to minimize errors due to numerical precision issues. The pairing algorithm attempts to minimize the peak gain of each biquadratic section. This is done by pairing poles with the nearest zeros, starting with the poles closest to the unit circle.

Algorithms
The current algorithms are designed specifically for use with digital filters. (The output coefficients are not correct for analog filters.)

The steps in the `pairing='nearest'` and `pairing='keep_odd'` algorithms are mostly shared. The nearest algorithm attempts to minimize the peak gain, while 'keep_odd' minimizes peak gain under the constraint that odd-order systems should retain one section as first order. The algorithm steps and are as follows:

As a pre-processing step, add poles or zeros to the origin as necessary to obtain the same number of poles and zeros for pairing. If `pairing == 'nearest'` and there are an odd number of poles, add an additional pole and a zero at the origin.

The following steps are then iterated over until no more poles or zeros remain:

1. Take the (next remaining) pole (complex or real) closest to the unit circle to begin a new filter section.

2. If the pole is real and there are no other remaining real poles, add the closest real zero to the section and leave it as a first order section. Note that after this step we are guaranteed to be left with an even number of real poles, complex poles, real zeros, and complex zeros for subsequent pairing iterations.

3. Else:

   (a) If the pole is complex and the zero is the only remaining real zero*, then pair the pole with the next closest zero (guaranteed to be complex). This is necessary to ensure that there will be a real zero remaining to eventually create a first-order section (thus keeping the odd order).

   (b) Else pair the pole with the closest remaining zero (complex or real).

   (c) Proceed to complete the second-order section by adding another pole and zero to the current pole and zero in the section:

      i. If the current pole and zero are both complex, add their conjugates.

      ii. Else if the pole is complex and the zero is real, add the conjugate pole and the next closest real zero.

      iii. Else if the pole is real and the zero is complex, add the conjugate zero and the real pole closest to those zeros.

      iv. Else (we must have a real pole and real zero) add the next real pole closest to the unit circle, and then add the real zero closest to that pole.

New in version 0.16.0.

Examples
Design a 6th order low-pass elliptic digital filter for a system with a sampling rate of 8000 Hz that has a pass-band corner frequency of 1000 Hz. The ripple in the pass-band should not exceed 0.087 dB, and the attenuation in the stop-band should be at least 90 dB.

---

* This conditional can only be met for specific odd-order inputs with the `pairing == 'keep_odd'` method.
In the following call to `signal.ellip`, we could use `output='sos'`, but for this example, we’ll use `output='zpk'`, and then convert to SOS format with `zpk2sos`:

```python
>>> from scipy import signal
data = signal.ellip(6, 0.087, 90, 1000/(0.5*8000), output='zpk')
```

Now convert to SOS format.

```python
>>> sos = signal.zpk2sos(z, p, k)
```

The coefficients of the numerators of the sections:

```python
>>> sos[:, :3]
array([[ 0.0014154 , 0.00248707, 0.0014154 ],
       [ 1. , 0.72965193, 1. ],
       [ 1. , 0.17594966, 1. ]])
```

The symmetry in the coefficients occurs because all the zeros are on the unit circle.

The coefficients of the denominators of the sections:

```python
>>> sos[:, 3:]
array([[ 1. , -1.32543251, 0.46989499],
       [ 1. , -1.26117915, 0.6262586 ],
       [ 1. , -1.25707217, 0.86199667]])
```

The next example shows the effect of the `pairing` option. We have a system with three poles and three zeros, so the SOS array will have shape (2, 6). The means there is, in effect, an extra pole and an extra zero at the origin in the SOS representation.

```python
>>> z1 = np.array([-1, -0.5-0.5j, -0.5+0.5j])
>>> p1 = np.array([0.75, 0.8+0.1j, 0.8-0.1j])
```

With `pairing='nearest'` (the default), we obtain

```python
>>> signal.zpk2sos(z1, p1, 1)
array([[ 1. , 1. , 0.5 , 1. , -0.75, 0. ],
       [ 1. , 1. , 0. , 1. , -1.6 , 0.65]])
```

The first section has the zeros {-0.5-0.5j, -0.5+0.5j} and the poles {0, 0.75}, and the second section has the zeros {-1, 0} and poles {0.8+0.1j, 0.8-0.1j}. Note that the extra pole and zero at the origin have been assigned to different sections.

With `pairing='keep_odd'`, we obtain:

```python
>>> signal.zpk2sos(z1, p1, 1, pairing='keep_odd')
array([[ 1. , 1. , 0.5 , 1. , -0.75, 0. ],
       [ 1. , 1. , 0.5 , 1. , -1.6 , 0.65]])
```

The extra pole and zero at the origin are in the same section. The first section is, in effect, a first-order section.

`scipy.signal.zpk2ss`

`scipy.signal.zpk2ss(z, p, k)`

Zero-pole-gain representation to state-space representation
**Parameters**

- **z, p** [sequence] Zeros and poles.
- **k** [float] System gain.

**Returns**

- **A, B, C, D** [ndarray] State space representation of the system, in controller canonical form.

`scipy.signal.ss2tf`

`scipy.signal.ss2tf(A, B, C, D, input=0)`  
State-space to transfer function.

A, B, C, D defines a linear state-space system with $p$ inputs, $q$ outputs, and $n$ state variables.

**Parameters**

- **A** [array_like] State (or system) matrix of shape $(n, n)$
- **B** [array_like] Input matrix of shape $(n, p)$
- **C** [array_like] Output matrix of shape $(q, n)$
- **D** [array_like] Feedthrough (or feedforward) matrix of shape $(q, p)$
- **input** [int, optional] For multiple-input systems, the index of the input to use.

**Returns**

- **num** [2-D ndarray] Numerator(s) of the resulting transfer function(s). `num` has one row for each of the system's outputs. Each row is a sequence representation of the numerator polynomial.
- **den** [1-D ndarray] Denominator of the resulting transfer function(s). `den` is a sequence representation of the denominator polynomial.

**Examples**

Convert the state-space representation:

$$\dot{x}(t) = \begin{bmatrix} -2 & -1 \\ 1 & 0 \end{bmatrix} x(t) + \begin{bmatrix} 1 \\ 0 \end{bmatrix} u(t)$$

$$y(t) = \begin{bmatrix} 1 & 2 \end{bmatrix} \begin{bmatrix} x(t) \end{bmatrix} + \begin{bmatrix} 1 \end{bmatrix} u(t)$$

```python
>>> A = [[-2, -1], [1, 0]]
>>> B = [[1], [0]]  # 2-dimensional column vector
>>> C = [[1, 2]]  # 2-dimensional row vector
>>> D = 1
```

to the transfer function:

$$H(s) = \frac{s^2 + 3s + 3}{s^2 + 2s + 1}$$

```python
>>> from scipy.signal import ss2tf
>>> ss2tf(A, B, C, D)
(array([[1, 3, 3]]), array([ 1., 2., 1.]))
```
scipy.signal.ss2zpk

scipy.signal.ss2zpk(A, B, C, D, input=0)

State-space representation to zero-pole-gain representation.

A, B, C, D defines a linear state-space system with \( p \) inputs, \( q \) outputs, and \( n \) state variables.

**Parameters**

- **A** [array_like] State (or system) matrix of shape \( (n, n) \)
- **B** [array_like] Input matrix of shape \( (n, p) \)
- **C** [array_like] Output matrix of shape \( (q, n) \)
- **D** [array_like] Feedthrough (or feedforward) matrix of shape \( (q, p) \)
- **input** [int, optional] For multiple-input systems, the index of the input to use.

**Returns**

- **z**, **p** [sequence] Zeros and poles.
- **k** [float] System gain.

scipy.signal.sos2zpk

scipy.signal.sos2zpk(sos)

Return zeros, poles, and gain of a series of second-order sections

**Parameters**

- **sos** [array_like] Array of second-order filter coefficients, must have shape \( (n\text{\_sections}, 6) \). See *sosfilt* for the SOS filter format specification.

**Returns**

- **z** [ndarray] Zeros of the transfer function.
- **p** [ndarray] Poles of the transfer function.
- **k** [float] System gain.

**Notes**

New in version 0.16.0.

scipy.signal.sos2tf

scipy.signal.sos2tf(sos)

Return a single transfer function from a series of second-order sections

**Parameters**

- **sos** [array_like] Array of second-order filter coefficients, must have shape \( (n\text{\_sections}, 6) \). See *sosfilt* for the SOS filter format specification.

**Returns**

- **b** [ndarray] Numerator polynomial coefficients.
- **a** [ndarray] Denominator polynomial coefficients.

**Notes**

New in version 0.16.0.
**scipy.signal.cont2discrete**

**scipy.signal.cont2discrete**(*system*, *dt*, *method='zoh', alpha=None*)

Transform a continuous to a discrete state-space system.

**Parameters**
- **system** [a tuple describing the system or an instance of *lti*] The following gives the number of elements in the tuple and the interpretation:
  - 1: (instance of *lti*)
  - 2: (num, den)
  - 3: (zeros, poles, gain)
  - 4: (A, B, C, D)
- **dt** [float] The discretization time step.
- **method** [{"gbt", "bilinear", "euler", "backward_diff", "zoh"}, optional] Which method to use:
  - gbt: generalized bilinear transformation
  - bilinear: Tustin’s approximation ("gbt" with alpha=0.5)
  - euler: Euler (or forward differencing) method ("gbt" with alpha=0)
  - backward_diff: Backwards differencing ("gbt" with alpha=1.0)
  - zoh: zero-order hold (default)
- **alpha** [float within [0, 1], optional] The generalized bilinear transformation weighting parameter, which should only be specified with method="gbt", and is ignored otherwise

**Returns**
- **sysd** [tuple containing the discrete system] Based on the input type, the output will be of the form
  - (num, den, dt) for transfer function input
  - (zeros, poles, gain, dt) for zeros-poles-gain input
  - (A, B, C, D, dt) for state-space system input

**Notes**
By default, the routine uses a Zero-Order Hold (zoh) method to perform the transformation. Alternatively, a generalized bilinear transformation may be used, which includes the common Tustin’s bilinear approximation, an Euler’s method technique, or a backwards differencing technique.

The Zero-Order Hold (zoh) method is based on [1], the generalized bilinear approximation is based on [2] and [3].

**References**
[1], [2], [3]

**scipy.signal.place_poles**

**scipy.signal.place_poles**(*A, B, poles*, *method='YT', rtol=0.001, maxiter=30*)

Compute K such that eigenvalues (A - dot(B, K))=poles.

K is the gain matrix such as the plant described by the linear system $AX + BU$ will have its closed-loop poles, i.e the eigenvalues $A - B*K$, as close as possible to those asked for in poles.

SISO, MISO and MIMO systems are supported.

**Parameters**
- **A, B** [ndarray] State-space representation of linear system $AX + BU$.
- **poles** [array_like] Desired real poles and/or complex conjugates poles. Complex poles are only supported with method="YT" (default).
method: {'YT', 'KNV0'}, optional
Which method to choose to find the gain matrix K. One of:
• 'YT': Yang Tits
• 'KNV0': Kautsky, Nichols, Van Dooren update method 0
See References and Notes for details on the algorithms.

rtol: float, optional
After each iteration the determinant of the eigenvectors of \( A - B*K \) is compared to its previous value, when the relative error between these two values becomes lower than rtol the algorithm stops. Default is 1e-3.

maxiter: int, optional
Maximum number of iterations to compute the gain matrix. Default is 30.

Returns

full_state_feedback
[Bunch object]
full_state_feedback is composed of:

gain_matrix
[1-D ndarray] The closed loop matrix K such as the eigenvalues of \( A + BK \) are as close as possible to the requested poles.

computed_poles
[1-D ndarray] The poles corresponding to \( A-BK \) sorted as first the real poles in increasing order, then the complex conjugates in lexicographic order.

requested_poles
[1-D ndarray] The poles the algorithm was asked to place sorted as above, they may differ from what was achieved.

X
[2-D ndarray] The transfer matrix such as \( X * \text{diag}(\text{poles}) = (A - BK)X \) (see Notes)

rtol
[float] The relative tolerance achieved on \( \det(X) \) (see Notes). rtol will be NaN if it is possible to solve the system \( \text{diag}(\text{poles}) = (A - BK) \), or 0 when the optimization algorithms can’t do anything i.e when B.shape[1] == 1.

nb_iter
[int] The number of iterations performed before converging. nb_iter will be NaN if it is possible to solve the system \( \text{diag}(\text{poles}) = (A - BK) \), or 0 when the optimization algorithms can’t do anything i.e when B.shape[1] == 1.

Notes
The Tits and Yang (YT), [2] paper is an update of the original Kautsky et al. (KNV) paper [1]. KNV relies on rank-1 updates to find the transfer matrix X such that \( X * \text{diag}(\text{poles}) = (A - BK)X \), whereas YT uses rank-2 updates. This yields on average more robust solutions (see [2] pp 21-22), furthermore the YT algorithm supports complex poles whereas KNV does not in its original version. Only update method 0 proposed by KNV has been implemented here, hence the name ‘KNV0’.

KNV extended to complex poles is used in Matlab’s place function, YT is distributed under a non-free licence by Slicot under the name robpole. It is unclear and undocumented how KNV0 has been extended to complex poles (Tits and Yang claim on page 14 of their paper that their method can not be used to extend KNV to complex poles), therefore only YT supports them in this implementation.

As the solution to the problem of pole placement is not unique for MIMO systems, both methods start with a tentative transfer matrix which is altered in various way to increase its determinant. Both methods have been proven to converge to a stable solution, however depending on the way the initial transfer matrix is chosen they will converge to different solutions and therefore there is absolutely no guarantee that using ‘KNV0’ will yield results similar to Matlab’s or any other implementation of these algorithms.
Using the default method 'YT' should be fine in most cases; 'KNV0' is only provided because it is needed by 'YT' in some specific cases. Furthermore 'YT' gives on average more robust results than 'KNV0' when \( \text{abs}(\text{det}(X)) \) is used as a robustness indicator.

[2] is available as a technical report on the following URL: https://hdl.handle.net/1903/5598

References
[1], [2]

Examples
A simple example demonstrating real pole placement using both KNV and YT algorithms. This is example number 1 from section 4 of the reference KNV publication ([1]):

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

>>> A = np.array([[1.380, -0.2077, 6.715, -5.676 ],
                ...                [-0.5814, -4.290, 0, 0.6750 ],
                ...                [1.067, 4.273, -6.654, 5.893 ],
                ...                [0.0480, 4.273, 1.343, -2.104 ]])
>>> B = np.array([[0, 5.679 ],
                ...                [1.136, 1.136 ],
                ...                [0, 0 ],
                ...                [-3.146, 0 ]])
>>> P = np.array([-0.2, -0.5, -5.0566, -8.6659])

Now compute K with KNV method 0, with the default YT method and with the YT method while forcing 100 iterations of the algorithm and print some results after each call.

```python
>>> fsf1 = signal.place_poles(A, B, P, method='KNV0')
>>> fsf1.gain_matrix
array([[ 0.20071427, -0.96665799, 0.24066128, -0.10279785],
       [ 0.50587268, 0.57779091, 0.51795763, -0.41991442]])

```python
>>> fsf2 = signal.place_poles(A, B, P) # uses YT method
>>> fsf2.computed_poles
array([-8.6659, -5.0566, -0.5 , -0.2 ])

```python
>>> fsf3 = signal.place_poles(A, B, P, rtol=-1, maxiter=100)
>>> fsf3.X
array([[ 0.52072442+0.j, -0.08409372+0.j, -0.56847937+0.j, 0.74823657+0.j],
       [-0.04977751+0.j, -0.80872954+0.j, 0.13566234+0.j, -0.29322906+0.j],
       [-0.82266932+0.j, -0.19168026+0.j, -0.56348322+0.j, -0.43815060+0.j],
       [ 0.22267347+0.j, 0.54967577+0.j, -0.58387806+0.j, -0.40271926+0.j]])

The absolute value of the determinant of X is a good indicator to check the robustness of the results, both 'KNV0' and 'YT' aim at maximizing it. Below a comparison of the robustness of the results above:

```python
>>> abs(np.linalg.det(fsf1.X)) < abs(np.linalg.det(fsf2.X))
True
>>> abs(np.linalg.det(fsf2.X)) < abs(np.linalg.det(fsf3.X))
True

Now a simple example for complex poles:
```python
>>> A = np.array([[0, 7/3., 0, 0],
                ...                   [0, 0, 0, 7/9.],
                ...                   [0, 0, 0, 0],
                ...                   [0, 0, 0, 0]])
>>> B = np.array([[0, 0],
                ...                   [0, 0],
                ...                   [1, 0],
                ...                   [0, 1]])
>>> P = np.array([-3, -1, -2-1j, -2+1j]) / 3.
>>> fsf = signal.place_poles(A, B, P, method='YT')
```

We can plot the desired and computed poles in the complex plane:

```python
>>> t = np.linspace(0, 2*np.pi, 401)
>>> plt.plot(np.cos(t), np.sin(t), 'k--')  # unit circle
>>> plt.plot(fsf.requested_poles.real, fsf.requested_poles.imag,
         ...         'wo', label='Desired')
>>> plt.plot(fsf.computed_poles.real, fsf.computed_poles.imag, 'bx',
         ...         label='Placed')
>>> plt.grid()
>>> plt.axis('image')
>>> plt.axis([-1.1, 1.1, -1.1, 1.1])
>>> plt.legend(bbox_to_anchor=(1.05, 1), loc=2, numpoints=1)
```

### 6.20.9 Waveforms

- `chirp(t, f0, t1, f1[, method, phi, vertex_zero])`: Frequency-swept cosine generator.
- `gausspulse(t[, fc, bw, bwr, tpr, retquad, ...])`: Return a Gaussian modulated sinusoid.
- `max_len_seq(nbits[, state, length, taps])`: Maximum length sequence (MLS) generator.
- `sawtooth(t[, width])`: Return a periodic sawtooth or triangle waveform.
- `square(t[, duty])`: Return a periodic square-wave waveform.
Table 161 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>sweep_poly(t, poly[, phi])</code></td>
<td>Frequency-swept cosine generator, with a time-dependent frequency.</td>
</tr>
<tr>
<td><code>unit_impulse(shape[, idx, dtype])</code></td>
<td>Unit impulse signal (discrete delta function) or unit basis vector.</td>
</tr>
</tbody>
</table>

**scipy.signal.chirp**

`scipy.signal.chirp(t, f0, t1, f1, method='linear', phi=0, vertex_zero=True)`

Frequency-swept cosine generator.

In the following, ‘Hz’ should be interpreted as ‘cycles per unit’; there is no requirement here that the unit is one second. The important distinction is that the units of rotation are cycles, not radians. Likewise, $t$ could be a measurement of space instead of time.

**Parameters**

- **t** [array_like] Times at which to evaluate the waveform.
- **f0** [float] Frequency (e.g. Hz) at time $t=0$.
- **t1** [float] Time at which $f1$ is specified.
- **f1** [float] Frequency (e.g. Hz) of the waveform at time $t1$.
- **phi** [float, optional] Phase offset, in degrees. Default is 0.
- **vertex_zero** [bool, optional] This parameter is only used when method is ‘quadratic’. It determines whether the vertex of the parabola that is the graph of the frequency is at $t=0$ or $t=t1$.

**Returns**

- **y** [ndarray] A numpy array containing the signal evaluated at $t$ with the requested time-varying frequency. More precisely, the function returns $\cos(\text{phase} + (\pi/180)\times\phi)$ where phase is the integral (from 0 to $t$) of $2\pi f(t)$. $f(t)$ is defined below.

**See also:**

`sweep_poly`

**Notes**

There are four options for the `method`. The following formulas give the instantaneous frequency (in Hz) of the signal generated by `chirp()`. For convenience, the shorter names shown below may also be used.

- **linear, lin, li:**

  $f(t) = f0 + (f1 - f0) \times t / t1$

- **quadratic, quad, q:**

  The graph of the frequency $f(t)$ is a parabola through $(0, f0)$ and $(t1, f1)$. By default, the vertex of the parabola is at $(0, f0)$. If `vertex_zero` is False, then the vertex is at $(t1, f1)$. The formula is: if `vertex_zero` is True:

  $f(t) = f0 + (f1 - f0) \times t**2 / t1**2$

  else:

  $f(t) = f1 - (f1 - f0) \times (t1 - t)**2 / t1**2$

  To use a more general quadratic function, or an arbitrary polynomial, use the function `scipy.signal.signal.waveforms.sweep_poly`.

- **logarithmic, log, lo:**
\[ f(t) = f_0 \times (f_1/f_0)^{(t/t_1)} \]
This signal is also known as a geometric or exponential chirp.

**Examples**
The following will be used in the examples:

```python
>>> from scipy.signal import chirp, spectrogram
>>> import matplotlib.pyplot as plt
```
For the first example, we’ll plot the waveform for a linear chirp from 6 Hz to 1 Hz over 10 seconds:

```python
>>> t = np.linspace(0, 10, 5001)
>>> w = chirp(t, f0=6, f1=1, t1=10, method='linear')
>>> plt.plot(t, w)
>>> plt.title("Linear Chirp, f(0)=6, f(10)=1")
>>> plt.xlabel('t (sec)')
>>> plt.show()
```

For the remaining examples, we’ll use higher frequency ranges, and demonstrate the result using `scipy.signal.spectrogram`. We’ll use a 10 second interval sampled at 8000 Hz.

```python
>>> fs = 8000
>>> T = 10
>>> t = np.linspace(0, T, T*fs, endpoint=False)
```

Quadratic chirp from 1500 Hz to 250 Hz over 10 seconds (vertex of the parabolic curve of the frequency is at t=0):

```python
>>> w = chirp(t, f0=1500, f1=250, t1=10, method='quadratic')
>>> ff, tt, Sxx = spectrogram(w, fs=fs, noverlap=256, nperseg=512,
```
(continues on next page)
Quadratic chirp from 1500 Hz to 250 Hz over 10 seconds (vertex of the parabolic curve of the frequency is at t=10):

```python
>>> w = chirp(t, f0=1500, f1=250, t1=10, method='quadratic',
... vertex_zero=False)
>>> ff, tt, Sxx = spectrogram(w, fs=fs, noverlap=256, nperseg=512,
... nfft=2048)
>>> plt.pcolormesh(tt, ff[:,513], Sxx[:,513], cmap='gray_r')
>>> plt.title('Quadratic Chirp, f(0)=1500, f(10)=250')
>>> plt.xlabel('t (sec)')
>>> plt.ylabel('Frequency (Hz)')
>>> plt.grid()
>>> plt.show()
```

Logarithmic chirp from 1500 Hz to 250 Hz over 10 seconds:

```python
>>> w = chirp(t, f0=1500, f1=250, t1=10, method='logarithmic')
>>> ff, tt, Sxx = spectrogram(w, fs=fs, noverlap=256, nperseg=512,
... nfft=2048)
>>> plt.pcolormesh(tt, ff[:,513], Sxx[:,513], cmap='gray_r')
>>> plt.title('Logarithmic Chirp, f(0)=1500, f(10)=250')
>>> plt.xlabel('t (sec)')
>>> plt.ylabel('Frequency (Hz)')
>>> plt.grid()
>>> plt.show()
```
Hyperbolic chirp from 1500 Hz to 250 Hz over 10 seconds:

```python
>>> w = chirp(t, f0=1500, f1=250, t1=10, method='hyperbolic')
>>> ff, tt, Sxx = spectrogram(w, fs=fs, noverlap=256, nperseg=512,
... nfft=2048)
>>> plt.pcolormesh(tt, ff[:513], Sxx[:513], cmap='gray_r')
>>> plt.title('Hyperbolic Chirp, f(0)=1500, f(10)=250')
>>> plt.xlabel('t (sec)')
>>> plt.ylabel('Frequency (Hz)')
>>> plt.grid()
>>> plt.show()
```
**scipy.signal.gausspulse**

```python
scipy.signal.gausspulse(t, fc=1000, bw=0.5, bwr=-6, tpr=-60, retquad=False, retenv=False)
```

Return a Gaussian modulated sinusoid:

$$\exp(-\alpha t^2) \exp(1j \cdot 2\pi \cdot fc \cdot t).$$

If `retquad` is True, then return the real and imaginary parts (in-phase and quadrature). If `retenv` is True, then return the envelope (unmodulated signal). Otherwise, return the real part of the modulated sinusoid.

**Parameters**

- **t** [ndarray or the string ‘cutoff’] Input array.
- **fc** [int, optional] Center frequency (e.g. Hz). Default is 1000.
- **bw** [float, optional] Fractional bandwidth in frequency domain of pulse (e.g. Hz). Default is 0.5.
- **bwr** [float, optional] Reference level at which fractional bandwidth is calculated (dB). Default is -6.
- **tpr** [float, optional] If `t` is ‘cutoff’, then the function returns the cutoff time for when the pulse amplitude falls below `tpr` (in dB). Default is -60.
- **retquad** [bool, optional] If True, return the quadrature (imaginary) as well as the real part of the signal. Default is False.
- **retenv** [bool, optional] If True, return the envelope of the signal. Default is False.

**Returns**

- **yI** [ndarray] Real part of signal. Always returned.
- **yQ** [ndarray] Imaginary part of signal. Only returned if `retquad` is True.
- **yenv** [ndarray] Envelope of signal. Only returned if `retenv` is True.

**See also:**

- `scipy.signal.morlet`

**Examples**

Plot real component, imaginary component, and envelope for a 5 Hz pulse, sampled at 100 Hz for 2 seconds:
from scipy import signal
import matplotlib.pyplot as plt
t = np.linspace(-1, 1, 2 * 100, endpoint=False)
i, q, e = signal.gausspulse(t, fc=5, retquad=True, retenv=True)
plt.plot(t, i, t, q, t, e, '--')

scipy.signal.max_len_seq

scipy.signal.max_len_seq(nbits, state=None, length=None, taps=None)
Maximum length sequence (MLS) generator.

Parameters

nbits [int] Number of bits to use. Length of the resulting sequence will be \((2^{nbits}) - 1\). Note that generating long sequences (e.g., greater than \(nbits == 16\)) can take a long time.

state [array_like, optional] If array, must be of length \(nbits\), and will be cast to binary (bool) representation. If None, a seed of ones will be used, producing a repeatable representation. If \(state\) is all zeros, an error is raised as this is invalid. Default: None.

length [int, optional] Number of samples to compute. If None, the entire length \((2^{nbits}) - 1\) is computed.

taps [array_like, optional] Polynomial taps to use (e.g., \([7, 6, 1]\) for an 8-bit sequence). If None, taps will be automatically selected (for up to \(nbits == 32\)).

Returns

seq [array] Resulting MLS sequence of 0’s and 1’s.
state [array] The final state of the shift register.

Notes
The algorithm for MLS generation is generically described in:

https://en.wikipedia.org/wiki/Maximum_length_sequence

The default values for taps are specifically taken from the first option listed for each value of \(nbits\) in:
New in version 0.15.0.

Examples

MLS uses binary convention:

```python
>>> from scipy.signal import max_len_seq
>>> max_len_seq(4)[0]
array([1, 1, 1, 0, 1, 0, 1, 0, 1, 0, 0, 0], dtype=int8)
```

MLS has a white spectrum (except for DC):

```python
>>> import matplotlib.pyplot as plt
>>> from numpy.fft import fft, ifft, fftshift, fftfreq
>>> seq = max_len_seq(6)[0] * 2 - 1  # +1 and -1
>>> spec = fft(seq)
>>> N = len(seq)
>>> plt.plot(fftshift(fftfreq(N)), fftshift(np.abs(spec)), '.-')
>>> plt.margins(0.1, 0.1)
>>> plt.grid(True)
>>> plt.show()
```

Circular autocorrelation of MLS is an impulse:

```python
>>> acorrcirc = ifft(spec * np.conj(spec)).real
>>> plt.figure()
>>> plt.plot(np.arange(-N/2+1, N/2+1), fftshift(acorrcirc), '.-')
>>> plt.margins(0.1, 0.1)
>>> plt.grid(True)
>>> plt.show()
```

Linear autocorrelation of MLS is approximately an impulse:
```python
>>> acorr = np.correlate(seq, seq, 'full')
>>> plt.figure()
>>> plt.plot(np.arange(-N+1, N), acorr, '.-')
>>> plt.margins(0.1, 0.1)
>>> plt.grid(True)
>>> plt.show()
```

**scipy.signal.sawtooth**

`scipy.signal.sawtooth(t, width=1)`

Return a periodic sawtooth or triangle waveform.

The sawtooth waveform has a period $2\pi$, rises from $-1$ to $1$ on the interval $0$ to $width\cdot2\pi$, then drops from $1$ to $-1$ on the interval $width\cdot2\pi$ to $2\pi$. $width$ must be in the interval $[0, 1]$. 
Note that this is not band-limited. It produces an infinite number of harmonics, which are aliased back and forth across the frequency spectrum.

**Parameters**

- `t`  
  [array_like] Time.

- `width`  
  [array_like, optional] Width of the rising ramp as a proportion of the total cycle. Default is 1, producing a rising ramp, while 0 produces a falling ramp. `width = 0.5` produces a triangle wave. If an array, causes wave shape to change over time, and must be the same length as `t`.

**Returns**

- `y`  
  [ndarray] Output array containing the sawtooth waveform.

**Examples**

A 5 Hz waveform sampled at 500 Hz for 1 second:

```python
def main():
    from scipy import signal
    import matplotlib.pyplot as plt
    t = np.linspace(0, 1, 500)
    y = signal.sawtooth(2 * np.pi * 5 * t)
    plt.plot(t, y)
    plt.show()

if __name__ == '__main__': main()
```

### scipy.signal.square

**scipy.signal.square**

- `t`  
  [array_like] The input time array.

- `duty`  
  [array_like, optional] Duty cycle. Default is 0.5 (50% duty cycle). If an array, causes wave shape to change over time, and must be the same length as `t`.

**Parameters**

- `duty`  
  [array_like, optional] Duty cycle. Default is 0.5 (50% duty cycle). If an array, causes wave shape to change over time, and must be the same length as `t`.

The square wave has a period $2\pi$, has value +1 from 0 to $2\pi \cdot \text{duty}$ and -1 from $2\pi \cdot \text{duty}$ to $2\pi$. `duty` must be in the interval $[0,1]$.

Note that this is not band-limited. It produces an infinite number of harmonics, which are aliased back and forth across the frequency spectrum.
Returns

\[y\] [ndarray] Output array containing the square waveform.

Examples

A 5 Hz waveform sampled at 500 Hz for 1 second:

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> t = np.linspace(0, 1, 500, endpoint=False)
>>> plt.plot(t, signal.square(2 * np.pi * 5 * t))
>>> plt.ylim(-2, 2)
```

A pulse-width modulated sine wave:

```python
>>> plt.figure()
>>> sig = np.sin(2 * np.pi * t)
>>> pwm = signal.square(2 * np.pi * 30 * t, duty=(sig + 1)/2)
>>> plt.subplot(2, 1, 1)
>>> plt.plot(t, sig)
>>> plt.subplot(2, 1, 2)
>>> plt.plot(t, pwm)
>>> plt.ylim(-1.5, 1.5)
```

```
0.0 0.2 0.4 0.6 0.8 1.0
-2 -1 0 1 2
```

**scipy.signal.sweep_poly**

**scipy.signal.sweep_poly** \((t, \text{poly}, \phi=0)\)

Frequency-swept cosine generator, with a time-dependent frequency.

This function generates a sinusoidal function whose instantaneous frequency varies with time. The frequency at time \(t\) is given by the polynomial \(\text{poly}\).

**Parameters**

- \(t\) [ndarray] Times at which to evaluate the waveform.
- \(\text{poly}\) [1-D array_like or instance of numpy.poly1d] The desired frequency expressed as a polynomial. If \(\text{poly}\) is a list or ndarray of length \(n\), then the elements of \(\text{poly}\) are the coefficients of the polynomial, and the instantaneous frequency is
f(t) = poly[0]*t**(n-1) + poly[1]*t**(n-2) + ... + poly[n-1]

If \( \text{poly} \) is an instance of numpy.poly1d, then the instantaneous frequency is

\[ f(t) = \text{poly}(t) \]

\( \phi \) [float, optional] Phase offset, in degrees, Default: 0.

**Returns**

sweep_poly

[ndarray] A numpy array containing the signal evaluated at \( t \) with the requested time-varying frequency. More precisely, the function returns \( \cos(\text{phase} + (\pi/180)*\phi) \), where \( \text{phase} \) is the integral (from 0 to \( t \)) of \( 2 * \pi * f(t) \); \( f(t) \) is defined above.

See also:

chirp

**Notes**

New in version 0.8.0.

If \( \text{poly} \) is a list or ndarray of length \( n \), then the elements of \( \text{poly} \) are the coefficients of the polynomial, and the instantaneous frequency is:

\[ f(t) = \text{poly}[0]*t**(n-1) + \text{poly}[1]*t**(n-2) + ... + \text{poly}[n-1] \]

If \( \text{poly} \) is an instance of numpy.poly1d, then the instantaneous frequency is:

\[ f(t) = \text{poly}(t) \]

Finally, the output \( s \) is:

\[ \cos(\text{phase} + (\pi/180)*\phi) \]

where \( \text{phase} \) is the integral from 0 to \( t \) of \( 2 * \pi * f(t) \); \( f(t) \) as defined above.

**Examples**

Compute the waveform with instantaneous frequency:

\[
f(t) = 0.025*t**3 - 0.36*t**2 + 1.25*t + 2
\]

over the interval \( 0 \leq t \leq 10 \).
```python
>>> from scipy.signal import sweep_poly
>>> p = np.poly1d([0.025, -0.36, 1.25, 2.0])
>>> t = np.linspace(0, 10, 5001)
>>> w = sweep_poly(t, p)

Plot it:
```
y  [ndarray] Output array containing an impulse signal.

Notes
The 1D case is also known as the Kronecker delta.
New in version 0.19.0.

Examples
An impulse at the 0th element ($\delta[n]$):

```python
>>> from scipy import signal
>>> signal.unit_impulse(8)
array([ 1., 0., 0., 0., 0., 0., 0., 0.])
```

Impulse offset by 2 samples ($\delta[n - 2]$):

```python
>>> signal.unit_impulse(7, 2)
array([ 0., 0., 1., 0., 0., 0., 0.])
```

2-dimensional impulse, centered:

```python
>>> signal.unit_impulse((3, 3), 'mid')
array([[ 0., 0., 0.],
       [ 0., 1., 0.],
       [ 0., 0., 0.]])
```

Impulse at (2, 2), using broadcasting:

```python
>>> signal.unit_impulse((4, 4), 2)
array([[ 0., 0., 0., 0.],
       [ 0., 0., 0., 0.],
       [ 0., 0., 1., 0.],
       [ 0., 0., 0., 0.]])
```

Plot the impulse response of a 4th-order Butterworth lowpass filter:

```python
>>> imp = signal.unit_impulse(100, 'mid')
>>> b, a = signal.butter(4, 0.2)
>>> response = signal.lfilter(b, a, imp)

>>> import matplotlib.pyplot as plt
>>> plt.plot(np.arange(-50, 50), imp)
>>> plt.plot(np.arange(-50, 50), response)
>>> plt.margins(0.1, 0.1)
>>> plt.xlabel('Time [samples]')
>>> plt.ylabel('Amplitude')
>>> plt.grid(True)
>>> plt.show()
```

6.20.10 Window functions

Most window functions are available in the `scipy.signal.windows` namespace, but we list them here for convenience:
<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
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<tbody>
<tr>
<td><code>get_window(window, Nx[, fftbins])</code></td>
<td>Return a window.</td>
</tr>
<tr>
<td><code>windows.barthann(M[, sym])</code></td>
<td>Return a modified Bartlett-Hann window.</td>
</tr>
<tr>
<td><code>windows.bartlett(M[, sym])</code></td>
<td>Return a Bartlett window.</td>
</tr>
<tr>
<td><code>windows.blackman(M[, sym])</code></td>
<td>Return a Blackman window.</td>
</tr>
<tr>
<td><code>windows.blackmanharris(M[, sym])</code></td>
<td>Return a minimum 4-term Blackman-Harris window.</td>
</tr>
<tr>
<td><code>windows.bohman(M[, sym])</code></td>
<td>Return a Bohman window.</td>
</tr>
<tr>
<td><code>windows.boxcar(M[, sym])</code></td>
<td>Return a boxcar or rectangular window.</td>
</tr>
<tr>
<td><code>windows.chebwin(M, at[, sym])</code></td>
<td>Return a Dolph-Chebyshev window.</td>
</tr>
<tr>
<td><code>windows.cosine(M[, sym])</code></td>
<td>Return a window with a simple cosine shape.</td>
</tr>
<tr>
<td><code>windows.dpss(M, NW[, Kmax, sym, norm, ...])</code></td>
<td>Compute the Discrete Prolate Spheroidal Sequences (DPSS).</td>
</tr>
<tr>
<td><code>windows.exponential(M[, center, tau, sym])</code></td>
<td>Return an exponential (or Poisson) window.</td>
</tr>
<tr>
<td><code>windows.flattop(M[, sym])</code></td>
<td>Return a flat top window.</td>
</tr>
<tr>
<td><code>windows.gaussian(M, std[, sym])</code></td>
<td>Return a Gaussian window.</td>
</tr>
<tr>
<td><code>windows.general_cosine(M, a[, sym])</code></td>
<td>Generic weighted sum of cosine terms window</td>
</tr>
<tr>
<td><code>windows.general_gaussian(M, p, sig[, sym])</code></td>
<td>Return a window with a generalized Gaussian shape.</td>
</tr>
<tr>
<td><code>windows.general_hamming(M, alpha[, sym])</code></td>
<td>Return a generalized Hamming window.</td>
</tr>
<tr>
<td><code>windows.hann(M[, , sym])</code></td>
<td>Return a Hann window.</td>
</tr>
<tr>
<td><code>windows.hanning(*args, **kwds)</code></td>
<td><code>hanning</code> is deprecated, use <code>scipy.signal.windows.hann</code> instead!</td>
</tr>
<tr>
<td><code>windows.kaiser(M, beta[, sym])</code></td>
<td>Return a Kaiser window.</td>
</tr>
<tr>
<td><code>windows.nuttall(M[, sym])</code></td>
<td>Return a minimum 4-term Blackman-Harris window according to Nuttall.</td>
</tr>
<tr>
<td><code>windows.parzen(M[, sym])</code></td>
<td>Return a Parzen window.</td>
</tr>
<tr>
<td><code>windows.slepian(M, width[, sym])</code></td>
<td>Return a digital Slepian (DPSS) window.</td>
</tr>
<tr>
<td><code>windows.triang(M[, sym])</code></td>
<td>Return a triangular window.</td>
</tr>
<tr>
<td><code>windows.tukey(M[, alpha, sym])</code></td>
<td>Return a Tukey window, also known as a tapered cosine window.</td>
</tr>
</tbody>
</table>

**scipy.signal.get_window**

`scipy.signal.get_window(window, Nx, fftbins=True)`  

1452 Return a window.

### Parameters

- **window** [string, float, or tuple] The type of window to create. See below for more details.
- **Nx** [int] The number of samples in the window.
- **fftbins** [bool, optional] If True (default), create a “periodic” window, ready to use with `ifftshift` and be multiplied by the result of an FFT (see also `fftpack.fftfreq`). If False, create a “symmetric” window, for use in filter design.
SciPy Reference Guide, Release 1.2.0

tion), **general_gaussian** (needs power, width), **slepian** (needs width), **dpss** (needs normalized half-bandwidth), **chebwin** (needs attenuation), **exponential** (needs decay scale), **tukey** (needs taper fraction)

If the window requires no parameters, then `window` can be a string.

If the window requires parameters, then `window` must be a tuple with the first argument the string name of the window, and the next arguments the needed parameters.

If `window` is a floating point number, it is interpreted as the beta parameter of the **kaiser** window.

Each of the window types listed above is also the name of a function that can be called directly to create a window of that type.

**Examples**

```python
>>> from scipy import signal
>>> signal.get_window('triang', 7)
array([ 0.125, 0.375, 0.625, 0.875, 0.875, 0.625, 0.375])
>>> signal.get_window(('kaiser', 4.0), 9)
array([ 0.08848053, 0.29425961, 0.56437221, 0.82160913, 0.97885093,
        0.97885093, 0.82160913, 0.56437221, 0.29425961])
>>> signal.get_window(4.0, 9)
array([ 0.08848053, 0.29425961, 0.56437221, 0.82160913, 0.97885093,
        0.97885093, 0.82160913, 0.56437221, 0.29425961])
```

**scipy.signal.windows.barthann**

**scipy.signal.windows.barthann**(*M*, **sym=True**)  
Return a modified Bartlett-Hann window.

**Parameters**

- **M** [int] Number of points in the output window. If zero or less, an empty array is returned.
- **sym** [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

**Returns**

- **w** [ndarray] The window, with the maximum value normalized to 1 (though the value 1 does not appear if *M* is even and **sym** is True).

**Examples**

Plot the window and its frequency response:

```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = signal.barthann(51)
>>> plt.plot(window)
>>> plt.title("Bartlett-Hann window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> A = fft(window, 2048) / (len(window)/2.0)
```
```python
code
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Bartlett-Hann window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```

```
Text

scipy.signal.windows.bartlett

scipy.signal.windows.bartlett(M, sym=True)

Return a Bartlett window.

The Bartlett window is very similar to a triangular window, except that the end points are at zero.

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```
It is often used in signal processing for tapering a signal, without generating too much ripple in the frequency domain.

**Parameters**

- **M** [int] Number of points in the output window. If zero or less, an empty array is returned.
- **sym** [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

**Returns**

- **w** [ndarray] The triangular window, with the first and last samples equal to zero and the maximum value normalized to 1 (though the value 1 does not appear if \( M \) is even and \( \text{sym} \) is True).

**See also:**

triang

A triangular window that does not touch zero at the ends

**Notes**

The Bartlett window is defined as

\[
    w(n) = \frac{2}{M - 1} \left( \frac{M - 1}{2} - \left| n - \frac{M - 1}{2} \right| \right)
\]

Most references to the Bartlett window come from the signal processing literature, where it is used as one of many windowing functions for smoothing values. Note that convolution with this window produces linear interpolation. It is also known as an apodization (which means “removing the foot”, i.e. smoothing discontinuities at the beginning and end of the sampled signal) or tapering function. The Fourier transform of the Bartlett is the product of two sinc functions. Note the excellent discussion in Kanasewich. [2]

**References**

[1], [2], [3], [4], [5]

**Examples**

Plot the window and its frequency response:

```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = signal.bartlett(51)
>>> plt.plot(window)
>>> plt.title("Bartlett window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Bartlett window")
```

(continues on next page)
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")

scipy.signal.windows.blackman

scipy.signal.windows.blackman(M, sym=True)

Return a Blackman window.

The Blackman window is a taper formed by using the first three terms of a summation of cosines. It was designed to have close to the minimal leakage possible. It is close to optimal, only slightly worse than a Kaiser window.

Parameters
M [int] Number of points in the output window. If zero or less, an empty array is returned.

sym [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

Returns

w [ndarray] The window, with the maximum value normalized to 1 (though the value 1 does not appear if $M$ is even and $sym$ is True).

Notes

The Blackman window is defined as

$$w(n) = 0.42 - 0.5 \cos(2\pi n/M) + 0.08 \cos(4\pi n/M)$$

The “exact Blackman” window was designed to null out the third and fourth sidelobes, but has discontinuities at the boundaries, resulting in a 6 dB/oct fall-off. This window is an approximation of the “exact” window, which does not null the sidelobes as well, but is smooth at the edges, improving the fall-off rate to 18 dB/oct. [3]

Most references to the Blackman window come from the signal processing literature, where it is used as one of many windowing functions for smoothing values. It is also known as an apodization (which means “removing the foot”, i.e. smoothing discontinuities at the beginning and end of the sampled signal) or tapering function. It is known as a “near optimal” tapering function, almost as good (by some measures) as the Kaiser window.

References

[1], [2], [3]

Examples

Plot the window and its frequency response:

```python
>>> from scipy import signal
cos(2\pi n/M) + 0.08 \cos(4\pi n/M)$$

Most references to the Blackman window come from the signal processing literature, where it is used as one of many windowing functions for smoothing values. It is also known as an apodization (which means “removing the foot”, i.e. smoothing discontinuities at the beginning and end of the sampled signal) or tapering function. It is known as a “near optimal” tapering function, almost as good (by some measures) as the Kaiser window.

References

[1], [2], [3]

Examples

Plot the window and its frequency response:

```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = signal.blackman(51)
>>> plt.plot(window)
>>> plt.title("Blackman window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Blackman window")
>>> plt.ylabel("Normalized magnitude [dB]"
>>> plt.xlabel("Normalized frequency [cycles per sample]

scipy.signal.windows.blackmanharris

scipy.signal.windows.blackmanharris(M, sym=True)

Return a minimum 4-term Blackman-Harris window.

Parameters

6.20. Signal processing (scipy.signal)
Blackman window

Normalized frequency [cycles per sample]

Normalized magnitude [dB]

Frequency response of the Blackman window

Sample

Amplitude

Normalized frequency [cycles per sample]
M  [int] Number of points in the output window. If zero or less, an empty array is returned.
sym [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

**Returns**
w [ndarray] The window, with the maximum value normalized to 1 (though the value 1 does not appear if M is even and sym is True).

**Examples**
Plot the window and its frequency response:

```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = signal.blackmanharris(51)
>>> plt.plot(window)
>>> plt.title("Blackman-Harris window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Blackman-Harris window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```

![Blackman-Harris window plot](image)
scipy.signal.windows.bohman

scipy.signal.windows.bohman(M, sym=True)

Return a Bohman window.

Parameters

- M [int] Number of points in the output window. If zero or less, an empty array is returned.
- sym [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

Returns

- w [ndarray] The window, with the maximum value normalized to 1 (though the value 1 does not appear if M is even and sym is True).

Examples

Plot the window and its frequency response:

```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = signal.bohman(51)
>>> plt.plot(window)
>>> plt.title("Bohman window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
```

(continues on next page)
```python
>>> plt.title("Frequency response of the Bohman window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```

**scipy.signal.windows.boxcar**

`scipy.signal.windows.boxcar(M, sym=True)`

Return a boxcar or rectangular window.

Also known as a rectangular window or Dirichlet window, this is equivalent to no window at all.

**Parameters**

- `M` [int] Number of points in the output window. If zero or less, an empty array is returned.
sym [bool, optional] Whether the window is symmetric. (Has no effect for boxcar.)

Returns

w [ndarray] The window, with the maximum value normalized to 1.

Examples
Plot the window and its frequency response:

```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = signal.boxcar(51)
>>> plt.plot(window)
>>> plt.title("Boxcar window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the boxcar window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```

scipy.signal.windows.chebwin

scipy.signal.windows.chebwin(M, at, sym=True)

Return a Dolph-Chebyshev window.

Parameters
**Frequency response of the boxcar window**

**M** [int] Number of points in the output window. If zero or less, an empty array is returned.

**at** [float] Attenuation (in dB).

**sym** [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

**Returns**

**w** [ndarray] The window, with the maximum value always normalized to 1

**Notes**

This window optimizes for the narrowest main lobe width for a given order $M$ and sidelobe equiripple attenuation $\text{at}$, using Chebyshev polynomials. It was originally developed by Dolph to optimize the directionality of radio antenna arrays.

Unlike most windows, the Dolph-Chebyshev is defined in terms of its frequency response:

$$W(k) = \frac{\cos\left\{M \cos^{-1}[\beta \cos\left(\frac{\pi k}{M}\right)]\right\}}{\cosh[M \cosh^{-1}(\beta)]}$$

where

$$\beta = \cosh\left[\frac{1}{M} \cosh^{-1}(10^{\text{at}/20})\right]$$

and $0 \leq \text{abs}(k) \leq M-1$. $\text{at}$ is the attenuation in decibels ($\text{at}$).

The time domain window is then generated using the IFFT, so power-of-two $M$ are the fastest to generate, and prime number $M$ are the slowest.

The equiripple condition in the frequency domain creates impulses in the time domain, which appear at the ends of the window.

**References**

[1], [2], [3]

**Examples**

Plot the window and its frequency response:
```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = signal.chebwin(51, at=100)
>>> plt.plot(window)
>>> plt.title("Dolph-Chebyshev window (100 dB)")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Dolph-Chebyshev window (100 dB)")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```

**scipy.signal.windows.cosine**

`scipy.signal.windows.cosine(M, sym=True)`

Return a window with a simple cosine shape.

**Parameters**

- **M**  
  [int] Number of points in the output window. If zero or less, an empty array is returned.

- **sym**  
  [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

**Returns**
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.. _windows.dpss:

scipy.signal.windows.dpss

.. _windows.dpss: scipy.signal.windows.

.. py:function:: dpss(M, NW, Kmax=None, sym=True, norm=None, return_ratios=False)

   Compute the Discrete Prolate Spheroidal Sequences (DPSS).

   DPSS (or Slepian sequences) are often used in multitaper power spectral density estimation (see [1]).

w

[ndarray] The window, with the maximum value normalized to 1 (though the value 1 does not appear if \( M \) is even and \( \text{sym} \) is True).

Notes

New in version 0.13.0.

Examples

Plot the window and its frequency response:

>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = signal.cosine(51)
>>> plt.plot(window)
>>> plt.title("Cosine window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the cosine window")
>>> plt.ylabel("Normalized magnitude [dB]"")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
>>> plt.show()
The first window in the sequence can be used to maximize the energy concentration in the main lobe, and is also called the Slepian window.

**Parameters**

- **M** [int] Window length.
- **NW** [float] Standardized half bandwidth corresponding to $2*NW = BW/f0 = BW*N*dt$ where $dt$ is taken as 1.
- **Kmax** [int | None, optional] Number of DPSS windows to return (orders 0 through Kmax-1). If None (default), return only a single window of shape $(M,)$ instead of an array of windows of shape $(Kmax, M)$.
- **sym** [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.
- **norm** [{2, 'approximate', 'subsample'} | None, optional] If ‘approximate’ or ‘subsample’, then the windows are normalized by the maximum, and a correction scale-factor for even-length windows is applied either using $M**2/(M**2+NW)$ (“approximate”) or a FFT-based subsample shift (“subsample”), see Notes for details. If None, then “approximate” is used when Kmax=None and 2 otherwise (which uses the I2 norm).
- **return_ratios** [bool, optional] If True, also return the concentration ratios in addition to the windows.

**Returns**

- **v** [ndarray, shape (Kmax, N) or (N,)] The DPSS windows. Will be 1D if Kmax is None.
- **r** [ndarray, shape (Kmax,) or float, optional] The concentration ratios for the windows. Only returned if return_ratios evaluates to True. Will be 0D if Kmax is None.

**Notes**

This computation uses the tridiagonal eigenvector formulation given in [2].

The default normalization for Kmax=None, i.e. window-generation mode, simply using the l-infinity norm would create a window with two unity values, which creates slight normalization differences between even and odd orders. The approximate correction of $M**2/float(M**2+NW)$ for even sample numbers is used to counteract this effect (see Examples below).

For very long signals (e.g., 1e6 elements), it can be useful to compute windows orders of magnitude shorter and use interpolation (e.g., scipy.interpolate.interp1d) to obtain tapers of length $M$, but this in general will not preserve orthogonality between the tapers.

New in version 1.1.

**References**

[1], [2], [3]

**Examples**

We can compare the window to kaiser, which was invented as an alternative that was easier to calculate [3] (example adapted from here):

```python
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> from scipy.signal import windows, freqz
>>> N = 51
>>> fig, axes = plt.subplots(3, 2, figsize=(5, 7))
>>> for ai, alpha in enumerate((1, 3, 5)):
...     win_dpss = windows.dpss(N, alpha)
...     beta = alpha*np.pi
(continues on next page)```
Using a standard $l_\infty$ norm would produce two unity values for even $M$, but only one unity value for odd $M$. This produces uneven window power that can be counteracted by the approximate correction $M*2/float(M*2+NW)$, which can be selected by using norm='approximate' (which is the same as norm=None when Kmax=None, as is the case here). Alternatively, the slower norm='subsample' can be used, which uses subsample shifting in the frequency domain (FFT) to compute the correction:

```python
>>> Ms = np.arange(1, 41)
>>> factors = (50, 20, 10, 5, 2.0001)
>>> energy = np.empty((3, len(Ms), len(factors)))
>>> for mi, M in enumerate(Ms):
...     for fi, factor in enumerate(factors):
...         NW = M / float(factor)
...         # Corrected using empirical approximation (default)
...         win = windows.dpss(M, NW)
...         energy[0, mi, fi] = np.sum(win ** 2) / np.sqrt(M)
...         # Corrected using subsample shifting
...         win = windows.dpss(M, NW, norm='subsample')
...         energy[1, mi, fi] = np.sum(win ** 2) / np.sqrt(M)
...         # Uncorrected (using $l_{\infty}$ norm)
...         win /= win.max()
...         energy[2, mi, fi] = np.sum(win ** 2) / np.sqrt(M)
```
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```python
>>> fig, ax = plt.subplots(1)
>>> hs = ax.plot(Ms, energy[2], '-o', markersize=4,
... markeredgecolor='none')
>>> leg = [hs[-1]]
>>> for hi, hh in enumerate(hs):
...     h1 = ax.plot(Ms, energy[0, :, hi], '-o', markersize=4,
...                 color=hh.get_color(), markeredgecolor='none',
...                 alpha=0.66)
...     h2 = ax.plot(Ms, energy[1, :, hi], '-o', markersize=4,
...                 color=hh.get_color(), markeredgecolor='none',
...                 alpha=0.33)
...     if hi == len(hs) - 1:
...         leg.insert(0, h1[0])
...         leg.insert(0, h2[0])
>>> ax.set(xlabel='M (samples)', ylabel=r'Power / $\sqrt{M}$')
>>> ax.legend(leg, ['Uncorrected', r'Corrected: $\frac{M^2}{M^2+NW}$',
... 'Corrected (subsample)'])
>>> fig.tight_layout()
```

**scipy.signal.windows.exponential**

Return an exponential (or Poisson) window.

**Parameters**

- **M** [int] Number of points in the output window. If zero or less, an empty array is returned.
- **center** [float, optional] Parameter defining the center location of the window function. The default value if not given is `center = (M-1) / 2`. This parameter must take its default value for symmetric windows.
- **tau** [float, optional] Parameter defining the decay. For `center = 0` use `tau = -(M-1) / ln(x)` if x is the fraction of the window remaining at the end.
sym

[bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

Returns

w

[ndarray] The window, with the maximum value normalized to 1 (though the value 1 does not appear if M is even and sym is True).

Notes

The Exponential window is defined as

\[ w(n) = e^{-|n-center|/\tau} \]

References


Examples

Plot the symmetric window and its frequency response:

```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> M = 51
>>> tau = 3.0
>>> window = signal.exponential(M, tau=tau)
>>> plt.plot(window)
>>> plt.title("Exponential Window (tau=3.0)"")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
```

(continues on next page)
This function can also generate non-symmetric windows:

```python
>>> tau2 = -(M-1) / np.log(0.01)
>>> window2 = signal.exponential(M, 0, tau2, False)
>>> plt.figure()
>>> plt.plot(window2)
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
```

---

**scipy.signal.windows.flattop**

`scipy.signal.windows.flattop(M, sym=True)`

Return a flat top window.

**Parameters**

- **M**  
  [int] Number of points in the output window. If zero or less, an empty array is returned.

- **sym**  
  [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

**Returns**

- **w**  
  [ndarray] The window, with the maximum value normalized to 1 (though the value 1 does not appear if M is even and sym is True).

**Notes**

Flat top windows are used for taking accurate measurements of signal amplitude in the frequency domain, with minimal scalloping error from the center of a frequency bin to its edges, compared to...
Frequency response of the Exponential window (tau=3.0)

Normalized magnitude [dB]

Normalized frequency [cycles per sample]

Amplitude

Sample
others. This is a 5th-order cosine window, with the 5 terms optimized to make the main lobe maximally flat. [1]

References
[1]

Examples
Plot the window and its frequency response:

```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = signal.flattop(51)
>>> plt.plot(window)
>>> plt.title("Flat top window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the flat top window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```

![Flat top window](image_url)

**scipy.signal.windows.gaussian**

`scipy.signal.windows.gaussian(M, std, sym=True)`

Return a Gaussian window.

**Parameters**
Normalized frequency [cycles per sample]

Normalized magnitude [dB]

Frequency response of the flat top window

M [int] Number of points in the output window. If zero or less, an empty array is returned.

std [float] The standard deviation, sigma.

sym [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

Returns

w [ndarray] The window, with the maximum value normalized to 1 (though the value 1 does not appear if M is even and sym is True).

Notes

The Gaussian window is defined as

\[ w(n) = e^{-\frac{1}{2}(\frac{n}{\sigma})^2} \]

Examples

Plot the window and its frequency response:

```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = signal.gaussian(51, std=7)
>>> plt.plot(window)
>>> plt.title(r"Gaussian window ($\sigma$=7)")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
```

(continues on next page)
```python
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title(r"Frequency response of the Gaussian window ($\sigma$=7)"")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```

![Gaussian window (\(\sigma=7\))](image1.png)

![Frequency response of the Gaussian window (\(\sigma=7\))]![image2.png)

**scipy.signal.windows.general_cosine**

```python
scipy.signal.windows.general_cosine(M, a, sym=True)
```

Generic weighted sum of cosine terms window

**Parameters**

- **M** [int] Number of points in the output window
SciPy Reference Guide, Release 1.2.0

a  [array_like] Sequence of weighting coefficients. This uses the convention of being centered on the origin, so these will typically all be positive numbers, not alternating sign.

sym  [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

References
[1], [2]

Examples
Heinzel describes a flat-top window named “HFT90D” with formula: [2]

\[ w_j = 1 - 1.942604 \cos(z) + 1.340318 \cos(2z) - 0.440811 \cos(3z) + 0.043097 \cos(4z) \]

where

\[ z = \frac{2\pi j}{N}, j = 0...N - 1 \]

Since this uses the convention of starting at the origin, to reproduce the window, we need to convert every other coefficient to a positive number:

```python
>>> HFT90D = [1, 1.942604, 1.340318, 0.440811, 0.043097]
```

The paper states that the highest sidelobe is at -90.2 dB. Reproduce Figure 42 by plotting the window and its frequency response, and confirm the sidelobe level in red:

```python
>>> from scipy.signal.windows import general_cosine
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = general_cosine(1000, HFT90D, sym=False)
>>> plt.plot(window)
>>> plt.title("HFT90D window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> A = fft(window, 10000) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-50/1000, 50/1000, -140, 0])
>>> plt.title("Frequency response of the HFT90D window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
>>> plt.axhline(-90.2, color='red')
>>> plt.show()
```

scipy.signal.windows.general_gaussian

scipy.signal.windows.general_gaussian(M, p, sig, sym=True)

Return a window with a generalized Gaussian shape.

Parameters

- M  [int] Number of points in the output window. If zero or less, an empty array is returned.
The diagram depicts the amplitude and frequency response of the HFT90D window. The amplitude plot shows a bell-shaped curve, indicating a central peak with decreasing values towards the edges. The frequency response indicates a sharp central peak, typical of a window designed to emphasize a specific frequency band, with significant attenuation at frequencies away from the central peak.
SciPy Reference Guide, Release 1.2.0

p [float] Shape parameter. p = 1 is identical to `gaussian`, p = 0.5 is the same shape as the Laplace distribution.

sig [float] The standard deviation, sigma.

sym [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

Returns

w [ndarray] The window, with the maximum value normalized to 1 (though the value 1 does not appear if M is even and sym is True).

Notes

The generalized Gaussian window is defined as

\[ w(n) = e^{-\frac{1}{2}|n|^p} \]

the half-power point is at

\[ (2\log(2))^{1/(2p)} \sigma \]

Examples

Plot the window and its frequency response:

```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = signal.general_gaussian(51, p=1.5, sig=7)
>>> plt.plot(window)
>>> plt.title(r"Generalized Gaussian window (p=1.5, $\sigma$=7)"
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = np.abs(fftshift(A / abs(A).max()))
>>> plt.plot(freq, response)
>>> plt.title(r"Freq. resp. of the gen. Gaussian "
... "window (p=1.5, $\sigma$=7)"
>>> plt.ylabel("Normalized magnitude [dB]"
>>> plt.xlabel("Normalized frequency [cycles per sample]"
```

scipy.signal.windows.general_hamming

scipy.signal.windows.general_hamming(M, alpha, sym=True)

Return a generalized Hamming window.

The generalized Hamming window is constructed by multiplying a rectangular window by one period of a cosine function [1].

Parameters

M [int] Number of points in the output window. If zero or less, an empty array is returned.

alpha [float] The window coefficient, \( \alpha \)
Generalized Gaussian window \((p=1.5, \sigma=7)\)

Freq. resp. of the gen. Gaussian window \((p=1.5, \sigma=7)\)
sym [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

Returns
w [ndarray] The window, with the maximum value normalized to 1 (though the value 1 does not appear if M is even and sym is True).

See also:
hamming, hann

Notes
The generalized Hamming window is defined as

\[ w(n) = \alpha - (1 - \alpha) \cos\left(\frac{2\pi n}{M-1}\right) \quad 0 \leq n \leq M - 1 \]

Both the common Hamming window and Hann window are special cases of the generalized Hamming window with \(\alpha = 0.54\) and \(\alpha = 0.5\), respectively [2].

References
[1], [2], [3], [4]

Examples
The Sentinel-1A/B Instrument Processing Facility uses generalized Hamming windows in the processing of spaceborne Synthetic Aperture Radar (SAR) data [3]. The facility uses various values for the \(\alpha\) parameter based on operating mode of the SAR instrument. Some common \(\alpha\) values include 0.75, 0.7 and 0.52 [4]. As an example, we plot these different windows.

```python
>>> from scipy.signal.windows import general_hamming
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> fig1, spatial_plot = plt.subplots()
>>> spatial_plot.set_title("Generalized Hamming Windows")
>>> spatial_plot.set_ylabel("Amplitude")
>>> spatial_plot.set_xlabel("Sample")

>>> fig2, freq_plot = plt.subplots()
>>> freq_plot.set_title("Frequency Responses")
>>> freq_plot.set_ylabel("Normalized magnitude [dB]")
>>> freq_plot.set_xlabel("Normalized frequency [cycles per sample]"

>>> for alpha in [0.75, 0.7, 0.52]:
...     window = general_hamming(41, alpha)
...     spatial_plot.plot(window, label="{:.2f}".format(alpha))
...     A = fft(window, 2048) / (len(window)/2.0)
...     freq = np.linspace(-0.5, 0.5, len(A))
...     response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
...     freq_plot.plot(freq, response, label="{:.2f}".format(alpha))

>>> freq_plot.legend(loc="upper right")
>>> spatial_plot.legend(loc="upper right")
```

scipy.signal.windows.hamming

scipy.signal.windows.hamming(M, sym=True)

Return a Hamming window.
Generalized Hamming Windows

![Graph of Generalized Hamming Windows](image)

Frequency Responses

![Graph of Frequency Responses](image)
The Hamming window is a taper formed by using a raised cosine with non-zero endpoints, optimized to minimize the nearest side lobe.

**Parameters**

- **M** [int] Number of points in the output window. If zero or less, an empty array is returned.
- **sym** [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

**Returns**

- **w** [ndarray] The window, with the maximum value normalized to 1 (though the value 1 does not appear if $M$ is even and $sym$ is True).

**Notes**

The Hamming window is defined as

$$w(n) = 0.54 - 0.46 \cos \left( \frac{2\pi n}{M - 1} \right) \quad 0 \leq n \leq M - 1$$

The Hamming was named for R. W. Hamming, an associate of J. W. Tukey and is described in Blackman and Tukey. It was recommended for smoothing the truncated autocovariance function in the time domain. Most references to the Hamming window come from the signal processing literature, where it is used as one of many windowing functions for smoothing values. It is also known as an apodization (which means “removing the foot”, i.e. smoothing discontinuities at the beginning and end of the sampled signal) or tapering function.

**References**

[1], [2], [3], [4]

**Examples**

Plot the window and its frequency response:

```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = signal.hamming(51)
>>> plt.plot(window)
>>> plt.title("Hamming window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Hamming window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample"]
```

scipy.signal.windows.hann

scipy.signal.windows.hann($M$, sym=True)

Return a Hann window.
Hamming window

Normalized frequency [cycles per sample]

Frequency response of the Hamming window

Normalized magnitude [dB]

Normalized frequency [cycles per sample]
The Hann window is a taper formed by using a raised cosine or sine-squared with ends that touch zero.

**Parameters**

- **M** [int] Number of points in the output window. If zero or less, an empty array is returned.
- **sym** [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

**Returns**

- **w** [ndarray] The window, with the maximum value normalized to 1 (though the value 1 does not appear if \(M\) is even and \(sym\) is True).

**Notes**

The Hann window is defined as

\[
    w(n) = 0.5 - 0.5 \cos\left(\frac{2\pi n}{M-1}\right) \quad 0 \leq n \leq M - 1
\]

The window was named for Julius von Hann, an Austrian meteorologist. It is also known as the Cosine Bell. It is sometimes erroneously referred to as the “Hanning” window, from the use of “hann” as a verb in the original paper and confusion with the very similar Hamming window.

Most references to the Hann window come from the signal processing literature, where it is used as one of many windowing functions for smoothing values. It is also known as an apodization (which means “removing the foot”, i.e. smoothing discontinuities at the beginning and end of the sampled signal) or tapering function.

**References**

[1], [2], [3], [4]

**Examples**

Plot the window and its frequency response:

```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = signal.hann(51)
>>> plt.plot(window)
>>> plt.title("Hann window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Hann window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```

**scipy.signal.windows.hanning**

scipy.signal.windows.hanning(*args, **kwds)

*hanning* is deprecated, use *scipy.signal.windows.hann* instead!
**scipy.signal.windows.kaiser**

**scipy.signal.windows.kaiser***(M, beta, sym=True)***

Return a Kaiser window.

The Kaiser window is a taper formed by using a Bessel function.

**Parameters**

- **M** [int] Number of points in the output window. If zero or less, an empty array is returned.
- **beta** [float] Shape parameter, determines trade-off between main-lobe width and side lobe level. As beta gets large, the window narrows.
- **sym** [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

**Returns**

- **w** [ndarray] The window, with the maximum value normalized to 1 (though the value 1 does not appear if M is even and sym is True).

**Notes**

The Kaiser window is defined as

\[
   w(n) = I_0 \left( \beta \sqrt{1 - \frac{4n^2}{(M-1)^2}} \right) / I_0(\beta)
\]

with

\[
   - \frac{M-1}{2} \leq n \leq \frac{M-1}{2},
\]

where \( I_0 \) is the modified zeroth-order Bessel function.

The Kaiser was named for Jim Kaiser, who discovered a simple approximation to the DPSS window based on Bessel functions. The Kaiser window is a very good approximation to the Digital Prolate Spheroidal Sequence, or Slepian window, which is the transform which maximizes the energy in the main lobe of the window relative to total energy.

The Kaiser can approximate other windows by varying the beta parameter. (Some literature uses alpha = beta/pi.) [4]

<table>
<thead>
<tr>
<th>beta</th>
<th>Window shape</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Rectangular</td>
</tr>
<tr>
<td>5</td>
<td>Similar to a Hamming</td>
</tr>
<tr>
<td>6</td>
<td>Similar to a Hann</td>
</tr>
<tr>
<td>8.6</td>
<td>Similar to a Blackman</td>
</tr>
</tbody>
</table>

A beta value of 14 is probably a good starting point. Note that as beta gets large, the window narrows, and so the number of samples needs to be large enough to sample the increasingly narrow spike, otherwise NaNs will be returned.

Most references to the Kaiser window come from the signal processing literature, where it is used as one of many windowing functions for smoothing values. It is also known as an apodization (which means “removing the foot”, i.e. smoothing discontinuities at the beginning and end of the sampled signal) or tapering function.

**References**

[1], [2], [3], [4]
Examples
Plot the window and its frequency response:

```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = signal.kaiser(51, beta=14)
>>> plt.plot(window)
>>> plt.title(r"Kaiser window ($\beta=14$)"")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title(r"Frequency response of the Kaiser window ($\beta=14$)"")
>>> plt.ylabel("Normalized magnitude [dB]"")
>>> plt.xlabel("Normalized frequency [cycles per sample]"")
```

![Kaiser window (β=14)](image)

scipy.signal.windows.nuttall

scipy.signal.windows.nuttall(M, sym=True)

Return a minimum 4-term Blackman-Harris window according to Nuttall.

This variation is called “Nuttall4c” by Heinzel. [2]

Parameters

- **M** [int] Number of points in the output window. If zero or less, an empty array is returned.
- **sym** [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.
Returns

\( w \)  [ndarray] The window, with the maximum value normalized to 1 (though the value 1 does not appear if \( M \) is even and \( \text{sym} \) is True).

References

[1], [2]

Examples

Plot the window and its frequency response:

```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = signal.nuttall(51)
>>> plt.plot(window)
>>> plt.title("Nuttall window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.title("Frequency response of the Nuttall window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```

**scipy.signal.windows.parzen**

\[ \text{scipy.signal.windows.parzen}(M, \text{sym}=True) \]

Return a Parzen window.
Nuttall window

Normalized magnitude [dB]

Frequency response of the Nuttall window

Normalized frequency [cycles per sample]
**Parameters**

- **M** [int] Number of points in the output window. If zero or less, an empty array is returned.
- **sym** [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

**Returns**

- **w** [ndarray] The window, with the maximum value normalized to 1 (though the value 1 does not appear if M is even and sym is True).

**References**

[1]

**Examples**

Plot the window and its frequency response:

```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = signal.parzen(51)
>>> plt.plot(window)
>>> plt.title("Parzen window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Parzen window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```

![Parzen window](image-url)
scipy.signal.windows.slepian

scipy.signal.windows.slepian(M, width, sym=True)

Return a digital Slepian (DPSS) window.

Used to maximize the energy concentration in the main lobe. Also called the digital prolate spheroidal sequence (DPSS).

Note: Deprecated in SciPy 1.1. `slepian` will be removed in a future version of SciPy, it is replaced by `dpss`, which uses the standard definition of a digital Slepian window.

Parameters

- M [int] Number of points in the output window. If zero or less, an empty array is returned.
- width [float] Bandwidth
- sym [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

Returns

- w [ndarray] The window, with the maximum value always normalized to 1

See also:

dpss

References

[1], [2]

Examples

Plot the window and its frequency response:

```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt
```
```python
>>> window = signal.slepian(51, width=0.3)
>>> plt.plot(window)
>>> plt.title("Slepian (DPSS) window (BW=0.3)"")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Slepian window (BW=0.3)"")
>>> plt.ylabel("Normalized magnitude [dB]"")
>>> plt.xlabel("Normalized frequency [cycles per sample]"")
```

**scipy.signal.windows.triang**

```python
scipy.signal.windows.triang(M, sym=True)
```

Return a triangular window.

**Parameters**

- **M** [int] Number of points in the output window. If zero or less, an empty array is returned.
- **sym** [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

**Returns**

- **w** [ndarray] The window, with the maximum value normalized to 1 (though the value 1 does not appear if M is even and sym is True).

**See also:**

- **bartlett**
A triangular window that touches zero

**Examples**

Plot the window and its frequency response:

```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = signal.triang(51)
>>> plt.plot(window)
>>> plt.title("Triangular window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")

>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the triangular window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```

**scipy.signal.windows.tukey**

`scipy.signal.windows.tukey(M, alpha=0.5, sym=True)`

Return a Tukey window, also known as a tapered cosine window.

**Parameters**

- `M` [int] Number of points in the output window. If zero or less, an empty array is returned.
Sample

0.0
0.2
0.4
0.6
0.8
1.0

Amplitude

Triangular window

Normalized frequency [cycles per sample]

0.4
0.2

Normalized magnitude [dB]

Frequency response of the triangular window

Normalized frequency [cycles per sample]

0.0 0.2 0.4

-120
-100
-80
-60
-40
-20
0

**alpha** [float, optional] Shape parameter of the Tukey window, representing the fraction of the window inside the cosine tapered region. If zero, the Tukey window is equivalent to a rectangular window. If one, the Tukey window is equivalent to a Hann window.

**sym** [bool, optional] When True (default), generates a symmetric window, for use in filter design. When False, generates a periodic window, for use in spectral analysis.

**Returns**

**w** [ndarray] The window, with the maximum value normalized to 1 (though the value 1 does not appear if \( M \) is even and \( sym \) is True).

**Examples**

Plot the window and its frequency response:

```python
>>> from scipy import signal
>>> from scipy.fftpack import fft, fftshift
>>> import matplotlib.pyplot as plt

>>> window = signal.tukey(51)
>>> plt.plot(window)
>>> plt.title("Tukey window")
>>> plt.ylabel("Amplitude")
>>> plt.xlabel("Sample")
>>> plt.ylim([0, 1.1])

>>> plt.figure()
>>> A = fft(window, 2048) / (len(window)/2.0)
>>> freq = np.linspace(-0.5, 0.5, len(A))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -120, 0])
>>> plt.title("Frequency response of the Tukey window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```

### 6.20.11 Wavelets

**cascade**(hk[, J]) Return (x, phi, psi) at dyadic points \( K/2^J \) from filter coefficients.

**daub**(p) The coefficients for the FIR low-pass filter producing Daubechies wavelets.

**morlet**(M[, w, s, complete]) Complex Morlet wavelet.

**qmf**(hk) Return high-pass qmf filter from low-pass

**ricker**(points, a) Return a Ricker wavelet, also known as the “Mexican hat wavelet”.

**cwt**(data, wavelet, widths) Continuous wavelet transform.

**scipy.signal.cascade**

`scipy.signal.cascade(hk, J=7)` Return (x, phi, psi) at dyadic points \( K/2^J \) from filter coefficients.
6.20. Signal processing (scipy.signal)

Tukey window

Frequency response of the Tukey window
Parameters

hk: [array_like] Coefficients of low-pass filter.
J: [int, optional] Values will be computed at grid points $K/2^{*}J$. Default is 7.

Returns

x: [ndarray] The dyadic points $K/2^{*}J$ for $K=0...N * (2^{*}J)-1$ where $\text{len}(hk) = \text{len}(gk) = N+1$.
phi: [ndarray] The scaling function $\phi(x)$ at $x$: $\phi(x) = \text{sum}(hk * \phi(2x-k))$, where $k$ is from 0 to $N$.
psi: [ndarray, optional] The wavelet function $\psi(x)$ at $x$: $\phi(x) = \text{sum}(gk * \phi(2x-k))$, where $k$ is from 0 to $N$. $\psi$ is only returned if $gk$ is not None.

Notes

The algorithm uses the vector cascade algorithm described by Strang and Nguyen in “Wavelets and Filter Banks”. It builds a dictionary of values and slices for quick reuse. Then inserts vectors into final vector at the end.

scipy.signal.daub

scipy.signal.daub(p)

The coefficients for the FIR low-pass filter producing Daubechies wavelets.

$p>=1$ gives the order of the zero at $f=1/2$. There are $2p$ filter coefficients.

Parameters

p: [int] Order of the zero at $f=1/2$, can have values from 1 to 34.

Returns

daub: [ndarray] Return

scipy.signal.morlet

scipy.signal.morlet(M, w=5.0, s=1.0, complete=True)

Complex Morlet wavelet.

Parameters

M: [int] Length of the wavelet.
w: [float, optional] Omega0. Default is 5
s: [float, optional] Scaling factor, windowed from $-s*2*pi$ to $+s*2*pi$. Default is 1.
complete: [bool, optional] Whether to use the complete or the standard version.

Returns

morlet: [(M,) ndarray]

See also:

scipy.signal.gausspulse

Notes

The standard version:

$$\pi^{*}-0.25 * \exp(1j*w*x) * \exp(-0.5*(x**2))$$

This commonly used wavelet is often referred to simply as the Morlet wavelet. Note that this simplified version can cause admissibility problems at low values of $w$.

The complete version:
This version has a correction term to improve admissibility. For \( w \) greater than 5, the correction term is negligible.

Note that the energy of the return wavelet is not normalised according to \( s \).

The fundamental frequency of this wavelet in Hz is given by \( f = 2s\omega r / M \) where \( r \) is the sampling rate.

Note: This function was created before \texttt{cwt} and is not compatible with it.

\begin{verbatim}
pi**-0.25 * (exp(1j*w*x) - exp(-0.5*(w**2))) * exp(-0.5*(x**2))
\end{verbatim}

\texttt{scipy.signal.qmf}

\texttt{scipy.signal.qmf(hk)}
Return high-pass qmf filter from low-pass

\textbf{Parameters}

- \texttt{hk} [array_like] Coefficients of high-pass filter.

\texttt{scipy.signal.ricker}

\texttt{scipy.signal.ricker(points, a)}
Return a Ricker wavelet, also known as the “Mexican hat wavelet”.

It models the function:

\[ A \left( 1 - \frac{x^2}{a^2} \right) \exp(-x^2/2 \ a^2), \]

where \( A = 2/\sqrt{3a} \pi^{1/4} \).

\textbf{Parameters}

- \texttt{points} [int] Number of points in \texttt{vector}. Will be centered around 0.
- \texttt{a} [scalar] Width parameter of the wavelet.

\textbf{Returns}

- \texttt{vector} [(N,) ndarray] Array of length \texttt{points} in shape of ricker curve.

\textbf{Examples}

\begin{verbatim}
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

>>> points = 100
>>> a = 4.0
>>> vec2 = signal.ricker(points, a)
>>> print(len(vec2))
100
>>> plt.plot(vec2)
>>> plt.show()
\end{verbatim}

\texttt{scipy.signal.cwt}

\texttt{scipy.signal.cwt(data, wavelet, widths)}
Continuous wavelet transform.

Performs a continuous wavelet transform on \texttt{data}, using the \texttt{wavelet} function. A CWT performs a convolution with \texttt{data} using the \texttt{wavelet} function, which is characterized by a width parameter and length parameter.
Parameters

- **data** *(N,)* ndarray: data on which to perform the transform.
- **wavelet** [function]: Wavelet function, which should take 2 arguments. The first argument is the number of points that the returned vector will have `(len(wavelet(length, width)) == length)`. The second is a width parameter, defining the size of the wavelet (e.g. standard deviation of a gaussian). See *ricker*, which satisfies these requirements.
- **widths** *(M,)* sequence: Widths to use for transform.

Returns

- **cwt**: *(M, N)* ndarray: Will have shape of `(len(widths), len(data))`.

Notes

```python
length = min(10 * width[ii], len(data))
cwt[ii, :] = signal.convolve(data, wavelet(length, width[ii]), mode='same')
```

Examples

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> t = np.linspace(-1, 1, 200, endpoint=False)
>>> sig = np.cos(2 * np.pi * 7 * t) + signal.gausspulse(t - 0.4, fc=2)
>>> widths = np.arange(1, 31)
>>> cwtmatr = signal.cwt(sig, signal.ricker, widths)
>>> plt.imshow(cwtmatr, extent=[-1, 1, 31, 1], cmap='PRGn', aspect='auto',
... vmax=abs(cwtmatr).max(), vmin=-abs(cwtmatr).max())
>>> plt.show()
```

6.20.12 Peak finding

- **argrelmin(data[, axis, order, mode])** Calculate the relative minima of `data`.
- **argrelextrema(data[, axis, order, mode])** Calculate the relative maxima of `data`. 

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**scipy.signal.argrelmin**

`scipy.signal.argrelmin(data, axis=0, order=1, mode='clip')`

Calculate the relative minima of `data`.

**Parameters**

- `data` [ndarray] Array in which to find the relative minima.
- `axis` [int, optional] Axis over which to select from `data`. Default is 0.
- `order` [int, optional] How many points on each side to use for the comparison to consider `comparator(n, n+x)` to be True.
- `mode` [str, optional] How the edges of the vector are treated. Available options are ‘wrap’ (wrap around) or ‘clip’ (treat overflow as the same as the last (or first) element). Default ‘clip’. See numpy.take

**Returns**

- `extrema` [tuple of ndarrays] Indices of the minima in arrays of integers. `extrema[k]` is the array of indices of axis `k` of `data`. Note that the return value is a tuple even when `data` is one-dimensional.

**See also:**

`argrelextrema, argrelmax, find_peaks`

**Notes**

This function uses `argrelextrema` with np.less as comparator. Therefore it requires a strict inequality on both sides of a value to consider it a minimum. This means flat minima (more than one sample wide) are not detected. In case of one-dimensional `data` `find_peaks` can be used to detect all local minima, including flat ones, by calling it with negated `data`.

New in version 0.11.0.

**Examples**

```python
>>> from scipy.signal import argrelmin
>>> x = np.array([2, 1, 2, 3, 2, 0, 1, 0])
>>> argrelmin(x)
(array([1, 5]),)
>>> y = np.array([[1, 2, 1, 2],
...               [2, 2, 0, 0],
...               [5, 3, 4, 4]])
...    ...
>>> argrelmin(y, axis=1)
(array([0], array([2, 1])))
```

**scipy.signal.argrelmax**

`scipy.signal.argrelmax(data, axis=0, order=1, mode='clip')`

Calculate the relative maxima of `data`.

**Parameters**

- `data` [ndarray] Array in which to find the relative maxima.
- `axis` [int, optional] Axis over which to select from `data`. Default is 0.
- `order` [int, optional] How many points on each side to use for the comparison to consider `comparator(n, n+x)` to be True.
- `mode` [str, optional] How the edges of the vector are treated. Available options are ‘wrap’ (wrap around) or ‘clip’ (treat overflow as the same as the last (or first) element). Default ‘clip’. See numpy.take

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data  [ndarray] Array in which to find the relative maxima.
axis  [int, optional] Axis over which to select from data. Default is 0.
order  [int, optional] How many points on each side to use for the comparison to consider
comparator(n, n+x) to be True.
mode  [str, optional] How the edges of the vector are treated. Available options are ‘wrap’
(wrap around) or ‘clip’ (treat overflow as the same as the last (or first) element). Default ‘clip’. See numpy.take.

Returns

extrema  [tuple of ndarrays] Indices of the maxima in arrays of integers. extrema[k] is the
array of indices of axis k of data. Note that the return value is a tuple even when
data is one-dimensional.

See also:

argrelextrema, argrelmin, find_peaks

Notes

This function uses argrelextrema with np.greater as comparator. Therefore it requires a strict in-
equality on both sides of a value to consider it a maximum. This means flat maxima (more than one
sample wide) are not detected. In case of one-dimensional data find_peaks can be used to detect all
local maxima, including flat ones.

New in version 0.11.0.

Examples

```python
>>> from scipy.signal import argrelmax
>>> x = np.array([2, 1, 2, 3, 2, 0, 1, 0])
>>> argrelmax(x)
(array([3, 6]),)
>>> y = np.array([[[1, 2, 1, 2],
...                [2, 2, 0, 0],
...                [5, 3, 4, 4]]])
... >>> argrelmax(y, axis=1)
(array([0]), array([1]))
```
scipy.signal.argrelextrema

`scipy.signal.argrelextrema(data, comparator, axis=0, order=1, mode='clip')`

Calculate the relative extrema of `data`.

**Parameters**

- `data` [ndarray] Array in which to find the relative extrema.
- `comparator` [callable] Function to use to compare two data points. Should take two arrays as arguments.
- `axis` [int, optional] Axis over which to select from `data`. Default is 0.
- `order` [int, optional] How many points on each side to use for the comparison to consider `comparator(n, n+x)` to be True.
- `mode` [str, optional] How the edges of the vector are treated. `‘wrap’` (wrap around) or `‘clip’` (treat overflow as the same as the last (or first) element). Default is `‘clip’`. See numpy.take.

**Returns**

- `extrema` [tuple of ndarrays] Indices of the maxima in arrays of integers. `extrema[k]` is the array of indices of axis `k` of `data`. Note that the return value is a tuple even when `data` is one-dimensional.

See also:

argrelmin, argrelmax

**Notes**

New in version 0.11.0.

**Examples**

```python
def main():
    from scipy.signal import find_peaks
    x = np.array([2, 1, 2, 3, 2, 0, 1, 0])
    peaks, props = find_peaks(x, height=1.5, height_percent=50, prominence=1)
    print(peaks, props)

if __name__ == '__main__':
    main()
```

scipy.signal.find_peaks

`scipy.signal.find_peaks(x, height=None, threshold=None, distance=None, prominence=None, width=None, wlen=None, rel_height=0.5, plateau_size=None)`

Find peaks inside a signal based on peak properties.

This function takes a one-dimensional array and finds all local maxima by simple comparison of neighbouring values. Optionally, a subset of these peaks can be selected by specifying conditions for a peak’s properties.

**Parameters**

- `x` [sequence] A signal with peaks.
- `height` [number or ndarray or sequence, optional] Required height of peaks. Either a number, `None`, an array matching `x` or a 2-element sequence of the former. The first element is always interpreted as the minimal and the second, if supplied, as the maximal required height.
threshold
[number or ndarray or sequence, optional] Required threshold of peaks, the vertical distance to its neighbouring samples. Either a number, None, an array matching x or a 2-element sequence of the former. The first element is always interpreted as the minimal and the second, if supplied, as the maximal required threshold.

distance [number, optional] Required minimal horizontal distance (>= 1) in samples between neighbouring peaks. The removal order is explained in the notes section.

prominence
[number or ndarray or sequence, optional] Required prominence of peaks. Either a number, None, an array matching x or a 2-element sequence of the former. The first element is always interpreted as the minimal and the second, if supplied, as the maximal required prominence.

width [number or ndarray or sequence, optional] Required width of peaks in samples. Either a number, None, an array matching x or a 2-element sequence of the former. The first element is always interpreted as the minimal and the second, if supplied, as the maximal required prominence.

wlen [int, optional] Used for calculation of the peaks prominences, thus it is only used if one of the arguments prominence or width is given. See argument wlen in peak_prominences for a full description of its effects.

rel_height [float, optional] Used for calculation of the peaks width, thus it is only used if width is given. See argument rel_height in peak_widths for a full description of its effects.

plateau_size [number or ndarray or sequence, optional] Required size of the flat top of peaks in samples. Either a number, None, an array matching x or a 2-element sequence of the former. The first element is always interpreted as the minimal and the second, if supplied as the maximal required plateau size.
New in version 1.2.0.

Returns

peaks [ndarray] Indices of peaks in x that satisfy all given conditions.

properties [dict] A dictionary containing properties of the returned peaks which were calculated as intermediate results during evaluation of the specified conditions:

• **peak_heights**
  If height is given, the height of each peak in x.

• **left_thresholds**, **right_thresholds**
  If threshold is given, these keys contain a peaks vertical distance to its neighbouring samples.

• **prominences**, **right_bases**, **left_bases**
  If prominence is given, these keys are accessible. See peak_prominences for a description of their content.

• **width_heights**, **left_ips**, **right_ips**
  If width is given, these keys are accessible. See peak_widths for a description of their content.

• **plateau_sizes**, **left_edges**, **right_edges**
  If plateau_size is given, these keys are accessible and contain the indices of a peak’s edges (edges are still part of the plateau) and the calculated plateau sizes.
New in version 1.2.0.

To calculate and return properties without excluding peaks, provide the open interval (None, None) as a value to the appropriate argument (excluding distance).
**Warns**

*PeakPropertyWarning*

Raised if a peak’s properties have unexpected values (see `peak_prominences` and `peak_widths`).

**Warning:** This function may return unexpected results for data containing NaNs. To avoid this, NaNs should either be removed or replaced.

See also:

- `find_peaks_cwt`  
  Find peaks using the wavelet transformation.
- `peak_prominences`  
  Directly calculate the prominence of peaks.
- `peak_widths`  
  Directly calculate the width of peaks.

Notes

In the context of this function, a peak or local maximum is defined as any sample whose two direct neighbours have a smaller amplitude. For flat peaks (more than one sample of equal amplitude wide) the index of the middle sample is returned (rounded down in case the number of samples is even). For noisy signals the peak locations can be off because the noise might change the position of local maxima. In those cases consider smoothing the signal before searching for peaks or use other peak finding and fitting methods (like `find_peaks_cwt`).

Some additional comments on specifying conditions:

- Almost all conditions (excluding `distance`) can be given as half-open or closed intervals, e.g. 1 or (1, None) defines the half-open interval [1, ∞) while (None, 1) defines the interval [−∞, 1]. The open interval (None, None) can be specified as well, which returns the matching properties without exclusion of peaks.
- The border is always included in the interval used to select valid peaks.
- For several conditions the interval borders can be specified with arrays matching `x` in shape which enables dynamic constrains based on the sample position.
- The conditions are evaluated in the following order: `plateau_size`, `height`, `threshold`, `distance`, `prominence`, `width`. In most cases this order is the fastest one because faster operations are applied first to reduce the number of peaks that need to be evaluated later.
- Satisfying the distance condition is accomplished by iterating over all peaks in descending order based on their height and removing all lower peaks that are too close.
- Use `wlen` to reduce the time it takes to evaluate the conditions for `prominence` or `width` if `x` is large or has many local maxima (see `peak_prominences`).

New in version 1.1.0.

Examples

To demonstrate this function’s usage we use a signal `x` supplied with SciPy (see `scipy.misc.electrocardiogram`). Let’s find all peaks (local maxima) in `x` whose amplitude lies above 0.
We can select peaks below 0 with `height=(None, 0)` or use arrays matching $x$ in size to reflect a changing condition for different parts of the signal.

```python
>>> border = np.sin(np.linspace(0, 3 * np.pi, x.size))
>>> peaks, _ = find_peaks(x, height=(-border, border))
>>> plt.plot(x)
>>> plt.plot(-border, "--", color="gray")
>>> plt.plot(border, ":", color="gray")
>>> plt.plot(peaks, x[peaks], "x")
>>> plt.show()
```

Another useful condition for periodic signals can be given with the `distance` argument. In this case we can easily select the positions of QRS complexes within the electrocardiogram (ECG) by demanding a distance of at least 150 samples.

```python
>>> peaks, _ = find_peaks(x, distance=150)
>>> np.diff(peaks)
array([186, 180, 177, 171, 177, 169, 167, 164, 158, 162, 172])
>>> plt.plot(x)
>>> plt.plot(peaks, x[peaks], "x")
>>> plt.show()
```

Especially for noisy signals peaks can be easily grouped by their prominence (see `peak_prominences`). E.g. we can select all peaks except for the mentioned QRS complexes by limiting the allowed prominence to 0.6.
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And finally let’s examine a different section of the ECG which contains beat forms of different shape. To select only the atypical heart beats we combine two conditions: a minimal prominence of 1 and width of at least 20 samples.

```python
>>> x = electrocardiogram()[17000:18000]
>>> peaks, properties = find_peaks(x, prominence=1, width=20)
>>> properties['prominences'], properties['widths']
(array([1.495, 2.3]), array([36.93773946, 39.32723577]))
>>> plt.plot(x)
>>> plt.plot(peaks, x[peaks], "x")
>>> plt.vlines(x=peaks, ymin=x[peaks] - properties['prominences'],
...           ymax=x[peaks], color = "C1")
>>> plt.hlines(y=properties['width_heights'], xmin=properties['left_ips'],
...           xmax=properties['right_ips'], color = "C1")
>>> plt.show()
```

**scipy.signal.find_peaks_cwt**

*scipy.signal.find_peaks_cwt(vector, widths, wavelet=None, max_distances=None, gap_thresh=None, min_length=None, min_snr=1, noise_perc=10)*

Find peaks in a 1-D array with wavelet transformation.

The general approach is to smooth `vector` by convolving it with `wavelet(width)` for each width in `widths`. Relative maxima which appear at enough length scales, and with sufficiently high SNR, are accepted.

**Parameters**

- `vector` [ndarray] 1-D array in which to find the peaks.
widths  [sequence]  1-D array of widths to use for calculating the CWT matrix. In general, this range should cover the expected width of peaks of interest.

wavelet  [callable, optional] Should take two parameters and return a 1-D array to convolve with vector. The first parameter determines the number of points of the returned wavelet array, the second parameter is the scale (width) of the wavelet. Should be normalized and symmetric. Default is the ricker wavelet.

max_distances  [ndarray, optional] At each row, a ridge line is only connected if the relative max at row[n] is within max_distances[n] from the relative max at row[n+1]. Default value is widths/4.

gap_thresh  [float, optional] If a relative maximum is not found within max_distances, there will be a gap. A ridge line is discontinued if there are more than gap_thresh points without connecting a new relative maximum. Default is the first value of the widths array i.e. widths[0].

min_length  [int, optional] Minimum length a ridge line needs to be acceptable. Default is cwt.shape[0] / 4, ie 1/4-th the number of widths.

min_snr  [float, optional] Minimum SNR ratio. Default 1. The signal is the value of the cwt matrix at the shortest length scale (cwt[0, loc]), the noise is the noise_perc’th percentile of datapoints contained within a window of window_size around cwt[0, loc].

noise_perc  [float, optional] When calculating the noise floor, percentile of data points examined below which to consider noise. Calculated using stats.scoreatpercentile. Default is 10.

Returns

peaks_indices  [ndarray] Indices of the locations in the vector where peaks were found. The list is sorted.

See also:

cwt
Continuous wavelet transform.

find_peaks

Find peaks inside a signal based on peak properties.

Notes
This approach was designed for finding sharp peaks among noisy data, however with proper parameter selection it should function well for different peak shapes.

The algorithm is as follows:

1. Perform a continuous wavelet transform on `vector`, for the supplied `widths`. This is a convolution of `vector` with `wavelet(width)` for each width in `widths`. See `cwt`
2. Identify “ridge lines” in the cwt matrix. These are relative maxima at each row, connected across adjacent rows. See `identify_ridge_lines`
3. Filter the ridge_lines using `filter_ridge_lines`.

New in version 0.11.0.

References
[1]

Examples

```python
>>> from scipy import signal
>>> xs = np.arange(0, np.pi, 0.05)
>>> data = np.sin(xs)
>>> peakind = signal.find_peaks_cwt(data, np.arange(1,10))
>>> peakind, xs[peakind], data[peakind]
([32], array([ 1.6]), array([ 0.9995736]))
```

scipy.signal.peak_prominences

**scipy.signal.peak_prominences**(*x*, *peaks*, *wlen=None*)

Calculate the prominence of each peak in a signal.

The prominence of a peak measures how much a peak stands out from the surrounding baseline of the signal and is defined as the vertical distance between the peak and its lowest contour line.

**Parameters**

- **x** : [sequence] A signal with peaks.
- **peaks** : [sequence] Indices of peaks in `x`.
- **wlen** : [int, optional] A window length in samples that optionally limits the evaluated area for each peak to a subset of `x`. The peak is always placed in the middle of the window therefore the given length is rounded up to the next odd integer. This parameter can speed up the calculation (see Notes).

**Returns**

- **prominences** : [ndarray] The calculated prominences for each peak in `peaks`.
- **left_bases, right_bases** : [ndarray] The peaks’ bases as indices in `x` to the left and right of each peak. The higher base of each pair is a peak’s lowest contour line.

**Raises**
ValueError

If a value in `peaks` is an invalid index for `x`.

Warns

PeakPropertyWarning

For indices in `peaks` that don’t point to valid local maxima in `x` the returned prominence will be 0 and this warning is raised. This also happens if `wlen` is smaller than the plateau size of a peak.

Warning: This function may return unexpected results for data containing NaNs. To avoid this, NaNs should either be removed or replaced.

See also:

`find_peaks`

Find peaks inside a signal based on peak properties.

`peak_widths`

Calculate the width of peaks.

Notes

Strategy to compute a peak’s prominence:

1. Extend a horizontal line from the current peak to the left and right until the line either reaches the window border (see `wlen`) or intersects the signal again at the slope of a higher peak. An intersection with a peak of the same height is ignored.

2. On each side find the minimal signal value within the interval defined above. These points are the peak’s bases.

3. The higher one of the two bases marks the peak’s lowest contour line. The prominence can then be calculated as the vertical difference between the peaks height itself and its lowest contour line.

Searching for the peak’s bases can be slow for large `x` with periodic behavior because large chunks or even the full signal need to be evaluated for the first algorithmic step. This evaluation area can be limited with the parameter `wlen` which restricts the algorithm to a window around the current peak and can shorten the calculation time if the window length is short in relation to `x`. However this may stop the algorithm from finding the true global contour line if the peak’s true bases are outside this window. Instead a higher contour line is found within the restricted window leading to a smaller calculated prominence. In practice this is only relevant for the highest set of peaks in `x`. This behavior may even be used intentionally to calculate “local” prominences.

New in version 1.1.0.

References

[1]

Examples

```python
>>> from scipy.signal import find_peaks, peak_prominences
>>> import matplotlib.pyplot as plt

Create a test signal with two overlayed harmonics

```
Find all peaks and calculate prominences

```python
>>> peaks, _ = find_peaks(x)
>>> prominences = peak_prominences(x, peaks)[0]
>>> prominences
array([1.24159486, 0.47840168, 0.28470524, 3.10716793, 0.284603 , 0.47822491, 2.48340261, 0.47822491])
```

Calculate the height of each peak’s contour line and plot the results

```python
>>> contour_heights = x[peaks] - prominences
>>> plt.plot(x)
>>> plt.plot(peaks, x[peaks], "x")
>>> plt.vlines(x=peaks, ymin=contour_heights, ymax=x[peaks])
>>> plt.show()
```

Let’s evaluate a second example that demonstrates several edge cases for one peak at index 5.

```python
>>> x = np.array([0, 1, 0, 3, 1, 3, 0, 4, 0])
>>> peaks = np.array([5])
>>> plt.plot(x)
>>> plt.plot(peaks, x[peaks], "x")
>>> plt.show()
```

```python
>>> peak_prominences(x, peaks)  # -> (prominences, left_bases, right_bases)
(array([3.]), array([4]), array([6]))
```

Note how the peak at index 3 of the same height is not considered as a border while searching for the left base. Instead two minima at 0 and 2 are found in which case the one closer to the evaluated peak is always chosen. On the right side however the base must be placed at 6 because the higher peak represents the right border to the evaluated area.

```python
>>> peak_prominences(x, peaks, wlen=3.1)
(array([2.]), array([4]), array([6]))
```
Here we restricted the algorithm to a window from 3 to 7 (the length is 5 samples because \textit{wlen} was rounded up to the next odd integer). Thus the only two candidates in the evaluated area are the two neighbouring samples and a smaller prominence is calculated.

\texttt{scipy.signal.peak_widths}

\texttt{scipy.signal.peak_widths(x, peaks, rel\_height=0.5, prominence\_data=None, wlen=None)}

Calculate the width of each peak in a signal.

This function calculates the width of a peak in samples at a relative distance to the peak’s height and prominence.

\textbf{Parameters}

\begin{itemize}
  \item \texttt{x} [sequence] A signal with peaks.
  \item \texttt{peaks} [sequence] Indices of peaks in \texttt{x}.
  \item \texttt{rel\_height} [float, optional] Chooses the relative height at which the peak width is measured as a percentage of its prominence. 1.0 calculates the width of the peak at its lowest contour line while 0.5 evaluates at half the prominence height. Must be at least 0. See notes for further explanation.
  \item \texttt{prominence\_data} [tuple, optional] A tuple of three arrays matching the output of \texttt{peak\_prominences} when called with the same arguments \texttt{x} and \texttt{peaks}. This data is calculated internally if not provided.
  \item \texttt{wlen} [int, optional] A window length in samples passed to \texttt{peak\_prominences} as an optional argument for internal calculation of \texttt{prominence\_data}. This argument is ignored if \texttt{prominence\_data} is given.
\end{itemize}

\textbf{Returns}

\begin{itemize}
  \item \texttt{widths} [ndarray] The widths for each peak in samples.
  \item \texttt{width\_heights} [ndarray] The height of the contour lines at which the \texttt{widths} where evaluated.
  \item \texttt{left\_ips, right\_ips} [ndarray] Interpolated positions of left and right intersection points of a horizontal line at the respective evaluation height.
\end{itemize}
Raises

ValueError

If prominence_data is supplied but doesn’t satisfy the condition 0 <= left_base <= peak <= right_base < x.shape[0] for each peak, has the wrong dtype, is not C-contiguous or does not have the same shape.

Warns

PeakPropertyWarning

Raised if any calculated width is 0. This may stem from the supplied prominence_data or if rel_height is set to 0.

Warning: This function may return unexpected results for data containing NaNs. To avoid this, NaNs should either be removed or replaced.

See also:

find_peaks

Find peaks inside a signal based on peak properties.

peak_prominences

Calculate the prominence of peaks.

Notes

The basic algorithm to calculate a peak’s width is as follows:

- Calculate the evaluation height \( h_{\text{eval}} \) with the formula \( h_{\text{eval}} = h_{\text{Peak}} - P \cdot R \), where \( h_{\text{Peak}} \) is the height of the peak itself, \( P \) is the peak’s prominence and \( R \) a positive ratio specified with the argument rel_height.

- Draw a horizontal line at the evaluation height to both sides, starting at the peak’s current vertical position until the lines either intersect a slope, the signal border or cross the vertical position of the peak’s base (see peak_prominences for an definition). For the first case, intersection with the signal, the true intersection point is estimated with linear interpolation.

- Calculate the width as the horizontal distance between the chosen endpoints on both sides. As a consequence of this the maximal possible width for each peak is the horizontal distance between its bases.

As shown above to calculate a peak’s width its prominence and bases must be known. You can supply these yourself with the argument prominence_data. Otherwise they are internally calculated (see peak_prominences).

New in version 1.1.0.

Examples

```python
>>> from scipy.signal import chirp, find_peaks, peak_widths
>>> import matplotlib.pyplot as plt

Create a test signal with two overlayed harmonics

```python
>>> x = np.linspace(0, 6 * np.pi, 1000)
>>> x = np.sin(x) + 0.6 * np.sin(2.6 * x)

Find all peaks and calculate their widths at the relative height of 0.5 (contour line at half the prominence height) and 1 (at the lowest contour line at full prominence height).
```
>>> peaks, _ = find_peaks(x)
>>> results_half = peak_widths(x, peaks, rel_height=0.5)
>>> results_half[0]  # widths
array([ 64.25172825,  41.29465463,  35.46943289, 104.71586081,
       35.46729324,  41.30429622, 181.93835853,  45.37078546])

Plot signal, peaks and contour lines at which the widths were calculated

```python
>>> plt.plot(x)
>>> plt.plot(peaks, x[peaks], "x")
>>> plt.hlines(*results_half[1:], color="C2")
>>> plt.hlines(*results_full[1:], color="C3")
>>> plt.show()
```

6.20.13 Spectral Analysis

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<td><code>csd(x, y, fs, window, nperseg, noverlap, ...)</code></td>
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<td>Check whether the Nonzero Overlap Add (NOLA) constraint is met.</td>
</tr>
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**scipy.signal.periodogram**

Estimate power spectral density using a periodogram.

**Parameters**

- **x** [array_like] Time series of measurement values
- **fs** [float, optional] Sampling frequency of the x time series. Defaults to 1.0.
- **window** [str or tuple or array_like, optional] Desired window to use. If window is a string or tuple, it is passed to `get_window` to generate the window values, which are DFT-even by default. See `get_window` for a list of windows and required parameters. If window is array_like it will be used directly as the window and its length must be nperseg. Defaults to ‘boxcar’.
- **nfft** [int, optional] Length of the FFT used. If None the length of x will be used.
- **detrend** [str or function or False, optional] Specifies how to detrend each segment. If detrend is a string, it is passed as the type argument to the detrend function. If it is a function, it takes a segment and returns a detrended segment. If detrend is False, no detrending is done. Defaults to ‘constant’.
- **return_onesided** [bool, optional] If True, return a one-sided spectrum for real data. If False return a two-sided spectrum. Note that for complex data, a two-sided spectrum is always returned.
- **scaling** [{‘density’, ‘spectrum’}, optional] Selects between computing the power spectral density (‘density’) where Pxx has units of V**2/Hz and computing the power spectrum (‘spectrum’) where Pxx has units of V**2, if x is measured in V and fs is measured in Hz. Defaults to ‘density’.
- **axis** [int, optional] Axis along which the periodogram is computed; the default is over the last axis (i.e. axis=-1).

**Returns**

- **f** [ndarray] Array of sample frequencies.
- **Pxx** [ndarray] Power spectral density or power spectrum of x.

**See also:**

- **welch**
  Estimate power spectral density using Welch’s method
- **lombscargle**
  Lomb-Scargle periodogram for unevenly sampled data
Notes
New in version 0.12.0.

Examples

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> np.random.seed(1234)

Generate a test signal, a 2 Vrms sine wave at 1234 Hz, corrupted by 0.001 V**2/Hz of white noise sampled at 10 kHz.

```python
>>> fs = 10e3
>>> N = 1e5
>>> amp = 2*np.sqrt(2)
>>> freq = 1234.0
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> x = amp*np.sin(2*np.pi*freq*time)
>>> x += np.random.normal(scale=np.sqrt(noise_power), size=time.shape)
```

Compute and plot the power spectral density.

```python
>>> f, Pxx_den = signal.periodogram(x, fs)
>>> plt.semilogy(f, Pxx_den)
>>> plt.ylim([1e-7, 1e2])
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('PSD [V**2/Hz]')
>>> plt.show()
```

If we average the last half of the spectral density, to exclude the peak, we can recover the noise power on the signal.

```python
>>> np.mean(Pxx_den[25000:])
0.00099728892368242854
```

Now compute and plot the power spectrum.
```python
>>> f, Pxx_spec = signal.periodogram(x, fs, 'flattop', scaling='spectrum')
>>> plt.figure()
>>> plt.semilogy(f, np.sqrt(Pxx_spec))
>>> plt.xlim([1e-4, 1e1])
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('Linear spectrum [V RMS]')
>>> plt.show()
```

The peak height in the power spectrum is an estimate of the RMS amplitude.

```python
>>> np.sqrt(Pxx_spec.max())
2.0077340678640727
```

### scipy.signal.welch

`scipy.signal.welch(x, fs=1.0, window='hann', nperseg=None, noverlap=None, nfft=None, detrend='constant', return_onesided=True, scaling='density', axis=-1, average='mean')`

Estimate power spectral density using Welch’s method.

Welch’s method \(^1\) computes an estimate of the power spectral density by dividing the data into overlapping segments, computing a modified periodogram for each segment and averaging the periodograms.

**Parameters**

- **x** [array_like] Time series of measurement values
- **fs** [float, optional] Sampling frequency of the `x` time series. Defaults to 1.0.
- **window** [str or tuple or array_like, optional] Desired window to use. If `window` is a string or tuple, it is passed to `get_window` to generate the window values, which are DFT-even by default. See `get_window` for a list of windows and required parameters. If `window` is array_like it will be used directly as the window and its length must be `nperseg`. Defaults to a Hann window.
- **nperseg** [int, optional] Length of each segment. Defaults to None, but if `window` is str or tuple, is set to 256, and if `window` is array_like, is set to the length of the window.
noverlap [int, optional] Number of points to overlap between segments. If None, noverlap = nperseg // 2. Defaults to None.

nfft [int, optional] Length of the FFT used, if a zero padded FFT is desired. If None, the FFT length is nperseg. Defaults to None.

detrend [str or function or False, optional] Specifies how to detrend each segment. If detrend is a string, it is passed as the type argument to the detrend function. If it is a function, it takes a segment and returns a detrended segment. If detrend is False, no detrending is done. Defaults to ‘constant’.

return_onesided [bool, optional] If True, return a one-sided spectrum for real data. If False return a two-sided spectrum. Note that for complex data, a two-sided spectrum is always returned.

scaling [{‘density’, ‘spectrum’}, optional] Selects between computing the power spectral density (‘density’) where \( P_{xx} \) has units of V**2/Hz and computing the power spectrum (‘spectrum’) where \( P_{xx} \) has units of V**2, if \( x \) is measured in V and \( f_s \) is measured in Hz. Defaults to ‘density’.

axis [int, optional] Axis along which the periodogram is computed; the default is over the last axis (i.e. axis=-1).

average [{‘mean’, ‘median’}, optional] Method to use when averaging periodograms. Defaults to ‘mean’.

New in version 1.2.0.

Returns

- Pxx [ndarray] Power spectral density or power spectrum of x.

See also:

- periodogram
- Lomb-Scargle periodogram for unevenly sampled data

Notes

An appropriate amount of overlap will depend on the choice of window and on your requirements. For the default Hann window an overlap of 50% is a reasonable trade off between accurately estimating the signal power, while not over counting any of the data. Narrower windows may require a larger overlap.

If noverlap is 0, this method is equivalent to Bartlett’s method [2].

New in version 0.12.0.

References

[1], [2]

Examples

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> np.random.seed(1234)
```

Generate a test signal, a 2 Vrms sine wave at 1234 Hz, corrupted by 0.001 V**2/Hz of white noise sampled at 10 kHz.
```python
>>> fs = 10e3
>>> N = 1e5
>>> amp = 2*np.sqrt(2)
>>> freq = 1234.0
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> x = amp*np.sin(2*np.pi*freq*time)
>>> x += np.random.normal(scale=np.sqrt(noise_power), size=time.shape)
```

Compute and plot the power spectral density.

```python
>>> f, Pxx_den = signal.welch(x, fs, nperseg=1024)
>>> plt.semilogy(f, Pxx_den)
>>> plt.ylim([0.5e-3, 1])
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('PSD [V**2/Hz]')
>>> plt.show()
```

If we average the last half of the spectral density, to exclude the peak, we can recover the noise power on the signal.

```python
>>> np.mean(Pxx_den[256:])
0.0009924865443739191
```

Now compute and plot the power spectrum.

```python
>>> f, Pxx_spec = signal.welch(x, fs, 'flattop', 1024, scaling='spectrum')
>>> plt.figure()
>>> plt.semilogy(f, np.sqrt(Pxx_spec))
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('Linear spectrum [V RMS]')
>>> plt.show()
```

The peak height in the power spectrum is an estimate of the RMS amplitude.
>>> np.sqrt(Pxx_spec.max())
2.0077340678640727

If we now introduce a discontinuity in the signal, by increasing the amplitude of a small portion of the signal by 50, we can see the corruption of the mean average power spectral density, but using a median average better estimates the normal behaviour.

```python
>>> f, Pxx_den = signal.welch(x, fs, nperseg=1024)
>>> f_med, Pxx_den_med = signal.welch(x, fs, nperseg=1024, average='median')
>>> plt.semilogy(f, Pxx_den, label='mean')
>>> plt.semilogy(f_med, Pxx_den_med, label='median')
>>> plt.ylim([0.5e-3, 1])
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('PSD [V**2/Hz]')
>>> plt.legend()
>>> plt.show()
```

**scipy.signal.csd**

Estimate the cross power spectral density, $P_{xy}$, using Welch’s method.

```python
scipy.signal.csd(x, y, fs=1.0, window='hann', nperseg=None, noverlap=None, nfft=None,
                   detrend='constant', return_onesided=True, scaling='density', axis=-1,
                   average='mean')
```

Estimate the cross power spectral density, $P_{xy}$, using Welch’s method.

**Parameters**

- **x** : [array_like] Time series of measurement values
- **y** : [array_like] Time series of measurement values
- **fs** : [float, optional] Sampling frequency of the $x$ and $y$ time series. Defaults to 1.0.
- **window** : [str or tuple or array_like, optional] Desired window to use. If `window` is a string or tuple, it is passed to `get_window` to generate the window values, which are DFT-even by default. See `get_window` for a list of windows and required parameters. If `window` is array_like it will be used directly as the window and its length must be nperseg. Defaults to a Hann window.

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npseg  [int, optional] Length of each segment. Defaults to None, but if window is str or
tuple, is set to 256, and if window is array_like, is set to the length of the window.

noverlap: int, optional
Number of points to overlap between segments. If None, overlap = npseg //
2. Defaults to None.

nfft  [int, optional] Length of the FFT used, if a zero padded FFT is desired. If None,
the FFT length is npseg. Defaults to None.

detrend  [str or function or False, optional] Specifies how to detrend each segment. If
detrend is a string, it is passed as the type argument to the detrend function.
If it is a function, it takes a segment and returns a detrended segment. If detrend
is False, no detrending is done. Defaults to 'constant'.

return_onesided
[bool, optional] If True, return a one-sided spectrum for real data. If False return
a two-sided spectrum. Note that for complex data, a two-sided spectrum is always
returned.

scaling  [{‘density’, ‘spectrum’}, optional] Selects between computing the cross spectral
density (‘density’) where \( \text{Pxy} \) has units of \( \text{V}^2/\text{Hz} \) and computing the cross spec-
trum (‘spectrum’) where \( \text{Pxy} \) has units of \( \text{V}^2 \), if x and y are measured in V and
fs is measured in Hz. Defaults to ‘density’

axis  [int, optional] Axis along which the CSD is computed for both inputs; the default
is over the last axis (i.e. axis=-1).

average  [{‘mean’, ‘median’}, optional] Method to use when averaging periodograms. De-
defaults to ‘mean’.
New in version 1.2.0.

Returns
f  [ndarray] Array of sample frequencies.
Pxy  [ndarray] Cross spectral density or cross power spectrum of x,y.

See also:

periodogram
Simple, optionally modified periodogram
lombscargle

Lomb-Scargle periodogram for unevenly sampled data

welch

Power spectral density by Welch’s method. [Equivalent to csd(x,x)]

coherence

Magnitude squared coherence by Welch’s method.

Notes

By convention, Pxy is computed with the conjugate FFT of X multiplied by the FFT of Y.

If the input series differ in length, the shorter series will be zero-padded to match.

An appropriate amount of overlap will depend on the choice of window and on your requirements. For
the default Hann window an overlap of 50% is a reasonable trade off between accurately estimating the
signal power, while not over counting any of the data. Narrower windows may require a larger overlap.

New in version 0.16.0.

References

[1], [2]

Examples

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

Generate two test signals with some common features.

```n
```python
>>> fs = 10e3
>>> N = 1e5
>>> amp = 20
>>> freq = 1234.0
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> b, a = signal.butter(2, 0.25, 'low')
>>> x = np.random.normal(scale=np.sqrt(noise_power), size=time.shape)
>>> y = signal.lfilter(b, a, x)
>>> x += amp*np.sin(2*np.pi*freq*time)
>>> y += np.random.normal(scale=0.1*np.sqrt(noise_power), size=time.shape)
```

Compute and plot the magnitude of the cross spectral density.

```python
>>> f, Pxy = signal.csd(x, y, fs, nperseg=1024)
>>> plt.semilogy(f, np.abs(Pxy))
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('CSD [V**2/Hz]')
>>> plt.show()
```

scipy.signal.coherence

Estimate the magnitude squared coherence estimate, Cxy, of discrete-time signals X and Y using
Welch’s method.
\[ C_{xy} = \frac{\text{abs}(P_{xy})^2}{P_{xx}P_{yy}} \], where \( P_{xx} \) and \( P_{yy} \) are power spectral density estimates of \( X \) and \( Y \), and \( P_{xy} \) is the cross spectral density estimate of \( X \) and \( Y \).

**Parameters**

- **x** [array_like] Time series of measurement values
- **y** [array_like] Time series of measurement values
- **fs** [float, optional] Sampling frequency of the \( x \) and \( y \) time series. Defaults to 1.0.
- **window** [str or tuple or array_like, optional] Desired window to use. If `window` is a string or tuple, it is passed to `get_window` to generate the window values, which are DFT-even by default. See `get_window` for a list of windows and required parameters. If `window` is array_like it will be used directly as the window and its length must be `nperseg`. Defaults to a Hann window.
- **nperseg** [int, optional] Length of each segment. Defaults to None, but if window is str or tuple, is set to 256, and if window is array_like, is set to the length of the window.
- **noverlap** [int, optional] Number of points to overlap between segments. If `None`, `noverlap = nperseg // 2`. Defaults to `None`.
- **nfft** [int, optional] Length of the FFT used, if a zero padded FFT is desired. If `None`, the FFT length is `nperseg`. Defaults to `None`.
- **detrend** [str or function or `False`, optional] Specifies how to detrend each segment. If `detrend` is a string, it is passed as the `type` argument to the `detrend` function. If it is a function, it takes a segment and returns a detrended segment. If `detrend` is `False`, no detrending is done. Defaults to ‘constant’.
- **axis** [int, optional] Axis along which the coherence is computed for both inputs; the default is over the last axis (i.e. `axis=-1`).

**Returns**

- **f** [ndarray] Array of sample frequencies.
- **Cxy** [ndarray] Magnitude squared coherence of \( x \) and \( y \).

**See also:**

- `periodogram`
  
  Simple, optionally modified periodogram
lombscargle
Lomb-Scargle periodogram for unevenly sampled data
welch
Power spectral density by Welch’s method.
csd
Cross spectral density by Welch’s method.

Notes
An appropriate amount of overlap will depend on the choice of window and on your requirements. For
the default Hann window an overlap of 50% is a reasonable trade off between accurately estimating the
signal power, while not over counting any of the data. Narrower windows may require a larger overlap.

New in version 0.16.0.

References
[1], [2]

Examples

```python
from scipy import signal
import matplotlib.pyplot as plt

Generate two test signals with some common features.

```>``` print(' from scipy import signal
>>> import matplotlib.pyplot as plt

```>``` print('Generate two test signals with some common features.
```>``` print('>>> fs = 10e3
>>> N = 1e5
>>> amp = 20
>>> freq = 1234.0
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> b, a = signal.butter(2, 0.25, 'low')
>>> x = np.random.normal(scale=np.sqrt(noise_power), size=time.shape)
>>> y = signal.lfilter(b, a, x)
>>> x += amp*np.sin(2*np.pi*freq*time)
>>> y += np.random.normal(scale=0.1*np.sqrt(noise_power), size=time.shape)

Compute and plot the coherence.

```>``` print('Compute and plot the coherence.
```>``` print('>>> f, Cxy = signal.coherence(x, y, fs, nperseg=1024)
>>> plt.semilogy(f, Cxy)
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('Coherence')
>>> plt.show()

scipy.signal.spectrogram
scipy.signal.spectrogram(x, fs=1.0, window=('tukey', 0.25), nperseg=None, noverlap=None, nfft=None, detrend='constant', return_onesided=True, scaling='density', axis=-1, mode='psd')

Compute a spectrogram with consecutive Fourier transforms.

Spectrograms can be used as a way of visualizing the change of a nonstationary signal’s frequency
content over time.

Parameters
x \ [array_like] \ Time \ series \ of \ measurement \ values
fs \ [float, \ optional] \ Sampling \ frequency \ of \ the \ x \ time \ series. \ Defaults \ to 1.0.
window \ [str \ or \ tuple \ or \ array_like, \ optional] \ Desired \ window \ to \ use. \ If \ window \ is \ a \ string \ or \ tuple, \ it \ is \ passed \ to \ get_window \ to \ generate \ the \ window \ values, \ which \ are \ DFT-even \ by \ default. \ See \ get_window \ for \ a \ list \ of \ windows \ and \ required \ parameters. \ If \ window \ is \ array_like \ it \ will \ be \ used \ directly \ as \ the \ window \ and \ its \ length \ must \ be \ nperseg. \ Defaults \ to \ a \ Tukey \ window \ with \ shape \ parameter \ of 0.25.
nperseg \ [int, \ optional] \ Length \ of \ each \ segment. \ Defaults \ to None, \ but \ if \ window \ is \ str \ or \ tuple, \ is \ set \ to 256, \ and \ if \ window \ is \ array_like, \ is \ set \ to \ the \ length \ of \ the \ window.
noverlap \ [int, \ optional] \ Number \ of \ points \ to \ overlap \ between \ segments. \ If \ None, nooverlap = nperseg // 8. \ Defaults \ to None.
nfft \ [int, \ optional] \ Length \ of \ the \ FFT \ used, \ if \ a \ zero \ padded \ FFT \ is \ desired. \ If \ None, \ the \ FFT \ length \ is nperseg. \ Defaults \ to None.
detrend \ [str \ or \ function \ or \ False, \ optional] \ Specifies \ how \ to \ detrend \ each \ segment. \ If \ detrend \ is \ a \ string, \ it \ is \ passed \ as \ the \ type \ argument \ to \ the \ detrend \ function. \ If \ it \ is \ a \ function, \ it \ takes \ a \ segment \ and \ returns \ a \ detrended \ segment. \ If \ detrend \ is False, \ no \ detrending \ is \ done. \ Defaults \ to \ ‘constant’.
return_onestided \ [bool, \ optional] \ If True, \ return \ a \ one-sided \ spectrum \ for \ real \ data. \ If False \ return \ a \ two-sided \ spectrum. \ Note \ that \ for \ complex \ data, \ a \ two-sided \ spectrum \ is \ always \ returned.
scaling \ [{‘density’, ‘spectrum’}, \ optional] \ Selects \ between \ computing \ the \ power \ spectral \ density \ (‘density’) \ where \ Sxx \ has \ units \ of \ V^2/Hz \ and \ computing \ the \ power \ spectrum \ (‘spectrum’) \ where \ Sxx \ has \ units \ of \ V^2, \ if \ x \ is \ measured \ in \ V \ and \ fs \ is \ measured \ in \ Hz. \ Defaults \ to \ ‘density’.
axis \ [int, \ optional] \ Axis \ along \ which \ the \ spectrogram \ is \ computed; \ the \ default \ is \ over \ the \ last \ axis \ (i.e. axis=-1).
mode \ [str, \ optional] \ Defines \ what \ kind \ of \ return \ values \ are \ expected. \ Options \ are \ [‘psd’, ‘complex’, ‘magnitude’, ‘angle’, ‘phase’]. \ ‘complex’ is equivalent to the output of stft with no padding or boundary extension. ‘magnitude’ returns the absolute magnitude of the STFT. ‘angle’ and ‘phase’ return the complex angle of the STFT, with and without unwrapping, respectively.

Returns
SciPy Reference Guide, Release 1.2.0

`f`  [ndarray] Array of sample frequencies.
`t`  [ndarray] Array of segment times.
`Sxx`  [ndarray] Spectrogram of x. By default, the last axis of Sxx corresponds to the segment times.

**See also:**

*periodogram*

Simple, optionally modified periodogram

*lombscargle*

Lomb-Scargle periodogram for unevenly sampled data

*welch*

Power spectral density by Welch’s method.

*csd*

Cross spectral density by Welch’s method.

**Notes**

An appropriate amount of overlap will depend on the choice of window and on your requirements. In contrast to Welch’s method, where the entire data stream is averaged over, one may wish to use a smaller overlap (or perhaps none at all) when computing a spectrogram, to maintain some statistical independence between individual segments. It is for this reason that the default window is a Tukey window with 1/8th of a window’s length overlap at each end.

New in version 0.16.0.

**References**

[1]

**Examples**

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

Generate a test signal, a 2 Vrms sine wave whose frequency is slowly modulated around 3kHz, corrupted by white noise of exponentially decreasing magnitude sampled at 10 kHz.

```python
>>> fs = 10e3
>>> N = 1e5
>>> amp = 2 * np.sqrt(2)
>>> noise_power = 0.01 * fs / 2
>>> time = np.arange(N) / float(fs)
>>> mod = 500*np.cos(2*np.pi*0.25*time)
>>> carrier = amp * np.sin(2*np.pi*3e3*time + mod)
>>> noise = np.random.normal(scale=np.sqrt(noise_power), size=time.shape)
>>> noise *= np.exp(-time/5)
>>> x = carrier + noise
```

Compute and plot the spectrogram.

```python
>>> f, t, Sxx = signal.spectrogram(x, fs)
>>> plt.pcolormesh(t, f, Sxx)
>>> plt.ylabel('Frequency [Hz]')
>>> plt.xlabel('Time [sec]')
>>> plt.show()
```
Note, if using output that is not one sided, then use the following:

```python
>>> f, t, Sxx = signal.spectrogram(x, fs, return_onesided=False)
>>> plt.pcolormesh(t, np.fft.fftshift(f), np.fft.fftshift(Sxx, axes=0))
>>> plt.ylabel('Frequency [Hz]')
>>> plt.xlabel('Time [sec]')
>>> plt.show()
```

**scipy.signal.lombscargle**

`scipy.signal.lombscargle(x, y, freqs)`

Computes the Lomb-Scargle periodogram.

The Lomb-Scargle periodogram was developed by Lomb [1] and further extended by Scargle [2] to find, and test the significance of weak periodic signals with uneven temporal sampling.
When `normalize` is False (default) the computed periodogram is unnormalized, it takes the value \((A^2) \times \frac{N}{4}\) for a harmonic signal with amplitude \(A\) for sufficiently large \(N\).

When `normalize` is True the computed periodogram is normalized by the residuals of the data around a constant reference model (at zero).

Input arrays should be one-dimensional and will be cast to float64.

**Parameters**

- **x** [array_like] Sample times.
- **y** [array_like] Measurement values.
- **freqs** [array_like] Angular frequencies for output periodogram.
- **precenter** [bool, optional] Pre-center amplitudes by subtracting the mean.
- **normalize** [bool, optional] Compute normalized periodogram.

**Returns**

- **pgram** [array_like] Lomb-Scargle periodogram.

**Raises**

- **ValueError**
  
  If the input arrays \(x\) and \(y\) do not have the same shape.

**See also:**

- **istft**
  
  Inverse Short Time Fourier Transform

- **check_COLA**

  Check whether the Constant OverLap Add (COLA) constraint is met

- **welch**

  Power spectral density by Welch’s method

- **spectrogram**

  Spectrogram by Welch’s method

- **csd**

  Cross spectral density by Welch’s method

**Notes**

This subroutine calculates the periodogram using a slightly modified algorithm due to Townsend [3] which allows the periodogram to be calculated using only a single pass through the input arrays for each frequency.

The algorithm running time scales roughly as \(O(x \times freqs)\) or \(O(N^{-2})\) for a large number of samples and frequencies.

**References**

[1], [2], [3]
Examples

```python
>>> import matplotlib.pyplot as plt

First define some input parameters for the signal:

```python
>>> A = 2.
>>> w = 1.
>>> phi = 0.5 * np.pi
>>> nin = 1000
>>> nout = 10000
>>> frac_points = 0.9 # Fraction of points to select
```

Randomly select a fraction of an array with timesteps:

```python
>>> r = np.random.rand(nin)
>>> x = np.linspace(0.01, 10*np.pi, nin)
>>> x = x[r > frac_points]
```

Plot a sine wave for the selected times:

```python
>>> y = A * np.sin(w*x+phi)
```

Define the array of frequencies for which to compute the periodogram:

```python
>>> f = np.linspace(0.01, 10, nout)
```

Calculate Lomb-Scargle periodogram:

```python
>>> import scipy.signal as signal
>>> pgram = signal.lombscargle(x, y, f, normalize=True)
```

Now make a plot of the input data:

```python
>>> plt.subplot(2, 1, 1)
>>> plt.plot(x, y, 'b+)
```

Then plot the normalized periodogram:

```python
>>> plt.subplot(2, 1, 2)
>>> plt.plot(f, pgram)
>>> plt.show()
```

### scipy.signal.vectorstrength

`scipy.signal.vectorstrength(events, period)`

Determine the vector strength of the events corresponding to the given period.

The vector strength is a measure of phase synchrony, how well the timing of the events is synchronized to a single period of a periodic signal.

If multiple periods are used, calculate the vector strength of each. This is called the “resonating vector strength”.

**Parameters**

- **events** [1D array_like] An array of time points containing the timing of the events.
period [float or array_like] The period of the signal that the events should synchronize to. The period is in the same units as events. It can also be an array of periods, in which case the outputs are arrays of the same length.

Returns

strength [float or 1D array] The strength of the synchronization. 1.0 is perfect synchronization and 0.0 is no synchronization. If period is an array, this is also an array with each element containing the vector strength at the corresponding period.

phase [float or array] The phase that the events are most strongly synchronized to in radians. If period is an array, this is also an array with each element containing the phase for the corresponding period.

References


scipy.signal.stft

scipy.signal.stft(x, fs=1.0, window='hann', nperseg=256, noverlap=None, nfft=None, detrend=False, return_onesided=True, boundary='zeros', padded=True, axis=-1)  
Compute the Short Time Fourier Transform (STFT).

STFTs can be used as a way of quantifying the change of a nonstationary signal’s frequency and phase content over time.

Parameters
x [array_like] Time series of measurement values
fs [float, optional] Sampling frequency of the x time series. Defaults to 1.0.
window [str or tuple or array_like, optional] Desired window to use. If window is a string or
tuple, it is passed to get_window to generate the window values, which are DFT-
even by default. See get_window for a list of windows and required parameters. If
window is array_like it will be used directly as the window and its length must be
nperseg. Defaults to a Hann window.
nperseg [int, optional] Length of each segment. Defaults to 256.
noverlap [int, optional] Number of points to overlap between segments. If None, noverlap
= nperseg // 2. Defaults to None. When specified, the COLA constraint must
be met (see Notes below).
nfft [int, optional] Length of the FFT used, if a zero padded FFT is desired. If None,
the FFT length is nperseg. Defaults to None.
detrend [str or function or False, optional] Specifies how to detrend each segment. If
detrend is a string, it is passed as the type argument to the detrend function.
If it is a function, it takes a segment and returns a detrended segment. If detrend
is False, no detrending is done. Defaults to False.
return_onesided [bool, optional] If True, return a one-sided spectrum for real data. If False return
a two-sided spectrum. Note that for complex data, a two-sided spectrum is always
returned. Defaults to True.
boundary [str or None, optional] Specifies whether the input signal is extended at both ends,
and how to generate the new values, in order to center the first windowed segment
on the first input point. This has the benefit of enabling reconstruction of the first
input point when the employed window function starts at zero. Valid options are
[’even’, ’odd’, ’constant’, ’zeros’, None]. Defaults to ’zeros’, for zero
padding extension. I.e. [1, 2, 3, 4] is extended to [0, 1, 2, 3, 4, 0] for
nperseg=3.
padded [bool, optional] Specifies whether the input signal is zero-padded at the end to
make the signal fit exactly into an integer number of window segments, so that
all of the signal is included in the output. Defaults to True. Padding occurs after
boundary extension, if boundary is not None, and padded is True, as is the default.
axis [int, optional] Axis along which the STFT is computed; the default is over the last
axis (i.e. axis=-1).

Returns
f [ndarray] Array of sample frequencies.
t [ndarray] Array of segment times.
Zxx [ndarray] STFT of x. By default, the last axis of Zxx corresponds to the segment
times.

See also:

istft
Inverse Short Time Fourier Transform

cHECK COLA
Check whether the Constant OverLap Add (COLA) constraint is met

cHECK NOLA
Check whether the Nonzero Overlap Add (NOLA) constraint is met
welch

Power spectral density by Welch’s method.

spectrogram

Spectrogram by Welch’s method.

csd

Cross spectral density by Welch’s method.

lombscargle

Lomb-Scargle periodogram for unevenly sampled data

Notes

In order to enable inversion of an STFT via the inverse STFT in istft, the signal windowing must obey the constraint of “Nonzero OverLap Add” (NOLA), and the input signal must have complete windowing coverage (i.e. (x.shape[axis] - nperseg) % (nperseg-noverlap) == 0). The padded argument may be used to accomplish this.

Given a time-domain signal x[n], a window w[n], and a hop size H = nperseg - noverlap, the windowed frame at time index t is given by

\[ x_t[n] = x[n]w[n - tH] \]

The overlap-add (OLA) reconstruction equation is given by

\[ x[n] = \frac{\sum_t x_t[n]w[n - tH]}{\sum_t w^2[n - tH]} \]

The NOLA constraint ensures that every normalization term that appears in the denominator of the OLA reconstruction equation is nonzero. Whether a choice of window, nperseg, and noverlap satisfy this constraint can be tested with check_NOLA.

New in version 0.19.0.

References

[1], [2]

Examples

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

Generate a test signal, a 2 Vrms sine wave whose frequency is slowly modulated around 3kHz, corrupted by white noise of exponentially decreasing magnitude sampled at 10 kHz.

```python
>>> fs = 10e3
>>> N = 1e5
>>> amp = 2 * np.sqrt(2)
>>> noise_power = 0.01 * fs / 2
>>> time = np.arange(N) / float(fs)
>>> mod = 500*np.cos(2*np.pi*0.25*time)
>>> carrier = amp * np.sin(2*np.pi*3e3*time + mod)
>>> noise = np.random.normal(scale=np.sqrt(noise_power), ...
                             size=time.shape)
>>> noise *= np.exp(-time/5)
>>> x = carrier + noise
```

Compute and plot the STFT’s magnitude.
```python
>>> f, t, Zxx = signal.stft(x, fs, nperseg=1000)
>>> plt.pcolormesh(t, f, np.abs(Zxx), vmin=0, vmax=amp)
>>> plt.title('STFT Magnitude')
>>> plt.ylabel('Frequency [Hz]')
>>> plt.xlabel('Time [sec]')
>>> plt.show()
```

![STFT Magnitude](image)

**scipy.signal.istft**

`scipy.signal.istft(Zxx, fs=1.0, window='hann', nperseg=None, noverlap=None, nfft=None, input_onesided=True, boundary=True, time_axis=-1, freq_axis=-2)`

Perform the inverse Short Time Fourier transform (iSTFT).

**Parameters**

- **Zxx** [array_like] STFT of the signal to be reconstructed. If a purely real array is passed, it will be cast to a complex data type.
- **fs** [float, optional] Sampling frequency of the time series. Defaults to 1.0.
- **window** [str or tuple or array_like, optional] Desired window to use. If `window` is a string or tuple, it is passed to `get_window` to generate the window values, which are DFT-even by default. See `get_window` for a list of windows and required parameters. If `window` is array_like it will be used directly as the window and its length must be `nperseg`. Defaults to a Hann window. Must match the window used to generate the STFT for faithful inversion.
- **nperseg** [int, optional] Number of data points corresponding to each STFT segment. This parameter must be specified if the number of data points per segment is odd, or if the STFT was padded via `nfft > nperseg`. If `None`, the value depends on the shape of `Zxx` and `input_onesided`. If `input_onesided` is True, `nperseg=2*(Zxx.shape[freq_axis] - 1)`. Otherwise, `nperseg=Zxx.shape[freq_axis]`. Defaults to `None`.
- **noverlap** [int, optional] Number of points to overlap between segments. If `None`, half of the segment length. Defaults to `None`. When specified, the COLA constraint must be met (see Notes below), and should match the parameter used to generate the STFT. Defaults to `None`.

---

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nfft

[int, optional] Number of FFT points corresponding to each STFT segment. This parameter must be specified if the STFT was padded via nfft > nperseg. If None, the default values are the same as for nperseg, detailed above, with one exception: if input_onesided is True and nperseg==2*Zxx.shape[freq_axis] - 1, nfft also takes on that value. This case allows the proper inversion of an odd-length unpadded STFT using nfft=None. Defaults to None.

input_onesided

[bool, optional] If True, interpret the input array as one-sided FFTs, such as is returned by stft with return_onesided=True and numpy.fft.rfft. If False, interpret the input as a a two-sided FFT. Defaults to True.

boundary

[bool, optional] Specifies whether the input signal was extended at its boundaries by supplying a non-None boundary argument to stft. Defaults to True.

time_axis

[int, optional] Where the time segments of the STFT is located; the default is the last axis (i.e. axis=-1).

freq_axis

[int, optional] Where the frequency axis of the STFT is located; the default is the penultimate axis (i.e. axis=-2).

Returns

- t [ndarray] Array of output data times.
- x [ndarray] iSTFT of Zxx.

See also:

stft

Short Time Fourier Transform

check_COLA

Check whether the Constant OverLap Add (COLA) constraint is met

check_NOLA

Check whether the Nonzero Overlap Add (NOLA) constraint is met

Notes

In order to enable inversion of an STFT via the inverse STFT with istft, the signal windowing must obey the constraint of “nonzero overlap add” (NOLA):

$$\sum_t w^2[n - tH] \neq 0$$

This ensures that the normalization factors that appear in the denominator of the overlap-add reconstruction equation

$$x[n] = \frac{\sum_t x_t[n]w[n - tH]}{\sum_t w^2[n - tH]}$$

are not zero. The NOLA constraint can be checked with the check_NOLA function.

An STFT which has been modified (via masking or otherwise) is not guaranteed to correspond to an exactly realizable signal. This function implements the iSTFT via the least-squares estimation algorithm detailed in [2], which produces a signal that minimizes the mean squared error between the STFT of the returned signal and the modified STFT.

New in version 0.19.0.
References
[1], [2]

Examples

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

Generate a test signal, a 2 Vrms sine wave at 50Hz corrupted by 0.001 V**2/Hz of white noise sampled at 1024 Hz.

```python
>>> fs = 1024
>>> N = 10*fs
>>> nperseg = 512
>>> amp = 2 * np.sqrt(2)
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / float(fs)
>>> carrier = amp * np.sin(2*np.pi*50*time)
>>> noise = np.random.normal(scale=np.sqrt(noise_power),
...                           size=time.shape)
>>> x = carrier + noise
```

Compute the STFT, and plot its magnitude

```python
>>> f, t, Zxx = signal.stft(x, fs=fs, nperseg=nperseg)
>>> plt.figure()
>>> plt.pcolormesh(t, f, np.abs(Zxx), vmin=0, vmax=amp)
>>> plt.ylim([f[1], f[-1]])
>>> plt.title('STFT Magnitude')
>>> plt.xlabel('Frequency [Hz]')
>>> plt.ylabel('Time [sec]')
>>> plt.yscale('log')
>>> plt.show()
```

Zero the components that are 10% or less of the carrier magnitude, then convert back to a time series via inverse STFT
>>> Zxx = np.where(np.abs(Zxx) >= amp/10, Zxx, 0)
>>> _, xrec = signal.istft(Zxx, fs)

Compare the cleaned signal with the original and true carrier signals.

```python
>>> plt.figure()
>>> plt.plot(time, x, time, xrec, time, carrier)
>>> plt.xlim([2, 2.1])
>>> plt.xlabel('Time [sec]')
>>> plt.ylabel('Signal')
>>> plt.legend(['Carrier + Noise', 'Filtered via STFT', 'True Carrier'])
>>> plt.show()
```

![Signal plot](image)

Note that the cleaned signal does not start as abruptly as the original, since some of the coefficients of the transient were also removed:

```python
>>> plt.figure()
>>> plt.plot(time, x, time, xrec, time, carrier)
>>> plt.xlim([0, 0.1])
>>> plt.xlabel('Time [sec]')
>>> plt.ylabel('Signal')
>>> plt.legend(['Carrier + Noise', 'Filtered via STFT', 'True Carrier'])
>>> plt.show()
```

`scipy.signal.check_COLA`

`scipy.signal.check_COLA(window, nperseg, noverlap, tol=1e-10)`

Check whether the Constant OverLap Add (COLA) constraint is met

**Parameters**

- `window` [str or tuple or array_like] Desired window to use. If `window` is a string or tuple, it is passed to `get_window` to generate the window values, which are DFT-even by default. See `get_window` for a list of windows and required parameters. If `window` is array_like it will be used directly as the window and its length must be `nperseg`. 

---

6.20. Signal processing (`scipy.signal`)
nperseg: [int] Length of each segment.
noverlap: [int] Number of points to overlap between segments.
tol: [float, optional] The allowed variance of a bin’s weighted sum from the median bin sum.

Returns
verdict: [bool] True if chosen combination satisfies COLA within tol, False otherwise

See also:
check_NOLA
Check whether the Nonzero Overlap Add (NOLA) constraint is met

stft
Short Time Fourier Transform

istft
Inverse Short Time Fourier Transform

Notes
In order to enable inversion of an STFT via the inverse STFT in istft, it is sufficient that the signal windowing obeys the constraint of “Constant OverLap Add” (COLA). This ensures that every point in the input data is equally weighted, thereby avoiding aliasing and allowing full reconstruction.

Some examples of windows that satisfy COLA:

- Rectangular window at overlap of 0, 1/2, 2/3, 3/4, ...
- Bartlett window at overlap of 1/2, 3/4, 5/6, ...
- Hann window at 1/2, 2/3, 3/4, ...
- Any Blackman family window at 2/3 overlap
- Any window with noverlap = nperseg-1
A very comprehensive list of other windows may be found in [2], wherein the COLA condition is satisfied when the “Amplitude Flatness” is unity.

New in version 0.19.0.

References
[1], [2]

Examples

```python
from scipy import signal

>>> signal.check_COLA(signal.boxcar(100), 100, 75)
True

COLA is not true for 25% (1/4) overlap, though:

>>> signal.check_COLA(signal.boxcar(100), 100, 25)
False

“Symmetrical” Hann window (for filter design) is not COLA:

>>> signal.check_COLA(signal.hann(120, sym=True), 120, 60)
False

“Periodic” or “DFT-even” Hann window (for FFT analysis) is COLA for overlap of 1/2, 2/3, 3/4, etc.:

>>> signal.check_COLA(signal.hann(120, sym=False), 120, 60)
True

>>> signal.check_COLA(signal.hann(120, sym=False), 120, 80)
True

>>> signal.check_COLA(signal.hann(120, sym=False), 120, 90)
True
```

**scipy.signal.check_NOLA**

scipy.signal.check_NOLA(window, nperseg, noverlap, tol=1e-10)

Check whether the Nonzero Overlap Add (NOLA) constraint is met

Parameters

- **window** [str or tuple or array_like] Desired window to use. If window is a string or tuple, it is passed to get_window to generate the window values, which are DFT-even by default. See get_window for a list of windows and required parameters. If window is array_like it will be used directly as the window and its length must be nperseg.
- **nperseg** [int] Length of each segment.
- **noverlap** [int] Number of points to overlap between segments.
- **tol** [float, optional] The allowed variance of a bin’s weighted sum from the median bin sum.

Returns

- **verdict** [bool] True if chosen combination satisfies the NOLA constraint within tol, False otherwise
See also:

check_COLA
Check whether the Constant OverLap Add (COLA) constraint is met

stft
Short Time Fourier Transform

istft
Inverse Short Time Fourier Transform

Notes
In order to enable inversion of an STFT via the inverse STFT in \texttt{istft}, the signal windowing must obey the constraint of “nonzero overlap add” (NOLA):

\[
\sum_t w^2[n - tH] \neq 0
\]

for all \(n\), where \(w\) is the window function, \(t\) is the frame index, and \(H\) is the hop size \((H = \text{nperseg} - \text{noverlap})\).

This ensures that the normalization factors in the denominator of the overlap-add inversion equation are not zero. Only very pathological windows will fail the NOLA constraint.

New in version 1.2.0.

References
[1], [2]

Examples

```python
>>> from scipy import signal

Confirm NOLA condition for rectangular window of 75\% (3/4) overlap:

```python
>>> signal.check_NOLA(signal.boxcar(100), 100, 75)
```

True

NOLA is also true for 25\% (1/4) overlap:

```python
>>> signal.check_NOLA(signal.boxcar(100), 100, 25)
```

True

“Symmetrical” Hann window (for filter design) is also NOLA:

```python
>>> signal.check_NOLA(signal.hann(120, sym=True), 120, 60)
```

True

As long as there is overlap, it takes quite a pathological window to fail NOLA:

```python
>>> w = np.ones(64, dtype="float")
>>> w[::2] = 0
>>> signal.check_NOLA(w, 64, 32)
```

False

If there is not enough overlap, a window with zeros at the ends will not work:
>>> signal.check_NOLA(signal.hann(64), 64, 0)
False
>>> signal.check_NOLA(signal.hann(64), 64, 1)
False
>>> signal.check_NOLA(signal.hann(64), 64, 2)
True

6.21 Sparse matrices (scipy.sparse)

SciPy 2-D sparse matrix package for numeric data.

6.21.1 Contents

Sparse matrix classes

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scipy.sparse.bsr_matrix

class scipy.sparse.bsr_matrix(arg1, shape=None, dtype=None, copy=False, blocksize=None)

Block Sparse Row matrix

This can be instantiated in several ways:

bsr_matrix(D, [blocksize=(R,C)])

where D is a dense matrix or 2-D ndarray.

bsr_matrix(S, [blocksize=(R,C)])

with another sparse matrix S (equivalent to S.tobsr())

bsr_matrix((M, N), [blocksize=(R,C), dtype])

to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype='d'.

bsr_matrix((data, ij), [blocksize=(R,C), shape=(M, N)])

where data and ij satisfy a[ij[0, k], ij[1, k]] = data[k]

bsr_matrix((data, indices, indptr), [shape=(M, N)])

is the standard BSR representation where the block column indices for row i are stored in indices[indptr[i]:indptr[i+1]] and their corresponding block values are stored in data[indptr[i]: indptr[i+1]] . If the shape parameter is not supplied, the matrix dimensions are inferred from the index arrays.
Notes
Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Summary of BSR format
The Block Compressed Row (BSR) format is very similar to the Compressed Sparse Row (CSR) format. BSR is appropriate for sparse matrices with dense sub matrices like the last example below. Block matrices often arise in vector-valued finite element discretizations. In such cases, BSR is considerably more efficient than CSR and CSC for many sparse arithmetic operations.

Blocksize
The blocksize (R,C) must evenly divide the shape of the matrix (M,N). That is, R and C must satisfy the relationship
\[ M \% R = 0 \] and \[ N \% C = 0 \].
If no blocksize is specified, a simple heuristic is applied to determine an appropriate blocksize.

Examples
```python
>>> from scipy.sparse import bsr_matrix

>>> bsr_matrix((3, 4), dtype=np.int8).toarray()
array([[0, 0, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]], dtype=int8)

>>> row = np.array([0, 0, 1, 2, 2])
>>> col = np.array([0, 2, 2, 0, 1])
>>> data = np.array([1, 2, 3, 4, 5])
>>> bsr_matrix((data, (row, col)), shape=(3, 3)).toarray()
array([[1, 0, 2],
       [0, 0, 3],
       [4, 5, 6]])

>>> indptr = np.array([0, 2, 3, 6])
>>> indices = np.array([0, 2, 2, 0, 1])
>>> data = np.array([1, 2, 3, 4, 5, 6]).repeat(4).reshape(6, 2, 2)
>>> bsr_matrix((data, indices, indptr), shape=(6, 6)).toarray()
array([[1, 1, 0, 0, 2, 2],
       [1, 1, 0, 0, 2, 2],
       [0, 0, 0, 0, 3, 3],
       [0, 0, 0, 0, 3, 3],
       [4, 4, 5, 5, 6, 6],
       [4, 4, 5, 5, 6, 6]])
```

Attributes
- **dtype** [dtype] Data type of the matrix
- **ndim** [int] Number of dimensions (this is always 2)
- **nnz** Number of stored values, including explicit zeros.
- **data** Data array of the matrix
- **indices** BSR format index array
- **indptr** BSR format index pointer array
- **blocksize** Block size of the matrix
- **has_sorted_indices** Determine whether the matrix has sorted indices
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**scipy.sparse.bsr_matrix.arcsin**

`bsr_matrix.arcsin()`  
Element-wise arcsin.

See numpy.arcsin for more information.
scipy.sparse.bsr_matrix.arcsinh

bsr_matrix.arcsinh()
   Element-wise arcsinh.
   See numpy.arcsinh for more information.

scipy.sparse.bsr_matrix.arctan

bsr_matrix.arctan()
   Element-wise arctan.
   See numpy.arctan for more information.

scipy.sparse.bsr_matrix.arctanh

bsr_matrix.arctanh()
   Element-wise arctanh.
   See numpy.arctanh for more information.

scipy.sparse.bsr_matrix.argmax

bsr_matrix.argmax(axis=None, out=None)
   Return indices of maximum elements along an axis.
   Implicit zero elements are also taken into account. If there are several maximum values, the index
   of the first occurrence is returned.

   Parameters
      axis  [{-2, -1, 0, 1, None}, optional] Axis along which the argmax is computed. If
            None (default), index of the maximum element in the flatten data is returned.
      out   [None, optional] This argument is in the signature solely for NumPy compat-
            ibility reasons. Do not pass in anything except for the default value, as this
            argument is not used.

   Returns
      ind   [np.matrix or int] Indices of maximum elements. If matrix, its size along axis
            is 1.

scipy.sparse.bsr_matrix.argmin

bsr_matrix.argmin(axis=None, out=None)
   Return indices of minimum elements along an axis.
   Implicit zero elements are also taken into account. If there are several minimum values, the index
   of the first occurrence is returned.

   Parameters
      axis  [{-2, -1, 0, 1, None}, optional] Axis along which the argmin is computed. If
            None (default), index of the minimum element in the flatten data is returned.
      out   [None, optional] This argument is in the signature solely for NumPy compat-
            ibility reasons. Do not pass in anything except for the default value, as this
            argument is not used.

   Returns
**scipy.sparse.bsr_matrix.asformat**

**bsr_matrix.asformat**(format, copy=False)

Return this matrix in the passed format.

**Parameters**

- **format**
  - [{str, None}] The desired matrix format ("csr", "csc", "lil", "dok", "array", ...) or None for no conversion.
- **copy**
  - [bool, optional] If True, the result is guaranteed to not share data with self.

**Returns**

- **A**
  - [This matrix in the passed format.]

**scipy.sparse.bsr_matrix.asfptype**

**bsr_matrix.asfptype()**

Upcast matrix to a floating point format (if necessary)

**scipy.sparse.bsr_matrix.astype**

**bsr_matrix.astype**(dtype, casting='unsafe', copy=True)

Cast the matrix elements to a specified type.

**Parameters**

- **dtype**
  - [string or numpy dtype] Typecode or data-type to which to cast the data.
- **casting**
  - [{'no', 'equiv', 'safe', 'same_kind', 'unsafe'}, optional] Controls what kind of data casting may occur. Defaults to ‘unsafe’ for backwards compatibility. ‘no’ means the data types should not be cast at all. ‘equiv’ means only byte-order changes are allowed. ‘safe’ means only casts which can preserve values are allowed. ‘same_kind’ means only safe casts or casts within a kind, like float64 to float32, are allowed. ‘unsafe’ means any data conversions may be done.
- **copy**
  - [bool, optional] If copy is False, the result might share some memory with this matrix. If copy is True, it is guaranteed that the result and this matrix do not share any memory.

**scipy.sparse.bsr_matrix.ceil**

**bsr_matrix.ceil()**

Element-wise ceil.

See numpy.ceil for more information.

**scipy.sparse.bsr_matrix.check_format**

**bsr_matrix.check_format**(full_check=True)

check whether the matrix format is valid

**Parameters:**

- **full_check**:
  - True - rigorous check, O(N) operations : default False - basic check, O(1) operations
scipy.sparse.bsr_matrix.conj

bsr_matrix.conj(copy=True)
   Element-wise complex conjugation.

   If the matrix is of non-complex data type and copy is False, this method does nothing and the
data is not copied.

   Parameters
   copy [bool, optional] If True, the result is guaranteed to not share data with self.

   Returns
   A [The element-wise complex conjugate.]

scipy.sparse.bsr_matrix.conjugate

bsr_matrix.conjugate(copy=True)
   Element-wise complex conjugation.

   If the matrix is of non-complex data type and copy is False, this method does nothing and the
data is not copied.

   Parameters
   copy [bool, optional] If True, the result is guaranteed to not share data with self.

   Returns
   A [The element-wise complex conjugate.]

scipy.sparse.bsr_matrix.copy

bsr_matrix.copy()
   Returns a copy of this matrix.

   No data/indices will be shared between the returned value and current matrix.

scipy.sparse.bsr_matrix.count_nonzero

bsr_matrix.count_nonzero()
   Number of non-zero entries, equivalent to
   np.count_nonzero(a.toarray())

   Unlike getnnz() and the nnz property, which return the number of stored entries (the length of
   the data attribute), this method counts the actual number of non-zero entries in data.

scipy.sparse.bsr_matrix.deg2rad

bsr_matrix.deg2rad()
   Element-wise deg2rad.

   See numpy.deg2rad for more information.
scipy.sparse.bsr_matrix.diagonal

bsr_matrix.diagonal(k=0)
Returns the k-th diagonal of the matrix.

Parameters

k [int, optional] Which diagonal to set, corresponding to elements a[i, i+k]. Default: 0 (the main diagonal).
New in version 1.0.

See also:

numpy.diagonal
Equivalent numpy function.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> A.diagonal()
array([1, 0, 5])
>>> A.diagonal(k=1)
array([2, 3])
```

scipy.sparse.bsr_matrix.dot

bsr_matrix.dot(other)
Ordinary dot product

Examples

```python
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

scipy.sparse.bsr_matrix.eliminate_zeros

bsr_matrix.eliminate_zeros()
Remove zero elements in-place.

scipy.sparse.bsr_matrix.expm1

bsr_matrix.expm1()
Element-wise expm1.
See numpy.expm1 for more information.

scipy.sparse.bsr_matrix.floor

bsr_matrix.floor()
Element-wise floor.
See numpy.floor for more information.
**scipy.sparse.bsr_matrix.getH**

bsr_matrix.getH()

Return the Hermitian transpose of this matrix.

**See also:**

**np.matrix.getH**

NumPy’s implementation of getH for matrices.

**scipy.sparse.bsr_matrix.get_shape**

bsr_matrix.get_shape()

Get shape of a matrix.

**scipy.sparse.bsr_matrix.getcol**

bsr_matrix.getcol(j)

Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

**scipy.sparse.bsr_matrix.getformat**

bsr_matrix.getformat()

Format of a matrix representation as a string.

**scipy.sparse.bsr_matrix.getmaxprint**

bsr_matrix.getmaxprint()

Maximum number of elements to display when printed.

**scipy.sparse.bsr_matrix.getnnz**

bsr_matrix.getnnz(axis=None)

Number of stored values, including explicit zeros.

**Parameters**

- **axis**: [None, 0, or 1] Select between the number of values across the whole matrix, in each column, or in each row.

**See also:**

**count_nonzero**

Number of non-zero entries.

**scipy.sparse.bsr_matrix.getrow**

bsr_matrix.getrow(i)

Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

**scipy.sparse.bsr_matrix.log1p**

bsr_matrix.log1p()

Element-wise log1p.

See numpy.log1p for more information.
**scipy.sparse.bsr_matrix.matmat**

```python
bsr_matrix.matmat(**kwds)
```

*matmat* is deprecated! BSR matmat is deprecated in scipy 0.19.0. Use * operator instead.

Multiply this sparse matrix by other matrix.

**scipy.sparse.bsr_matrix.matvec**

```python
bsr_matrix.matvec(**kwds)
```

*matvec* is deprecated! BSR matvec is deprecated in scipy 0.19.0. Use * operator instead.

Multiply matrix by vector.

**scipy.sparse.bsr_matrix.max**

```python
bsr_matrix.max(axis=None, out=None)
```

Return the maximum of the matrix or maximum along an axis. This takes all elements into account, not just the non-zero ones.

**Parameters**

- **axis**
  - `{[-2, -1, 0, 1, None] optional}` Axis along which the sum is computed. The default is to compute the maximum over all the matrix elements, returning a scalar (i.e. *axis* = *None*).

- **out**
  - `[None, optional]` This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

**Returns**

- **amax**
  - `[coo_matrix or scalar]` Maximum of *a*. If *axis* is None, the result is a scalar value. If *axis* is given, the result is a sparse.coo_matrix of dimension *a.ndim* - 1.

**See also:**

- **min**
  - The minimum value of a sparse matrix along a given axis.

- **np.matrix.max**
  - NumPy’s implementation of ‘max’ for matrices

**scipy.sparse.bsr_matrix.maximum**

```python
bsr_matrix.maximum(other)
```

Element-wise maximum between this and another matrix.

**scipy.sparse.bsr_matrix.mean**

```python
bsr_matrix.mean(axis=None, dtype=None, out=None)
```

Compute the arithmetic mean along the specified axis.

Returns the average of the matrix elements. The average is taken over all elements in the matrix by default, otherwise over the specified axis. *float64* intermediate and return values are used for integer inputs.

**Parameters**

- **axis**
  - `{[-2, -1, 0, 1, None] optional}` Axis along which the sum is computed. The default is to compute the maximum over all the matrix elements, returning a scalar (i.e. *axis* = *None*).

- **dtype**
  - `[None, optional]` This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

- **out**
  - `[None, optional]` This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.
axis [{-2, -1, 0, 1, None} optional] Axis along which the mean is computed. The default is to compute the mean of all elements in the matrix (i.e. axis = None).
dtype [data-type, optional] Type to use in computing the mean. For integer inputs, the default is float64; for floating point inputs, it is the same as the input dtype.
out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.

Returns
m [np.matrix]

See also:

np.matrix.mean
NumPy’s implementation of ‘mean’ for matrices

scipy.sparse.bsr_matrix.min

bsr_matrix.min(axis=None, out=None)
Return the minimum of the matrix or maximum along an axis. This takes all elements into account, not just the non-zero ones.

Parameters
axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the minimum over all the matrix elements, returning a scalar (i.e. axis = None).
out [None, optional] This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns
amin [coo_matrix or scalar] Minimum of a. If axis is None, the result is a scalar value. If axis is given, the result is a sparse.coo_matrix of dimension a.ndim - 1.

See also:

max
The maximum value of a sparse matrix along a given axis.

np.matrix.min
NumPy’s implementation of ‘min’ for matrices

scipy.sparse.bsr_matrix.minimum

bsr_matrix.minimum(other)
Element-wise minimum between this and another matrix.
scipy.sparse.bsr_matrix.multiply

bsr_matrix.multiply(other)
Point-wise multiplication by another matrix, vector, or scalar.

scipy.sparse.bsr_matrix.nonzero

bsr_matrix.nonzero()
nonzero indices
Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

scipy.sparse.bsr_matrix.power

bsr_matrix.power(n, dtype=None)
This function performs element-wise power.

Parameters

- n [n is a scalar]
- dtype [If dtype is not specified, the current dtype will be preserved.]

scipy.sparse.bsr_matrix.prune

bsr_matrix.prune()
Remove empty space after all non-zero elements.

scipy.sparse.bsr_matrix.rad2deg

bsr_matrix.rad2deg()
Element-wise rad2deg.
See numpy.rad2deg for more information.

scipy.sparse.bsr_matrix.reshape

bsr_matrix.reshape(self, shape, order='C', copy=False)
Gives a new shape to a sparse matrix without changing its data.

Parameters

- shape [length-2 tuple of ints] The new shape should be compatible with the original shape.
- order [{‘C’, ‘F’}, optional] Read the elements using this index order. ‘C’ means to read and write the elements using C-like index order; e.g. read entire first row, then second row, etc. ‘F’ means to read and write the elements using Fortran-like index order; e.g. read entire first column, then second column, etc.
- copy [bool, optional] Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.
**Returns**

`reshaped_matrix`

[sparse matrix] A sparse matrix with the given `shape`, not necessarily of the same format as the current object.

**See also:**

`np.matrix.reshape`

NumPy’s implementation of ‘reshape’ for matrices

**scipy.sparse.bsr_matrix.resize**

`bsr_matrix.resize(*shape)`

Resize the matrix in-place to dimensions given by `shape`

Any elements that lie within the new shape will remain at the same indices, while non-zero elements lying outside the new shape are removed.

**Parameters**

`shape`  
[(int, int)] number of rows and columns in the new matrix

**Notes**

The semantics are not identical to `numpy.ndarray.resize` or `numpy.resize`. Here, the same data will be maintained at each index before and after reshape, if that index is within the new bounds. In numpy, resizing maintains contiguity of the array, moving elements around in the logical matrix but not within a flattened representation.

We give no guarantees about whether the underlying data attributes (arrays, etc.) will be modified in place or replaced with new objects.

**scipy.sparse.bsr_matrix.rint**

`bsr_matrix.rint()`  
Element-wise rint.

See numpy.rint for more information.

**scipy.sparse.bsr_matrix.set_shape**

`bsr_matrix.set_shape(shape)`  
See `reshape`.

**scipy.sparse.bsr_matrix.setdiag**

`bsr_matrix.setdiag(values, k=0)`  
Set diagonal or off-diagonal elements of the array.

**Parameters**

`values`  
[array_like] New values of the diagonal elements. Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values if longer than the diagonal, then the remaining values are ignored. If a scalar value is given, all of the diagonal is set to it.

`k`  
[int, optional] Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).
scipy.sparse.bsr_matrix.sign

bsr_matrix.sign()

Element-wise sign.

See numpy.sign for more information.

scipy.sparse.bsr_matrix.sin

bsr_matrix.sin()

Element-wise sin.

See numpy.sin for more information.

scipy.sparse.bsr_matrix.sinh

bsr_matrix.sinh()

Element-wise sinh.

See numpy.sinh for more information.

scipy.sparse.bsr_matrix.sort_indices

bsr_matrix.sort_indices()

Sort the indices of this matrix in place

scipy.sparse.bsr_matrix.sorted_indices

bsr_matrix.sorted_indices()

Return a copy of this matrix with sorted indices

scipy.sparse.bsr_matrix.sqrt

bsr_matrix.sqrt()

Element-wise sqrt.

See numpy.sqrt for more information.

scipy.sparse.bsr_matrix.sum

bsr_matrix.sum(axis=None, dtype=None, out=None)

Sum the matrix elements over a given axis.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the sum of all the matrix elements, returning a scalar (i.e. axis = None).

dtype [dtype, optional] The type of the returned matrix and of the accumulator in which the elements are summed. The dtype of a is used by default unless a has an integer dtype of less precision than the default platform integer. In that case, if a is signed then the platform integer is used while if a is unsigned then an unsigned integer of the same precision as the platform integer is used. New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.
New in version 0.18.0.

**Returns**

`sum_along_axis`

[np.matrix] A matrix with the same shape as `self`, with the specified axis removed.

**See also:**

`np.matrix.sum`

NumPy's implementation of 'sum' for matrices

### scipy.sparse.bsr_matrix.sum_duplicates

`bsr_matrix.sum_duplicates()`

Eliminate duplicate matrix entries by adding them together

The is an *in place* operation

### scipy.sparse.bsr_matrix.tan

`bsr_matrix.tan()`

Element-wise tan.

See `numpy.tan` for more information.

### scipy.sparse.bsr_matrix.tanh

`bsr_matrix.tanh()`

Element-wise tanh.

See `numpy.tanh` for more information.

### scipy.sparse.bsr_matrix.toarray

`bsr_matrix.toarray(order=None, out=None)`

Return a dense ndarray representation of this matrix.

**Parameters**

- `order` [{‘C’, ‘F’}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is ‘None’, indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the `out` argument.

- `out` [ndarray, 2-dimensional, optional] If specified, uses this array as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method. For most sparse types, `out` is required to be memory contiguous (either C or Fortran ordered).

**Returns**

- `arr` [ndarray, 2-dimensional] An array with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If `out` was passed, the same object is returned after being modified in-place to contain the appropriate values.
scipy.sparse.bsr_matrix.tobsr

bsr_matrix.tobsr(blocksize=None, copy=False)

Convert this matrix into Block Sparse Row Format.

With copy=False, the data/indices may be shared between this matrix and the resultant bsr_matrix.

If blocksize=(R, C) is provided, it will be used for determining block size of the bsr_matrix.

scipy.sparse.bsr_matrix.tocoo

bsr_matrix.tocoo(copy=True)

Convert this matrix to COOrdinate format.

When copy=False the data array will be shared between this matrix and the resultant coo_matrix.

scipy.sparse.bsr_matrix.tocsc

bsr_matrix.tocsc(copy=False)

Convert this matrix to Compressed Sparse Column format.

With copy=False, the data/indices may be shared between this matrix and the resultant csc_matrix.

scipy.sparse.bsr_matrix.tocsr

bsr_matrix.tocsr(copy=False)

Convert this matrix to Compressed Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant csr_matrix.

scipy.sparse.bsr_matrix.todense

bsr_matrix.todense(order=None, out=None)

Return a dense matrix representation of this matrix.

Parameters

order [{‘C’, ‘F’}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is ‘None’, indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the out argument.

out [ndarray, 2-dimensional, optional] If specified, uses this array (or numpy.matrix) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.

Returns

arr [numpy.matrix, 2-dimensional] A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If out was passed and was an array (rather than a numpy.matrix), it will be filled with the appropriate values and returned wrapped in a numpy.matrix object that shares the same memory.
scipy.sparse.bsr_matrix.todia

bsr_matrix.todia(copy=False)
    Convert this matrix to sparse DIAgonal format.
    With copy=False, the data/indices may be shared between this matrix and the resultant dia_matrix.

scipy.sparse.bsr_matrix.todok

bsr_matrix.todok(copy=False)
    Convert this matrix to Dictionary Of Keys format.
    With copy=False, the data/indices may be shared between this matrix and the resultant dok_matrix.

scipy.sparse.bsr_matrix.tolil

bsr_matrix.tolil(copy=False)
    Convert this matrix to LInked List format.
    With copy=False, the data/indices may be shared between this matrix and the resultant lil_matrix.

scipy.sparse.bsr_matrix.transpose

bsr_matrix.transpose(axes=None, copy=False)
    Reverses the dimensions of the sparse matrix.

    Parameters
    axes [None, optional] This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value.
    copy [bool, optional] Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

    Returns
    p [self with the dimensions reversed.]

    See also:

    np.matrix.transpose
        NumPy's implementation of 'transpose' for matrices

scipy.sparse.bsr_matrix.trunc

bsr_matrix.trunc()
    Element-wise trunc.
    See numpy.trunc for more information.

scipy.sparse.coo_matrix

class scipy.sparse.coo_matrix(arg1, shape=None, dtype=None, copy=False)
    A sparse matrix in COOrdinate format.
    Also known as the 'ijv' or 'triplet' format.

    This can be instantiated in several ways:
coo_matrix(D)
    with a dense matrix D

coo_matrix(S)
    with another sparse matrix S (equivalent to S.tocoo())

coo_matrix((M, N), [dtype])
    to construct an empty matrix with shape (M, N) dtype is optional, defaulting to
dtype='d'.

coo_matrix((data, (i, j)), [shape=(M, N)])
    to construct from three arrays:
    1. data[:,:] the entries of the matrix, in any order
    2. i[:] the row indices of the matrix entries
    3. j[:] the column indices of the matrix entries

    Where A[i[k], j[k]] = data[k]. When shape is not specified, it is inferred from the
    index arrays

Notes
Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication,
division, and matrix power.

Advantages of the COO format

• facilitates fast conversion among sparse formats
• permits duplicate entries (see example)
• very fast conversion to and from CSR/CSC formats

Disadvantages of the COO format

• does not directly support:
  – arithmetic operations
  – slicing

Intended Usage

• COO is a fast format for constructing sparse matrices
• Once a matrix has been constructed, convert to CSR or CSC format for fast arithmetic and
  matrix vector operations
• By default when converting to CSR or CSC format, duplicate (i,j) entries will be summed
  together. This facilitates efficient construction of finite element matrices and the like. (see
  example)

Examples
>>> # Constructing an empty matrix
>>> from scipy.sparse import coo_matrix
>>> coo_matrix((3, 4), dtype=np.int8).toarray()
array([[0, 0, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]], dtype=int8)

>>> # Constructing a matrix using ijv format
>>> row = np.array([0, 3, 1, 0])
>>> col = np.array([0, 3, 1, 2])
>>> data = np.array([4, 5, 7, 9])
>>> coo_matrix((data, (row, col)), shape=(4, 4)).toarray()
array([[4, 0, 9, 0],
       [0, 7, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 5]])

>>> # Constructing a matrix with duplicate indices
>>> row = np.array([0, 0, 1, 3, 1, 0])
>>> col = np.array([0, 2, 1, 3, 1, 0])
>>> data = np.array([1, 1, 1, 1, 1, 1])
>>> coo = coo_matrix((data, (row, col)), shape=(4, 4))
>>> # Duplicate indices are maintained until implicitly or explicitly summed
>>> np.max(coo.data)
1
>>> coo.toarray()
array([[3, 0, 1, 0],
       [0, 2, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 1]])

Attributes

dtype  [dtype] Data type of the matrix
ndim   [int] Number of dimensions (this is always 2)
nnz    Number of stored values, including explicit zeros.
data    COO format data array of the matrix
row    COO format row index array of the matrix
col    COO format column index array of the matrix

Methods

arcsin()
Element-wise arcsin.
arcsinh()
Element-wise arcsinh.
arctan()
Element-wise arctan.
arctanh()
Element-wise arctanh.
argmax([axis, out])
Return indices of maximum elements along an axis.
argmin([axis, out])
Return indices of minimum elements along an axis.
asformat(format[, copy])
Return this matrix in the passed format.

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<td><code>conj([copy])</code></td>
<td>Element-wise complex conjugation.</td>
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<td><code>getrow(i)</code></td>
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<td>Return the maximum of the matrix or maximum along an axis.</td>
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<tr>
<td><code>maximum(other)</code></td>
<td>Element-wise maximum between this and another matrix.</td>
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<td>Convert this matrix to COOrdinate format.</td>
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<td><code>tocsc(copy)</code></td>
<td>Convert this matrix to Compressed Sparse Column format</td>
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<td><code>tocsr(copy)</code></td>
<td>Convert this matrix to Compressed Sparse Row format</td>
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<td><code>todense(order, out)</code></td>
<td>Return a dense matrix representation of this matrix.</td>
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<td><code>todia(copy)</code></td>
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<td><code>todok(copy)</code></td>
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<td><code>tolil(copy)</code></td>
<td>Convert this matrix to Linked List format.</td>
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<td><code>transpose(axes, copy)</code></td>
<td>Reverses the dimensions of the sparse matrix.</td>
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<td><code>trunc()</code></td>
<td>Element-wise trunc.</td>
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**scipy.sparse.coo_matrix.arcsin**

```python
coo_matrix.arcsin()
```

Element-wise arcsin.

See `numpy.arcsin` for more information.

**scipy.sparse.coo_matrix.arcsinh**

```python
coo_matrix.arcsinh()
```

Element-wise arcsinh.

See `numpy.arcsinh` for more information.

**scipy.sparse.coo_matrix.arctan**

```python
coo_matrix.arctan()
```

Element-wise arctan.

See `numpy.arctan` for more information.

**scipy.sparse.coo_matrix.arctanh**

```python
coo_matrix.arctanh()
```

Element-wise arctanh.

See `numpy.arctanh` for more information.

**scipy.sparse.coo_matrix.argmax**

```python
coo_matrix.argmax(axis=None, out=None)
```

Return indices of maximum elements along an axis.
Implicit zero elements are also taken into account. If there are several maximum values, the index of the first occurrence is returned.

**Parameters**

- **axis**
  
  [{-2, -1, 0, 1, None}, optional] Axis along which the argmax is computed. If None (default), index of the maximum element in the flatten data is returned.

- **out**
  
  [None, optional] This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

**Returns**

- **ind**
  
  [np.matrix or int] Indices of maximum elements. If matrix, its size along axis is 1.

*scipy.sparse.coo_matrix.argmax*

coo_matrix.argmax(*axis=None, out=None*)

Return indices of minimum elements along an axis.

Implicit zero elements are also taken into account. If there are several minimum values, the index of the first occurrence is returned.

**Parameters**

- **axis**
  
  [{-2, -1, 0, 1, None}, optional] Axis along which the argmin is computed. If None (default), index of the minimum element in the flatten data is returned.

- **out**
  
  [None, optional] This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

**Returns**

- **ind**
  
  [np.matrix or int] Indices of minimum elements. If matrix, its size along axis is 1.

*scipy.sparse.coo_matrix.asformat*

coo_matrix.asformat(*format, copy=False*)

Return this matrix in the passed format.

**Parameters**

- **format**
  
  [{str, None}] The desired matrix format (“csr”, “csc”, “lil”, “dok”, “array”, …) or None for no conversion.

- **copy**
  
  [bool, optional] If True, the result is guaranteed to not share data with self.

**Returns**

**A**

[This matrix in the passed format.]

*scipy.sparse.coo_matrix.asfptype*

coo_matrix.asfptype()

Upcast matrix to a floating point format (if necessary)
scipy.sparse.coo_matrix.astype

coo_matrix.astype(dtype, casting='unsafe', copy=True)

Cast the matrix elements to a specified type.

Parameters

dtype [string or numpy dtype] Typecode or data-type to which to cast the data.

casting [{‘no’, ‘equiv’, ‘safe’, ‘same_kind’, ‘unsafe’}, optional] Controls what kind of
data casting may occur. Defaults to ‘unsafe’ for backwards compatibility. ‘no’
means the data types should not be cast at all. ‘equiv’ means only byte-order
changes are allowed. ‘safe’ means only casts which can preserve values are
allowed. ‘same_kind’ means only safe casts or casts within a kind, like float64
to float32, are allowed. ‘unsafe’ means any data conversions may be done.

copy [bool, optional] If copy is False, the result might share some memory with this
matrix. If copy is True, it is guaranteed that the result and this matrix do not
share any memory.

scipy.sparse.coo_matrix.ceil

coo_matrix.ceil()

Element-wise ceil.

See numpy.ceil for more information.

scipy.sparse.coo_matrix.conj

coo_matrix.conj(copy=True)

Element-wise complex conjugation.

If the matrix is of non-complex data type and copy is False, this method does nothing and the
data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.coo_matrix.conjugate

coo_matrix.conjugate(copy=True)

Element-wise complex conjugation.

If the matrix is of non-complex data type and copy is False, this method does nothing and the
data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]
scipy.sparse.coo_matrix.copy

coo_matrix.copy()

Returns a copy of this matrix.

No data/indices will be shared between the returned value and current matrix.

scipy.sparse.coo_matrix.count_nonzero

coo_matrix.count_nonzero()

Number of non-zero entries, equivalent to

np.count_nonzero(a.toarray())

Unlike getnnz() and the nnz property, which return the number of stored entries (the length of
the data attribute), this method counts the actual number of non-zero entries in data.

scipy.sparse.coo_matrix.deg2rad

coo_matrix.deg2rad()

Element-wise deg2rad.

See numpy.deg2rad for more information.

scipy.sparse.coo_matrix.diagonal

coo_matrix.diagonal(k=0)

Returns the k-th diagonal of the matrix.

Parameters

k [int, optional] Which diagonal to set, corresponding to elements a[i, i+k]. De-
default: 0 (the main diagonal).

New in version 1.0.

See also:

numpy.diagonal

Equivalent numpy function.

Examples

>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> A.diagonal()
array([1, 0, 5])
>>> A.diagonal(k=1)
array([2, 3])

scipy.sparse.coo_matrix.dot

coo_matrix.dot(other)

Ordinary dot product

Examples
```python
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

**scipy.sparse.coo_matrix.eliminate_zeros**

`coo_matrix.eliminate_zeros()`  
Remove zero entries from the matrix  
This is an *in place* operation

**scipy.sparse.coo_matrix.expm1**

`coo_matrix.expm1()`  
Element-wise expm1.  
See numpy.expm1 for more information.

**scipy.sparse.coo_matrix.floor**

`coo_matrix.floor()`  
Element-wise floor.  
See numpy.floor for more information.

**scipy.sparse.coo_matrix.getH**

`coo_matrix.getH()`  
Return the Hermitian transpose of this matrix.  
See also:

`np.matrix.getH`

NumPy's implementation of *getH* for matrices

**scipy.sparse.coo_matrix.get_shape**

`coo_matrix.get_shape()`  
Get shape of a matrix.

**scipy.sparse.coo_matrix.getcol**

`coo_matrix.getcol(j)`  
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

**scipy.sparse.coo_matrix.getformat**

`coo_matrix.getformat()`  
Format of a matrix representation as a string.
**scipy.sparse.coo_matrix.getmaxprint**

```python
coo_matrix.getmaxprint()
```

Maximum number of elements to display when printed.

**scipy.sparse.coo_matrix.getnnz**

```python
coo_matrix.getnnz(axis=None)
```

Number of stored values, including explicit zeros.

**Parameters**

- `axis` : [None, 0, or 1] Select between the number of values across the whole matrix, in each column, or in each row.

**See also:**

- `count_nonzero`

  Number of non-zero entries

**scipy.sparse.coo_matrix.getrow**

```python
coo_matrix.getrow(i)
```

Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

**scipy.sparse.coo_matrix.log1p**

```python
coo_matrix.log1p()
```

Element-wise log1p.

See `numpy.log1p` for more information.

**scipy.sparse.coo_matrix.max**

```python
coo_matrix.max(axis=None, out=None)
```

Return the maximum of the matrix or maximum along an axis. This takes all elements into account, not just the non-zero ones.

**Parameters**

- `axis` : [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the maximum over all the matrix elements, returning a scalar (i.e. `axis = None`).
- `out` : [None, optional] This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

**Returns**

- `amax` : [coo_matrix or scalar] Maximum of `a`. If `axis` is None, the result is a scalar value. If `axis` is given, the result is a `coo_matrix` of dimension `a.ndim - 1`.

**See also:**

- `min`

  The minimum value of a sparse matrix along a given axis.
np.matrix.max

NumPy's implementation of 'max' for matrices

scipy.sparse.coo_matrix.maximum

coo_matrix.maximum(other)

Element-wise maximum between this and another matrix.

scipy.sparse.coo_matrix.mean

coo_matrix.mean(axis=None, dtype=None, out=None)

Compute the arithmetic mean along the specified axis.

Returns the average of the matrix elements. The average is taken over all elements in the matrix by default, otherwise over the specified axis. float64 intermediate and return values are used for integer inputs.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the mean is computed. The default is to compute the mean of all elements in the matrix (i.e. axis = None).

dtype [data-type, optional] Type to use in computing the mean. For integer inputs, the default is float64; for floating point inputs, it is the same as the input dtype.

New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.

New in version 0.18.0.

Returns

m [np.matrix]

See also:

np.matrix.mean

NumPy's implementation of 'mean' for matrices

scipy.sparse.coo_matrix.min

coo_matrix.min(axis=None, out=None)

Return the minimum of the matrix or maximum along an axis. This takes all elements into account, not just the non-zero ones.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the minimum over all the matrix elements, returning a scalar (i.e. axis = None).

out [None, optional] This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns
amin [coo_matrix or scalar] Minimum of a. If axis is None, the result is a scalar value. If axis is given, the result is a sparse.coo_matrix of dimension a.ndim - 1.

See also:

max

The maximum value of a sparse matrix along a given axis.

np.matrix.min

NumPy’s implementation of ‘min’ for matrices

scipy.sparse.coo_matrix.minimum

coo_matrix.minimum(other)

Element-wise minimum between this and another matrix.

scipy.sparse.coo_matrix.multiply

coo_matrix.multiply(other)

Point-wise multiplication by another matrix

scipy.sparse.coo_matrix.nonzero

coo_matrix.nonzero()

nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

scipy.sparse.coo_matrix.power

coo_matrix.power(n, dtype=None)

This function performs element-wise power.

Parameters

n [n is a scalar]
dtype [If dtype is not specified, the current dtype will be preserved.]

scipy.sparse.coo_matrix.rad2deg

coo_matrix.rad2deg()

Element-wise rad2deg.

See numpy.rad2deg for more information.
**scipy.sparse.coo_matrix.reshape**

**coo_matrix.reshape**(self, shape, order='C', copy=False)

Gives a new shape to a sparse matrix without changing its data.

**Parameters**

- **shape**: [length-2 tuple of ints] The new shape should be compatible with the original shape.
- **order**: [{‘C’, ‘F’}, optional] Read the elements using this index order. ‘C’ means to read and write the elements using C-like index order; e.g., read entire first row, then second row, etc. ‘F’ means to read and write the elements using Fortran-like index order; e.g., read entire first column, then second column, etc.
- **copy**: [bool, optional] Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

**Returns**

- **reshaped_matrix**: [sparse matrix] A sparse matrix with the given shape, not necessarily of the same format as the current object.

See also:

- **np.matrix.reshape**
  NumPy's implementation of 'reshape' for matrices

**scipy.sparse.coo_matrix.resize**

**coo_matrix.resize**(shape)

Resize the matrix in-place to dimensions given by shape

Any elements that lie within the new shape will remain at the same indices, while non-zero elements lying outside the new shape are removed.

**Parameters**

- **shape**: [(int, int)] number of rows and columns in the new matrix

**Notes**

The semantics are not identical to numpy.ndarray.resize or numpy.resize. Here, the same data will be maintained at each index before and after reshape, if that index is within the new bounds. In numpy, resizing maintains contiguity of the array, moving elements around in the logical matrix but not within a flattened representation.

We give no guarantees about whether the underlying data attributes (arrays, etc.) will be modified in place or replaced with new objects.

**scipy.sparse.coo_matrix.rint**

**coo_matrix.rint**()

Element-wise rint.

See numpy.rint for more information.
**scipy.sparse.coo_matrix.set_shape**

```python
coo_matrix.set_shape(shape)
```

See `reshape`.

**scipy.sparse.coo_matrix.setdiag**

```python
coo_matrix.setdiag(values, k=0)
```

Set diagonal or off-diagonal elements of the array.

**Parameters**

- `values` [array_like] New values of the diagonal elements. Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values if longer than the diagonal, then the remaining values are ignored. If a scalar value is given, all of the diagonal is set to it.
- `k` [int, optional] Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).

**scipy.sparse.coo_matrix.sign**

```python
coo_matrix.sign()
```

Element-wise sign. See `numpy.sign` for more information.

**scipy.sparse.coo_matrix.sin**

```python
coo_matrix.sin()
```

Element-wise sin. See `numpy.sin` for more information.

**scipy.sparse.coo_matrix.sinh**

```python
coo_matrix.sinh()
```

Element-wise sinh. See `numpy.sinh` for more information.

**scipy.sparse.coo_matrix.sqrt**

```python
coo_matrix.sqrt()
```

Element-wise sqrt. See `numpy.sqrt` for more information.

**scipy.sparse.coo_matrix.sum**

```python
coo_matrix.sum(axis=None, dtype=None, out=None)
```

Sum the matrix elements over a given axis.

**Parameters**

- `axis` [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the sum of all the matrix elements, returning a scalar (i.e. `axis = None`).
**dtype**

[dttype, optional] The type of the returned matrix and of the accumulator in which the elements are summed. The dttype of a is used by default unless a has an integer dttype of less precision than the default platform integer. In that case, if a is signed then the platform integer is used while if a is unsigned then an unsigned integer of the same precision as the platform integer is used. New in version 0.18.0.

**out**

[np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary. New in version 0.18.0.

**Returns**

**sum_along_axis**

[np.matrix] A matrix with the same shape as self, with the specified axis removed.

**See also:**

np.matrix.sum

NumPy’s implementation of ‘sum’ for matrices

scipy.sparse.coo_matrix.sum_duplicates

coo_matrix.sum_duplicates()

Eliminate duplicate matrix entries by adding them together

This is an in place operation

scipy.sparse.coo_matrix.tan

coo_matrix.tan()

Element-wise tan.

See numpy.tan for more information.

scipy.sparse.coo_matrix.tanh

coo_matrix.tanh()

Element-wise tanh.

See numpy.tanh for more information.

scipy.sparse.coo_matrix.toarray

coo_matrix.toarray(order=None, out=None)

See the docstring for spmatrix.toarray.

scipy.sparse.coo_matrix.tobsr

coo_matrix.tobsr(blocksize=None, copy=False)

Convert this matrix to Block Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant bsr_matrix.

When blocksize=(R, C) is provided, it will be used for construction of the bsr_matrix.
scipy.sparse.coo_matrix.tocoo
c
coo_matrix.tocoo(copy=False)
Convert this matrix to COOrdinate format.
With copy=False, the data/indices may be shared between this matrix and the resultant coo_matrix.

scipy.sparse.coo_matrix.tocsc
c
coo_matrix.tocsc(copy=False)
Convert this matrix to Compressed Sparse Column format
Duplicate entries will be summed together.

Examples
```python
>>> from numpy import array
>>> from scipy.sparse import coo_matrix
>>> row = array([0, 0, 1, 3, 1, 0])
>>> col = array([0, 2, 1, 3, 1, 0])
>>> data = array([1, 1, 1, 1, 1, 1])
>>> A = coo_matrix((data, (row, col)), shape=(4, 4)).tocsc()
>>> A.todense()
array([[3, 0, 1, 0],
        [0, 2, 0, 0],
        [0, 0, 0, 0],
        [0, 0, 0, 1]])
```

scipy.sparse.coo_matrix.tocsr
c
coo_matrix.tocsr(copy=False)
Convert this matrix to Compressed Sparse Row format
Duplicate entries will be summed together.

Examples
```python
>>> from numpy import array
>>> from scipy.sparse import coo_matrix
>>> row = array([0, 0, 1, 3, 1, 0])
>>> col = array([0, 2, 1, 3, 1, 0])
>>> data = array([1, 1, 1, 1, 1, 1])
>>> A = coo_matrix((data, (row, col)), shape=(4, 4)).tocsr()
>>> A.todense()
array([[3, 0, 1, 0],
        [0, 2, 0, 0],
        [0, 0, 0, 0],
        [0, 0, 0, 1]])
```

scipy.sparse.coo_matrix.todense
c
coo_matrix.todense(order=None, out=None)
Return a dense matrix representation of this matrix.

Parameters
```
order [{'C', 'F'}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating
```
the NumPy default of C-ordered. Cannot be specified in conjunction with the
out argument.

```
out
```
[ndarray, 2-dimensional, optional] If specified, uses this array (or numpy.
`matrix`) as the output buffer instead of allocating a new array to return. The
provided array must have the same shape and dtype as the sparse matrix on
which you are calling the method.

**Returns**

```
arr
```
[numpy.matrix, 2-dimensional] A NumPy matrix object with the same shape
and containing the same data represented by the sparse matrix, with the re-
quested memory order. If out was passed and was an array (rather than a
numpy.matrix), it will be filled with the appropriate values and returned
wrapped in a numpy.matrix object that shares the same memory.

**scipy.sparse.coo_matrix.todia**

```
coo_matrix.todia(copy=False)
```
Convert this matrix to sparse DIAgonal format.

With copy=False, the data/indices may be shared between this matrix and the resultant
dia_matrix.

**scipy.sparse.coo_matrix.todok**

```
coo_matrix.todok(copy=False)
```
Convert this matrix to Dictionary Of Keys format.

With copy=False, the data/indices may be shared between this matrix and the resultant
dok_matrix.

**scipy.sparse.coo_matrix.tolil**

```
coo_matrix.tolil(copy=False)
```
Convert this matrix to Linked List format.

With copy=False, the data/indices may be shared between this matrix and the resultant
lil_matrix.

**scipy.sparse.coo_matrix.transpose**

```
coo_matrix.transpose(axes=None, copy=False)
```
Reverses the dimensions of the sparse matrix.

**Parameters**

```
axes
```
[None, optional] This argument is in the signature solely for NumPy compati-
bility reasons. Do not pass in anything except for the default value.

```
copy
```
[bool, optional] Indicates whether or not attributes of `self` should be copied
whenever possible. The degree to which attributes are copied varies depending
on the type of sparse matrix being used.

**Returns**

```
p
```
[self with the dimensions reversed.]

**See also:**
**np.matrix.transpose**

NumPy's implementation of 'transpose' for matrices

**scipy.sparse.coo_matrix.trunc**

coo_matrix.trunc()

Element-wise trunc.

See numpy.trunc for more information.

**scipy.sparse.csc_matrix**

class scipy.sparse.csc_matrix(arg1, shape=None, dtype=None, copy=False)

Compressed Sparse Column matrix

This can be instantiated in several ways:

- `csc_matrix(D)` with a dense matrix or rank-2 ndarray D
- `csc_matrix(S)` with another sparse matrix S (equivalent to S.tocsc())
- `csc_matrix((M, N), [dtype])` to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype='d'.
- `csc_matrix((data, (row_ind, col_ind)), [shape=(M, N)])` where data, row_ind and col_ind satisfy the relationship a[row_ind[k], col_ind[k]] = data[k].
- `csc_matrix((data, indices, indptr), [shape=(M, N)])` is the standard CSC representation where the row indices for column i are stored in indices[indptr[i]:indptr[i+1]] and their corresponding values are stored in data[indptr[i]:indptr[i+1]]. If the shape parameter is not supplied, the matrix dimensions are inferred from the index arrays.

**Notes**

Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

**Advantages of the CSC format**

- efficient arithmetic operations CSC + CSC, CSC * CSC, etc.
- efficient column slicing
- fast matrix vector products (CSR, BSR may be faster)

**Disadvantages of the CSC format**

- slow row slicing operations (consider CSR)
- changes to the sparsity structure are expensive (consider LIL or DOK)

**Examples**

```python
>>> import numpy as np
>>> from scipy.sparse import csc_matrix
>>> csc_matrix((3, 4), dtype=np.int8).toarray()
array([[0, 0, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]], dtype=int8)
```
```python
>>> row = np.array([0, 2, 2, 0, 1, 2])
>>> col = np.array([0, 0, 1, 2, 2, 2])
>>> data = np.array([1, 2, 3, 4, 5, 6])
>>> csc_matrix((data, (row, col)), shape=(3, 3)).toarray()
array([[1, 0, 4],
[0, 0, 5],
[2, 3, 6]])
```

```python
>>> indptr = np.array([0, 2, 3, 6])
>>> indices = np.array([0, 2, 2, 0, 1, 2])
>>> data = np.array([1, 2, 3, 4, 5, 6])
>>> csc_matrix((data, indices, indptr), shape=(3, 3)).toarray()
array([[1, 0, 4],
[0, 0, 5],
[2, 3, 6]])
```

**Attributes**

- `dtype`  
  Data type of the matrix

- `shape`  

- `ndim`  
  [int] Number of dimensions (this is always 2)

- `nnz`  
  Number of stored values, including explicit zeros.

- `data`  
  Data array of the matrix

- `indices`  
  CSC format index array

- `indptr`  
  CSC format index pointer array

- `has_sorted_indices`

  Determine whether the matrix has sorted indices

**Methods**

- `arcsin()`  
  Element-wise arcsin.

- `arcsinh()`  
  Element-wise arcsinh.

- `arctan()`  
  Element-wise arctan.

- `arctanh()`  
  Element-wise arctanh.

- `argmax(axis, out)`  
  Return indices of maximum elements along an axis.

- `argmin(axis, out)`  
  Return indices of minimum elements along an axis.

- `asformat(format[, copy])`  
  Return this matrix in the passed format.

- `asfptype()`  
  Upcast matrix to a floating point format (if necessary)

- `astype(dtype[, casting, copy])`  
  Cast the matrix elements to a specified type.

- `ceil()`  
  Element-wise floor.

- `check_format([full_check])`  
  Check whether the matrix format is valid

- `conj([copy])`  
  Element-wise complex conjugation.

- `conjugate([copy])`  
  Element-wise complex conjugation.

- `copy()`  
  Returns a copy of this matrix.

- `count_nonzero()`  
  Number of non-zero entries, equivalent to

- `deg2rad()`  
  Element-wise deg2rad.

- `diagonal([k])`  
  Returns the k-th diagonal of the matrix.

- `dot(other)`  
  Ordinary dot product

- `eliminate_zeros()`  
  Remove zero entries from the matrix

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### scipy.sparse.csc_matrix.arcsin

```python
csc_matrix.arcsin()
```

Element-wise arcsin. See :func:`numpy.arcsin` for more information.

### scipy.sparse.csc_matrix.arcsinh

```python
csc_matrix.arcsinh()
```


### scipy.sparse.csc_matrix.arctan

```python
csc_matrix.arctan()
```

Element-wise arctan. See :func:`numpy.arctan` for more information.

### scipy.sparse.csc_matrix.arctanh

```python
csc_matrix.arctanh()
```

Element-wise arctanh. See :func:`numpy.arctanh` for more information.

### scipy.sparse.csc_matrix.argmax

```python
csc_matrix.argmax(axis=None, out=None)
```

Return indices of maximum elements along an axis. Implicit zero elements are also taken into account. If there are several maximum values, the index of the first occurrence is returned.

**Parameters**

- **axis** \([-2, -1, 0, 1, \text{None}], \text{optional}\) Axis along which the argmax is computed. If None (default), index of the maximum element in the flatten data is returned.
out  [None, optional] This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

ind  [np.matrix or int] Indices of maximum elements. If matrix, its size along axis is 1.

scipy.sparse.csc_matrix.argmin

csc_matrix.argmin(axis=None, out=None)

Return indices of minimum elements along an axis.

Implicit zero elements are also taken into account. If there are several minimum values, the index of the first occurrence is returned.

Parameters

axis  [{-2, -1, 0, 1, None}, optional] Axis along which the argmin is computed. If None (default), index of the minimum element in the flatten data is returned.

out  [None, optional] This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

ind  [np.matrix or int] Indices of minimum elements. If matrix, its size along axis is 1.

scipy.sparse.csc_matrix.asformat

csc_matrix.asformat(format, copy=False)

Return this matrix in the passed format.

Parameters

format  [{str, None}] The desired matrix format ("csr", "csc", "lil", "dok", "array", ...) or None for no conversion.

copy  [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A  [This matrix in the passed format.]

scipy.sparse.csc_matrix.asfptype

csc_matrix.asfptype()

Upcast matrix to a floating point format (if necessary)

scipy.sparse.csc_matrix.astype

csc_matrix.astype(dtype, casting='unsafe', copy=True)

Cast the matrix elements to a specified type.

Parameters

dtype  [string or numpy dtype] Typecode or data-type to which to cast the data.
casting

Parameters

copy

Notes

Examples

References

scipy.sparse.csc_matrix.ceil

csc_matrix.ceil()

Element-wise ceil.

See numpy.ceil for more information.

scipy.sparse.csc_matrix.check_format

csc_matrix.check_format(full_check=True)

check whether the matrix format is valid

Parameters

full_check

[bool, optional] If True, rigorous check, O(N) operations. Otherwise basic check, O(1) operations (default True).

scipy.sparse.csc_matrix.conj

csc_matrix.conj(copy=True)

Element-wise complex conjugation.

If the matrix is of non-complex data type and copy is False, this method does nothing and the data is not copied.

Parameters

copy

[bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.csc_matrix.conjugate

csc_matrix.conjugate(copy=True)

Element-wise complex conjugation.

If the matrix is of non-complex data type and copy is False, this method does nothing and the data is not copied.

Parameters

copy

[bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]
scipy.sparse.csc_matrix.copy

csc_matrix.copy()

Returns a copy of this matrix.

No data/indices will be shared between the returned value and current matrix.

scipy.sparse.csc_matrix.count_nonzero

csc_matrix.count_nonzero()

Number of non-zero entries, equivalent to

np.count_nonzero(a.toarray())

Unlike getnnz() and the nnz property, which return the number of stored entries (the length of
the data attribute), this method counts the actual number of non-zero entries in data.

scipy.sparse.csc_matrix.deg2rad

csc_matrix.deg2rad()

Element-wise deg2rad.

See numpy.deg2rad for more information.

scipy.sparse.csc_matrix.diagonal

csc_matrix.diagonal(k=0)

Returns the k-th diagonal of the matrix.

Parameters

k [int, optional] Which diagonal to set, corresponding to elements a[i, i+k]. De-
default: 0 (the main diagonal).

New in version 1.0.

See also:

numpy.diagonal

Equivalent numpy function.

Examples

>>> from scipy.sparse import csr_matrix

>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])

>>> A.diagonal()
array([1, 0, 5])

>>> A.diagonal(k=1)
array([2, 3])

scipy.sparse.csc_matrix.dot

csc_matrix.dot(other)

Ordinary dot product

Examples
```python
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

scipy.sparse.csc_matrix.eliminate_zeros

`csc_matrix.eliminate_zeros()`

Remove zero entries from the matrix

This is an in place operation

scipy.sparse.csc_matrix.expm1

`csc_matrix.expm1()`

Element-wise expm1.

See numpy.expm1 for more information.

scipy.sparse.csc_matrix.floor

`csc_matrix.floor()`

Element-wise floor.

See numpy.floor for more information.

scipy.sparse.csc_matrix.getH

`csc_matrix.getH()`

Return the Hermitian transpose of this matrix.

See also:

np.matrix.getH

NumPy’s implementation of getH for matrices

scipy.sparse.csc_matrix.get_shape

`csc_matrix.get_shape()`

Get shape of a matrix.

scipy.sparse.csc_matrix.getcol

`csc_matrix.getcol(i)`

Returns a copy of column i of the matrix, as a (m x 1) CSC matrix (column vector).

scipy.sparse.csc_matrix.getformat

`csc_matrix.getformat()`

Format of a matrix representation as a string.
scipy.sparse.csc_matrix.getmaxprint

csc_matrix.getmaxprint()
    Maximum number of elements to display when printed.

scipy.sparse.csc_matrix.getnnz

csc_matrix.getnnz(axis=None)
    Number of stored values, including explicit zeros.

    Parameters
    axis    [None, 0, or 1] Select between the number of values across the whole matrix,
            in each column, or in each row.

    See also:

    count_nonzero
        Number of non-zero entries

scipy.sparse.csc_matrix.getrow

csc_matrix.getrow(i)
    Returns a copy of row i of the matrix, as a (1 x n) CSR matrix (row vector).

scipy.sparse.csc_matrix.log1p

csc_matrix.log1p()
    Element-wise log1p.

    See numpy.log1p for more information.

scipy.sparse.csc_matrix.max

csc_matrix.max(axis=None, out=None)
    Return the maximum of the matrix or maximum along an axis. This takes all elements into
    account, not just the non-zero ones.

    Parameters
    axis    [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The
default is to compute the maximum over all the matrix elements, returning a
scalar (i.e. axis = None).
    out      [None, optional] This argument is in the signature solely for NumPy compat-
            ibility reasons. Do not pass in anything except for the default value, as this
            argument is not used.

    Returns
    amax    [coo_matrix or scalar] Maximum of a. If axis is None, the result is a scalar
            value. If axis is given, the result is a sparse.coo_matrix of dimension a.ndim
            - 1.

    See also:

    min
        The minimum value of a sparse matrix along a given axis.
np.matrix.max

NumPy’s implementation of ‘max’ for matrices

scipy.sparse.csc_matrix.maximum

csc_matrix.maximum(other)

Element-wise maximum between this and another matrix.

scipy.sparse.csc_matrix.mean

csc_matrix.mean(axis=None, dtype=None, out=None)

Compute the arithmetic mean along the specified axis.

Returns the average of the matrix elements. The average is taken over all elements in the matrix by default, otherwise over the specified axis. float64 intermediate and return values are used for integer inputs.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the mean is computed. The default is to compute the mean of all elements in the matrix (i.e. axis = None).
dtype [data-type, optional] Type to use in computing the mean. For integer inputs, the default is float64; for floating point inputs, it is the same as the input dtype.
out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.

Returns

m [np.matrix]

See also:

np.matrix.mean

NumPy’s implementation of ‘mean’ for matrices

scipy.sparse.csc_matrix.min

csc_matrix.min(axis=None, out=None)

Return the minimum of the matrix or maximum along an axis. This takes all elements into account, not just the non-zero ones.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the minimum over all the matrix elements, returning a scalar (i.e. axis = None).
out [None, optional] This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns
amin  [coo_matrix or scalar] Minimum of a. If axis is None, the result is a scalar value. If axis is given, the result is a sparse.coo_matrix of dimension a.ndim - 1.

See also:

max

The maximum value of a sparse matrix along a given axis.

np.matrix.min

NumPy’s implementation of ‘min’ for matrices

scipy.sparse.csc_matrix.minimum

csc_matrix.minimum(other)

Element-wise minimum between this and another matrix.

scipy.sparse.csc_matrix.multiply

csc_matrix.multiply(other)

Point-wise multiplication by another matrix, vector, or scalar.

scipy.sparse.csc_matrix.nonzero

csc_matrix.nonzero()

nonzero indices

Returns a tuple of arrays (row, col) containing the indices of the non-zero elements of the matrix.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

scipy.sparse.csc_matrix.power

csc_matrix.power(n, dtype=None)

This function performs element-wise power.

Parameters

- n  [n is a scalar]
- dtype  [If dtype is not specified, the current dtype will be preserved.]

scipy.sparse.csc_matrix.prune

csc_matrix.prune()

Remove empty space after all non-zero elements.

scipy.sparse.csc_matrix.rad2deg

csc_matrix.rad2deg()

Element-wise rad2deg.

See numpy.rad2deg for more information.
scipy.sparse.csc_matrix.reshape

csc_matrix.reshape(self, shape, order='C', copy=False)

Gives a new shape to a sparse matrix without changing its data.

Parameters

- shape (length-2 tuple of ints) The new shape should be compatible with the original shape.
- order ([{'C', 'F'}, optional]) Read the elements using this index order. 'C' means to read and write the elements using C-like index order; e.g. read entire first row, then second row, etc. ‘F’ means to read and write the elements using Fortran-like index order; e.g. read entire first column, then second column, etc.
- copy (bool, optional) Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

- reshaped_matrix (sparse matrix) A sparse matrix with the given shape, not necessarily of the same format as the current object.

See also:

- np.matrix.reshape

NumPy's implementation of 'reshape' for matrices

scipy.sparse.csc_matrix.resize

csc_matrix.resize(*shape)

Resize the matrix in-place to dimensions given by shape

Any elements that lie within the new shape will remain at the same indices, while non-zero elements lying outside the new shape are removed.

Parameters

- shape [(int, int)] number of rows and columns in the new matrix

Notes

The semantics are not identical to numpy.ndarray.resize or numpy.resize. Here, the same data will be maintained at each index before and after reshape, if that index is within the new bounds. In numpy, resizing maintains contiguity of the array, moving elements around in the logical matrix but not within a flattened representation.

We give no guarantees about whether the underlying data attributes (arrays, etc.) will be modified in place or replaced with new objects.

scipy.sparse.csc_matrix.rint

csc_matrix.rint()

Element-wise rint.

See numpy.rint for more information.
scipy.sparse.csc_matrix.set_shape

csc_matrix.set_shape(shape)
    See reshape.

scipy.sparse.csc_matrix.setdiag

csc_matrix.setdiag(values, k=0)
    Set diagonal or off-diagonal elements of the array.

    Parameters:
    values ([array_like]) New values of the diagonal elements.
    Values may have any length. If the diagonal is longer than values, then the
    remaining diagonal entries will not be set. If values if longer than the diagonal,
    then the remaining values are ignored.
    If a scalar value is given, all of the diagonal is set to it.
    k (int, optional) Which off-diagonal to set, corresponding to elements a[i,i+k].
    Default: 0 (the main diagonal).

scipy.sparse.csc_matrix.sign

csc_matrix.sign()
    Element-wise sign.
    See numpy.sign for more information.

scipy.sparse.csc_matrix.sin

csc_matrix.sin()
    Element-wise sin.
    See numpy.sin for more information.

scipy.sparse.csc_matrix.sinh

csc_matrix.sinh()
    Element-wise sinh.
    See numpy.sinh for more information.

scipy.sparse.csc_matrix.sort_indices

csc_matrix.sort_indices()
    Sort the indices of this matrix in place

scipy.sparse.csc_matrix.sorted_indices

csc_matrix.sorted_indices()
    Return a copy of this matrix with sorted indices

scipy.sparse.csc_matrix.sqrt

csc_matrix.sqrt()
    Element-wise sqrt.
    See numpy.sqrt for more information.
scipy.sparse.csc_matrix.sum

csc_matrix.sum(axis=None, dtype=None, out=None)
Sum the matrix elements over a given axis.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the sum of all the matrix elements, returning a scalar (i.e. axis = None).

dtype [dtype, optional] The type of the returned matrix and of the accumulator in which the elements are summed. The dtype of a is used by default unless a has an integer dtype of less precision than the default platform integer. In that case, if a is signed then the platform integer is used while if a is unsigned then an unsigned integer of the same precision as the platform integer is used. New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary. New in version 0.18.0.

Returns

sum_along_axis [np.matrix] A matrix with the same shape as self, with the specified axis removed.

See also:

np.matrix.sum
NumPy’s implementation of ‘sum’ for matrices

scipy.sparse.csc_matrix.sum_duplicates

csc_matrix.sum_duplicates()
Eliminate duplicate matrix entries by adding them together

The is an in place operation

scipy.sparse.csc_matrix.tan

csc_matrix.tan()
Element-wise tan.

See numpy.tan for more information.

scipy.sparse.csc_matrix.tanh

csc_matrix.tanh()
Element-wise tanh.

See numpy.tanh for more information.

scipy.sparse.csc_matrix.toarray

csc_matrix.toarray(order=None, out=None)
Return a dense ndarray representation of this matrix.
Parameters

order  [{‘C’, ‘F’}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is ‘None’, indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the out argument.

out  [ndarray, 2-dimensional, optional] If specified, uses this array as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method. For most sparse types, out is required to be memory contiguous (either C or Fortran ordered).

Returns

arr  [ndarray, 2-dimensional] An array with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If out was passed, the same object is returned after being modified in-place to contain the appropriate values.

scipy.sparse.csc_matrix.tobsr

csc_matrix.tobsr(blocksize=None, copy=False)
Convert this matrix to Block Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant bsr_matrix.

When blocksize=(R, C) is provided, it will be used for construction of the bsr_matrix.

scipy.sparse.csc_matrix.tocoo

csc_matrix.tocoo(copy=True)
Convert this matrix to COOrdinate format.

With copy=False, the data/indices may be shared between this matrix and the resultant coo_matrix.

scipy.sparse.csc_matrix.tocsc

csc_matrix.tocsc(copy=False)
Convert this matrix to Compressed Sparse Column format.

With copy=False, the data/indices may be shared between this matrix and the resultant csc_matrix.

scipy.sparse.csc_matrix.tocsr

csc_matrix.tocsr(copy=False)
Convert this matrix to Compressed Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant csr_matrix.

scipy.sparse.csc_matrix.todense

csc_matrix.todense(order=None, out=None)
Return a dense matrix representation of this matrix.

Parameters
order  [{‘C’, ‘F’}, optional] Whether to store multi-dimensional data in C (row-major)
(or Fortran (column-major) order in memory. The default is ‘None’, indicating
the NumPy default of C-ordered. Cannot be specified in conjunction with the
out argument.

out  [ndarray, 2-dimensional, optional] If specified, uses this array (or numpy.
matrix) as the output buffer instead of allocating a new array to return. The
provided array must have the same shape and dtype as the sparse matrix on
which you are calling the method.

Returns
arr  [numpy.matrix, 2-dimensional] A NumPy matrix object with the same shape
and containing the same data represented by the sparse matrix, with the re-
quested memory order. If out was passed and was an array (rather than a
numpy.matrix), it will be filled with the appropriate values and returned
wrapped in a numpy.matrix object that shares the same memory.

scipy.sparse.csc_matrix.todia

csc_matrix.todia(copy=False)
Convert this matrix to sparse DIAgonal format.
With copy=False, the data/indices may be shared between this matrix and the resultant
dia_matrix.

scipy.sparse.csc_matrix.todok

csc_matrix.todok(copy=False)
Convert this matrix to Dictionary Of Keys format.
With copy=False, the data/indices may be shared between this matrix and the resultant
dok_matrix.

scipy.sparse.csc_matrix.tolil

csc_matrix.tolil(copy=False)
Convert this matrix to LInked List format.
With copy=False, the data/indices may be shared between this matrix and the resultant
lil_matrix.

scipy.sparse.csc_matrix.transpose

csc_matrix.transpose(axes=None, copy=False)
Reverses the dimensions of the sparse matrix.

Parameters
axes  [None, optional] This argument is in the signature solely for NumPy compati-
bility reasons. Do not pass in anything except for the default value.
copy  [bool, optional] Indicates whether or not attributes of self should be copied
whenever possible. The degree to which attributes are copied varies depending
on the type of sparse matrix being used.

Returns
p  [self with the dimensions reversed.]
See also:
np.matrix.transpose

NumPy’s implementation of ‘transpose’ for matrices

scipy.sparse.csc_matrix.trunc

sc_matrix.trunc()

Element-wise trunc.

See numpy.trunc for more information.

scipy.sparse.csr_matrix

class scipy.sparse.csr_matrix(arg1, shape=None, dtype=None, copy=False)

Compressed Sparse Row matrix

This can be instantiated in several ways:

csr_matrix(D)

with a dense matrix or rank-2 ndarray D

csr_matrix(S)

with another sparse matrix S (equivalent to S.tocsr())

csr_matrix((M, N), [dtype])

%to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype=’d’.

csr_matrix((data, (row_ind, col_ind)), [shape=(M, N)])

where data, row_ind and col_ind satisfy the relationship a[row_ind[k], col_ind[k]] = data[k].

csr_matrix((data, indices, indptr), [shape=(M, N)])

is the standard CSR representation where the column indices for row i are stored in indices[indptr[i]:indptr[i+1]] and their corresponding values are stored in data[indptr[i]:indptr[i+1]]. If the shape parameter is not supplied, the matrix dimensions are inferred from the index arrays.

Notes
Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Advantages of the CSR format

• efficient arithmetic operations CSR + CSR, CSR * CSR, etc.
• efficient row slicing
• fast matrix vector products

Disadvantages of the CSR format

• slow column slicing operations (consider CSC)
• changes to the sparsity structure are expensive (consider LIL or DOK)
Examples

```python
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> csr_matrix(([3, 4], dtype=np.int8)).toarray()
array([[0, 0, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]], dtype=int8)

>>> row = np.array([0, 0, 1, 2, 2])
>>> col = np.array([0, 2, 2, 0, 1, 2])
>>> data = np.array([1, 2, 3, 4, 5, 6])
>>> csr_matrix((data, (row, col)), shape=(3, 3)).toarray()
array([[1, 0, 2],
       [0, 0, 3],
       [4, 5, 6]])

>>> indptr = np.array([0, 2, 3, 6])
>>> indices = np.array([0, 2, 2, 0, 1, 2])
>>> data = np.array([1, 2, 3, 4, 5, 6])
>>> csr_matrix((data, indices, indptr), shape=(3, 3)).toarray()
array([[1, 0, 2],
       [0, 0, 3],
       [4, 5, 6]])
```

As an example of how to construct a CSR matrix incrementally, the following snippet builds a term-document matrix from texts:

```python
>>> docs = [['hello', 'world', 'hello'], ['goodbye', 'cruel', 'world']]
>>> indptr = [0]
>>> indices = []
>>> data = []
>>> vocabulary = {}
>>> for d in docs:
...     for term in d:
...         index = vocabulary.setdefault(term, len(vocabulary))
...         indices.append(index)
...         data.append(1)
...     indptr.append(len(indices))
... >>> csr_matrix((data, indices, indptr), dtype=int).toarray()
array([[2, 1, 0, 0],
       [0, 1, 1, 1]])
```

Attributes

- **dtype** [dtype] Data type of the matrix
- **ndim** [int] Number of dimensions (this is always 2)
- **nnz** Number of stored values, including explicit zeros.
- **data** CSR format data array of the matrix
- **indices** CSR format index array of the matrix
- **indptr** CSR format index pointer array of the matrix
- **has_sorted_indices**
Determine whether the matrix has sorted indices

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<tr>
<td><code>mean(axis, dtype, out)</code></td>
<td>Compute the arithmetic mean along the specified axis.</td>
</tr>
<tr>
<td><code>min(axis, out)</code></td>
<td>Return the minimum of the matrix or maximum along an axis.</td>
</tr>
<tr>
<td><code>minimum(other)</code></td>
<td>Element-wise minimum between this and another matrix.</td>
</tr>
<tr>
<td><code>multiply(other)</code></td>
<td>Point-wise multiplication by another matrix, vector, or scalar.</td>
</tr>
<tr>
<td><code>nonzero()</code></td>
<td>nonzero indices</td>
</tr>
</tbody>
</table>

Continued on next page
Table 170 — continued from previous page

- **power(n[, dtype])**: This function performs element-wise power.
- **prune()**: Remove empty space after all non-zero elements.
- **rad2deg()**: Element-wise rad2deg.
- **reshape(self, shape[, order, copy])**: Gives a new shape to a sparse matrix without changing its data.
- **resize(*shape)**: Resize the matrix in-place to dimensions given by *shape*
- **rint()**: Element-wise rint.
- **set_shape(shape)**: See reshape.
- **setdiag(values[, k])**: Set diagonal or off-diagonal elements of the array.
- **sign()**: Element-wise sign.
- **sin()**: Element-wise sin.
- **sinh()**: Element-wise sinh.
- **sort_indices()**: Sort the indices of this matrix in place.
- **sorted_indices()**: Return a copy of this matrix with sorted indices.
- **sqrt()**: Element-wise sqrt.
- **sum(axis, dtype, out)**: Sum the matrix elements over a given axis.
- **sum_duplicates()**: Eliminate duplicate matrix entries by adding them together.
- **tan()**: Element-wise tan.
- **tanh()**: Element-wise tanh.
- **toarray([order, out])**: Return a dense ndarray representation of this matrix.
- **tobsr([blocksize, copy])**: Convert this matrix to Block Sparse Row format.
- **tocoo([copy])**: Convert this matrix to COOrdinate format.
- **tocsc([copy])**: Convert this matrix to Compressed Sparse Column format.
- **tocsr([copy])**: Convert this matrix to Compressed Sparse Row format.
- **todense([order, out])**: Return a dense matrix representation of this matrix.
- **todia([copy])**: Convert this matrix to sparse DIAgonal format.
- **todok([copy])**: Convert this matrix to Dictionary Of Keys format.
- **tolil([copy])**: Convert this matrix to LInked List format.
- **transpose([axes, copy])**: Reverses the dimensions of the sparse matrix.
- **trunc()**: Element-wise trunc.

**scipy.sparse.csr_matrix.arcsin**

- **csr_matrix.arcsin()**: Element-wise arcsin.
  
  See numpy.arcsin for more information.

**scipy.sparse.csr_matrix.arcsinh**

- **csr_matrix.arcsinh()**: Element-wise arcsinh.
  
  See numpy.arcsinh for more information.
scipy.sparse.csr_matrix.arctan
csr_matrix.arctan()
   Element-wise arctan.
   See numpy.arctan for more information.

scipy.sparse.csr_matrix.arctanh
csr_matrix.arctanh()
   Element-wise arctanh.
   See numpy.arctanh for more information.

scipy.sparse.csr_matrix.argmax
csr_matrix.argmax(axis=None, out=None)
   Return indices of maximum elements along an axis.
   Implicit zero elements are also taken into account. If there are several maximum values, the index
   of the first occurrence is returned.

   Parameters
   axis  [{-2, -1, 0, 1, None}, optional] Axis along which the argmax is computed. If
         None (default), index of the maximum element in the flatten data is returned.
   out   [None, optional] This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

   Returns
   ind   [np.matrix or int] Indices of maximum elements. If matrix, its size along axis
         is 1.

scipy.sparse.csr_matrix.argmin
csr_matrix.argmin(axis=None, out=None)
   Return indices of minimum elements along an axis.
   Implicit zero elements are also taken into account. If there are several minimum values, the index
   of the first occurrence is returned.

   Parameters
   axis  [{-2, -1, 0, 1, None}, optional] Axis along which the argmin is computed. If
         None (default), index of the minimum element in the flatten data is returned.
   out   [None, optional] This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

   Returns
   ind   [np.matrix or int] Indices of minimum elements. If matrix, its size along axis
         is 1.
scipy.sparse.csr_matrix.asformat

csr_matrix.asformat(format, copy=False)

Return this matrix in the passed format.

Parameters

- format: [{str, None}] The desired matrix format (“csr”, “csc”, “lil”, “dok”, “array”, …) or None for no conversion.
- copy: [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

- A: [This matrix in the passed format.]

scipy.sparse.csr_matrix.asfptype

csr_matrix.asfptype()

Upcast matrix to a floating point format (if necessary)

scipy.sparse.csr_matrix.astype

csr_matrix.astype(dtype, casting='unsafe', copy=True)

Cast the matrix elements to a specified type.

Parameters

- dtype: [string or numpy dtype] Typecode or data-type to which to cast the data.
- casting: [{‘no’, ‘equiv’, ‘safe’, ‘same_kind’, ‘unsafe’}, optional] Controls what kind of data casting may occur. Defaults to ‘unsafe’ for backwards compatibility. ‘no’ means the data types should not be cast at all. ‘equiv’ means only byte-order changes are allowed. ‘safe’ means only casts which can preserve values are allowed. ‘same_kind’ means only safe casts or casts within a kind, like float64 to float32, are allowed. ‘unsafe’ means any data conversions may be done.
- copy: [bool, optional] If copy is False, the result might share some memory with this matrix. If copy is True, it is guaranteed that the result and this matrix do not share any memory.

scipy.sparse.csr_matrix.ceil

csr_matrix.ceil()

Element-wise ceil.

See numpy.ceil for more information.

scipy.sparse.csr_matrix.check_format

csr_matrix.check_format(full_check=True)

check whether the matrix format is valid

Parameters

- full_check: [bool, optional] If True, rigorous check, O(N) operations. Otherwise basic check, O(1) operations (default True).
scipy.sparse.csr_matrix.conj

csr_matrix.conj(copy=True)
Element-wise complex conjugation.

If the matrix is of non-complex data type and copy is False, this method does nothing and the data is not copied.

Parameters
- copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns
- A [The element-wise complex conjugate.]

scipy.sparse.csr_matrix.conjugate

csr_matrix.conjugate(copy=True)
Element-wise complex conjugation.

If the matrix is of non-complex data type and copy is False, this method does nothing and the data is not copied.

Parameters
- copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns
- A [The element-wise complex conjugate.]

scipy.sparse.csr_matrix.copy

csr_matrix.copy()
Returns a copy of this matrix.

No data/indices will be shared between the returned value and current matrix.

scipy.sparse.csr_matrix.count_nonzero

csr_matrix.count_nonzero()
Number of non-zero entries, equivalent to
np.count_nonzero(a.toarray())

Unlike getnnz() and the nz property, which return the number of stored entries (the length of the data attribute), this method counts the actual number of non-zero entries in data.

scipy.sparse.csr_matrix.deg2rad

csr_matrix.deg2rad()
Element-wise deg2rad.

See numpy.deg2rad for more information.
scipy.sparse.csr_matrix.diagonal

csr_matrix.diagonal(k=0)
Returns the k-th diagonal of the matrix.

Parameters
  k [int, optional] Which diagonal to set, corresponding to elements a[i, i+k].
  Default: 0 (the main diagonal).
  New in version 1.0.

See also:
numpy.diagonal
  Equivalent numpy function.

Examples
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> A.diagonal()  
array([1, 0, 5])
>>> A.diagonal(k=1)
array([2, 3])

scipy.sparse.csr_matrix.dot

csr_matrix.dot(other)
Ordinary dot product.

Examples
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)

scipy.sparse.csr_matrix.eliminate_zeros

csr_matrix.eliminate_zeros()
Remove zero entries from the matrix
  This is an \textit{in place} operation.

scipy.sparse.csr_matrix.expm1

csr_matrix.expm1()
Element-wise expm1.
  See numpy.expm1 for more information.

scipy.sparse.csr_matrix.floor

csr_matrix.floor()
Element-wise floor.
See numpy.floor for more information.

**scipy.sparse.csr_matrix.getH**

csr_matrix.getH()

Return the Hermitian transpose of this matrix.

**See also:**

np.matrix.getH

NumPy's implementation of getH for matrices

**scipy.sparse.csr_matrix.get_shape**

csr_matrix.get_shape()

Get shape of a matrix.

**scipy.sparse.csr_matrix.getcol**

csr_matrix.getcol(i)

Returns a copy of column i of the matrix, as a (m x 1) CSR matrix (column vector).

**scipy.sparse.csr_matrix.getformat**

csr_matrix.getformat()

Format of a matrix representation as a string.

**scipy.sparse.csr_matrix.getmaxprint**

csr_matrix.getmaxprint()

Maximum number of elements to display when printed.

**scipy.sparse.csr_matrix.getnnz**

csr_matrix.getnnz(axis=None)

Number of stored values, including explicit zeros.

**Parameters**

axis [None, 0, or 1] Select between the number of values across the whole matrix, in each column, or in each row.

**See also:**

count_nonzero

Number of non-zero entries

**scipy.sparse.csr_matrix.getrow**

csr_matrix.getrow(i)

Returns a copy of row i of the matrix, as a (1 x n) CSR matrix (row vector).
scipy.sparse.csr_matrix.log1p

csr_matrix.log1p()

Element-wise log1p.

See numpy.log1p for more information.

scipy.sparse.csr_matrix.max

csr_matrix.max(axis=None, out=None)

Return the maximum of the matrix or maximum along an axis. This takes all elements into account, not just the non-zero ones.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the maximum over all the matrix elements, returning a scalar (i.e. axis = None).

out [None, optional] This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

amax [coo_matrix or scalar] Maximum of a. If axis is None, the result is a scalar value. If axis is given, the result is a sparse.coo_matrix of dimension a.ndim - 1.

See also:

min

The minimum value of a sparse matrix along a given axis.

np.matrix.max

NumPy’s implementation of ‘max’ for matrices

scipy.sparse.csr_matrix.maximum

csr_matrix.maximum(other)

Element-wise maximum between this and another matrix.

scipy.sparse.csr_matrix.mean

csr_matrix.mean(axis=None, dtype=None, out=None)

Compute the arithmetic mean along the specified axis.

Returns the average of the matrix elements. The average is taken over all elements in the matrix by default, otherwise over the specified axis. float64 intermediate and return values are used for integer inputs.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the mean is computed. The default is to compute the mean of all elements in the matrix (i.e. axis = None).

dtype [data-type, optional] Type to use in computing the mean. For integer inputs, the default is float64; for floating point inputs, it is the same as the input dtype.

New in version 0.18.0.
out | [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary. New in version 0.18.0.

Returns
m | [np.matrix]

See also:

np.matrix.mean
NumPy’s implementation of ‘mean’ for matrices

scipy.sparse.csr_matrix.min
csr_matrix.min(axis=None, out=None)
Return the minimum of the matrix or maximum along an axis. This takes all elements into account, not just the non-zero ones.

Parameters
axis | [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the minimum over all the matrix elements, returning a scalar (i.e. axis = None).
out | [None, optional] This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns
amin | [coo_matrix or scalar] Minimum of a. If axis is None, the result is a scalar value. If axis is given, the result is a sparse.coo_matrix of dimension a.ndim - 1.

See also:

max
The maximum value of a sparse matrix along a given axis.

np.matrix.min
NumPy’s implementation of ‘min’ for matrices

scipy.sparse.csr_matrix.minimum
csr_matrix.minimum(other)
Element-wise minimum between this and another matrix.

scipy.sparse.csr_matrix.multiply
csr_matrix.multiply(other)
Point-wise multiplication by another matrix, vector, or scalar.
**scipy.sparse.csr_matrix.nonzero**

`csr_matrix.nonzero()`

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

**Examples**

```python
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

**scipy.sparse.csr_matrix.power**

`csr_matrix.power(n, dtype=None)`

This function performs element-wise power.

**Parameters**

- `n` [n is a scalar]
- `dtype` [If dtype is not specified, the current dtype will be preserved.]

**scipy.sparse.csr_matrix.prune**

`csr_matrix.prune()`

Remove empty space after all non-zero elements.

**scipy.sparse.csr_matrix.rad2deg**

`csr_matrix.rad2deg()`

Element-wise rad2deg.

See numpy.rad2deg for more information.

**scipy.sparse.csr_matrix.reshape**

`csr_matrix.reshape(self, shape, order='C', copy=False)`

Gives a new shape to a sparse matrix without changing its data.

**Parameters**

- `shape` [length-2 tuple of ints] The new shape should be compatible with the original shape.
- `order` [{‘C’, ‘F’}, optional] Read the elements using this index order. ‘C’ means to read and write the elements using C-like index order; e.g. read entire first row, then second row, etc. ‘F’ means to read and write the elements using Fortran-like index order; e.g. read entire first column, then second column, etc.
- `copy` [bool, optional] Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

**Returns**

- `reshaped_matrix` [sparse matrix] A sparse matrix with the given `shape`, not necessarily of the same format as the current object.
See also:

**np.matrix.reshape**

NumPy's implementation of 'reshape' for matrices

**scipy.sparse.csr_matrix.resize**

`csr_matrix.resize(*shape)`

Resize the matrix in-place to dimensions given by `shape`

Any elements that lie within the new shape will remain at the same indices, while non-zero elements lying outside the new shape are removed.

**Parameters**

- `shape` [(int, int)] number of rows and columns in the new matrix

**Notes**

The semantics are not identical to `numpy.ndarray.resize` or `numpy.resize`. Here, the same data will be maintained at each index before and after reshape, if that index is within the new bounds. In numpy, resizing maintains contiguity of the array, moving elements around in the logical matrix but not within a flattened representation.

We give no guarantees about whether the underlying data attributes (arrays, etc.) will be modified in place or replaced with new objects.

**scipy.sparse.csr_matrix.rint**

`csr_matrix.rint()`

Element-wise rint.

See `numpy.rint` for more information.

**scipy.sparse.csr_matrix.set_shape**

`csr_matrix.set_shape(shape)`

See `reshape`.

**scipy.sparse.csr_matrix.setdiag**

`csr_matrix.setdiag(values, k=0)`

Set diagonal or off-diagonal elements of the array.

**Parameters**

- `values` [array_like] New values of the diagonal elements.
  Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values if longer than the diagonal, then the remaining values are ignored.
  If a scalar value is given, all of the diagonal is set to it.

- `k` [int, optional] Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).
scipy.sparse.csr_matrix.sign

csr_matrix.sign()

Element-wise sign.

See numpy.sign for more information.

scipy.sparse.csr_matrix.sin

csr_matrix.sin()

Element-wise sin.

See numpy.sin for more information.

scipy.sparse.csr_matrix.sinh

csr_matrix.sinh()

Element-wise sinh.

See numpy.sinh for more information.

scipy.sparse.csr_matrix.sort_indices

csr_matrix.sort_indices()

Sort the indices of this matrix in place

scipy.sparse.csr_matrix.sorted_indices

csr_matrix.sorted_indices()

Return a copy of this matrix with sorted indices

scipy.sparse.csr_matrix.sqrt

csr_matrix.sqrt()

Element-wise sqrt.

See numpy.sqrt for more information.

scipy.sparse.csr_matrix.sum

csr_matrix.sum(axis=None, dtype=None, out=None)

Sum the matrix elements over a given axis.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The
default is to compute the sum of all the matrix elements, returning a scalar
(i.e. axis = None).

dtype [dtype, optional] The type of the returned matrix and of the accumulator in
which the elements are summed. The dtype of a is used by default unless a
has an integer dtype of less precision than the default platform integer. In
that case, if a is signed then the platform integer is used while if a is unsigned
then an unsigned integer of the same precision as the platform integer is used.
New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It
must have the same shape as the expected output, but the type of the output
values will be cast if necessary.
New in version 0.18.0.

**Returns**

`sum_along_axis`

[np.matrix] A matrix with the same shape as `self`, with the specified axis removed.

**See also:**

* np.matrix.sum
  
  NumPy's implementation of 'sum' for matrices

* scipy.sparse.csr_matrix.sum_duplicates

  csr_matrix.sum_duplicates()

  Eliminate duplicate matrix entries by adding them together

  The is an *in place* operation

* scipy.sparse.csr_matrix.tan

  csr_matrix.tan()

  Element-wise tan.

  See numpy.tan for more information.

* scipy.sparse.csr_matrix.tanh

  csr_matrix.tanh()

  Element-wise tanh.

  See numpy.tanh for more information.

* scipy.sparse.csr_matrix.toarray

  csr_matrix.toarray(order=None, out=None)

  Return a dense ndarray representation of this matrix.

  **Parameters**

  order [{‘C’, ‘F’}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is ‘None’, indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the `out` argument.

  out [ndarray, 2-dimensional, optional] If specified, uses this array as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method. For most sparse types, `out` is required to be memory contiguous (either C or Fortran ordered).

  **Returns**

  arr [ndarray, 2-dimensional] An array with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If `out` was passed, the same object is returned after being modified in-place to contain the appropriate values.
scipy.sparse.csr_matrix.tobsr

```python
csr_matrix.tobsr(blocksize=None, copy=True)
```
Convert this matrix to Block Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant bsr_matrix.

When blocksize=(R, C) is provided, it will be used for construction of the bsr_matrix.

scipy.sparse.csr_matrix.tocoo

```python
csr_matrix.tocoo(copy=True)
```
Convert this matrix to COOrdinate format.

With copy=False, the data/indices may be shared between this matrix and the resultant coo_matrix.

scipy.sparse.csr_matrix.tocsc

```python
csr_matrix.tocsc(copy=False)
```
Convert this matrix to Compressed Sparse Column format.

With copy=False, the data/indices may be shared between this matrix and the resultant csc_matrix.

scipy.sparse.csr_matrix.tocsr

```python
csr_matrix.tocsr(copy=False)
```
Convert this matrix to Compressed Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant csr_matrix.

scipy.sparse.csr_matrix.todense

```python
csr_matrix.todense(order=None, out=None)
```
Return a dense matrix representation of this matrix.

**Parameters**

- `order`: [{'C', 'F'}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is ‘None’, indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the `out` argument.
- `out`: [ndarray, 2-dimensional, optional] If specified, uses this array (or `numpy.matrix`) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.

**Returns**

- `arr`: [numpy.matrix, 2-dimensional] A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If `out` was passed and was an array (rather than a `numpy.matrix`), it will be filled with the appropriate values and returned wrapped in a `numpy.matrix` object that shares the same memory.

6.21. Sparse matrices (scipy.sparse)
scipy.sparse.csr_matrix.todia

csr_matrix.todia(copy=False)
Convert this matrix to sparse DIAGONAL format.

With copy=False, the data/indices may be shared between this matrix and the resultant
dia_matrix.

scipy.sparse.csr_matrix.todok

csr_matrix.todok(copy=False)
Convert this matrix to Dictionary Of Keys format.

With copy=False, the data/indices may be shared between this matrix and the resultant
dok_matrix.

scipy.sparse.csr_matrix.tolil

csr_matrix.tolil(copy=False)
Convert this matrix to LInked List format.

With copy=False, the data/indices may be shared between this matrix and the resultant
lil_matrix.

scipy.sparse.csr_matrix.transpose

csr_matrix.transpose(axes=None, copy=False)
Reverses the dimensions of the sparse matrix.

Parameters

axes [None, optional] This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value.
copy [bool, optional] Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

p [self with the dimensions reversed.]

See also:

np.matrix.transpose
 NumPy’s implementation of ‘transpose' for matrices

scipy.sparse.csr_matrix.trunc

csr_matrix.trunc()
Element-wise trunc.

See numpy.trunc for more information.

scipy.sparse.dia_matrix

class scipy.sparse.dia_matrix(arg1, shape=None, dtype=None, copy=False)
Sparse matrix with DIAGONAL storage

This can be instantiated in several ways:
dia_matrix(D)

with a dense matrix

dia_matrix(S)

with another sparse matrix S (equivalent to S.todia())

dia_matrix((M, N), [dtype])

to construct an empty matrix with shape (M, N), dtype is optional, defaulting to
dtype='d'.

dia_matrix((data, offsets), shape=(M, N))

where the data[k,:] stores the diagonal entries for diagonal offsets[k] (See example
below)

Notes
Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Examples

```python
>>> import numpy as np
>>> from scipy.sparse import dia_matrix
>>> dia_matrix((3, 4), dtype=np.int8).toarray()
array([[0, 0, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]], dtype=int8)

>>> data = np.array([[1, 2, 3, 4]]).repeat(3, axis=0)
>>> offsets = np.array([0, -1, 2])
>>> dia_matrix((data, offsets), shape=(4, 4)).toarray()
array([[1, 0, 3, 0],
       [1, 2, 0, 4],
       [0, 2, 3, 0],
       [0, 0, 3, 4]])
```

Attributes

dtype [dtype] Data type of the matrix
ndim [int] Number of dimensions (this is always 2)
nnz Number of stored values, including explicit zeros.
data DIA format data array of the matrix
offsets DIA format offset array of the matrix

Methods

- arcsin()
- arcsinh()
- arctan()
- arctanh()
- asformat()
- astype()
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<th>Function</th>
<th>Description</th>
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<td><code>ceil()</code></td>
<td>Element-wise ceiling</td>
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<tr>
<td><code>conj([copy])</code></td>
<td>Element-wise complex conjugation</td>
</tr>
<tr>
<td><code>conjugate([copy])</code></td>
<td>Element-wise complex conjugation</td>
</tr>
<tr>
<td><code>copy()</code></td>
<td>Returns a copy of this matrix.</td>
</tr>
<tr>
<td><code>count_nonzero()</code></td>
<td>Number of non-zero entries, equivalent to</td>
</tr>
<tr>
<td><code>deg2rad()</code></td>
<td>Element-wise deg2rad</td>
</tr>
<tr>
<td><code>diagonal([k])</code></td>
<td>Returns the k-th diagonal of the matrix.</td>
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**scipy.sparse.dia_matrix.arcsin**

`dia_matrix.arcsin()`  
Element-wise arcsin.  
See numpy.arcsin for more information.

**scipy.sparse.dia_matrix.arcsinh**

`dia_matrix.arcsinh()`  
Element-wise arcsinh.  
See numpy.arcsinh for more information.

**scipy.sparse.dia_matrix.arctan**

`dia_matrix.arctan()`  
Element-wise arctan.  
See numpy.arctan for more information.

**scipy.sparse.dia_matrix.arctanh**

`dia_matrix.arctanh()`  
Element-wise arctanh.  
See numpy.arctanh for more information.

**scipy.sparse.dia_matrix.asformat**

`dia_matrix.asformat(format, copy=False)`  
Return this matrix in the passed format.

**Parameters**

- `format`  
  (str, None] The desired matrix format ("csr", "csc", "lil", "dok", "array", ...) or None for no conversion.
- `copy`  
  [bool, optional] If True, the result is guaranteed to not share data with self.

**Returns**

- `A`  
  [This matrix in the passed format.]
**scipy.sparse.dia_matrix.asfptype**

```python
dia_matrix.asfptype()
```
Upcast matrix to a floating point format (if necessary)

**scipy.sparse.dia_matrix.astype**

```python
dia_matrix.astype(dtype, casting='unsafe', copy=True)
```
Cast the matrix elements to a specified type.

**Parameters**

- **dtype** [string or numpy dtype] Typecode or data-type to which to cast the data.
- **casting** [{{'no', 'equiv', 'safe', 'same_kind', 'unsafe'}, optional] Controls what kind of data casting may occur. Defaults to 'unsafe' for backwards compatibility. ‘no’ means the data types should not be cast at all. ‘equiv’ means only byte-order changes are allowed. ‘safe’ means only casts which can preserve values are allowed. ‘same_kind’ means only safe casts or casts within a kind, like float64 to float32, are allowed. ‘unsafe’ means any data conversions may be done.
- **copy** [bool, optional] If `copy` is `False`, the result might share some memory with this matrix. If `copy` is `True`, it is guaranteed that the result and this matrix do not share any memory.

**scipy.sparse.dia_matrix.ceil**

```python
dia_matrix.ceil()
```
Element-wise ceiling.

See numpy.ceil for more information.

**scipy.sparse.dia_matrix.conj**

```python
dia_matrix.conj(copy=True)
```
Element-wise complex conjugation.

If the matrix is of non-complex data type and `copy` is `False`, this method does nothing and the data is not copied.

**Parameters**

- **copy** [bool, optional] If True, the result is guaranteed to not share data with self.

**Returns**

- **A** [The element-wise complex conjugate.]

**scipy.sparse.dia_matrix.conjugate**

```python
dia_matrix.conjugate(copy=True)
```
Element-wise complex conjugation.

If the matrix is of non-complex data type and `copy` is `False`, this method does nothing and the data is not copied.

**Parameters**

- **copy** [bool, optional] If True, the result is guaranteed to not share data with self.

**Returns**

- **A** [The element-wise complex conjugate.]
**scipy.sparse.dia_matrix.copy**

dia_matrix.copy()

Returns a copy of this matrix.

No data/indices will be shared between the returned value and current matrix.

**scipy.sparse.dia_matrix.count_nonzero**

dia_matrix.count_nonzero()

Number of non-zero entries, equivalent to

np.count_nonzero(a.toarray())

Unlike getnnz() and the nnz property, which return the number of stored entries (the length of
the data attribute), this method counts the actual number of non-zero entries in data.

**scipy.sparse.dia_matrix.deg2rad**

dia_matrix.deg2rad()

Element-wise deg2rad.

See numpy.deg2rad for more information.

**scipy.sparse.dia_matrix.diagonal**

dia_matrix.diagonal(k=0)

Returns the k-th diagonal of the matrix.

**Parameters**

k [int, optional] Which diagonal to set, corresponding to elements a[i, i+k]. Default: 0 (the main diagonal).

New in version 1.0.

**See also:**

numpy.diagonal

Equivalent numpy function.

**Examples**

```python
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> A.diagonal()
array([1, 0, 5])
>>> A.diagonal(k=1)
array([2, 3])
```

**scipy.sparse.dia_matrix.dot**

dia_matrix.dot(other)

Ordinary dot product

**Examples**
```python
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

**scipy.sparse.dia_matrix.expm1**

`dia_matrix.expm1()`  
Element-wise expm1.  
See `numpy.expm1` for more information.

**scipy.sparse.dia_matrix.floor**

`dia_matrix.floor()`  
Element-wise floor.  
See `numpy.floor` for more information.

**scipy.sparse.dia_matrix.getH**

`dia_matrix.getH()`  
Return the Hermitian transpose of this matrix.  
See also:

`np.matrix.getH`  
NumPy’s implementation of `getH` for matrices

**scipy.sparse.dia_matrix.get_shape**

`dia_matrix.get_shape()`  
Get shape of a matrix.

**scipy.sparse.dia_matrix.getcol**

`dia_matrix.getcol(j)`  
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

**scipy.sparse.dia_matrix.getformat**

`dia_matrix.getformat()`  
Format of a matrix representation as a string.

**scipy.sparse.dia_matrix.getmaxprint**

`dia_matrix.getmaxprint()`  
Maximum number of elements to display when printed.
scipy.sparse.dia_matrix.getnnz

dia_matrix.getnnz(axis=None)
Number of stored values, including explicit zeros.

Parameters

axis [None, 0, or 1] Select between the number of values across the whole matrix, in each column, or in each row.

See also:

count_nonzero
Number of non-zero entries

scipy.sparse.dia_matrix.getrow

dia_matrix.getrow(i)
Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

scipy.sparse.dia_matrix.log1p

dia_matrix.log1p()
Element-wise log1p.
See numpy.log1p for more information.

scipy.sparse.dia_matrix.maximum

dia_matrix.maximum(other)
Element-wise maximum between this and another matrix.

scipy.sparse.dia_matrix.mean

dia_matrix.mean(axis=None, dtype=None, out=None)
Compute the arithmetic mean along the specified axis.

Returns the average of the matrix elements. The average is taken over all elements in the matrix by default, otherwise over the specified axis. float64 intermediate and return values are used for integer inputs.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the mean is computed. The default is to compute the mean of all elements in the matrix (i.e. axis = None).
dtype [data-type, optional] Type to use in computing the mean. For integer inputs, the default is float64; for floating point inputs, it is the same as the input dtype.
out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.

Returns

m [np.matrix]

See also:
np.matrix.mean

NumPy’s implementation of ‘mean’ for matrices

scipy.sparse.dia_matrix.minimum

dia_matrix.minimum(other)
Element-wise minimum between this and another matrix.

scipy.sparse.dia_matrix.multiply

dia_matrix.multiply(other)
Point-wise multiplication by another matrix

scipy.sparse.dia_matrix.nonzero

dia_matrix.nonzero()
nonzero indices

Returns a tuple of arrays (row, col) containing the indices of the non-zero elements of the matrix.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

scipy.sparse.dia_matrix.power

dia_matrix.power(n, dtype=None)
This function performs element-wise power.

Parameters

- **n** [n is a scalar]
- **dtype** [If dtype is not specified, the current dtype will be preserved.]

scipy.sparse.dia_matrix.rad2deg

dia_matrix.rad2deg()
Element-wise rad2deg.

See numpy.rad2deg for more information.

scipy.sparse.dia_matrix.reshape

dia_matrix.reshape(self, shape, order='C', copy=False)
Gives a new shape to a sparse matrix without changing its data.

Parameters

- **shape** [length-2 tuple of ints] The new shape should be compatible with the original shape.
- **order** [{‘C’, ‘F’}, optional] Read the elements using this index order. ‘C’ means to read and write the elements using C-like index order; e.g. read entire first row, then second row, etc. ‘F’ means to read and write the elements using Fortran-like index order; e.g. read entire first column, then second column, etc.
copy [bool, optional] Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

reshaped_matrix [sparse matrix] A sparse matrix with the given shape, not necessarily of the same format as the current object.

See also:

np.matrix.reshape
NumPy’s implementation of ‘reshape’ for matrices

scipy.sparse.dia_matrix.resize
dia_matrix.resize(*shape)
Reshape the matrix in-place to dimensions given by shape

Any elements that lie within the new shape will remain at the same indices, while non-zero elements lying outside the new shape are removed.

Parameters

shape [(int, int)] number of rows and columns in the new matrix

Notes
The semantics are not identical to numpy.ndarray.resize or numpy.resize. Here, the same data will be maintained at each index before and after reshape, if that index is within the new bounds. In numpy, resizing maintains contiguity of the array, moving elements around in the logical matrix but not within a flattened representation.

We give no guarantees about whether the underlying data attributes (arrays, etc.) will be modified in place or replaced with new objects.

scipy.sparse.dia_matrix.rint
dia_matrix.rint()
Element-wise rint.

See numpy.rint for more information.

scipy.sparse.dia_matrix.set_shape
dia_matrix.set_shape(shape)
See reshape.

scipy.sparse.dia_matrix.setdiag
dia_matrix.setdiag(values, k=0)
Set diagonal or off-diagonal elements of the array.

Parameters

values [array_like] New values of the diagonal elements.
Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values if longer than the diagonal, then the remaining values are ignored.
If a scalar value is given, all of the diagonal is set to it.

\( k \) [int, optional] Which off-diagonal to set, corresponding to elements \( a[i,i+k] \).
Default: 0 (the main diagonal).

```python
scipy.sparse.dia_matrix.sign
```

```
dia_matrix.sign()
```

Element-wise sign.

See numpy.sign for more information.

```python
scipy.sparse.dia_matrix.sin
```

```
dia_matrix.sin()
```

Element-wise sin.

See numpy.sin for more information.

```python
scipy.sparse.dia_matrix.sinh
```

```
dia_matrix.sinh()
```

Element-wise sinh.

See numpy.sinh for more information.

```python
scipy.sparse.dia_matrix.sqrt
```

```
dia_matrix.sqrt()
```

Element-wise sqrt.

See numpy.sqrt for more information.

```python
scipy.sparse.dia_matrix.sum
```

```
dia_matrix.sum(axis=None, dtype=None, out=None)
```

Sum the matrix elements over a given axis.

**Parameters**

- **axis** [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the sum of all the matrix elements, returning a scalar (i.e. \( axis = None \)).

- **dtype** [dtype, optional] The type of the returned matrix and of the accumulator in which the elements are summed. The dtype of \( a \) is used by default unless \( a \) has an integer dtype of less precision than the default platform integer. In that case, if \( a \) is signed then the platform integer is used while if \( a \) is unsigned then an unsigned integer of the same precision as the platform integer is used. New in version 0.18.0.

- **out** [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary. New in version 0.18.0.

**Returns**

- **sum_along_axis** [np.matrix] A matrix with the same shape as \( self \), with the specified axis removed.
See also:

*np.matrix.sum*

NumPy's implementation of 'sum' for matrices

```
scipy.sparse.dia_matrix.tan
dia_matrix.tan()
```

Element-wise tan.

See `numpy.tan` for more information.

```
scipy.sparse.dia_matrix.tanh
dia_matrix.tanh()
```

Element-wise tanh.

See `numpy.tanh` for more information.

```
scipy.sparse.dia_matrix.toarray
dia_matrix.toarray(order=None, out=None)
```

Return a dense ndarray representation of this matrix.

**Parameters**

- `order` [{`C`, `F`}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is ‘None’, indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the `out` argument.

- `out` [ndarray, 2-dimensional, optional] If specified, uses this array as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method. For most sparse types, `out` is required to be memory contiguous (either C or Fortran ordered).

**Returns**

- `arr` [ndarray, 2-dimensional] An array with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If `out` was passed, the same object is returned after being modified in-place to contain the appropriate values.

```
scipy.sparse.dia_matrix.tobsr
dia_matrix.tobsr(blocksize=None, copy=False)
```

Convert this matrix to Block Sparse Row format.

With `copy=False`, the data/indices may be shared between this matrix and the resultant `bsr_matrix`.

When `blocksize=(R, C)` is provided, it will be used for construction of the `bsr_matrix`. 
scipy.sparse.dia_matrix.tocoo

dia_matrix.tocoo(copy=False)
    Convert this matrix to COOrdinate format.
    With copy=False, the data/indices may be shared between this matrix and the resultant coo_matrix.

scipy.sparse.dia_matrix.tocsc

dia_matrix.tocsc(copy=False)
    Convert this matrix to Compressed Sparse Column format.
    With copy=False, the data/indices may be shared between this matrix and the resultant csc_matrix.

scipy.sparse.dia_matrix.tocsr

dia_matrix.tocsr(copy=False)
    Convert this matrix to Compressed Sparse Row format.
    With copy=False, the data/indices may be shared between this matrix and the resultant csr_matrix.

scipy.sparse.dia_matrix.todense

dia_matrix.todense(order=None, out=None)
    Return a dense matrix representation of this matrix.
    
    Parameters
    ----------
    order : {'C', 'F'}, optional
        Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the out argument.
    out : ndarray, 2-dimensional, optional
        If specified, uses this array (or numpy.matrix) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.
    
    Returns
    -------
    arr : numpy.matrix, 2-dimensional
        A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If out was passed and was an array (rather than a numpy.matrix), it will be filled with the appropriate values and returned wrapped in a numpy.matrix object that shares the same memory.

scipy.sparse.dia_matrix.todia

dia_matrix.todia(copy=False)
    Convert this matrix to sparse DIAgonal format.
    With copy=False, the data/indices may be shared between this matrix and the resultant dia_matrix.
**scipy.sparse.dia_matrix.todok**

`dia_matrix.todok(copy=False)`

Convert this matrix to Dictionary Of Keys format.

With `copy=False`, the data/indices may be shared between this matrix and the resultant `dok_matrix`.

**scipy.sparse.dia_matrix.tolil**

`dia_matrix.tolil(copy=False)`

Convert this matrix to LInked List format.

With `copy=False`, the data/indices may be shared between this matrix and the resultant `lil_matrix`.

**scipy.sparse.dia_matrix.transpose**

`dia_matrix.transpose(axes=None, copy=False)`

Reverses the dimensions of the sparse matrix.

**Parameters**

- `axes` [None, optional] This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value.
- `copy` [bool, optional] Indicates whether or not attributes of `self` should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

**Returns**

- `p` [self with the dimensions reversed.]

**See also:**

- `np.matrix.transpose`
  
  NumPy’s implementation of ‘transpose’ for matrices

**scipy.sparse.dia_matrix.trunc**

`dia_matrix.trunc()`

Element-wise trunc.

See `numpy.trunc` for more information.

**scipy.sparse.dok_matrix**

Class `scipy.sparse.dok_matrix(arg1, shape=None, dtype=None, copy=False)`

Dictionary Of Keys based sparse matrix.

This is an efficient structure for constructing sparse matrices incrementally.

This can be instantiated in several ways:

- `dok_matrix(D)` with a dense matrix, D
- `dok_matrix(S)` with a sparse matrix, S
dok_matrix((M,N), [dtype])

create the matrix with initial shape (M,N) dtype is optional, defaulting to dtype='d'

Notes
Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Allows for efficient O(1) access of individual elements. Duplicates are not allowed. Can be efficiently converted to a coo_matrix once constructed.

Examples

```python
>>> import numpy as np
>>> from scipy.sparse import dok_matrix
>>> S = dok_matrix((5, 5), dtype=np.float32)
>>> for i in range(5):
...     for j in range(5):
...         S[i, j] = i + j  # Update element
```

Attributes

dtype [dtype] Data type of the matrix
nndim [int] Number of dimensions (this is always 2)
nnz Number of stored values, including explicit zeros.

Methods

asformat(format[, copy]) Return this matrix in the passed format.
asfptype() Upcast matrix to a floating point format (if necessary)
astype(dtype[, casting, copy]) Cast the matrix elements to a specified type.
clear()
conj([copy]) Element-wise complex conjugation.
conjtransp() Return the conjugate transpose.
conjugate([copy]) Element-wise complex conjugation.
copy() Returns a copy of this matrix.
count_nonzero() Number of non-zero entries, equivalent to
diagonal([k]) Returns the k-th diagonal of the matrix.
dot(other) Ordinary dot product
fromkeys($type, iterable[, value]) Returns a new dict with keys from iterable and values equal to value.
get(key[, default]) This overrides the dict.get method, providing type checking but otherwise equivalent functionality.
getH() Return the Hermitian transpose of this matrix.
get_shape() Get shape of a matrix.
getcol(j) Returns the j-th column as a (m x 1) DOK matrix.
getformat() Format of a matrix representation as a string.
getmaxprint() Maximum number of elements to display when printed.
getnnz([axis]) Number of stored values, including explicit zeros.
getrow(i) Returns the i-th row as a (1 x n) DOK matrix.
items()  
keys()  
maximum(other)  
mean(axis, dtype, out)  
minimum(other)  
multiply(other)  
nonzero()  
pop(k[, d])  
popitem()  
power(n[, dtype])  
reshape(self, shape[, order, copy])  
resize(*shape)  
set_shape(shape)  
setdefault(k[, d])  
setdiag(values[, k])  
sum(axis, dtype, out)  
toarray([order, out])  
tobsr([blocksize, copy])  
tocoo([copy])  
tocsc([copy])  
tocsr([copy])  
todense([order, out])  
todia([copy])  
todok([copy])  
tolil([copy])  
transpose([axes, copy])  
update([E, **F])  
values()  

**scipy.sparse.dok_matrix.asformat**  

**dok_matrix.asformat**(format, copy=False)  
Return this matrix in the passed format.

**Parameters**  
format  

6.21. Sparse matrices (**scipy.sparse**)  

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or None for no conversion.

**copy**  [bool, optional] If True, the result is guaranteed to not share data with self.

**Returns**

A  [This matrix in the passed format.]

---

**scipy.sparse.dok_matrix.asfptype**

dok_matrix.asfptype()

Upcast matrix to a floating point format (if necessary)

---

**scipy.sparse.dok_matrix.astype**

dok_matrix.astype(dtype, casting='unsafe', copy=True)

Cast the matrix elements to a specified type.

**Parameters**

dtype  [string or numpy dtype] Typecode or data-type to which to cast the data.

casting  [{'no', 'equiv', 'safe', 'same_kind', 'unsafe'}, optional] Controls what kind of data casting may occur. Defaults to ‘unsafe’ for backwards compatibility. ‘no’ means the data types should not be cast at all. ‘equiv’ means only byte-order changes are allowed. ‘safe’ means only casts which can preserve values are allowed. ‘same_kind’ means only safe casts or casts within a kind, like float64 to float32, are allowed. ‘unsafe’ means any data conversions may be done.

copy  [bool, optional] If copy is False, the result might share some memory with this matrix. If copy is True, it is guaranteed that the result and this matrix do not share any memory.

---

**scipy.sparse.dok_matrix.clear**

dok_matrix.clear() → None. Remove all items from D.

---

**scipy.sparse.dok_matrix.conj**

dok_matrix.conj(copy=True)

Element-wise complex conjugation.

If the matrix is of non-complex data type and copy is False, this method does nothing and the data is not copied.

**Parameters**

copy  [bool, optional] If True, the result is guaranteed to not share data with self.

**Returns**

A  [The element-wise complex conjugate.]

---

**scipy.sparse.dok_matrix.conjtransp**

dok_matrix.conjtransp()

Return the conjugate transpose.
scipy.sparse.dok_matrix.conjugate

dok_matrix.conjugate(copy=True)

Element-wise complex conjugation.

If the matrix is of non-complex data type and copy is False, this method does nothing and the data is not copied.

Parameters

- copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

- A [The element-wise complex conjugate.]

scipy.sparse.dok_matrix.copy

dok_matrix.copy()

Returns a copy of this matrix.

No data/indices will be shared between the returned value and current matrix.

scipy.sparse.dok_matrix.count_nonzero

dok_matrix.count_nonzero()

Number of non-zero entries, equivalent to

np.count_nonzero(a.toarray())

Unlike getnnz() and the nnz property, which return the number of stored entries (the length of the data attribute), this method counts the actual number of non-zero entries in data.

scipy.sparse.dok_matrix.diagonal

dok_matrix.diagonal(k=0)

Returns the k-th diagonal of the matrix.

Parameters

- k [int, optional] Which diagonal to set, corresponding to elements a[i, i+k]. Default: 0 (the main diagonal).

New in version 1.0.

See also:

numpy.diagonal

Equivalent numpy function.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> A.diagonal()
array([1, 0, 5])
>>> A.diagonal(k=1)
array([2, 3])
```
scipy.sparse.dok_matrix.dot

dok_matrix.dot(other)
   Ordinary dot product

Examples
   >>> import numpy as np
   >>> from scipy.sparse import csr_matrix
   >>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
   >>> v = np.array([1, 0, -1])
   >>> A.dot(v)
   array([ 1, -3, -1], dtype=int64)

scipy.sparse.dok_matrix.fromkeys

dok_matrix.fromkeys($type, iterable, value=None, /)
   Returns a new dict with keys from iterable and values equal to value.

scipy.sparse.dok_matrix.get

dok_matrix.get(key, default=0.0)
   This overrides the dict.get method, providing type checking but otherwise equivalent functionality.

scipy.sparse.dok_matrix.getH

dok_matrix.getH()
   Return the Hermitian transpose of this matrix.
   See also:

   np.matrix.getH
      NumPy’s implementation of getH for matrices

scipy.sparse.dok_matrix.get_shape

dok_matrix.get_shape()
   Get shape of a matrix.

scipy.sparse.dok_matrix.getcol

dok_matrix.getcol(j)
   Returns the j-th column as a (m x 1) DOK matrix.

scipy.sparse.dok_matrix.getformat

dok_matrix.getformat()
   Format of a matrix representation as a string.

scipy.sparse.dok_matrix.getmaxprint

dok_matrix.getmaxprint()
   Maximum number of elements to display when printed.
**scipy.sparse.dok_matrix.getnnz**

_dok_matrix.getnnz(axis=None)_  
Number of stored values, including explicit zeros.

**Parameters**

- **axis**  
  [None, 0, or 1] Select between the number of values across the whole matrix, in each column, or in each row.

**See also:**

- **count_nonzero**  
  Number of non-zero entries

**scipy.sparse.dok_matrix.getrow**

dok_matrix.getrow(i)  
Returns the i-th row as a (1 x n) DOK matrix.

**scipy.sparse.dok_matrix.items**

dok_matrix.items() → a set-like object providing a view on D’s items

**scipy.sparse.dok_matrix.keys**

dok_matrix.keys() → a set-like object providing a view on D’s keys

**scipy.sparse.dok_matrix.maximum**

dok_matrix.maximum(other)  
Element-wise maximum between this and another matrix.

**scipy.sparse.dok_matrix.mean**

dok_matrix.mean(axis=None, dtype=None, out=None)  
Compute the arithmetic mean along the specified axis. Returns the average of the matrix elements. The average is taken over all elements in the matrix by default, otherwise over the specified axis. float64 intermediate and return values are used for integer inputs.

**Parameters**

- **axis**  
  [{-2, -1, 0, 1, None} optional] Axis along which the mean is computed. The default is to compute the mean of all elements in the matrix (i.e. axis = None).
- **dtype**  
  [data-type, optional] Type to use in computing the mean. For integer inputs, the default is float64; for floating point inputs, it is the same as the input dtype. New in version 0.18.0.
- **out**  
  [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary. New in version 0.18.0.

**Returns**

- **m**  
  [np.matrix]
See also:

np.matrix.mean

NumPy's implementation of 'mean' for matrices

scipy.sparse.dok_matrix.minimum
dok_matrix.minimum(other)

Element-wise minimum between this and another matrix.

scipy.sparse.dok_matrix.multiply
dok_matrix.multiply(other)

Point-wise multiplication by another matrix

scipy.sparse.dok_matrix.nonzero
dok_matrix.nonzero()

nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 1, 2]), array([0, 1, 2]))
```

scipy.sparse.dok_matrix.pop
dok_matrix.pop(k[, d]) → v, remove specified key and return the corresponding value.

If key is not found, d is returned if given, otherwise KeyError is raised

scipy.sparse.dok_matrix.popitem
dok_matrix.popitem() → (k, v), remove and return some (key, value) pair as a 2-tuple; but raise KeyError if D is empty.

scipy.sparse.dok_matrix.power
dok_matrix.power(n, dtype=None)

Element-wise power.

scipy.sparse.dok_matrix.reshape
dok_matrix.reshape(self, shape, order='C', copy=False)

Gives a new shape to a sparse matrix without changing its data.

Parameters

shape  [length-2 tuple of ints] The new shape should be compatible with the original shape.
order [{‘C’, ‘F’}, optional] Read the elements using this index order. ‘C’ means to read and write the elements using C-like index order; e.g. read entire first row, then second row, etc. ‘F’ means to read and write the elements using Fortran-like index order; e.g. read entire first column, then second column, etc.

copy [bool, optional] Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

reshaped_matrix [sparse matrix] A sparse matrix with the given shape, not necessarily of the same format as the current object.

See also:

np.matrix.reshape

NumPy’s implementation of ‘reshape’ for matrices

scipy.sparse.dok_matrix.resize
dok_matrix.resize(*shape)

Resize the matrix in-place to dimensions given by shape

Any elements that lie within the new shape will remain at the same indices, while non-zero elements lying outside the new shape are removed.

Parameters

shape [(int, int)] number of rows and columns in the new matrix

Notes

The semantics are not identical to numpy.ndarray.resize or numpy.resize. Here, the same data will be maintained at each index before and after reshape, if that index is within the new bounds. In numpy, resizing maintains contiguity of the array, moving elements around in the logical matrix but not within a flattened representation.

We give no guarantees about whether the underlying data attributes (arrays, etc.) will be modified in place or replaced with new objects.

scipy.sparse.dok_matrix.set_shape
dok_matrix.set_shape(shape)

See reshape.

scipy.sparse.dok_matrix.setdefault
dok_matrix.setdefault(k[, d]) → D.get(k,d), also set D[k]=d if k not in D

scipy.sparse.dok_matrix.setdiag
dok_matrix.setdiag(values, k=0)

Set diagonal or off-diagonal elements of the array.

Parameters
values [array_like] New values of the diagonal elements. Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values if longer than the diagonal, then the remaining values are ignored. If a scalar value is given, all of the diagonal is set to it.

k [int, optional] Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).

scipy.sparse.dok_matrix.sum
dok_matrix.sum(axis=None, dtype=None, out=None)
Sum the matrix elements over a given axis.

Parameters
axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the sum of all the matrix elements, returning a scalar (i.e. axis = None).
dtype [dtype, optional] The type of the returned matrix and of the accumulator in which the elements are summed. The dtype of a is used by default unless a has an integer dtype of less precision than the default platform integer. In that case, if a is signed then the platform integer is used while if a is unsigned then an unsigned integer of the same precision as the platform integer is used. New in version 0.18.0.
out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary. New in version 0.18.0.

Returns
sum_along_axis [np.matrix] A matrix with the same shape as self, with the specified axis removed.

See also:
np.matrix.sum
NumPy’s implementation of ‘sum’ for matrices

scipy.sparse.dok_matrix.toarray
dok_matrix.toarray(order=None, out=None)
Return a dense ndarray representation of this matrix.

Parameters
order [{‘C’, ‘F’}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is ‘None’, indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the out argument.
out [ndarray, 2-dimensional, optional] If specified, uses this array as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method. For most sparse types, out is required to be memory contiguous (either C or Fortran ordered).
**Returns**

`arr` [ndarray, 2-dimensional] An array with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If `out` was passed, the same object is returned after being modified in-place to contain the appropriate values.

**scipy.sparse.dok_matrix.tobsr**

`dok_matrix.tobsr(blocksize=None, copy=False)`  
Convert this matrix to Block Sparse Row format.

With `copy=False`, the data/indices may be shared between this matrix and the resultant `bsr_matrix`.

When `blocksize=(R, C)` is provided, it will be used for construction of the `bsr_matrix`.

**scipy.sparse.dok_matrix.tocoo**

`dok_matrix.tocoo(copy=False)`  
Convert this matrix to COOrdinate format.

With `copy=False`, the data/indices may be shared between this matrix and the resultant `coo_matrix`.

**scipy.sparse.dok_matrix.tocsc**

`dok_matrix.tocsc(copy=False)`  
Convert this matrix to Compressed Sparse Column format.

With `copy=False`, the data/indices may be shared between this matrix and the resultant `csc_matrix`.

**scipy.sparse.dok_matrix.tocsr**

`dok_matrix.tocsr(copy=False)`  
Convert this matrix to Compressed Sparse Row format.

With `copy=False`, the data/indices may be shared between this matrix and the resultant `csr_matrix`.

**scipy.sparse.dok_matrix.todense**

`dok_matrix.todense(order=None, out=None)`  
Return a dense matrix representation of this matrix.

**Parameters**

- `order` [{‘C’, ‘F’}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is ‘None’, indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the `out` argument.

- `out` [ndarray, 2-dimensional, optional] If specified, uses this array (or `numpy.matrix`) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and `dtype` as the sparse matrix on which you are calling the method.

**Returns**
arr [numpy.matrix, 2-dimensional] A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If out was passed and was an array (rather than a numpy.matrix), it will be filled with the appropriate values and returned wrapped in a numpy.matrix object that shares the same memory.

scipy.sparse.dok_matrix.todia
dok_matrix.todia(copy=False)
Convert this matrix to sparse DIAgonal format.
With copy=False, the data/indices may be shared between this matrix and the resultant dia_matrix.

scipy.sparse.dok_matrix.todok
dok_matrix.todok(copy=False)
Convert this matrix to Dictionary Of Keys format.
With copy=False, the data/indices may be shared between this matrix and the resultant dok_matrix.

scipy.sparse.dok_matrix.tolil
dok_matrix.tolil(copy=False)
Convert this matrix to LInked List format.
With copy=False, the data/indices may be shared between this matrix and the resultant lil_matrix.

scipy.sparse.dok_matrix.transpose
dok_matrix.transpose(axes=None, copy=False)
Reverses the dimensions of the sparse matrix.

Parameters
axes [None, optional] This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value.
copy [bool, optional] Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns
p [self with the dimensions reversed.]

See also:

np.matrix.transpose
NumPy's implementation of 'transpose' for matrices

scipy.sparse.dok_matrix.update
dok_matrix.update([E], **F) → None. Update D from dict/iterable E and F.
If E is present and has a .keys() method, then does: for k in E: D[k] = E[k] If E is present and
lacks a .keys() method, then does: for k, v in E: D[k] = v. In either case, this is followed by: for k in F: D[k] = F[k].

```python
scipy.sparse.dok_matrix.values
```

```python
dok_matrix.values() → an object providing a view on D’s values
```

```python
scipy.sparse.lil_matrix
```

```python
class scipy.sparse.lil_matrix(arg1, shape=None, dtype=None, copy=False)
```

Row-based linked list sparse matrix

This is a structure for constructing sparse matrices incrementally. Note that inserting a single item can take linear time in the worst case; to construct a matrix efficiently, make sure the items are pre-sorted by index, per row.

This can be instantiated in several ways:

```python
lil_matrix(D)
```

with a dense matrix or rank-2 ndarray D

```python
lil_matrix(S)
```

with another sparse matrix S (equivalent to S.tolil())

```python
lil_matrix((M, N), [dtype])
```

to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype='d'.

Notes

Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Advantages of the LIL format

• supports flexible slicing
• changes to the matrix sparsity structure are efficient

Disadvantages of the LIL format

• arithmetic operations LIL + LIL are slow (consider CSR or CSC)
• slow column slicing (consider CSC)
• slow matrix vector products (consider CSR or CSC)

Intended Usage

• LIL is a convenient format for constructing sparse matrices
• once a matrix has been constructed, convert to CSR or CSC format for fast arithmetic and matrix vector operations
• consider using the COO format when constructing large matrices

Data Structure

• An array (self.rows) of rows, each of which is a sorted list of column indices of non-zero elements.
The corresponding nonzero values are stored in similar fashion in `self.data`.

**Attributes**

- `dtype` [dtype] Data type of the matrix
- `ndim` [int] Number of dimensions (this is always 2)
- `nnz` Number of stored values, including explicit zeros.
- `data` LIL format data array of the matrix
- `rows` LIL format row index array of the matrix

**Methods**

- `asformat(format[, copy])` Return this matrix in the passed format.
- `astype()` Upcast matrix to a floating point format (if necessary)
- `astype(dtype[, casting, copy])` Cast the matrix elements to a specified type.
- `conj([copy])` Element-wise complex conjugation.
- `conjugate([copy])` Element-wise complex conjugation.
- `copy()` Returns a copy of this matrix.
- `count_nonzero()` Number of non-zero entries, equivalent to
- `diagonal([k])` Returns the k-th diagonal of the matrix.
- `dot(other)` Ordinary dot product
- `getH()` Return the Hermitian transpose of this matrix.
- `get_shape()` Get shape of a matrix.
- `getcol(j)` Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).
- `getformat()` Format of a matrix representation as a string.
- `getmaxprint()` Maximum number of elements to display when printed.
- `getnnz([axis])` Number of stored values, including explicit zeros.
- `getrow(i)` Returns a copy of the 'i'th row.
- `getrowview(i)` Returns a view of the 'i'th row (without copying).
- `maximum(other)` Element-wise maximum between this and another matrix.
- `mean([axis, dtype, out])` Compute the arithmetic mean along the specified axis.
- `minimum(other)` Element-wise minimum between this and another matrix.
- `multiply(other)` Point-wise multiplication by another matrix
- `nonzero()` non-zero indices
- `power(n[, dtype])` Element-wise power.
- `reshape(self, shape[, order, copy])` Gives a new shape to a sparse matrix without changing its data.
- `resize(*shape)` Resize the matrix in-place to dimensions given by `shape`
- `set_shape(shape)` See `reshape`.
- `setdiag(values[, k])` Set diagonal or off-diagonal elements of the array.
- `sum([axis, dtype, out])` Sum the matrix elements over a given axis.
- `toarray([order, out])` Return a dense ndarray representation of this matrix.

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<th>Description</th>
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<td>Convert this matrix to Block Sparse Row format.</td>
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<td>Convert this matrix to COOrdinate format.</td>
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<td><code>tocsc([copy])</code></td>
<td>Convert this matrix to Compressed Sparse Column format.</td>
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<td><code>tocsr([copy])</code></td>
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<td><code>todense([order, out])</code></td>
<td>Return a dense matrix representation of this matrix.</td>
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<td><code>todia([copy])</code></td>
<td>Convert this matrix to sparse DIAgonal format.</td>
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<td>Reverses the dimensions of the sparse matrix.</td>
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#### scipy.sparse.lil_matrix.asformat

`lil_matrix.asformat(format, copy=False)`

Return this matrix in the passed format.

**Parameters**

- `format` ([str, None]) The desired matrix format ("csr", "csc", "lil", "dok", "array", ...) or None for no conversion.
- `copy` [bool, optional] If True, the result is guaranteed to not share data with self.

**Returns**

- `A` [This matrix in the passed format.]

#### scipy.sparse.lil_matrix.asfptype

`lil_matrix.asfptype()`

Upcast matrix to a floating point format (if necessary)

#### scipy.sparse.lil_matrix.astype

`lil_matrix.astype(dtype, casting='unsafe', copy=True)`

Cast the matrix elements to a specified type.

**Parameters**

- `dtype` [string or numpy dtype] Typecode or data-type to which to cast the data.
- `casting` [{‘no’, ‘equiv’, ‘safe’, ‘same_kind’, ‘unsafe’}, optional] Controls what kind of data casting may occur. Defaults to ‘unsafe’ for backwards compatibility. ‘no’ means the data types should not be cast at all. ‘equiv’ means only byte-order changes are allowed. ‘safe’ means only casts which can preserve values are allowed. ‘same_kind’ means only safe casts or casts within a kind, like float64 to float32, are allowed. ‘unsafe’ means any data conversions may be done.
- `copy` [bool, optional] If copy is False, the result might share some memory with this matrix. If copy is True, it is guaranteed that the result and this matrix do not share any memory.

#### scipy.sparse.lil_matrix.conj

`lil_matrix.conj(copy=True)`

Element-wise complex conjugation.
If the matrix is of non-complex data type and \textit{copy} is False, this method does nothing and the data is not copied.

\textbf{Parameters}

\textit{copy} \hspace{1cm} \text{[bool, optional]} If True, the result is guaranteed to not share data with self.

\textbf{Returns}

\textit{A} \hspace{1cm} \text{[The element-wise complex conjugate.]}  

\texttt{scipy.sparse.lil_matrix.conjugate}

\texttt{lil_matrix.conjugate}(\textit{copy}=\texttt{True})  
Element-wise complex conjugation.

If the matrix is of non-complex data type and \textit{copy} is False, this method does nothing and the data is not copied.

\textbf{Parameters}

\textit{copy} \hspace{1cm} \text{[bool, optional]} If True, the result is guaranteed to not share data with self.

\textbf{Returns}

\textit{A} \hspace{1cm} \text{[The element-wise complex conjugate.]}  

\texttt{scipy.sparse.lil_matrix.copy}

\texttt{lil_matrix.copy()}  
Returns a copy of this matrix.

No data/indices will be shared between the returned value and current matrix.

\texttt{scipy.sparse.lil_matrix.count_nonzero}

\texttt{lil_matrix.count_nonzero()}  
Number of non-zero entries, equivalent to  
np.count_nonzero(a.toarray())  
Unlike \texttt{getnnz()} and the \texttt{nnz} property, which return the number of stored entries (the length of the data attribute), this method counts the actual number of non-zero entries in data.

\texttt{scipy.sparse.lil_matrix.diagonal}

\texttt{lil_matrix.diagonal}(\textit{k}=0)  
Returns the \textit{k}-th diagonal of the matrix.

\textbf{Parameters}

\textit{k} \hspace{1cm} \text{[int, optional]} Which diagonal to set, corresponding to elements \texttt{a[i, i+k]}. Default: 0 (the main diagonal).  
New in version 1.0.

\textbf{See also:}

\texttt{numpy.diagonal}  
Equivalent numpy function.
Examples

```python
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> A.diagonal()
array([1, 0, 5])
>>> A.diagonal(k=1)
array([2, 3])
```

**scipy.sparse.lil_matrix.dot**

lil_matrix.dot(other)
Ordinary dot product

**Examples**

```python
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

**scipy.sparse.lil_matrix.getH**

lil_matrix.getH()
Return the Hermitian transpose of this matrix.

See also:

**np.matrix.getH**
NumPy's implementation of getH for matrices

**scipy.sparse.lil_matrix.get_shape**

lil_matrix.get_shape()
Get shape of a matrix.

**scipy.sparse.lil_matrix.getcol**

lil_matrix.getcol(j)
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

**scipy.sparse.lil_matrix.getformat**

lil_matrix.getformat()
Format of a matrix representation as a string.

**scipy.sparse.lil_matrix.getmaxprint**

lil_matrix.getmaxprint()
Maximum number of elements to display when printed.
**scipy.sparse.lil_matrix.getnnz**

`lil_matrix.getnnz(axis=None)`

Number of stored values, including explicit zeros.

**Parameters**

- `axis` : [None, 0, 1] Select between the number of values across the whole matrix, in each column, or in each row.

**See also:**

- `count_nonzero`
  
  Number of non-zero entries

**scipy.sparse.lil_matrix.getrow**

`lil_matrix.getrow(i)`

Returns a copy of the ‘i’th row.

**scipy.sparse.lil_matrix.getrowview**

`lil_matrix.getrowview(i)`

Returns a view of the ‘i’th row (without copying).

**scipy.sparse.lil_matrix.maximum**

`lil_matrix.maximum(other)`

Element-wise maximum between this and another matrix.

**scipy.sparse.lil_matrix.mean**

`lil_matrix.mean(axis=None, dtype=None, out=None)`

Compute the arithmetic mean along the specified axis.

Returns the average of the matrix elements. The average is taken over all elements in the matrix by default, otherwise over the specified axis. `float64` intermediate and return values are used for integer inputs.

**Parameters**

- `axis` : [{-2, -1, 0, 1, None} optional] Axis along which the mean is computed. The default is to compute the mean of all elements in the matrix (i.e. `axis = None`).
- `dtype` : [data-type, optional] Type to use in computing the mean. For integer inputs, the default is `float64`; for floating point inputs, it is the same as the input dtype. New in version 0.18.0.
- `out` : [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary. New in version 0.18.0.

**Returns**

- `m` : [np.matrix]

**See also:**
np.matrix.mean

NumPy’s implementation of ‘mean’ for matrices

scipy.sparse.lil_matrix.minimum

lil_matrix.minimum(other)
Element-wise minimum between this and another matrix.

scipy.sparse.lil_matrix.multiply

lil_matrix.multiply(other)
Point-wise multiplication by another matrix.

scipy.sparse.lil_matrix.nonzero

lil_matrix.nonzero()
nonzero indices
Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

scipy.sparse.lil_matrix.power

lil_matrix.power(n, dtype=None)
Element-wise power.

scipy.sparse.lil_matrix.reshape

lil_matrix.reshape(self, shape, order='C', copy=False)
Gives a new shape to a sparse matrix without changing its data.

Parameters

- **shape** [length-2 tuple of ints] The new shape should be compatible with the original shape.

- **order** [{‘C’, ‘F’}, optional] Read the elements using this index order. ‘C’ means to read and write the elements using C-like index order; e.g. read entire first row, then second row, etc. ‘F’ means to read and write the elements using Fortran-like index order; e.g. read entire first column, then second column, etc.

- **copy** [bool, optional] Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

- **reshaped_matrix** [sparse matrix] A sparse matrix with the given shape, not necessarily of the same format as the current object.

See also:
np.matrix.reshape

NumPy’s implementation of ‘reshape’ for matrices

scipy.sparse.lil_matrix.resize

lil_matrix.resize(*shape)

Resize the matrix in-place to dimensions given by shape

Any elements that lie within the new shape will remain at the same indices, while non-zero elements lying outside the new shape are removed.

Parameters

shape [(int, int)] number of rows and columns in the new matrix

Notes

The semantics are not identical to numpy.ndarray.resize or numpy.resize. Here, the same data will be maintained at each index before and after reshape, if that index is within the new bounds. In numpy, resizing maintains contiguity of the array, moving elements around in the logical matrix but not within a flattened representation.

We give no guarantees about whether the underlying data attributes (arrays, etc.) will be modified in place or replaced with new objects.

scipy.sparse.lil_matrix.set_shape

lil_matrix.set_shape(shape)

See reshape.

scipy.sparse.lil_matrix.setdiag

lil_matrix.setdiag(values, k=0)

Set diagonal or off-diagonal elements of the array.

Parameters

values [array_like] New values of the diagonal elements. Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values if longer than the diagonal, then the remaining values are ignored. If a scalar value is given, all of the diagonal is set to it.

k [int, optional] Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).

scipy.sparse.lil_matrix.sum

lil_matrix.sum(axis=None, dtype=None, out=None)

Sum the matrix elements over a given axis.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the sum of all the matrix elements, returning a scalar (i.e. axis = None).

dtype [dtype, optional] The type of the returned matrix and of the accumulator in which the elements are summed. The dtype of a is used by default unless a has an integer dtype of less precision than the default platform integer. In
that case, if $a$ is signed then the platform integer is used while if $a$ is unsigned then an unsigned integer of the same precision as the platform integer is used. New in version 0.18.0.

**out**
[np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary. New in version 0.18.0.

**Returns**

**sum_along_axis**
[np.matrix] A matrix with the same shape as self, with the specified axis removed.

**See also:**

`np.matrix.sum`
NumPy’s implementation of ‘sum’ for matrices

**scipy.sparse.lil_matrix.tocoo**

**lil_matrix.tocoo**(order=None, out=None)
Return a dense ndarray representation of this matrix.

**Parameters**

**order**
[{'C', 'F'}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is ‘None’, indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the `out` argument.

**out**
[ndarray, 2-dimensional, optional] If specified, uses this array as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method. For most sparse types, `out` is required to be memory contiguous (either C or Fortran ordered).

**Returns**

**arr**
[ndarray, 2-dimensional] An array with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If `out` was passed, the same object is returned after being modified in-place to contain the appropriate values.

**scipy.sparse.lil_matrix.tobsr**

**lil_matrix.tobsr**(blocksize=None, copy=False)
Convert this matrix to Block Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant `bsr_matrix`.

When blocksize=(R, C) is provided, it will be used for construction of the `bsr_matrix`.

**scipy.sparse.lil_matrix.tocoo**

**lil_matrix.tocoo**(copy=False)
Convert this matrix to COOrdinate format.
With copy=False, the data/indices may be shared between this matrix and the resultant coo_matrix.

**scipy.sparse.lil_matrix.tocsc**

lil_matrix.tocsc(copy=False)

Convert this matrix to Compressed Sparse Column format.

With copy=False, the data/indices may be shared between this matrix and the resultant csc_matrix.

**scipy.sparse.lil_matrix.tocsr**

lil_matrix.tocsr(copy=False)

Convert this matrix to Compressed Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant csr_matrix.

**scipy.sparse.lil_matrix.todense**

lil_matrix.todense(order=None, out=None)

Return a dense matrix representation of this matrix.

**Parameters**

- **order** [{‘C’, ‘F’}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is ‘None’, indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the out argument.
- **out** [ndarray, 2-dimensional, optional] If specified, uses this array (or numpy.matrix) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.

**Returns**

- **arr** [numpy.matrix, 2-dimensional] A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If out was passed and was an array (rather than a numpy.matrix), it will be filled with the appropriate values and returned wrapped in a numpy.matrix object that shares the same memory.

**scipy.sparse.lil_matrix.todia**

lil_matrix.todia(copy=False)

Convert this matrix to sparse DIAgonal format.

With copy=False, the data/indices may be shared between this matrix and the resultant dia_matrix.

**scipy.sparse.lil_matrix.todok**

lil_matrix.todok(copy=False)

Convert this matrix to Dictionary Of Keys format.

With copy=False, the data/indices may be shared between this matrix and the resultant dok_matrix.
### scipy.sparse.lil_matrix.tolil

`lil_matrix.tolil(copy=False)`

Convert this matrix to Linked List format.

With `copy=False`, the data/indices may be shared between this matrix and the resultant `lil_matrix`.

### scipy.sparse.lil_matrix.transpose

`lil_matrix.transpose(axes=None, copy=False)`

Reverses the dimensions of the sparse matrix.

**Parameters**

- `axes` ([None, optional]) This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value.
- `copy` ([bool, optional]) Indicates whether or not attributes of `self` should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

**Returns**

- `p` ([`self` with the dimensions reversed.]

**See also:**

- `np.matrix.transpose`
  
  NumPy's implementation of 'transpose' for matrices

### scipy.sparse.spmatrix

#### class scipy.sparse.spmatrix(maxprint=50)

This class provides a base class for all sparse matrices. It cannot be instantiated. Most of the work is provided by subclasses.

**Attributes**

- `nnz` Number of stored values, including explicit zeros.
- `shape` Get shape of a matrix.

**Methods**

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**scipy.sparse.spmatrix.asformat**

`spmatrix.asformat(format, copy=False)`

Return this matrix in the passed format.

**Parameters**

- **format** [{str, None}] The desired matrix format ("csr", "csc", "lil", "dok", "array", ...) or None for no conversion.
- **copy** [bool, optional] If True, the result is guaranteed to not share data with self.

**Returns**

- **A** [This matrix in the passed format.]
scipy.sparse.spmatrix.asfptype

spmatrix.asfptype()
Upcast matrix to a floating point format (if necessary)

scipy.sparse.spmatrix.astype

spmatrix.astype(dtype, casting='unsafe', copy=True)
Cast the matrix elements to a specified type.

Parameters

dtype [string or numpy dtype] Typecode or data-type to which to cast the data.
casting [{‘no’, ‘equiv’, ‘safe’, ‘same_kind’, ‘unsafe’}, optional] Controls what kind of
data casting may occur. Defaults to ‘unsafe’ for backwards compatibility. ‘no’
means the data types should not be cast at all. ‘equiv’ means only byte-order
changes are allowed. ‘safe’ means only casts which can preserve values are
allowed. ‘same_kind’ means only safe casts or casts within a kind, like float64
to float32, are allowed. ‘unsafe’ means any data conversions may be done.
copy [bool, optional] If copy is False, the result might share some memory with this
matrix. If copy is True, it is guaranteed that the result and this matrix do not
share any memory.

scipy.sparse.spmatrix.conj

spmatrix.conj(copy=True)
Element-wise complex conjugation.

If the matrix is of non-complex data type and copy is False, this method does nothing and the
data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.spmatrix.conjugate

spmatrix.conjugate(copy=True)
Element-wise complex conjugation.

If the matrix is of non-complex data type and copy is False, this method does nothing and the
data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.spmatrix.copy

spmatrix.copy()
Returns a copy of this matrix.

No data/indices will be shared between the returned value and current matrix.
**scipy.sparse.spmatrix.count_nonzero**

`spmatrix.count_nonzero()`  
Number of non-zero entries, equivalent to  
`np.count_nonzero(a.toarray())`  
Unlike getnnz() and the nnz property, which return the number of stored entries (the length of the data attribute), this method counts the actual number of non-zero entries in data.

**scipy.sparse.spmatrix.diagonal**

`spmatrix.diagonal(k=0)`  
Returns the k-th diagonal of the matrix.

**Parameters**

- `k` : [int, optional] Which diagonal to set, corresponding to elements `a[i, i+k]`. Default: 0 (the main diagonal). New in version 1.0.

**See also:**

- `numpy.diagonal`  
  Equivalent numpy function.

**Examples**

```python  
>>> from scipy.sparse import csr_matrix  
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])  
>>> A.diagonal()  
array([1, 0, 5])  
>>> A.diagonal(k=1)  
array([2, 3])  
```

**scipy.sparse.spmatrix.dot**

`spmatrix.dot(other)`  
Ordinary dot product

**Examples**

```python  
>>> import numpy as np  
>>> from scipy.sparse import csr_matrix  
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])  
>>> v = np.array([1, 0, -1])  
>>> A.dot(v)  
array([ 1, -3, -1], dtype=int64)  
```

**scipy.sparse.spmatrix.getH**

`spmatrix.getH()`  
Return the Hermitian transpose of this matrix.

**See also:**

- `np.matrix.getH`  
  NumPy’s implementation of `getH` for matrices
scipy.sparse.spmatrix.get_shape

spmatrix.get_shape()
    Get shape of a matrix.

scipy.sparse.spmatrix.getcol

spmatrix.getcol(j)
    Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

scipy.sparse.spmatrix.getformat

spmatrix.getformat()
    Format of a matrix representation as a string.

scipy.sparse.spmatrix.getmaxprint

spmatrix.getmaxprint()
    Maximum number of elements to display when printed.

scipy.sparse.spmatrix.getnnz

spmatrix.getnnz(axis=None)
    Number of stored values, including explicit zeros.

    Parameters
    axis [None, 0, or 1] Select between the number of values across the whole matrix,
                   in each column, or in each row.

    See also:

    count_nonzero
        Number of non-zero entries

scipy.sparse.spmatrix.getrow

spmatrix.getrow(i)
    Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

scipy.sparse.spmatrix.maximum

spmatrix.maximum(other)
    Element-wise maximum between this and another matrix.

scipy.sparse.spmatrix.mean

spmatrix.mean(axis=None, dtype=None, out=None)
    Compute the arithmetic mean along the specified axis.

    Returns the average of the matrix elements. The average is taken over all elements in the matrix
    by default, otherwise over the specified axis. float64 intermediate and return values are used for
    integer inputs.

    Parameters
axis [{-2, -1, 0, 1, None} optional] Axis along which the mean is computed. The
default is to compute the mean of all elements in the matrix (i.e. axis = None).
dtype [data-type, optional] Type to use in computing the mean. For integer inputs,
the default is float64; for floating point inputs, it is the same as the input
dtype.
out [np.matrix, optional] Alternative output matrix in which to place the result. It
must have the same shape as the expected output, but the type of the output
values will be cast if necessary.
New in version 0.18.0.

Returns

m [np.matrix]
See also:

np.matrix.mean

NumPy’s implementation of ‘mean’ for matrices

scipy.sparse.spmatrix.minimum

spmatrix.minimum(other)
Element-wise minimum between this and another matrix.

scipy.sparse.spmatrix.multiply

spmatrix.multiply(other)
Point-wise multiplication by another matrix

scipy.sparse.spmatrix.nonzero

spmatrix.nonzero()
nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

scipy.sparse.spmatrix.power

spmatrix.power(n, dtype=None)
Element-wise power.

scipy.sparse.spmatrix.reshape

spmatrix.reshape(self, shape, order='C', copy=False)

Gives a new shape to a sparse matrix without changing its data.

Parameters
shape [length-2 tuple of ints] The new shape should be compatible with the original shape.

order [{‘C’, ‘F’}, optional] Read the elements using this index order. ‘C’ means to read and write the elements using C-like index order; e.g. read entire first row, then second row, etc. ‘F’ means to read and write the elements using Fortran-like index order; e.g. read entire first column, then second column, etc.

copy [bool, optional] Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

reshaped_matrix [sparse matrix] A sparse matrix with the given shape, not necessarily of the same format as the current object.

See also:

np.matrix.reshape NumPy’s implementation of ‘reshape’ for matrices

scipy.sparse.spmatrix.resize

spmatrix.resize(shape) Resize the matrix in-place to dimensions given by shape

Any elements that lie within the new shape will remain at the same indices, while non-zero elements lying outside the new shape are removed.

Parameters

shape [(int, int)] number of rows and columns in the new matrix

Notes

The semantics are not identical to numpy.ndarray.resize or numpy.resize. Here, the same data will be maintained at each index before and after reshape, if that index is within the new bounds. In numpy, resizing maintains contiguity of the array, moving elements around in the logical matrix but not within a flattened representation.

We give no guarantees about whether the underlying data attributes (arrays, etc.) will be modified in place or replaced with new objects.

scipy.sparse.spmatrix.set_shape

spmatrix.set_shape(shape) See reshape.

scipy.sparse.spmatrix.setdiag

spmatrix.setdiag(values, k=0) Set diagonal or off-diagonal elements of the array.

Parameters

values [array_like] New values of the diagonal elements. Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values if longer than the diagonal, then the remaining values are ignored.
If a scalar value is given, all of the diagonal is set to it.

\[ k \quad [\text{int, optional}] \] Which off-diagonal to set, corresponding to elements \( a[i, i+k] \).
Default: 0 (the main diagonal).

**scipy.sparse.spmatrix.sum**

**spmatrix.sum**(*axis=None, dtype=None, out=None*)

Sum the matrix elements over a given axis.

**Parameters**

- **axis** [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the sum of all the matrix elements, returning a scalar (i.e. \( \text{axis} = \text{None} \)).
- **dtype** [dtype, optional] The type of the returned matrix and of the accumulator in which the elements are summed. The dtype of \( a \) is used by default unless \( a \) has an integer dtype of less precision than the default platform integer. In that case, if \( a \) is signed then the platform integer is used while if \( a \) is unsigned then an unsigned integer of the same precision as the platform integer is used. New in version 0.18.0.
- **out** [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary. New in version 0.18.0.

**Returns**

- **sum_along_axis** [np.matrix] A matrix with the same shape as \( \text{self} \), with the specified axis removed.

**See also:**

- **np.matrix.sum**

  NumPy’s implementation of ‘sum’ for matrices

**scipy.sparse.spmatrix.toarray**

**spmatrix.toarray**(*order=None, out=None*)

Return a dense ndarray representation of this matrix.

**Parameters**

- **order** [{‘C’, ‘F’}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is ‘None’, indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the \( \text{out} \) argument.
- **out** [ndarray, 2-dimensional, optional] If specified, uses this array as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method. For most sparse types, \( \text{out} \) is required to be memory contiguous (either C or Fortran ordered).

**Returns**

- **arr** [ndarray, 2-dimensional] An array with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If
When `out` was passed, the same object is returned after being modified in-place to contain the appropriate values.

**scipy.sparse.spmatrix.tobsr**

`spmatrix.tobsr(blocksize=None, copy=False)`  
Convert this matrix to Block Sparse Row format.  

With `copy=False`, the data/indices may be shared between this matrix and the resultant `bsr_matrix`.  

When `blocksize=(R, C)` is provided, it will be used for construction of the `bsr_matrix`.

**scipy.sparse.spmatrix.tocoo**

`spmatrix.tocoo(copy=False)`  
Convert this matrix to COOrdinate format.  

With `copy=False`, the data/indices may be shared between this matrix and the resultant `coo_matrix`.

**scipy.sparse.spmatrix.tocsc**

`spmatrix.tocsc(copy=False)`  
Convert this matrix to Compressed Sparse Column format.  

With `copy=False`, the data/indices may be shared between this matrix and the resultant `csc_matrix`.

**scipy.sparse.spmatrix.tocsr**

`spmatrix.tocsr(copy=False)`  
Convert this matrix to Compressed Sparse Row format.  

With `copy=False`, the data/indices may be shared between this matrix and the resultant `csr_matrix`.

**scipy.sparse.spmatrix.todense**

`spmatrix.todense(order=None, out=None)`  
Return a dense matrix representation of this matrix.

**Parameters**

- `order`: [{‘C’, ‘F’}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is ‘None’, indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the `out` argument.
- `out`: [ndarray, 2-dimensional, optional] If specified, uses this array (or `numpy.matrix`) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.

**Returns**

- `arr`: [numpy.matrix, 2-dimensional] A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If `out` was passed and was an array (rather than
a `numpy.matrix`), it will be filled with the appropriate values and returned wrapped in a `numpy.matrix` object that shares the same memory.

**scipy.sparse.spmatrix.todia**

```python
spmatrix.todia(copy=False)
```

Convert this matrix to sparse DIAgonal format.

With `copy=False`, the data/indices may be shared between this matrix and the resultant `dia_matrix`.

**scipy.sparse.spmatrix.todok**

```python
spmatrix.todok(copy=False)
```

Convert this matrix to Dictionary Of Keys format.

With `copy=False`, the data/indices may be shared between this matrix and the resultant `dok_matrix`.

**scipy.sparse.spmatrix.tolil**

```python
spmatrix.tolil(copy=False)
```

Convert this matrix to LInked List format.

With `copy=False`, the data/indices may be shared between this matrix and the resultant `lil_matrix`.

**scipy.sparse.spmatrix.transpose**

```python
spmatrix.transpose(axes=None, copy=False)
```

Reverses the dimensions of the sparse matrix.

**Parameters**

- `axes` [None, optional] This argument is in the signature solely for NumPy compatibility reasons. Do not pass in anything except for the default value.
- `copy` [bool, optional] Indicates whether or not attributes of `self` should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

**Returns**

- `p` `self` with the dimensions reversed.

**See also:**

- `np.matrix.transpose`

NumPy’s implementation of ‘transpose’ for matrices

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### scipy.sparse.eye

**scipy.sparse.eye**

`scipy.sparse.eye(m, n=None, k=0, dtype=<class 'float'>, format=None)`

Sparse matrix with ones on diagonal

Returns a sparse (m x n) matrix where the k-th diagonal is all ones and everything else is zeros.

**Parameters**

- `m`  
  int] Number of rows in the matrix.

- `n`  
  int, optional] Number of columns. Default: m.

- `k`  
  int, optional] Diagonal to place ones on. Default: 0 (main diagonal).

- `dtype`  
  [dtype, optional] Data type of the matrix.

- `format`  
  [str, optional] Sparse format of the result, e.g. format=”csr”, etc.

**Examples**

```python
>>> from scipy import sparse
>>> sparse.eye(3).toarray()
array([[ 1., 0., 0.],
       [ 0., 1., 0.],
       [ 0., 0., 1.]])
>>> sparse.eye(3, dtype=np.int8)
<3x3 sparse matrix of type '<class 'numpy.int8'>'
with 3 stored elements (1 diagonals) in DIAgonal format>
```

### scipy.sparse.identity

**scipy.sparse.identity**

`scipy.sparse.identity(n, dtype='d', format=None)`

Identity matrix in sparse format

Returns an identity matrix with shape (n,n) using a given sparse format and dtype.

**Parameters**

- `n`  
  [int] Shape of the identity matrix.

- `dtype`  
  [dtype, optional] Data type of the matrix.

- `format`  
  [str, optional] Sparse format of the result, e.g. format=”csr”, etc.

**Examples**

```python
```
```python
>>> from scipy.sparse import identity
>>> identity(3).toarray()
array([[ 1.,  0.,  0.],
       [ 0.,  1.,  0.],
       [ 0.,  0.,  1.]])
>>> identity(3, dtype='int8', format='dia')
<3x3 sparse matrix of type '<class 'numpy.int8'>'
with 3 stored elements (1 diagonals) in DIAgonal format>
```

**scipy.sparse.kron**

scipy.sparse.kron(A, B, format=None)

Kronecker product of sparse matrices A and B

**Parameters**

A  [sparse or dense matrix] first matrix of the product  
B  [sparse or dense matrix] second matrix of the product  
format [str, optional] format of the result (e.g. “csr”)

**Returns**

Kronecker product in a sparse matrix format

**Examples**

```python
>>> from scipy import sparse
>>> A = sparse.csr_matrix(np.array([[0, 2], [5, 0]]))
>>> B = sparse.csr_matrix(np.array([[1, 2], [3, 4]]))
>>> sparse.kron(A, B).toarray()
array([[ 0,  0,  2,  4],
       [ 0,  0,  6,  8],
       [ 5, 10,  0,  0],
       [15, 20,  0,  0]])
```

```python
>>> sparse.kron(A, [[1, 2], [3, 4]]).toarray()
array([[ 0,  0,  2,  4],
       [ 0,  0,  6,  8],
       [ 5, 10,  0,  0],
       [15, 20,  0,  0]])
```

**scipy.sparse.kronsum**

scipy.sparse.kronsum(A, B, format=None)

Kronecker sum of sparse matrices A and B

Kronecker sum of two sparse matrices is a sum of two Kronecker products kron(I_n,A) + kron(B,I_m)
where A has shape (m,m) and B has shape (n,n) and I_m and I_n are identity matrices of shape (m,m) and (n,n) respectively.

**Parameters**

A  square matrix  
B  square matrix  
format [str] format of the result (e.g. “csr”)

**Returns**

Kronecker sum in a sparse matrix format
construct a sparse matrix from diagonals.

Parameters

diagonals
[sequence of array_like] Sequence of arrays containing the matrix diagonals, corresponding to offsets.

offsets
[sequence of int or an int, optional]

Diagonals to set:

- k = 0 the main diagonal (default)
- k > 0 the k-th upper diagonal
- k < 0 the k-th lower diagonal

shape
[tuple of int, optional] Shape of the result. If omitted, a square matrix large enough to contain the diagonals is returned.

format
[{“dia”, “csr”, “csc”, “lil”, ...}, optional] Matrix format of the result. By default (format=None) an appropriate sparse matrix format is returned. This choice is subject to change.

dtype
[dtype, optional] Data type of the matrix.

See also:

spdiags
construct matrix from diagonals

Notes
This function differs from spdiags in the way it handles off-diagonals.

The result from diags is the sparse equivalent of:

```python
np.diag(diagonals[0], offsets[0])
+ ...
+ np.diag(diagonals[k], offsets[k])
```

Repeated diagonal offsets are disallowed.

New in version 0.11.

Examples

```python
>>> from scipy.sparse import diags
>>> diagonals = [[1, 2, 3, 4], [1, 2, 3], [1, 2]]
>>> diags(diagonals, [0, -1, 2]).toarray()
array([[1, 0, 1, 0],
       [1, 2, 0, 2],
       [0, 2, 3, 0],
       [0, 0, 3, 4]])
```

Broadcasting of scalars is supported (but shape needs to be specified):

```python
>>> diags([[1, -2, 1], [-1, 0, 1], shape=(4, 4)).toarray()
array([[1., -2., 1., 0., 0.],
       [-1., 1., 0., 0., 0.],
       [1., -2., 1., 0., 0.],
       [0., 1., -2., 1., 0.],
       [0., 0., 1., -2., 1.]])
```
If only one diagonal is wanted (as in `numpy.diag`), the following works as well:

```python
>>> diags([[1, 2, 3], [1, 2, 3], [1, 2, 3]]).toarray()
array([[0., 1., 0., 0.],
       [0., 0., 2., 0.],
       [0., 0., 0., 3.],
       [0., 0., 0., 0.]])
```

**scipy.sparse.spdiags**

Return a sparse matrix from diagonals.

**Parameters**

- `data` ([array_like] matrix diagonals stored row-wise)
- `diags` ([diagonals to set])
  - `k = 0` the main diagonal
  - `k > 0` the k-th upper diagonal
  - `k < 0` the k-th lower diagonal
- `m, n` ([int] shape of the result)
- `format` ([str, optional] Format of the result. By default (format=None) an appropriate sparse matrix format is returned. This choice is subject to change.

See also:

- `diags` more convenient form of this function
- `dia_matrix` the sparse DIAGONAL format.

**Examples**

```python
>>> from scipy.sparse import spdiags
>>> data = np.array([[1, 2, 3, 4], [1, 2, 3, 4], [1, 2, 3, 4]])
>>> diags = np.array([0, -1, 2])
>>> spdiags(data, diags, 4, 4).toarray()
array([[1, 0, 3, 0],
       [1, 2, 0, 4],
       [0, 2, 3, 0],
       [0, 0, 3, 4]])
```

**scipy.sparse.block_diag**

Build a block diagonal sparse matrix from provided matrices.

**Parameters**

- `mats` ([sequence of matrices] Input matrices)
- `format` ([str, optional] The sparse format of the result (e.g. “csr”). If not given, the matrix is returned in “coo” format.
- `dtype` ([dtype specifier, optional] The data-type of the output matrix. If not given, the dtype is determined from that of blocks)

**Returns**

- `res` ([sparse matrix])
See also:

```
bmat, diags
```

Notes
New in version 0.11.0.

Examples

```python
>>> from scipy.sparse import coo_matrix, block_diag
>>> A = coo_matrix([[1, 2], [3, 4]])
>>> B = coo_matrix([[5, 6]])
>>> C = coo_matrix([[7]])
>>> block_diag((A, B, C)).toarray()
array([[1, 2, 0, 0],
       [3, 4, 0, 0],
       [0, 0, 5, 0],
       [0, 0, 6, 0],
       [0, 0, 0, 7]])
```

Scipy.sparse.tril

scipy.sparse.tril(A, k=0, format=None)

Return the lower triangular portion of a matrix in sparse format

*Returns the elements on or below the k-th diagonal of the matrix A.*

- k = 0 corresponds to the main diagonal
- k > 0 is above the main diagonal
- k < 0 is below the main diagonal

Parameters

- A [dense or sparse matrix] Matrix whose lower triangular portion is desired.
- k [integer] The top-most diagonal of the lower triangle.
- format [string] Sparse format of the result, e.g. format=“csr”, etc.

Returns

- L [sparse matrix] Lower triangular portion of A in sparse format.

See also:

```
triu
```

upper triangle in sparse format

Examples

```python
>>> from scipy.sparse import csr_matrix, tril
>>> A = csr_matrix([[1, 2, 0, 0, 3], [4, 5, 0, 6, 7],
                  [0, 0, 8, 9, 0]],
                  dtype='int32')
>>> A.toarray()
array([[1, 2, 0, 0, 3],
       [4, 5, 0, 6, 7],
       [0, 0, 8, 9, 0]])
>>> tril(A).toarray()
array([[1, 0, 0, 0, 0],
       [4, 5, 0, 0, 0],
       [0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0]])
```

(continues on next page)
>>> tril(A).nnz
4
>>> tril(A, k=1).toarray()
array([[1, 2, 0, 0, 0],
       [4, 5, 0, 0, 0],
       [0, 0, 8, 9, 0]])
>>> tril(A, k=-1).toarray()
array([[0, 0, 0, 0, 0],
       [4, 0, 0, 0, 0],
       [0, 0, 0, 0, 0]])
>>> tril(A, format='csc')
<3x5 sparse matrix of type '<class 'numpy.int32'>'
 with 4 stored elements in Compressed Sparse Column format>

scipy.sparse.triu
scipy.sparse.triu(A, k=0, format=None)
Return the upper triangular portion of a matrix in sparse format

Returns the elements on or above the k-th diagonal of the matrix A.

- k = 0 corresponds to the main diagonal
- k > 0 is above the main diagonal
- k < 0 is below the main diagonal

Parameters

- **A** [dense or sparse matrix] Matrix whose upper triangular portion is desired.
- **k** [integer] The bottom-most diagonal of the upper triangle.
- **format** [string] Sparse format of the result, e.g. format="csr", etc.

Returns

- **L** [sparse matrix] Upper triangular portion of A in sparse format.

See also:

tril
lower triangle in sparse format

Examples

>>> from scipy.sparse import csr_matrix, triu
>>> A = csr_matrix([[1, 2, 0, 0, 3], [4, 5, 0, 6, 7], [0, 0, 8, 9, 0]],
                 dtype='int32')
>>> A.toarray()
array([[1, 2, 0, 0, 3],
       [4, 5, 0, 6, 7],
       [0, 0, 8, 9, 0]])
>>> triu(A).toarray()
array([[1, 2, 0, 0, 3],
       [0, 5, 0, 6, 7],
       [0, 0, 8, 9, 0]])
>>> triu(A).nnz
8
>>> triu(A, k=1).toarray()
array([[0, 2, 0, 0, 3],
       [0, 0, 0, 6, 7],
       [0, 0, 0, 9, 0]])
>>> triu(A, k=-1).toarray()
array([[4, 5, 0, 6, 7],
       [0, 0, 8, 9, 0]])
>>> triu(A, format='csc')
<3x5 sparse matrix of type '<class 'numpy.int32'>'
      with 8 stored elements in Compressed Sparse Column format>

scipy.sparse.bmat

scipy.sparse.bmat(blocks, format=None, dtype=None)

Build a sparse matrix from sparse sub-blocks

Parameters

blocks [array_like] Grid of sparse matrices with compatible shapes. An entry of None implies an all-zero matrix.
format [{‘bsr’, ‘coo’, ‘csc’, ‘csr’, ‘dia’, ‘dok’, ‘lil’}, optional] The sparse format of the result (e.g. ‘csr’). By default an appropriate sparse matrix format is returned. This choice is subject to change.
dtype [dtype, optional] The data-type of the output matrix. If not given, the dtype is determined from that of blocks.

Returns

bmat [sparse matrix]

See also:

block_diag, diags

Examples

```python
>>> from scipy.sparse import coo_matrix, bmat
>>> A = coo_matrix([[1, 2], [3, 4]])
>>> B = coo_matrix([[5], [6]])
>>> C = coo_matrix([[7]])
>>> bmat([[A, B], [None, C]]).toarray()
array([[1, 2, 5],
       [3, 4, 0],
       [0, 0, 7]])
```

```python
>>> bmat([[A, None], [None, C]]).toarray()
array([[1, 2, 0],
       [3, 4, 0],
       [0, 0, 7]])
```

scipy.sparse.hstack

scipy.sparse.hstack(blocks, format=None, dtype=None)

Stack sparse matrices horizontally (column wise)

Parameters
blocks sequence of sparse matrices with compatible shapes
format [str] sparse format of the result (e.g. “csr”) by default an appropriate sparse matrix format is returned. This choice is subject to change.
dtype [dtype, optional] The data-type of the output matrix. If not given, the dtype is determined from that of blocks.

See also:

vstack

stack sparse matrices vertically (row wise)

Examples

```python
>>> from scipy.sparse import coo_matrix, hstack
>>> A = coo_matrix(([1, 2], ([3, 4])))
>>> B = coo_matrix(([5], [6]))
>>> hstack([A, B]).toarray()
array([[1, 2],
       [3, 4, 6]])
```

scipy.sparse.vstack
scipy.sparse.vstack(blocks, format=None, dtype=None)

Stack sparse matrices vertically (row wise)

Parameters

blocks sequence of sparse matrices with compatible shapes
format [str, optional] sparse format of the result (e.g. “csr”) by default an appropriate sparse matrix format is returned. This choice is subject to change.
dtype [dtype, optional] The data-type of the output matrix. If not given, the dtype is determined from that of blocks.

See also:

hstack

stack sparse matrices horizontally (column wise)

Examples

```python
>>> from scipy.sparse import coo_matrix, vstack
>>> A = coo_matrix(([1, 2], ([3, 4])))
>>> B = coo_matrix(([5], [6]))
>>> vstack([A, B]).toarray()
array([[1, 2],
       [3, 4],
       [5, 6]])
```

scipy.sparse.rand
scipy.sparse.rand(m, n, density=0.01, format='coo', dtype=None, random_state=None)

Generate a sparse matrix of the given shape and density with uniformly distributed values.

Parameters

m, n [int] shape of the matrix
density [real, optional] density of the generated matrix: density equal to one means a full matrix, density of 0 means a matrix with no non-zero items.
format [str, optional] sparse matrix format.
dtype [dtype, optional] type of the returned matrix values.
random_state

[{numpy.random.RandomState, int}, optional] Random number generator or random seed. If not given, the singleton numpy.random will be used.

Returns

res [sparse matrix]

See also:

scipy.sparse.random

Similar function that allows a user-specified random data source.

Notes

Only float types are supported for now.

Examples

```python
>>> from scipy.sparse import rand
>>> matrix = rand(3, 4, density=0.25, format="csr", random_state=42)
>>> matrix
<3x4 sparse matrix of type '<class 'numpy.float64'>'
with 3 stored elements in Compressed Sparse Row format>
>>> matrix.todense()
matrix([[0.05641158, 0.0, 0.0, 0.65088847],
        [0.0, 0.0, 0.0, 0.14286682],
        [0.0, 0.0, 0.0, 0.0]])
```

scipy.sparse.random

scipy.sparse.random(m, n, density=0.01, format='coo', dtype=None, random_state=None, data_rvs=None)

Generate a sparse matrix of the given shape and density with randomly distributed values.

Parameters

m, n [int] shape of the matrix
density [real, optional] density of the generated matrix: density equal to one means a full matrix, density of 0 means a matrix with no non-zero items.
format [str, optional] sparse matrix format.
dtype [dtype, optional] type of the returned matrix values.
random_state [{numpy.random.RandomState, int}, optional] Random number generator or random seed. If not given, the singleton numpy.random will be used. This random state will be used for sampling the sparsity structure, but not necessarily for sampling the values of the structurally nonzero entries of the matrix.
data_rvs [callable, optional] Samples a requested number of random values. This function should take a single argument specifying the length of the ndarray that it will return. The structurally nonzero entries of the sparse random matrix will be taken from the array sampled by this function. By default, uniform [0, 1) random values will be sampled using the same random state as is used for sampling the sparsity structure.

Returns

res [sparse matrix]

Notes

Only float types are supported for now.
Examples

```python
>>> from scipy.sparse import random
>>> from scipy import stats

>>> class CustomRandomState(np.random.RandomState):
...    def randint(self, k):
...        i = np.random.randint(k)
...        return i - i % 2

>>> np.random.seed(12345)

>>> rs = CustomRandomState()

>>> rvs = stats.poisson(25, loc=10).rvs

>>> S = random([3, 4], density=0.25, random_state=rs, data_rvs=rvs)

>>> S.A
array([[ 36.,  0.,  33.,  0.],  # random
       [  0.,  0.,  0.,  0.],
       [  0.,  0.,  36.,  0.]]))
```

```python
>>> from scipy.sparse import random
>>> from scipy.stats import rv_continuous

>>> class CustomDistribution(rv_continuous):
...    def _rvs(self, *args, **kwargs):
...        return self._random_state.randn(*self._size)

>>> X = CustomDistribution(seed=2906)

>>> Y = X()  # get a frozen version of the distribution

>>> S = random([3, 4], density=0.25, random_state=2906, data_rvs=Y.rvs)

>>> S.A
array([[ 0. ,  0. ,  0. ,  0. ],
       [ 0.13569738,  1.9467163 , -0.81205367,  0. ],
       [ 0. ,  0. ,  0. ,  0. ]])
```

Save and load sparse matrices:

```python
save_npz(file, matrix[, compressed]) Save a sparse matrix to a file using .npz format.
load_npz(file) Load a sparse matrix from a file using .npz format.
```

**scipy.sparse.save_npz**

**scipy.sparse.save_npz**(*file, matrix, compressed=**True***)
Save a sparse matrix to a file using .npz format.

**Parameters**

- **file**
  [str or file-like object] Either the file name (string) or an open file (file-like object) where the data will be saved. If file is a string, the .npz extension will be appended to the file name if it is not already there.

- **matrix**: spmatrix (format: “csc”, “csr”, “bsr”, “dia” or “coo”)
  The sparse matrix to save.

- **compressed**
  [bool, optional] Allow compressing the file. Default: True

**See also:**

**scipy.sparse.load_npz**
Load a sparse matrix from a file using .npz format.
**numpy.savez**

Save several arrays into a .npz archive.

**numpy.savez_compressed**

Save several arrays into a compressed .npz archive.

**Examples**

Store sparse matrix to disk, and load it again:

```python
>>> import scipy.sparse

>>> sparse_matrix = scipy.sparse.csc_matrix(np.array([[0, 0, 3], [4, 0, 0]]))

>>> sparse_matrix
<2x3 sparse matrix of type '<class 'numpy.int64'>'
 with 2 stored elements in Compressed Sparse Column format>

>>> sparse_matrix.todense()
matrix([[0, 0, 3],
 [4, 0, 0]], dtype=int64)

>>> scipy.sparse.save_npz('/tmp/sparse_matrix.npz', sparse_matrix)

>>> sparse_matrix = scipy.sparse.load_npz('/tmp/sparse_matrix.npz')

>>> sparse_matrix
<2x3 sparse matrix of type '<class 'numpy.int64'>'
 with 2 stored elements in Compressed Sparse Column format>

>>> sparse_matrix.todense()
matrix([[0, 0, 3],
 [4, 0, 0]], dtype=int64)
```

### scipy.sparse.load_npz

**scipy.sparse.load_npz(file)**

Load a sparse matrix from a file using .npz format.

**Parameters**

- **file** [str or file-like object] Either the file name (string) or an open file (file-like object) where the data will be loaded.

**Returns**

- **result** [csc_matrix, csr_matrix, bsr_matrix, dia_matrix or coo_matrix] A sparse matrix containing the loaded data.

**Raises**

- IOError If the input file does not exist or cannot be read.

**See also:**

- **scipy.sparse.save_npz**
  
  Save a sparse matrix to a file using .npz format.

- **numpy.load**
  
  Load several arrays from a .npz archive.
Examples
Store sparse matrix to disk, and load it again:

```python
>>> import scipy.sparse
>>> sparse_matrix = scipy.sparse.csc_matrix(np.array([[0, 0, 3], [4, 0, 0]]))
>>> sparse_matrix
<2x3 sparse matrix of type '<class 'numpy.int64'>'
    with 2 stored elements in Compressed Sparse Column format>
>>> sparse_matrix.todense()
matrix([[0, 0, 3],
        [4, 0, 0]], dtype=int64)
```

```python
>>> scipy.sparse.save_npz('/tmp/sparse_matrix.npz', sparse_matrix)
>>> sparse_matrix = scipy.sparse.load_npz('/tmp/sparse_matrix.npz')
```

Sparse matrix tools:

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<tr>
<td><code>find(A)</code></td>
<td>Return the indices and values of the nonzero elements of a matrix</td>
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**scipy.sparse.find**

`scipy.sparse.find(A)`

Return the indices and values of the nonzero elements of a matrix

**Parameters**

- **A** [dense or sparse matrix] Matrix whose nonzero elements are desired.

**Returns**

- **(I,J,V)** [tuple of arrays] I,J, and V contain the row indices, column indices, and values of the nonzero matrix entries.

**Examples**

```python
>>> from scipy.sparse import csr_matrix, find
>>> A = csr_matrix([[7., 8., 0], [0, 0, 9.]])
>>> find(A)
(array([0, 0, 1], dtype=int32), array([0, 1, 2], dtype=int32), array([ 7., 8., 9., ...]))
```

Identifying sparse matrices:

<table>
<thead>
<tr>
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<tbody>
<tr>
<td><code>issparse(x)</code></td>
<td>Is x of a sparse matrix type?</td>
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<tr>
<td><code>isspmatrix(x)</code></td>
<td>Is x of a sparse matrix type?</td>
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<td><code>isspmatrix_csc(x)</code></td>
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<td><code>isspmatrix_bsr(x)</code></td>
<td>Is x of a bsr_matrix type?</td>
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<td><code>isspmatrix_lil(x)</code></td>
<td>Is x of lil_matrix type?</td>
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<tr>
<td><code>isspmatrix_dok(x)</code></td>
<td>Is x of dok_matrix type?</td>
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<tr>
<td><code>isspmatrix_coo(x)</code></td>
<td>Is x of coo_matrix type?</td>
</tr>
<tr>
<td><code>isspmatrix_dia(x)</code></td>
<td>Is x of dia_matrix type?</td>
</tr>
</tbody>
</table>

**scipy.sparse.issparse**

**scipy.sparse.issparse(x)**

Is x of a sparse matrix type?

*Parameters*

- `x` object to check for being a sparse matrix

*Returns*

- `bool` True if x is a sparse matrix, False otherwise

*Notes*

issparse and isspmatrix are aliases for the same function.

*Examples*

```python
>>> from scipy.sparse import csr_matrix, isspmatrix
>>> isspmatrix(csr_matrix([[5]]))
True

>>> from scipy.sparse import isspmatrix
>>> isspmatrix(5)
False
```

**scipy.sparse.isspmatrix**

**scipy.sparse.isspmatrix(x)**

Is x of a sparse matrix type?

*Parameters*

- `x` object to check for being a sparse matrix

*Returns*

- `bool` True if x is a sparse matrix, False otherwise

*Notes*

issparse and isspmatrix are aliases for the same function.

*Examples*

```python
>>> from scipy.sparse import csr_matrix, isspmatrix
>>> isspmatrix(csr_matrix([[5]]))
True

>>> from scipy.sparse import isspmatrix
>>> isspmatrix(5)
False
```

**scipy.sparse.isspmatrix_csc**

**scipy.sparse.isspmatrix_csc(x)**

Is x of csc_matrix type?

*Parameters*
object to check for being a csc matrix

**Returns**

bool True if x is a csc matrix, False otherwise

**Examples**

```python
>>> from scipy.sparse import csc_matrix, isspmatrix_csc
>>> isspmatrix_csc(csc_matrix([[5]]))
True
```

```python
>>> from scipy.sparse import csr_matrix, isspmatrix_csc
>>> isspmatrix_csc(csr_matrix([[5]]))
False
```

`scipy.sparse.isspmatrix_csr`

`scipy.sparse.isspmatrix_csr(x)`

Is x of csr_matrix type?

**Parameters**

x object to check for being a csr matrix

**Returns**

bool True if x is a csr matrix, False otherwise

**Examples**

```python
>>> from scipy.sparse import csr_matrix, isspmatrix_csr
>>> isspmatrix_csr(csr_matrix([[5]]))
True
```

```python
>>> from scipy.sparse import csc_matrix, csr_matrix, isspmatrix_csc
>>> isspmatrix_csc(csc_matrix([[5]]))
False
```

`scipy.sparse.isspmatrix_bsr`

`scipy.sparse.isspmatrix_bsr(x)`

Is x of a bsr_matrix type?

**Parameters**

x object to check for being a bsr matrix

**Returns**

bool True if x is a bsr matrix, False otherwise

**Examples**

```python
>>> from scipy.sparse import bsr_matrix, isspmatrix_bsr
>>> isspmatrix_bsr(bsr_matrix([[5]]))
True
```

```python
>>> from scipy.sparse import bsr_matrix, csr_matrix, isspmatrix_bsr
>>> isspmatrix_bsr(csr_matrix([[5]]))
False
```
scipy.sparse.isspmatrix_lil
scipy.sparse.isspmatrix_lil(x)
Is x of lil_matrix type?

Parameters
x object to check for being a lil matrix

Returns
bool True if x is a lil matrix, False otherwise

Examples
>>> from scipy.sparse import lil_matrix, isspmatrix_lil
>>> isspmatrix_lil(lil_matrix([[5]]))
True

>>> from scipy.sparse import lil_matrix, csr_matrix, isspmatrix_lil
>>> isspmatrix_lil(csr_matrix([[5]]))
False

scipy.sparse.isspmatrix_dok
scipy.sparse.isspmatrix_dok(x)
Is x of dok_matrix type?

Parameters
x object to check for being a dok matrix

Returns
bool True if x is a dok matrix, False otherwise

Examples
>>> from scipy.sparse import dok_matrix, isspmatrix_dok
>>> isspmatrix_dok(dok_matrix([[5]]))
True

>>> from scipy.sparse import dok_matrix, csr_matrix, isspmatrix_dok
>>> isspmatrix_dok(csr_matrix([[5]]))
False

scipy.sparse.isspmatrix_coo
scipy.sparse.isspmatrix_coo(x)
Is x of coo_matrix type?

Parameters
x object to check for being a coo matrix

Returns
bool True if x is a coo matrix, False otherwise

Examples
>>> from scipy.sparse import coo_matrix, isspmatrix_coo
>>> isspmatrix_coo(coo_matrix([[5]]))
True
```python
>>> from scipy.sparse import coo_matrix, csr_matrix, isspmatrix_coo
csr_matrix([[5]])
False
```

### scipy.sparse.isspmatrix_coo

Is x of coo_matrix type?

**Parameters**

- `x` : object to check for being a coo matrix

**Returns**

- `bool` : True if x is a coo matrix, False otherwise

### Examples

```python
>>> from scipy.sparse import coo_matrix, isspmatrix_coo
csr_matrix([[5]])
```

```python
>>> from scipy.sparse import coo_matrix, isspmatrix_coo
csr_matrix([[5]])
```

### Scipy Reference Guide, Release 1.2.0

Fast graph algorithms based on sparse matrix representations.

#### Contents

- `connected_components` : Analyze the connected components of a sparse graph
- `laplacian` : Return the Laplacian matrix of a directed graph
- `shortest_path` : Perform a shortest-path graph search on a positive directed or undirected graph
- `dijkstra` : Dijkstra algorithm using Fibonacci Heaps
- `floyd_warshall` : Compute the shortest path lengths using the Floyd-Warshall algorithm
- `bellman_ford` : Compute the shortest path lengths using the Bellman-Ford algorithm

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- `johnson(csgraph[, directed, indices, ...])` Compute the shortest path lengths using Johnson’s algorithm.
- `breadth_first_order(csgraph, i_start[, ...])` Return a breadth-first ordering starting with specified node.
- `depth_first_order(csgraph, i_start[, ...])` Return a depth-first ordering starting with specified node.
- `breadth_first_tree(csgraph, i_start[, directed])` Return the tree generated by a breadth-first search.
- `depth_first_tree(csgraph, i_start[, directed])` Return a tree generated by a depth-first search.
- `minimum_spanning_tree(csgraph[, overwrite])` Return a minimum spanning tree of an undirected graph.
- `reverse_cuthill_mckee(graph[, symmetric_mode])` Returns the permutation array that orders a sparse CSR or CSC matrix in Reverse-Cuthill McKee ordering.
- `maximum_bipartite_matching(graph[, perm_type])` Returns an array of row or column permutations that makes the diagonal of a nonsingular square CSC sparse matrix zero free.
- `structural_rank(graph)` Compute the structural rank of a graph (matrix) with a given sparsity pattern.

`NegativeCycleError`

**scipy.sparse.csgraph.connected_components**

`scipy.sparse.csgraph.connected_components(csgraph, directed=True, connection='weak', return_labels=True)`

Analyze the connected components of a sparse graph.

New in version 0.11.0.

**Parameters**

- `csgraph` [array_like or sparse matrix] The N x N matrix representing the compressed sparse graph. The input csgraph will be converted to csr format for the calculation.
- `directed` [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].
- `connection` [str, optional] [‘weak’|’strong’]. For directed graphs, the type of connection to use. Nodes i and j are strongly connected if a path exists both from i to j and from j to i. Nodes i and j are weakly connected if only one of these paths exists. If directed == False, this keyword is not referenced.
- `return_labels` [bool, optional] If True (default), then return the labels for each of the connected components.

**Returns**

- `n_components`: int
  The number of connected components.
- `labels`: ndarray
  The length-N array of labels of the connected components.

**References**

[1]
Examples

```python
from scipy.sparse import csr_matrix
from scipy.sparse.csgraph import connected_components

graph = [
    ... [0, 1, 1, 0, 0],
    ... [0, 0, 1, 0, 0],
    ... [0, 0, 0, 0, 0],
    ... [0, 0, 0, 1],
    ... [0, 0, 0, 0]
    ... ]

graph = csr_matrix(graph)
print(graph)

(0, 1) 1
(0, 2) 1
(1, 2) 1
(3, 4) 1

n_components, labels = connected_components(csgraph=graph, directed=False,
                                          return_labels=True)

n_components
2
labels
array([0, 0, 0, 1, 1], dtype=int32)
```

scipy.sparse.csgraph.laplacian

```python
scipy.sparse.csgraph.laplacian(csgraph, normed=False, return_diag=False,
                               use_out_degree=False)
```

Return the Laplacian matrix of a directed graph.

**Parameters**

- `csgraph` : array_like or sparse matrix, 2 dimensions] compressed-sparse graph, with shape (N, N).
- `normed` : bool, optional] If True, then compute normalized Laplacian.
- `return_diag` : bool, optional] If True, then also return an array related to vertex degrees.
- `use_out_degree` : bool, optional] If True, then use out-degree instead of in-degree. This distinction matters only if the graph is asymmetric. Default: False.

**Returns**

- `lap` : ndarray or sparse matrix] The N x N laplacian matrix of csgraph. It will be a numpy array (dense) if the input was dense, or a sparse matrix otherwise.
- `diag` : ndarray, optional] The length-N diagonal of the Laplacian matrix. For the normalized Laplacian, this is the array of square roots of vertex degrees or 1 if the degree is zero.

**Notes**

The Laplacian matrix of a graph is sometimes referred to as the “Kirchoff matrix” or the “admittance matrix”, and is useful in many parts of spectral graph theory. In particular, the eigen-decomposition of the laplacian matrix can give insight into many properties of the graph.
Examples

```python
>>> from scipy.sparse import csgraph
>>> G = np.arange(5) * np.arange(5)[..., np.newaxis]
>>> G
array([[ 0,  0,  0,  0,  0],
       [ 0,  1,  2,  3,  4],
       [ 0,  2,  4,  6,  8],
       [ 0,  3,  6,  9, 12],
       [ 0,  4,  8, 12, 16]])
>>> csgraph.laplacian(G, normed=False)
array([[ 0,  0,  0,  0,  0],
       [ 0,  9, -2, -3, -4],
       [ 0, -2, 16, -6, -8],
       [ 0, -3, -6, 21, -12],
       [ 0, -4, -8, -12, 24]])
```

`scipy.sparse.csgraph.shortest_path`

Perform a shortest-path graph search on a positive directed or undirected graph.

New in version 0.11.0.

Parameters

- **csgraph** [array, matrix, or sparse matrix, 2 dimensions] The N x N array of distances representing the input graph.
- **method** [string ['auto'|'FW'|'D'], optional] Algorithm to use for shortest paths. Options are:
  - 'auto' – (default) select the best among ‘FW’, ‘D’, ‘BF’, or ‘J’ based on the input data.
  - ‘FW’ – Floyd-Warshall algorithm. Computational cost is approximately $O[N^3]$. The input csgraph will be converted to a dense representation.
  - ‘D’ – Dijkstra’s algorithm with Fibonacci heaps. Computational cost is approximately $O[N(N*k + N*log(N))]$, where $k$ is the average number of connected edges per node. The input csgraph will be converted to a csr representation.
  - ‘BF’ – Bellman-Ford algorithm. This algorithm can be used when weights are negative. If a negative cycle is encountered, an error will be raised. Computational cost is approximately $O[N(N^2 2 k)]$, where $k$ is the average number of connected edges per node. The input csgraph will be converted to a csr representation.
  - ‘J’ – Johnson’s algorithm. Like the Bellman-Ford algorithm, Johnson’s algorithm is designed for use when the weights are negative. It combines the Bellman-Ford algorithm with Dijkstra’s algorithm for faster computation.
- **directed** [bool, optional] If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]
- **return_predecessors** [bool, optional] If True, return the size (N, N) predecessor matrix.
unweighted:
[bool, optional] If True, then find unweighted distances. That is, rather than finding
the path between each point such that the sum of weights is minimized, find the
path such that the number of edges is minimized.

overwrite:
[bool, optional] If True, overwrite csgraph with the result. This applies only if
method == 'FW' and csgraph is a dense, c-ordered array with dtype=float64.

indices:
[array_like or int, optional] If specified, only compute the paths for the points at
the given indices. Incompatible with method == 'FW'.

Returns:

dist_matrix:
[ndarray] The N x N matrix of distances between graph nodes. dist_matrix[i,j]
gives the shortest distance from point i to point j along the graph.

predecessors:
[ndarray] Returned only if return_predecessors == True. The N x N matrix of
predecessors, which can be used to reconstruct the shortest paths. Row i of the
predecessor matrix contains information on the shortest paths from point i: each
entry predecessors[i, j] gives the index of the previous node in the path from point
i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Raises:

NegativeCycleError:
if there are negative cycles in the graph

Notes:
As currently implemented, Dijkstra’s algorithm and Johnson’s algorithm do not work for graphs with
direction-dependent distances when directed == False. i.e., if csgraph[i,j] and csgraph[j,i] are non-equal
edges, method=`D` may yield an incorrect result.

Examples:

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import shortest_path

>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [2, 0, 0, 3],
... [0, 0, 0, 0]
... ]

>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 3) 1
(2, 0) 2
(2, 3) 3

>>> dist_matrix, predecessors = shortest_path(csgraph=graph, directed=False,
... indices=0, return_predecessors=True)

>>> dist_matrix
array([ 0., 1., 2., 2.])

>>> predecessors
array([-9999, 0, 0, 1], dtype=int32)
```
scipy.sparse.csgraph.dijkstra

scipy.sparse.csgraph.dijkstra(csgraph, directed=True, indices=None, return_predecessors=False, unweighted=False, limit=np.inf)

Dijkstra algorithm using Fibonacci Heaps

New in version 0.11.0.

Parameters

- **csgraph** [array, matrix, or sparse matrix, 2 dimensions] The N x N array of non-negative distances representing the input graph.
- **directed** [bool, optional] If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j] and from point j to i along paths csgraph[j, i]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j or j to i along either csgraph[i, j] or csgraph[j, i].
- **indices** [array_like or int, optional] if specified, only compute the paths for the points at the given indices.
- **return_predecessors** [bool, optional] If True, return the size (N, N) predecessor matrix
- **unweighted** [bool, optional] If True, return unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.
- **limit** [float, optional] The maximum distance to calculate, must be >= 0. Using a smaller limit will decrease computation time by aborting calculations between pairs that are separated by a distance > limit. For such pairs, the distance will be equal to np.inf (i.e., not connected). New in version 0.14.0.

Returns

- **dist_matrix** [ndarray] The matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.
- **predecessors** [ndarray] Returned only if return_predecessors == True. The matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Notes

As currently implemented, Dijkstra’s algorithm does not work for graphs with direction-dependent distances when directed == False. i.e., if csgraph[i,j] and csgraph[j,i] are not equal and both are nonzero, setting directed=False will not yield the correct result.

Also, this routine does not work for graphs with negative distances. Negative distances can lead to infinite cycles that must be handled by specialized algorithms such as Bellman-Ford’s algorithm or Johnson’s algorithm.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import dijkstra
```
```python
>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 3) 1
(2, 3) 3
```

```python
>>> dist_matrix, predecessors = dijkstra(csgraph=graph, directed=False, indices=0,
... return_predecessors=True)
>>> dist_matrix
array([ 0., 1., 2., 2.])
>>> predecessors
array([-9999, 0, 0, 1], dtype=int32)
```

`scipy.sparse.csgraph.floyd_warshall`

`scipy.sparse.csgraph.floyd_warshall(csgraph, directed=True, return_predecessors=False, unweighted=False, overwrite=False)`

Compute the shortest path lengths using the Floyd-Warshall algorithm

New in version 0.11.0.

**Parameters**

- `csgraph` [array, matrix, or sparse matrix, 2 dimensions] The N x N array of distances representing the input graph.
- `directed` [bool, optional] If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]
- `return_predecessors` [bool, optional] If True, return the size (N, N) predecessor matrix
- `unweighted` [bool, optional] If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.
- `overwrite` [bool, optional] If True, overwrite csgraph with the result. This applies only if csgraph is a dense, c-ordered array with dtype=’float64’.

**Returns**

- `dist_matrix` [ndarray] The N x N matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.
- `predecessors` [ndarray] Returned only if return_predecessors == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each
entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

**Raises**

NegativeCycleError:
if there are negative cycles in the graph

**Examples**

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import floyd_warshall

>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 1],
... [2, 0, 3],
... [0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 3) 1
(2, 0) 2
(2, 3) 3

>>> dist_matrix, predecessors = floyd_warshall(csgraph=graph, directed=False,
... return_predecessors=True)
>>> dist_matrix
array([[ 0., 1., 2., 2.],
[ 1., 0., 3., 1.],
[ 2., 3., 0., 3.],
[ 2., 1., 3., 0.]])
>>> predecessors
array([[-9999, 0, 0, 1],
[ 1, -9999, 0, 1],
[ 2, 0, -9999, 2],
[ 1, 3, 3, -9999]], dtype=int32)
```

**scipy.sparse.csgraph.bellman_ford**

Compute the shortest path lengths using the Bellman-Ford algorithm.

The Bellman-ford algorithm can robustly deal with graphs with negative weights. If a negative cycle is detected, an error is raised. For graphs without negative edge weights, dijkstra’s algorithm may be faster.

New in version 0.11.0.

**Parameters**

- **csgraph** [array, matrix, or sparse matrix, 2 dimensions] The N x N array of distances representing the input graph.
directed [bool, optional] If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

indices [array_like or int, optional] if specified, only compute the paths for the points at the given indices.

return_predecessors [bool, optional] If True, return the size (N, N) predecessor matrix

unweighted [bool, optional] If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

Returns

dist_matrix [ndarray] The N x N matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.

predecessors [ndarray] Returned only if return_predecessors == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Raises

NegativeCycleError: if there are negative cycles in the graph

Notes
This routine is specially designed for graphs with negative edge weights. If all edge weights are positive, then Dijkstra’s algorithm is a better choice.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import bellman_ford

>>> graph = [
... [0, 1 , 2, 0],
... [0, 0, 0, 1],
... [2, 0, 0, 3],
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 3) 1
(2, 0) 2
(2, 3) 3

>>> dist_matrix, predecessors = bellman_ford(csgraph=graph, directed=False,
... indices=0, return_predecessors=True)
>>> dist_matrix
```

(continues on next page)
array([[ 0.,  1.,  2.,  2.],
       [-9999,  0,  0,  1], dtype=int32)

scipy.sparse.csgraph.johnson

scipy.sparse.csgraph.johnson(csgraph, directed=True, indices=None, return_predecessors=False, unweighted=False)

Compute the shortest path lengths using Johnson's algorithm.

Johnson’s algorithm combines the Bellman-Ford algorithm and Dijkstra’s algorithm to quickly find shortest paths in a way that is robust to the presence of negative cycles. If a negative cycle is detected, an error is raised. For graphs without negative edge weights, dijkstra() may be faster.

New in version 0.11.0.

Parameters

- csgraph [array, matrix, or sparse matrix, 2 dimensions] The N x N array of distances representing the input graph.
- directed [bool, optional] If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]
- indices [array_like or int, optional] if specified, only compute the paths for the points at the given indices.
- return_predecessors [bool, optional] If True, return the size (N, N) predecessor matrix
- unweighted [bool, optional] If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

Returns

- dist_matrix [ndarray] The N x N matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.
- predecessors [ndarray] Returned only if return_predecessors == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Raises

- NegativeCycleError: if there are negative cycles in the graph

Notes

This routine is specially designed for graphs with negative edge weights. If all edge weights are positive, then Dijkstra’s algorithm is a better choice.
Examples

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import johnson

>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 1, 0],
... [2, 0, 0, 3],
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 3) 1
(2, 0) 2
(2, 3) 3

>>> dist_matrix, predecessors = johnson(csgraph=graph, directed=False, indices=0,
... return_predecessors=True)
>>> dist_matrix
array([ 0., 1., 2., 2.])
>>> predecessors
array([-9999, 0, 0, 1], dtype=int32)
```

scipy.sparse.csgraph.breadth_first_order

`scipy.sparse.csgraph.breadth_first_order(csgraph, i_start, directed=True, return_predecessors=True)`

Return a breadth-first ordering starting with specified node.

Note that a breadth-first order is not unique, but the tree which it generates is unique.

New in version 0.11.0.

**Parameters**

- `csgraph` [array_like or sparse matrix] The N x N compressed sparse graph. The input csgraph will be converted to csr format for the calculation.
- `i_start` [int] The index of starting node.
- `directed` [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].
- `return_predecessors` [bool, optional] If True (default), then return the predecessor array (see below).

**Returns**

- `node_array` [ndarray, one dimension] The breadth-first list of nodes, starting with specified node. The length of node_array is the number of nodes reachable from the specified node.
- `predecessors` [ndarray, one dimension] Returned only if return_predecessors is True. The length-N list of predecessors of each node in a breadth-first tree. If node i is in the tree,
then its parent is given by predecessors[i]. If node i is not in the tree (and for the parent node) then predecessors[i] = -9999.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import breadth_first_order

>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [2, 0, 0, 3],
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 3) 1
(2, 0) 2
(2, 3) 3

>>> breadth_first_order(graph, 0)
(array([0, 1, 2, 3], dtype=int32), array([-9999, 0, 0, 1], dtype=int32))
```

scipy.sparse.csgraph.breadth_first_order

`scipy.sparse.csgraph.breadth_first_order(csgraph, i_start, directed=True, return_predecessors=True)`

Return a breadth-first ordering starting with specified node.

Note that a breadth-first order is not unique. Furthermore, for graphs with cycles, the tree generated by a breadth-first search is not unique either.

New in version 0.11.0.

Parameters

- `csgraph` [array_like or sparse matrix] The N x N compressed sparse graph. The input csgraph will be converted to csr format for the calculation.
- `i_start` [int] The index of starting node.
- `directed` [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].
- `return_predecessors` [bool, optional] If True (default), then return the predecessor array (see below).

Returns

- `node_array` [ndarray, one dimension] The breadth-first list of nodes, starting with specified node. The length of node_array is the number of nodes reachable from the specified node.
- `predecessors` [ndarray, one dimension] Returned only if return_predecessors is True. The length-N list of predecessors of each node in a breadth-first tree. If node i is in the tree,
then its parent is given by predecessors[i]. If node i is not in the tree (and for
the parent node) then predecessors[i] = -9999.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import depth_first_order

>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 1],
... [2, 0, 3],
... [0, 0, 0]
... ]

>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 3) 1
(2, 0) 2
(2, 3) 3

>>> depth_first_order(graph, 0)
(array([0, 1, 3, 2], dtype=int32), array([-9999, 0, 0, 1], dtype=int32))
```

`scipy.sparse.csgraph.breadth_first_tree`

**scipy.sparse.csgraph.breadth_first_tree** *(csgraph, i_start, directed=True)*

Return the tree generated by a breadth-first search

Note that a breadth-first tree from a specified node is unique.

New in version 0.11.0.

**Parameters**

- `csgraph` [array_like or sparse matrix] The N x N matrix representing the compressed sparse graph. The input csgraph will be converted to csr format for the calculation.
- `i_start` [int] The index of starting node.
- `directed` [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

**Returns**

- `cstree` [csr matrix] The N x N directed compressed-sparse representation of the breadth-first tree drawn from csgraph, starting at the specified node.

**Examples**

The following example shows the computation of a depth-first tree over a simple four-component graph, starting at node 0:

```
input  graph        breadth first tree from (0)

(0)                (0)
/ \                  / \ 
```

(continues on next page)
In compressed sparse representation, the solution looks like this:

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import breadth_first_tree
>>> X = csr_matrix([[0, 8, 0, 3],
...                  [0, 0, 2, 0],
...                  [0, 0, 0, 6],
...                  [0, 0, 0, 0]])
>>> Tcsr = breadth_first_tree(X, 0, directed=False)
>>> Tcsr.toarray().astype(int)
array([[0, 8, 0, 3],
       [0, 0, 2, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]])
```

Note that the resulting graph is a Directed Acyclic Graph which spans the graph. A breadth-first tree from a given node is unique.

**scipy.sparse.csgraph.depth_first_tree**

Return a tree generated by a depth-first search.

Note that a tree generated by a depth-first search is not unique: it depends on the order that the children of each node are searched.

New in version 0.11.0.

**Parameters**

- `csgraph` [array_like or sparse matrix] The N x N matrix representing the compressed sparse graph. The input csgraph will be converted to csr format for the calculation.

- `i_start` [int] The index of starting node.

- `directed` [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

**Returns**

- `cstree` [csr matrix] The N x N directed compressed-sparse representation of the depth-first tree drawn from csgraph, starting at the specified node.

**Examples**

The following example shows the computation of a depth-first tree over a simple four-component graph, starting at node 0:
In compressed sparse representation, the solution looks like this:

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import depth_first_tree
>>> X = csr_matrix([[0, 8, 0, 3],
                 ... [0, 0, 2, 5],
                 ... [0, 0, 0, 6],
                 ... [0, 0, 0, 0]])
>>> Tcsr = depth_first_tree(X, 0, directed=False)
>>> Tcsr.todense().astype(int)
aarray([[0, 8, 0, 0],
        [0, 0, 2, 0],
        [0, 0, 0, 6],
        [0, 0, 0, 0]])
```

Note that the resulting graph is a Directed Acyclic Graph which spans the graph. Unlike a breadth-first tree, a depth-first tree of a given graph is not unique if the graph contains cycles. If the above solution had begun with the edge connecting nodes 0 and 3, the result would have been different.

**scipy.sparse.csgraph.minimum_spanning_tree**

A minimum spanning tree is a graph consisting of the subset of edges which together connect all connected nodes, while minimizing the total sum of weights on the edges. This is computed using the Kruskal algorithm.

New in version 0.11.0.

**Parameters**

- `csgraph` : array_like or sparse matrix, 2 dimensions
  The N x N matrix representing an undirected graph over N nodes (see notes below).

- `overwrite` : bool, optional
  If true, then parts of the input graph will be overwritten for efficiency.

**Returns**

- `span_tree` : csr_matrix
  The N x N compressed-sparse representation of the undirected minimum spanning tree over the input (see notes below).
Notes
This routine uses undirected graphs as input and output. That is, if graph[i, j] and graph[j, i] are both zero, then nodes i and j do not have an edge connecting them. If either is nonzero, then the two are connected by the minimum nonzero value of the two.

Examples
The following example shows the computation of a minimum spanning tree over a simple four-component graph:

```
input graph               minimum spanning tree

(0)          (0)
/ \          /
3  8 3
/ \          /
(3)---5---(1) (3)---5---(1)
\ /          /
6  2 2
\ /          /
(2)          (2)
```

It is easy to see from inspection that the minimum spanning tree involves removing the edges with weights 8 and 6. In compressed sparse representation, the solution looks like this:

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import minimum_spanning_tree
>>> X = csr_matrix([[0, 8, 0, 3],
                  ... [0, 0, 2, 5],
                  ... [0, 0, 6, 0],
                  ... [0, 0, 0, 0]])
>>> Tcsr = minimum_spanning_tree(X)
>>> Tcsr.toarray().astype(int)
array([[0, 0, 0, 3],
       [0, 0, 2, 5],
       [0, 0, 0, 0],
       [0, 0, 0, 0]])
```

**scipy.sparse.csgraph.reverse_cuthill_mckee**

The `scipy.sparse.csgraph.reverse_cuthill_mckee` function returns the permutation array that orders a sparse CSR or CSC matrix in Reverse-Cuthill McKee ordering.

It is assumed by default, `symmetric_mode=False`, that the input matrix is not symmetric and works on the matrix `A+A.T`. If you are guaranteed that the matrix is symmetric in structure (values of matrix elements do not matter) then set `symmetric_mode=True`.

**Parameters**

- `graph` [sparse matrix] Input sparse in CSC or CSR sparse matrix format.
- `symmetric_mode` [bool, optional] Is input matrix guaranteed to be symmetric.

**Returns**

- `perm` [ndarray] Array of permuted row and column indices.
Notes
New in version 0.15.0.

References

Examples
```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import reverse_cuthill_mckee

>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 1],
... [2, 0, 3],
... [0, 0, 0]
...]

>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 3) 1
(2, 0) 2
(2, 3) 3

>>> reverse_cuthill_mckee(graph)
array([3, 2, 1, 0], dtype=int32)
```

```
sparse.csgraph.maximum_bipartite_matching

scipy.sparse.csgraph.maximum_bipartite_matching(graph, perm_type='row')

Returns an array of row or column permutations that makes the diagonal of a nonsingular square CSC sparse matrix zero free.

Such a permutation is always possible provided that the matrix is nonsingular. This function looks at the structure of the matrix only. The input matrix will be converted to CSC matrix format if necessary.

Parameters

- graph [sparse matrix] Input sparse in CSC format
- perm_type [str, {'row', 'column'}] Type of permutation to generate.

Returns

- perm [ndarray] Array of row or column permutations.

Notes

This function relies on a maximum cardinality bipartite matching algorithm based on a breadth-first search (BFS) of the underlying graph.

New in version 0.15.0.

References

```
Examples

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import maximum_bipartite_matching

>>> graph = [
... [0, 1, 2, 0],
... [1, 0, 0, 1],
... [2, 0, 0, 3],
... [0, 1, 3, 0]
... ]
```

```python
>>> graph = csr_matrix(graph)
>>> print(graph)
 (0, 1) 1
 (0, 2) 2
 (1, 0) 1
 (1, 3) 1
 (2, 0) 2
 (2, 3) 3
 (3, 1) 1
 (3, 2) 3
```

```python
>>> maximum_bipartite_matching(graph, perm_type='row')
array([1, 0, 3, 2], dtype=int32)
```

**scipy.sparse.csgraph.structural_rank**

scipy.sparse.csgraph.structural_rank(graph)

Compute the structural rank of a graph (matrix) with a given sparsity pattern.

The structural rank of a matrix is the number of entries in the maximum transversal of the corresponding bipartite graph, and is an upper bound on the numerical rank of the matrix. A graph has full structural rank if it is possible to permute the elements to make the diagonal zero-free.

New in version 0.19.0.

**Parameters**

- graph : [sparse matrix] Input sparse matrix.

**Returns**

- rank : [int] The structural rank of the sparse graph.

**References**

[1], [2]

**Examples**

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import structural_rank

>>> graph = [
... [0, 1, 2, 0],
... [1, 0, 0, 1],
... [2, 0, 0, 3],
... [0, 1, 3, 0]
... ]
```

(continues on next page)


```python
>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 0) 1
(1, 3) 1
(2, 0) 2
(2, 3) 3
(3, 1) 1
(3, 2) 3
```

```python
>>> structural_rank(graph)
4
```

**scipy.sparse.csgraph.NegativeCycleError**

*exception scipy.sparse.csgraph.NegativeCycleError*

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**scipy.sparse.csgraph.construct_dist_matrix**

*scipy.sparse.csgraph.construct_dist_matrix(graph, predecessors, directed=True, null_value=np.inf)*

Construct distance matrix from a predecessor matrix

New in version 0.11.0.

**Parameters**

- **graph** [array_like or sparse] The N x N matrix representation of a directed or undirected graph. If dense, then non-edges are indicated by zeros or infinities.
- **predecessors** [array_like] The N x N matrix of predecessors of each node (see Notes below).
- **directed** [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then operate on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].
null_value
[bool, optional] value to use for distances between unconnected nodes. Default is np.inf

Returns
dist_matrix
[ndarray] The N x N matrix of distances between nodes along the path specified by the predecessor matrix. If no path exists, the distance is zero.

Notes
The predecessor matrix is of the form returned by graph_shortest_path. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Examples
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import construct_dist_matrix

>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(csr_matrix(graph))
(0, 1) 1
(0, 2) 2
(1, 3) 1
(2, 3) 3

>>> pred = np.array([[-9999, 0, 0, 2],
... [1, -9999, 0, 1],
... [2, 0, -9999, 2],
... [1, 3, 3, -9999]], dtype=np.int32)

>>> construct_dist_matrix(graph=graph, predecessors=pred, directed=False)
array([[ 0., 1., 2., 5.],
[ 1., 0., 3., 1.],
[ 2., 3., 0., 3.],
[ 2., 1., 3., 0.]])

scipy.sparse.csgraph.csgraph_from_dense

scipy.sparse.csgraph.csgraph_from_dense(graph, null_value=0, nan_null=True, infin-
ity_null=True)

Construct a CSR-format sparse graph from a dense matrix.

Parameters

graph [array_like] Input graph. Shape should be (n_nodes, n_nodes).
null_value

[float or None (optional)] Value that denotes non-edges in the graph. Default is zero.

infinity_null

[bool] If True (default), then infinite entries (both positive and negative) are treated as null edges.

nan_null

[bool] If True (default), then NaN entries are treated as non-edges

Returns

`csgraph`

[csr_matrix] Compressed sparse representation of graph,

Examples

```python
>>> from scipy.sparse.csgraph import csgraph_from_dense

>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... ]

>>> csgraph_from_dense(graph)
<4x4 sparse matrix of type '<class 'numpy.float64'>'
    with 4 stored elements in Compressed Sparse Row format>
```

`scipy.sparse.csgraph.csgraph_from_masked`

`scipy.sparse.csgraph.csgraph_from_masked(graph)`

Construct a CSR-format graph from a masked array.

New in version 0.11.0.

Parameters

`graph` [MaskedArray] Input graph. Shape should be (n_nodes, n_nodes).

Returns

`csgraph` [csr_matrix] Compressed sparse representation of graph,

Examples

```python
>>> import numpy as np

>>> from scipy.sparse.csgraph import csgraph_from_masked

>>> graph_masked = np.ma.masked_array(data=[
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... ],
... mask=[[ True, False, False , True],
... [ True, True , True, False],
... [ True, True , True, False],
... ]

(continues on next page)
```
>>> csgraph_from_masked(graph_masked)
<4x4 sparse matrix of type '<class 'numpy.float64'>'
   with 4 stored elements in Compressed Sparse Row format>

scipy.sparse.csgraph.csgraph_masked_from_dense

scipy.sparse.csgraph.csgraph_masked_from_dense(graph, null_value=0, nan_null=True, infinity_null=True, copy=True)

Construct a masked array graph representation from a dense matrix.

New in version 0.11.0.

Parameters

- **graph** [array_like] Input graph. Shape should be (n_nodes, n_nodes).
- **null_value** [float or None (optional)] Value that denotes non-edges in the graph. Default is zero.
- **infinity_null** [bool] If True (default), then infinite entries (both positive and negative) are treated as null edges.
- **nan_null** [bool] If True (default), then NaN entries are treated as non-edges

Returns

- **csgraph** [MaskedArray] masked array representation of graph

Examples

```python
>>> from scipy.sparse.csgraph import csgraph_masked_from_dense
```

```python
>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... ]
```

```python
>>> csgraph_masked_from_dense(graph)
masked_array(
data=[[-- 1, 2, --],
     [-- -- -- 1],
     [-- -- -- 3],
     [-- -- -- --]],
mask=[[ True, False, False, True],
      [ True, True, True, False],
      [ True, True, True, False],
      [ True, True, True, True]],
fill_value=0)
```
scipy.sparse.csgraph.csgraph_to_dense

scipy.sparse.csgraph.csgraph_to_dense(csgraph, null_value=0)

Convert a sparse graph representation to a dense representation

New in version 0.11.0.

Parameters

- csgraph [csr_matrix, csc_matrix, or lil_matrix] Sparse representation of a graph.
- null_value [float, optional] The value used to indicate null edges in the dense representation. Default is 0.

Returns


Notes

For normal sparse graph representations, calling csgraph_to_dense with null_value=0 produces an equivalent result to using dense format conversions in the main sparse package. When the sparse representations have repeated values, however, the results will differ. The tools in scipy.sparse will add repeating values to obtain a final value. This function will select the minimum among repeating values to obtain a final value. For example, here we’ll create a two-node directed sparse graph with multiple edges from node 0 to node 1, of weights 2 and 3. This illustrates the difference in behavior:

```python
>>> from scipy.sparse import csr_matrix, csgraph
>>> data = np.array([2, 3])
>>> indices = np.array([1, 1])
>>> indptr = np.array([0, 2, 2])
>>> M = csr_matrix((data, indices, indptr), shape=(2, 2))
>>> M.toarray()
array([[0, 5],
       [0, 0]])
>>> csgraph.csgraph_to_dense(M)
array([[0., 2.],
       [0., 0.]])
```

The reason for this difference is to allow a compressed sparse graph to represent multiple edges between any two nodes. As most sparse graph algorithms are concerned with the single lowest-cost edge between any two nodes, the default scipy.sparse behavior of summing multiple weights does not make sense in this context.

The other reason for using this routine is to allow for graphs with zero-weight edges. Let’s look at the example of a two-node directed graph, connected by an edge of weight zero:

```python
>>> from scipy.sparse import csr_matrix, csgraph
>>> data = np.array([0.0])
>>> indices = np.array([1])
>>> indptr = np.array([0, 1, 1])
>>> M = csr_matrix((data, indices, indptr), shape=(2, 2))
>>> M.toarray()
array([[0, 0],
       [0, 0]])
>>> csgraph.csgraph_to_dense(M, np.inf)
array([[inf, 0.],
       [inf, inf]])
```
In the first case, the zero-weight edge gets lost in the dense representation. In the second case, we can choose a different null value and see the true form of the graph.

**Examples**

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import csgraph_to_dense

>>> graph = csr_matrix([  
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... ])
>>> graph
<4x4 sparse matrix of type '<class 'numpy.int64'>'
with 4 stored elements in Compressed Sparse Row format>

>>> csgraph_to_dense(graph)
array([[ 0., 1., 2., 0.],
       [ 0., 0., 0., 1.],
       [ 0., 0., 0., 3.],
       [ 0., 0., 0., 0.]])
```

**scipy.sparse.csgraph.csgraph_to_masked**

*scipy.sparse.csgraph.csgraph_to_masked(csgraph)*

Convert a sparse graph representation to a masked array representation

New in version 0.11.0.

**Parameters**

- csgraph [csr_matrix, csc_matrix, or lil_matrix] Sparse representation of a graph.

**Returns**

- graph [MaskedArray] The masked dense representation of the sparse graph.

**Examples**

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import csgraph_to_masked

>>> graph = csr_matrix([  
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... ])
>>> graph
<4x4 sparse matrix of type '<class 'numpy.int64'>'
with 4 stored elements in Compressed Sparse Row format>

>>> csgraph_to_masked(graph)
masked_array(
    data=[[-, 1.0, 2.0, -],
          [-, 0.0, 0.0, -],
          [-, 0.0, 0.0, -],
          [-, 0.0, 0.0, -]],
    mask=[[-, True, True, -],
           [-, True, True, -],
           [-, True, True, -],
           [-, True, True, -]],
    fill_value=999999)
```

(continues on next page)
scipy.sparse.csgraph.reconstruct_path

scipy.sparse.csgraph.reconstruct_path(csgraph, predecessors, directed=True)

Construct a tree from a graph and a predecessor list.

New in version 0.11.0.

Parameters

csgraph : [array_like or sparse matrix] The N x N matrix representing the directed or undirected graph from which the predecessors are drawn.

predecessors : [array_like, one dimension] The length-N array of indices of predecessors for the tree. The index of the parent of node i is given by predecessors[i].

directed : [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then operate on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

Returns
cstree : [csr matrix] The N x N directed compressed-sparse representation of the tree drawn from csgraph which is encoded by the predecessor list.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import reconstruct_path

>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
...]
>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 3) 1
(2, 3) 3

>>> pred = np.array([-9999, 0, 0, 1], dtype=np.int32)
```
Graph Representations

This module uses graphs which are stored in a matrix format. A graph with N nodes can be represented by an (N x N) adjacency matrix G. If there is a connection from node i to node j, then G[i, j] = w, where w is the weight of the connection. For nodes i and j which are not connected, the value depends on the representation:

- for dense array representations, non-edges are represented by G[i, j] = 0, infinity, or NaN.
- for dense masked representations (of type np.ma.MaskedArray), non-edges are represented by masked values. This can be useful when graphs with zero-weight edges are desired.
- for sparse array representations, non-edges are represented by non-entries in the matrix. This sort of sparse representation also allows for edges with zero weights.

As a concrete example, imagine that you would like to represent the following undirected graph:

```
G
(0) /
\ 1 2
/  \
(2) (1)
```

This graph has three nodes, where node 0 and 1 are connected by an edge of weight 2, and nodes 0 and 2 are connected by an edge of weight 1. We can construct the dense, masked, and sparse representations as follows, keeping in mind that an undirected graph is represented by a symmetric matrix:

```
>>> G_dense = np.array([[0, 2, 1],
                      ... [2, 0, 0],
                      ... [1, 0, 0]])
>>> G_masked = np.ma.masked_values(G_dense, 0)
>>> from scipy.sparse import csr_matrix
>>> G_sparse = csr_matrix(G_dense)
```

This becomes more difficult when zero edges are significant. For example, consider the situation when we slightly modify the above graph:

```
G2
(0) /
\ 0 2
/  \
(2) (1)
```

This is identical to the previous graph, except nodes 0 and 2 are connected by an edge of zero weight. In this case, the dense representation above leads to ambiguities: how can non-edges be represented if zero is
a meaningful value? In this case, either a masked or sparse representation must be used to eliminate the
ambiguity:

```python
>>> G2_data = np.array([[np.inf, 2, 0],
                      [2, np.inf, np.inf],
                      [0, np.inf, np.inf]])
>>> G2_masked = np.ma.masked_invalid(G2_data)
>>> from scipy.sparse.csgraph import csgraph_from_dense
>>> # G2_sparse = csr_matrix(G2_data) would give the wrong result
>>> G2_sparse = csgraph_from_dense(G2_data, null_value=np.inf)
>>> G2_sparse.data
array([ 2., 0., 2., 0.])
```

Here we have used a utility routine from the csgraph submodule in order to convert the dense representation
to a sparse representation which can be understood by the algorithms in submodule. By viewing the data
array, we can see that the zero values are explicitly encoded in the graph.

**Directed vs. Undirected**

Matrices may represent either directed or undirected graphs. This is specified throughout the csgraph module
by a boolean keyword. Graphs are assumed to be directed by default. In a directed graph, traversal from
node i to node j can be accomplished over the edge G[i, j], but not the edge G[j, i]. Consider the following
dense graph:

```python
>>> G_dense = np.array([[0, 1, 0],
                      [2, 0, 3],
                      [0, 4, 0]])
```

When `directed=True` we get the graph:

```
---1--> ---3-->  
(0) (1) (2)  
<--2--- <--4---
```

In a non-directed graph, traversal from node i to node j can be accomplished over either G[i, j] or G[j, i]. If
both edges are not null, and the two have unequal weights, then the smaller of the two is used.

So for the same graph, when `directed=False` we get the graph:

```
(0)--1--(1)--2--(2)
```

Note that a symmetric matrix will represent an undirected graph, regardless of whether the ‘directed’ keyword
is set to True or False. In this case, using `directed=True` generally leads to more efficient computation.

The routines in this module accept as input either scipy.sparse representations (csr, csc, or lil format), masked
representations, or dense representations with non-edges indicated by zeros, infinities, and NaN entries.

**scipy.sparse.linalg**

Sparse linear algebra (**scipy.sparse.linalg**)

**Abstract linear operators**

<table>
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<th><code>LinearOperator</code>(dtype, shape)</th>
<th>Common interface for performing matrix vector products</th>
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<tr>
<td><code>aslinearoperator</code>(A)</td>
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</table>
scipy.sparse.linalg.LinearOperator

class scipy.sparse.linalg.LinearOperator(dtype, shape)

Common interface for performing matrix vector products

Many iterative methods (e.g. cg, gmres) do not need to know the individual entries of a matrix to
solve a linear system A*x=b. Such solvers only require the computation of matrix vector products,
A*v where v is a dense vector. This class serves as an abstract interface between iterative solvers and
matrix-like objects.

To construct a concrete LinearOperator, either pass appropriate callables to the constructor of this
class, or subclass it.

A subclass must implement either one of the methods _matvec and _matmat, and the at-
tributes/properties shape (pair of integers) and dtype (may be None). It may call the __init__
on this class to have these attributes validated. Implementing _matvec automatically implements
_matmat (using a naive algorithm) and vice-versa.

Optionally, a subclass may implement _rmatvec or _adjoint to implement the Hermitian adjoint
(conjugate transpose). As with _matvec and _matmat, implementing either _rmatvec or _adjoint
implements the other automatically. Implementing _adjoint is preferable; _rmatvec is mostly there
for backwards compatibility.

Parameters

- matvec: [callable f(v)] Returns returns A * v.
- rmatvec: [callable f(v)] Returns A^H * v, where A^H is the conjugate transpose of A.
- matmat: [callable f(V)] Returns A * V, where V is a dense matrix with dimensions (N,K).
- dtype: [dtype] Data type of the matrix.

See also:

aslinearoperator

Construct LinearOperators

Notes

The user-defined matvec() function must properly handle the case where v has shape (N,) as well as
the (N,1) case. The shape of the return type is handled internally by LinearOperator.

LinearOperator instances can also be multiplied, added with each other and exponentiated, all lazily:
the result of these operations is always a new, composite LinearOperator, that defers linear operations
to the original operators and combines the results.

Examples

```python
>>> import numpy as np
>>> from scipy.sparse.linalg import LinearOperator
>>> def mv(v):
...     return np.array([2*v[0], 3*v[1]])
...
>>> A = LinearOperator(((2, 2), matvec=mv)
>>> A
<2x2 _CustomLinearOperator with dtype= float64>
>>> A.matvec(np.ones(2))
array([ 2.,  3.])
>>> A * np.ones(2)
array([ 2.,  3.])
```
Attributes

*args

tuple* For linear operators describing products etc. of other linear operators, the operands of the binary operation.

Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
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<td><strong>call</strong></td>
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<td>Matrix-matrix multiplication.</td>
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<td>rmatvec(x)</td>
<td>Adjoint matrix-vector multiplication.</td>
</tr>
<tr>
<td>transpose()</td>
<td>Transpose this linear operator.</td>
</tr>
</tbody>
</table>

**scipy.sparse.linalg.LinearOperator.__call__**

LinearOperator.__call__(x)

Call self as a function.

**scipy.sparse.linalg.LinearOperator.adjoint**

LinearOperator.adjoint()

Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

*Returns*


**scipy.sparse.linalg.LinearOperator.dot**

LinearOperator.dot(x)

Matrix-matrix or matrix-vector multiplication.

*Parameters*

x  [array_like] 1-d or 2-d array, representing a vector or matrix.

*Returns*

**Ax**  [array] 1-d or 2-d array (depending on the shape of x) that represents the result of applying this linear operator on x.

**scipy.sparse.linalg.LinearOperator.matmat**

LinearOperator.matmat(X)

Matrix-matrix multiplication.

Performs the operation y=A*X where A is an MxN linear operator and X dense N*K matrix or ndarray.

*Parameters*

X  [{matrix, ndarray}] An array with shape (N,K).

*Returns*
\[ Y \] A matrix or ndarray with shape \((M,K)\) depending on the type of the \(X\) argument.

**Notes**
This matmat wraps any user-specified matmat routine or overridden \_matmat method to ensure that \(y\) has the correct type.

**scipy.sparse.linalg.LinearOperator.matvec**

\[
\text{LinearOperator.matvec}(x)
\]
Matrix-vector multiplication.
Perform the operation \(y = A \times x\) where \(A\) is an \(M\times N\) linear operator and \(x\) is a column vector or 1-d array.

**Parameters**
- \(x\) An array with shape \((N,)\) or \((N,1)\).

**Returns**
- \(y\) A matrix or ndarray with shape \((M,)\) or \((M,1)\) depending on the type and shape of the \(x\) argument.

**Notes**
This matvec wraps the user-specified matvec routine or overridden \_matvec method to ensure that \(y\) has the correct shape and type.

**scipy.sparse.linalg.LinearOperator.rmatvec**

\[
\text{LinearOperator.rmatvec}(x)
\]
Adjoint matrix-vector multiplication.
Perform the operation \(y = A^H \times x\) where \(A\) is an \(M\times N\) linear operator and \(x\) is a column vector or 1-d array.

**Parameters**
- \(x\) An array with shape \((M,)\) or \((M,1)\).

**Returns**
- \(y\) A matrix or ndarray with shape \((N,)\) or \((N,1)\) depending on the type and shape of the \(x\) argument.

**Notes**
This rmatvec wraps the user-specified rmatvec routine or overridden \_rmatvec method to ensure that \(y\) has the correct shape and type.

**scipy.sparse.linalg.LinearOperator.transpose**

\[
\text{LinearOperator.transpose}()
\]
Transpose this linear operator.
Returns a LinearOperator that represents the transpose of this one. Can be abbreviated \(self.T\) instead of \(self.transpose()\).
scipy.sparse.linalg.aslinearoperator

scipy.sparse.linalg.aslinearoperator(A)

Return A as a LinearOperator.

‘A’ may be any of the following types:

- ndarray
- matrix
- sparse matrix (e.g. csr_matrix, lil_matrix, etc.)
- LinearOperator
- An object with .shape and .matvec attributes

See the LinearOperator documentation for additional information.

Notes
If ‘A’ has no .dtype attribute, the data type is determined by calling LinearOperator.matvec - set the .dtype attribute to prevent this call upon the linear operator creation.

Examples

```python
>>> from scipy.sparse.linalg import aslinearoperator
>>> M = np.array(([1, 2, 3], [4, 5, 6]), dtype=np.int32)
>>> aslinearoperator(M)
<2x3 MatrixLinearOperator with dtype=int32>
```

Matrix Operations

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
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<td>inv(A)</td>
<td>Compute the inverse of a sparse matrix</td>
</tr>
<tr>
<td>expm(A)</td>
<td>Compute the matrix exponential using Pade approximation.</td>
</tr>
<tr>
<td>expm_multiply(A, B[, start, stop, num, endpoint])</td>
<td>Compute the action of the matrix exponential of A on B.</td>
</tr>
</tbody>
</table>

scipy.sparse.linalg.inv

scipy.sparse.linalg.inv(A)

Compute the inverse of a sparse matrix

Parameters

- A  

[(M,M) ndarray or sparse matrix] square matrix to be inverted

Returns

- Ainv  

[(M,M) ndarray or sparse matrix] inverse of A

Notes

This computes the sparse inverse of A. If the inverse of A is expected to be non-sparse, it will likely be faster to convert A to dense and use scipy.linalg.inv.

Examples

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import inv
>>> A = csc_matrix(([1., 0.], [1., 2.]))
```
>>> Ainv = inv(A)
>>> Ainv
<2x2 sparse matrix of type '<class 'numpy.float64'>'
   with 3 stored elements in Compressed Sparse Column format>
>>> A.dot(Ainv)
<2x2 sparse matrix of type '<class 'numpy.float64'>'
   with 2 stored elements in Compressed Sparse Column format>
```
```
New in version 0.12.0.

**scipy.sparse.linalg.expm**

The function `scipy.sparse.linalg.expm(A)` computes the matrix exponential using Pade approximation.

**Parameters**

- `A`: [(M,M) array_like or sparse matrix] 2D Array or Matrix (sparse or dense) to be exponentiated.

**Returns**

- `expA`: [(M,M) ndarray] Matrix exponential of A.

**Notes**

This is algorithm (6.1) which is a simplification of algorithm (5.1).

New in version 0.12.0.

**References**

[1]

**Examples**

```
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import expm
>>> A = csc_matrix([[1, 0, 0], [0, 2, 0], [0, 0, 3]])
>>> A.todense()
matrix([[ 1., 0.],
        [ 0., 2.],
        [ 0., 3.]], dtype=int64)
>>> Aexp = expm(A)
>>> Aexp
<3x3 sparse matrix of type '<class 'numpy.float64'>'
   with 3 stored elements in Compressed Sparse Column format>
>>> Aexp.todense()
matrix([[ 2.71828183,  0.        ,  0.        ],
       [ 0.        ,  7.3890561 ,  0.        ],
       [ 0.        ,  0.        , 20.08553692]])
```

**scipy.sparse.linalg.expm_multiply**

The function `scipy.sparse.linalg.expm_multiply(A, B, start=None, stop=None, num=None, endpoint=None)` computes the action of the matrix exponential of A on B.

6.21. Sparse matrices (scipy.sparse)
Parameters

- **A** [transposable linear operator] The operator whose exponential is of interest.
- **B** [ndarray] The matrix or vector to be multiplied by the matrix exponential of A.
- **start** [scalar, optional] The starting time point of the sequence.
- **stop** [scalar, optional] The end time point of the sequence, unless `endpoint` is set to False. In that case, the sequence consists of all but the last of `num + 1` evenly spaced time points, so that `stop` is excluded. Note that the step size changes when `endpoint` is False.
- **num** [int, optional] Number of time points to use.
- **endpoint** [bool, optional] If True, `stop` is the last time point. Otherwise, it is not included.

Returns

- **expm_A_B** [ndarray] The result of the action $e^{tkA}B$.

Notes

The optional arguments defining the sequence of evenly spaced time points are compatible with the arguments of `numpy.linspace`.

The output ndarray shape is somewhat complicated so I explain it here. The ndim of the output could be either 1, 2, or 3. It would be 1 if you are computing the expm action on a single vector at a single time point. It would be 2 if you are computing the expm action on a vector at multiple time points, or if you are computing the expm action on a matrix at a single time point. It would be 3 if you want the action on a matrix with multiple columns at multiple time points. If multiple time points are requested, `expm_A_B[0]` will always be the action of the expm at the first time point, regardless of whether the action is on a vector or a matrix.

References

[1], [2]

Examples

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import expm, expm_multiply
>>> A = csc_matrix([[1, 0], [0, 1]])
>>> A.todense()
matrix([[1, 0],
        [0, 1]], dtype=int64)
>>> B = np.array([np.exp(-1.), np.exp(-2.)])
>>> B
array([ 0.36787944, 0.13533528])
>>> expm_multiply(A, B, start=1, stop=2, num=3, endpoint=True)
array([[ 1.0  , 0.36787944],
       [ 1.64872127, 0.60653066],
       [ 2.71828183, 1.        ]])
>>> expm(A).dot(B)  # Verify 1st timestep
array([ 1.0  , 0.36787944])
>>> expm(1.5*A).dot(B)  # Verify 2nd timestep
array([ 1.64872127, 0.60653066])
>>> expm(2*A).dot(B)  # Verify 3rd timestep
array([ 2.71828183, 1.        ])```

Matrix norms
scipy.sparse.linalg.norm

**scipy.sparse.linalg.norm**(*x*, *ord=None, axis=None*)

Norm of a sparse matrix

This function is able to return one of seven different matrix norms, depending on the value of the *ord* parameter.

**Parameters**

- **x**  
  [a sparse matrix] Input sparse matrix.

- **ord**  

- **axis**  
  [{int, 2-tuple of ints, None}, optional] If *axis* is an integer, it specifies the axis of *x* along which to compute the vector norms. If *axis* is a 2-tuple, it specifies the axes that hold 2-D matrices, and the matrix norms of these matrices are computed. If *axis* is None then either a vector norm (when *x* is 1-D) or a matrix norm (when *x* is 2-D) is returned.

**Returns**

- **n**  
  [float or ndarray]

**Notes**

Some of the ord are not implemented because some associated functions like, _multi_svd_norm, are not yet available for sparse matrix.

This docstring is modified based on numpy.linalg.norm. https://github.com/numpy/numpy/blob/master/numpy/linalg/linalg/linalg.py

The following norms can be calculated:

<table>
<thead>
<tr>
<th>ord</th>
<th>norm for sparse matrices</th>
</tr>
</thead>
<tbody>
<tr>
<td>None</td>
<td>Frobenius norm</td>
</tr>
<tr>
<td>‘fro’</td>
<td>Frobenius norm</td>
</tr>
<tr>
<td>inf</td>
<td>max(sum(abs(x), axis=1))</td>
</tr>
<tr>
<td>-inf</td>
<td>min(sum(abs(x), axis=1))</td>
</tr>
<tr>
<td>0</td>
<td>abs(x).sum(axis=axis)</td>
</tr>
<tr>
<td>1</td>
<td>max(sum(abs(x), axis=0))</td>
</tr>
<tr>
<td>-1</td>
<td>min(sum(abs(x), axis=0))</td>
</tr>
<tr>
<td>2</td>
<td>Not implemented</td>
</tr>
<tr>
<td>-2</td>
<td>Not implemented</td>
</tr>
<tr>
<td>other</td>
<td>Not implemented</td>
</tr>
</tbody>
</table>

The Frobenius norm is given by /1/:  

\[ ||A||_F = \left( \sum_{i,j} abs(a_{i,j})^2 \right)^{1/2} \]

**References**

/1/

**Examples**
```python
>>> from scipy.sparse import *
>>> import numpy as np
>>> from scipy.sparse.linalg import norm
>>> a = np.arange(9) - 4
>>> a
array([-4, -3, -2, -1, 0, 1, 2, 3, 4])
>>> b = a.reshape((3, 3))
>>> b
array([[ 4, -4, -3],
       [ 2,  0,  1],
       [ 3, -1, -2]])
>>> b = csr_matrix(b)
>>> norm(b)
7.745966692414834
>>> norm(b, 'fro')
7.745966692414834
>>> norm(b, np.inf)
9
>>> norm(b, -np.inf)
2
>>> norm(b, 1)
7
>>> norm(b, -1)
6
```

**scipy.sparse.linalg.onenormest**

`scipy.sparse.linalg.onenormest(A, t=2, itmax=5, compute_v=False, compute_w=False)`

Compute a lower bound of the 1-norm of a sparse matrix.

**Parameters**

- `A` [ndarray or other linear operator] A linear operator that can be transposed and that can produce matrix products.
- `t` [int, optional] A positive parameter controlling the tradeoff between accuracy versus time and memory usage. Larger values take longer and use more memory but give more accurate output.
- `itmax` [int, optional] Use at most this many iterations.
- `compute_v` [bool, optional] Request a norm-maximizing linear operator input vector if True.
- `compute_w` [bool, optional] Request a norm-maximizing linear operator output vector if True.

**Returns**

- `est` [float] An underestimate of the 1-norm of the sparse matrix.
- `v` [ndarray, optional] The vector such that `||Av||_1 == est*||v||_1`. It can be thought of as an input to the linear operator that gives an output with particularly large norm.
- `w` [ndarray, optional] The vector `Av` which has relatively large 1-norm. It can be thought of as an output of the linear operator that is relatively large in norm compared to the input.
Notes
This is algorithm 2.4 of [1].

In [2] it is described as follows. “This algorithm typically requires the evaluation of about 4t matrix-vector products and almost invariably produces a norm estimate (which is, in fact, a lower bound on the norm) correct to within a factor 3.”

New in version 0.13.0.

References
[1], [2]

Examples

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import onenormest
>>> A = csc_matrix([[1., 0., 0.], [5., 8., 2.], [0., -1., 0.]], dtype=float)
>>> A.todense()
matrix([[ 1., 0., 0.],
        [ 5., 8., 2.],
        [ 0., -1., 0.]])
>>> onenormest(A)
9.0
>>> np.linalg.norm(A.todense(), ord=1)
9.0
```

Solving linear problems

Direct methods for linear equation systems:

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>spsolve(A, b[, permc_spec, use_umfpack])</code></td>
<td>Solve the sparse linear system $Ax=b$, where $b$ may be a vector or a matrix.</td>
</tr>
<tr>
<td><code>spsolve_triangular(A, b[, lower, ...])</code></td>
<td>Solve the equation $A x = b$ for $x$, assuming $A$ is a triangular matrix.</td>
</tr>
<tr>
<td><code>factorized(A)</code></td>
<td>Return a function for solving a sparse linear system, with $A$ pre-factorized.</td>
</tr>
</tbody>
</table>

MatrixRankWarning

`use_solver(**kwargs)` Select default sparse direct solver to be used.

scipy.sparse.linalg.spsolve

`scipy.sparse.linalg.spsolve(A, b, permc_spec=None, use_umfpack=True)` Solve the sparse linear system $Ax=b$, where $b$ may be a vector or a matrix.

Parameters

- **A** [ndarray or sparse matrix] The square matrix $A$ will be converted into CSC or CSR form
- **b** [ndarray or sparse matrix] The matrix or vector representing the right hand side of the equation. If a vector, $b$.shape must be (n,) or (n, 1).
- **permc_spec** [str, optional] How to permute the columns of the matrix for sparsity preservation. (default: ‘COLAMD’)
  - **NATURAL**: natural ordering.
  - **MMD_ATA**: minimum degree ordering on the structure of $A^T A$.
  - **MMD_AT_PLUS_A**: minimum degree ordering on the structure of $A^T + A$.
  - **COLAMD**: approximate minimum degree column ordering
use_umfpack

[bool, optional] if True (default) then use umfpack for the solution. This is only referenced if b is a vector and scikit-umfpack is installed.

Returns

x

[ndarray or sparse matrix] the solution of the sparse linear equation. If b is a vector, then x is a vector of size A.shape[1] If b is a matrix, then x is a matrix of size (A.shape[1], b.shape[1])

Notes

For solving the matrix expression AX = B, this solver assumes the resulting matrix X is sparse, as is often the case for very sparse inputs. If the resulting X is dense, the construction of this sparse result will be relatively expensive. In that case, consider converting A to a dense matrix and using scipy.linalg.solve or its variants.

Examples

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import spsolve
>>> A = csc_matrix([[3, 2, 0], [1, -1, 0], [0, 5, 1]], dtype=float)
>>> B = csc_matrix([[2, 0], [-1, 0], [2, 0]], dtype=float)
>>> x = spsolve(A, B)
>>> np.allclose(A.dot(x).todense(), B.todense())
True
```

scipy.sparse.linalg.sp.solve_triangular

scipy.sparse.linalg.sp.solve_triangular(A, b, lower=True, overwrite_A=False, overwrite_b=False)

Solve the equation $A x = b$ for $x$, assuming $A$ is a triangular matrix.

Parameters

- A
- b
  - [(M,) or (M, N) array_like] Right-hand side matrix in $A x = b$
- lower
  - [bool, optional] Whether $A$ is a lower or upper triangular matrix. Default is lower triangular matrix.
- overwrite_A
  - [bool, optional] Allow changing $A$. The indices of $A$ are going to be sorted and zero entries are going to be removed. Enabling gives a performance gain. Default is False.
- overwrite_b
  - [bool, optional] Allow overwriting data in $b$. Enabling gives a performance gain. Default is False. If overwrite_b is True, it should be ensured that $b$ has an appropriate dtype to be able to store the result.

Returns

- x
  - [(M,) or (M, N) ndarray] Solution to the system $A x = b$. Shape of return matches shape of $b$.

Raises

- LinAlgError
  - If $A$ is singular or not triangular.
- ValueError
  - If shape of $A$ or shape of $b$ do not match the requirements.
Notes
New in version 0.19.0.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.linalg import spsolve_triangular
>>> A = csr_matrix([[3, 0, 0], [1, -1, 0], [2, 0, 1]], dtype=float)
>>> B = np.array([[2, 0], [-1, 0], [2, 0]], dtype=float)
>>> x = spsolve_triangular(A, B)
>>> np.allclose(A.dot(x), B)
True
```

scipy.sparse.linalg.factorized

scipy.sparse.linalg.factorized(A)

Return a function for solving a sparse linear system, with A pre-factorized.

Parameters
A [(N, N) array_like] Input.

Returns
solve [callable] To solve the linear system of equations given in A, the solve callable should be passed an ndarray of shape (N,).

Examples

```python
>>> from scipy.sparse.linalg import factorized
>>> A = np.array([[3., 2., -1.],
...                [2., -2., 4.],
...                [-1., 0.5, -1.]])
>>> solve = factorized(A)  # Makes LU decomposition.
>>> rhs1 = np.array([1, -2, 0])
>>> solve(rhs1)  # Uses the LU factors.
array([ 1., -2., -2.])
```

scipy.sparse.linalg.MatrixRankWarning

exception scipy.sparse.linalg.MatrixRankWarning

scipy.sparse.linalg.use_solver

scipy.sparse.linalg.use_solver(**kwargs)

Select default sparse direct solver to be used.

Parameters
useUmfpack [bool, optional] Use UMFPACK over SuperLU. Has effect only if scikits.umfpack is installed. Default: True
assumeSortedIndices [bool, optional] Allow UMFPACK to skip the step of sorting indices for a CSR/CSC matrix. Has effect only if useUmfpack is True and scikits.umfpack is installed. Default: False
Notes
The default sparse solver is umfpack when available (scikits.umfpack is installed). This can be changed by passing useUmfpack = False, which then causes the always present SuperLU based solver to be used.

Umfpack requires a CSR/CSC matrix to have sorted column/row indices. If sure that the matrix fulfills this, pass assumeSortedIndices=True to gain some speed.

Iterative methods for linear equation systems:

- **bicg**
  - (A, b[, x0, tol, maxiter, M, callback, atol])
  - Use BIConjugate Gradient iteration to solve $Ax = b$.

- **bicgstab**
  - (A, b[, x0, tol, maxiter, M, ...])
  - Use BIConjugate Gradient STABilized iteration to solve $Ax = b$.

- **cg**
  - (A, b[, x0, tol, maxiter, M, callback, atol])
  - Use Conjugate Gradient iteration to solve $Ax = b$.

- **cgs**
  - (A, b[, x0, tol, maxiter, M, callback, atol])
  - Use Conjugate Gradient Squared iteration to solve $Ax = b$.

- **gmres**
  - (A, b[, x0, tol, restart, maxiter, M, ...])
  - Use Generalized Minimal RESidual iteration to solve $Ax = b$.

- **lgmres**
  - (A, b[, x0, tol, maxiter, M, ...])
  - Solve a matrix equation using the LGMRES algorithm.

- **minres**
  - (A, b[, x0, shift, tol, maxiter, M, ...])
  - Use MINimum RESidual iteration to solve $Ax=b$.

- **qmr**
  - (A, b[, x0, tol, maxiter, M1, M2, ...])
  - Use Quasi-Minimal Residual iteration to solve $Ax = b$.

- **gcrotmk**
  - (A, b[, x0, tol, maxiter, M, ...])
  - Solve a matrix equation using flexible GCROT(m,k) algorithm.

**scipy.sparse.linalg.bicg**

- **scipy.sparse.linalg.bicg**(A, b, x0=None, tol=1e-05, maxiter=None, M=None, callback=None, atol=None)
  - Use BIConjugate Gradient iteration to solve $Ax = b$.

**Parameters**

- **A**
  - [[sparse matrix, dense matrix, LinearOperator]] The real or complex N-by-N matrix of the linear system. It is required that the linear operator can produce $Ax$ and $A^T x$.

- **b**
  - [[array, matrix]] Right hand side of the linear system. Has shape (N,) or (N,1).

**Returns**

- **x**
  - [[array, matrix]] The converged solution.

- **info**
  - [integer]

  **Provides convergence information:**
  
  - 0 : successful exit
  - >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

**Other Parameters**

- **x0**
  - [[array, matrix]] Starting guess for the solution.

- **tol, atol**
  - [float, optional] Tolerances for convergence, $\text{norm(residual)} \leq \max(\text{tol} \cdot \text{norm(b)}, \text{atol})$. The default for atol is 'legacy', which emulates a different legacy behavior.

**Warning:** The default value for atol will be changed in a future release. For future compatibility, specify atol explicitly.
**maxiter** [integer] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

**M** [{sparse matrix, dense matrix, LinearOperator}] Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

**callback** [function] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

scipy.sparse.linalg.bicgstab

```python
scipy.sparse.linalg.bicgstab(A, b, x0=None, tol=1e-05, maxiter=None, M=None, callback=None, atol=None)
```

Use BiConjugate Gradient STABilized iteration to solve \( Ax = b \).

**Parameters**

**A** [{sparse matrix, dense matrix, LinearOperator}] The real or complex \( N \times N \) matrix of the linear system.

**b** [{array, matrix}] Right hand side of the linear system. Has shape \( (N,) \) or \( (N,1) \).

**Returns**

**x** [{array, matrix}] The converged solution.

**info** [integer] Provides convergence information:

- 0 : successful exit
- >0 : convergence not achieved, number of iterations
- <0 : illegal input or breakdown

**Other Parameters**

**x0** [{array, matrix}] Starting guess for the solution.

**tol, atol** [float, optional] Tolerances for convergence, \( \text{norm}(\text{residual}) \leq \max(\text{tol} \cdot \text{norm}(b), \text{atol}) \). The default for \( \text{atol} \) is 'legacy', which emulates a different legacy behavior.

---

**Warning:** The default value for \( \text{atol} \) will be changed in a future release. For future compatibility, specify \( \text{atol} \) explicitly.

**maxiter** [integer] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

**M** [{sparse matrix, dense matrix, LinearOperator}] Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

**callback** [function] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

scipy.sparse.linalg.cg

```python
scipy.sparse.linalg.cg(A, b, x0=None, tol=1e-05, maxiter=None, M=None, callback=None, atol=None)
```

Use Conjugate Gradient iteration to solve \( Ax = b \).

**Parameters**

**A** [{sparse matrix, dense matrix, LinearOperator}] The real or complex \( N \times N \) matrix of the linear system. \( A \) must represent a hermitian, positive definite matrix.
SciPy Reference Guide, Release 1.2.0

b [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

Returns

x [{array, matrix}] The converged solution.
info [integer]

Provides convergence information:

0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

Other Parameters

x0 [{array, matrix}] Starting guess for the solution.
tol, atol [float, optional] Tolerances for convergence, \( \text{norm(residual)} \leq \max(\text{tol} \cdot \text{norm(b)}, \text{atol}) \). The default for \( \text{atol} \) is 'legacy', which emulates a different legacy behavior.

Warning: The default value for \( \text{atol} \) will be changed in a future release. For future compatibility, specify \( \text{atol} \) explicitly.

maxiter [integer] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.
M [{sparse matrix, dense matrix, LinearOperator}] Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.
callback [function] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

scipy.sparse.linalg.cgs

scipy.sparse.linalg.cgs(A, b, x0=None, tol=1e-05, maxiter=None, M=None, callback=None, atol=None)

Use Conjugate Gradient Squared iteration to solve \( Ax = b \).

Parameters

Parameters

A [{sparse matrix, dense matrix, LinearOperator}] The real-valued N-by-N matrix of the linear system.
b [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

Returns

x [{array, matrix}] The converged solution.
info [integer]

Provides convergence information:

0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

Other Parameters

x0 [{array, matrix}] Starting guess for the solution.
tol, atol [float, optional] Tolerances for convergence, \( \text{norm(residual)} \leq \max(\text{tol} \cdot \text{norm(b)}, \text{atol}) \). The default for \( \text{atol} \) is 'legacy', which emulates a different legacy behavior.

Warning: The default value for \( \text{atol} \) will be changed in a future release. For future compatibility, specify \( \text{atol} \) explicitly.
maxiter [integer] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M [(sparse matrix, dense matrix, LinearOperator)] Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback [function] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

scipy.sparse.linalg.gmres

scipy.sparse.linalg.gmres(A, b, x0=None, tol=1e-05, restart=None, maxiter=None, M=None, callback=None, restrt=None, atol=None)

Use Generalized Minimal RESidual iteration to solve $Ax = b$.

**Parameters**

A [(sparse matrix, dense matrix, LinearOperator)] The real or complex N-by-N matrix of the linear system.

b [(array, matrix)] Right hand side of the linear system. Has shape (N,) or (N,1).

**Returns**

x [(array, matrix)] The converged solution.

info [int] Provides convergence information:

- 0 : successful exit
- >0 : convergence to tolerance not achieved, number of iterations
- <0 : illegal input or breakdown

**Other Parameters**

x0 [(array, matrix)] Starting guess for the solution (a vector of zeros by default).

tol, atol [float, optional] Tolerances for convergence, $\operatorname{norm}(\text{residual}) \leq \max(\text{tol}\times\operatorname{norm}(b), \text{atol})$. The default for atol is 'legacy', which emulates a different legacy behavior.

**Warning:** The default value for atol will be changed in a future release. For future compatibility, specify atol explicitly.

restart [int, optional] Number of iterations between restarts. Larger values increase iteration cost, but may be necessary for convergence. Default is 20.

maxiter [int, optional] Maximum number of iterations (restart cycles). Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M [(sparse matrix, dense matrix, LinearOperator)] Inverse of the preconditioner of A. M should approximate the inverse of A and be easy to solve for (see Notes). Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance. By default, no preconditioner is used.

callback [function] User-supplied function to call after each iteration. It is called as callback(rk), where rk is the current residual vector.

restrt [int, optional] DEPRECATED - use restart instead.

See also:

LinearOperator
Notes
A preconditioner, P, is chosen such that P is close to A but easy to solve for. The preconditioner parameter required by this routine is $M = P^{-1}$. The inverse should preferably not be calculated explicitly. Rather, use the following template to produce M:

```
# Construct a linear operator that computes P^-1 * x.
import scipy.sparse.linalg as spla
M_x = lambda x: spla.spsolve(P, x)
M = spla.LinearOperator((n, n), M_x)
```

Examples
```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import gmres
>>> A = csc_matrix([[3, 2, 0], [1, -1, 0], [0, 5, 1]], dtype=float)
>>> b = np.array([2, 4, -1], dtype=float)
>>> x, exitCode = gmres(A, b)
>>> print(exitCode)  # 0 indicates successful convergence
0
>>> np.allclose(A.dot(x), b)
True
```

scipy.sparse.linalg.lgmres

Solve a matrix equation using the LGMRES algorithm.

The LGMRES algorithm \[1\] \[2\] is designed to avoid some problems in the convergence in restarted GMRES, and often converges in fewer iterations.

**Parameters**

- **A** [{sparse matrix, dense matrix, LinearOperator}] The real or complex N-by-N matrix of the linear system.
- **b** [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).
- **x0** [{array, matrix}] Starting guess for the solution.
- **tol, atol** [float, optional] Tolerances for convergence, $\|r\| \leq \max(tol \cdot \|b\|, atol)$. The default for atol is tol.
- **maxiter** [int, optional] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.
- **M** [{sparse matrix, dense matrix, LinearOperator}, optional] Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.
- **callback** [function, optional] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.
- **inner_m** [int, optional] Number of inner GMRES iterations per each outer iteration.
- **outer_k** [int, optional] Number of vectors to carry between inner GMRES iterations. According to \[1\], good values are in the range of 1…3. However, note that if you want

---

**Warning:** The default value for atol will be changed in a future release. For future compatibility, specify atol explicitly.
to use the additional vectors to accelerate solving multiple similar problems, larger values may be beneficial.

**outer_v**  
[list of tuples, optional] List containing tuples \((\mathbf{v}, \mathbf{Av})\) of vectors and corresponding matrix-vector products, used to augment the Krylov subspace, and carried between inner GMRES iterations. The element \(\mathbf{Av}\) can be \(\text{None}\) if the matrix-vector product should be re-evaluated. This parameter is modified in-place by \(\text{lgmres}\), and can be used to pass “guess” vectors in and out of the algorithm when solving similar problems.

**store_outer_Av**  
[bool, optional] Whether LGMRES should store also \(\mathbf{A^*v}\) in addition to vectors \(\mathbf{v}\) in the \(\text{outer}_v\) list. Default is True.

**prepend_outer_v**  
[bool, optional] Whether to put \(\text{outer_v}\) augmentation vectors before Krylov iterates. In standard LGMRES, \(\text{prepend}_\text{outer_v}=\text{False}\).

**Returns**

- **x**  
[array or matrix] The converged solution.

- **info**  
[int] Provides convergence information:
  • 0 : successful exit
  • >0 : convergence to tolerance not achieved, number of iterations
  • <0 : illegal input or breakdown

**Notes**

The LGMRES algorithm \([1] [2]\) is designed to avoid the slowing of convergence in restarted GMRES, due to alternating residual vectors. Typically, it often outperforms GMRES(m) of comparable memory requirements by some measure, or at least is not much worse.

Another advantage in this algorithm is that you can supply it with ‘guess’ vectors in the \(\text{outer}_v\) argument that augment the Krylov subspace. If the solution lies close to the span of these vectors, the algorithm converges faster. This can be useful if several very similar matrices need to be inverted one after another, such as in Newton-Krylov iteration where the Jacobian matrix often changes little in the nonlinear steps.

**References**

\([1] [2]\)

**Examples**

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import lgmres
>>> A = csc_matrix([[3, 2, 0], [1, -1, 0], [0, 5, 1]], dtype=float)
>>> b = np.array([2, 4, -1], dtype=float)
>>> x, exitCode = lgmres(A, b)
>>> print(exitCode)  # 0 indicates successful convergence
0
>>> np.allclose(A.dot(x), b)
True
```

**scipy.sparse.linalg.minres**

Use MINimum RESidual iteration to solve \(\mathbf{Ax=b}\)

MINRES minimizes \(\|\mathbf{A^*x - b}\|\) for a real symmetric matrix \(\mathbf{A}\). Unlike the Conjugate Gradient method, \(\mathbf{A}\) can be indefinite or singular.

If \(\text{shift}=0\) then the method solves \((\mathbf{A} - \text{shift*I})\mathbf{x} = \mathbf{b}\)
Parameters

A  [{sparse matrix, dense matrix, LinearOperator}] The real symmetric N-by-N matrix of the linear system

b  [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x  [{array, matrix}] The converged solution.

info  [integer]

Provides convergence information:
- 0 : successful exit
- >0 : convergence to tolerance not achieved, number of iterations
- <0 : illegal input or breakdown

Other Parameters

x0  [{array, matrix}] Starting guess for the solution.

tol  [float] Tolerance to achieve. The algorithm terminates when the relative residual is below tol.

maxiter  [integer] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M  [{sparse matrix, dense matrix, LinearOperator}] Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback  [function] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

References

Solution of sparse indefinite systems of linear equations,

This file is a translation of the following MATLAB implementation:
https://web.stanford.edu/group/SOL/software/minres/minres-matlab.zip

scipy.sparse.linalg.qmr

scipy.sparse.linalg.qmr(A, b, x0=None, tol=1e-05, maxiter=None, M1=None, M2=None, callback=None, atol=None)

Use Quasi-Minimal Residual iteration to solve \( Ax = b \).

Parameters

A  [{sparse matrix, dense matrix, LinearOperator}] The real-valued N-by-N matrix of the linear system. It is required that the linear operator can produce \( Ax \) and \( A^T x \).

b  [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x  [{array, matrix}] The converged solution.

info  [integer]

Provides convergence information:
- 0 : successful exit
- >0 : convergence to tolerance not achieved, number of iterations
- <0 : illegal input or breakdown

Other Parameters

x0  [{array, matrix}] Starting guess for the solution.
tol, atol [float, optional] Tolerances for convergence, \( \text{norm(residual)} \leq \max(\text{tol} \cdot \text{norm(b)}, \text{atol}) \). The default for atol is 'legacy', which emulates a different legacy behavior.

**Warning:** The default value for atol will be changed in a future release. For future compatibility, specify atol explicitly.

maxiter [integer] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M1 [(sparse matrix, dense matrix, LinearOperator)] Left preconditioner for A.

M2 [(sparse matrix, dense matrix, LinearOperator)] Right preconditioner for A. Used together with the left preconditioner M1. The matrix M1*A*M2 should have better conditioned than A alone.

callback [function] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

See also: LinearOperator

**Examples**

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import qmr
>>> A = csc_matrix([[3, 2, 0], [1, -1, 0], [0, 5, 1]], dtype=float)
>>> b = np.array([2, 4, -1], dtype=float)
>>> x, exitCode = qmr(A, b)
>>> print(exitCode)   # 0 indicates successful convergence
0
>>> np.allclose(A.dot(x), b)
True
```

scipy.sparse.linalg.gcrotmk

scipy.sparse.linalg.gcrotmk(A, b, x0=None, tol=1e-05, maxiter=1000, M=None, callback=None, m=20, k=None, CU=None, discard_C=False, truncate='oldest', atol=None)

Solve a matrix equation using flexible GCROT(m,k) algorithm.

**Parameters**

A [(sparse matrix, dense matrix, LinearOperator)] The real or complex N-by-N matrix of the linear system.

b [(array, matrix)] Right hand side of the linear system. Has shape (N,) or (N,1).

x0 [(array, matrix)] Starting guess for the solution.

tol, atol [float, optional] Tolerances for convergence, \( \text{norm(residual)} \leq \max(\text{tol} \cdot \text{norm(b)}, \text{atol}) \). The default for atol is tol.

**Warning:** The default value for atol will be changed in a future release. For future compatibility, specify atol explicitly.

maxiter [int, optional] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M [(sparse matrix, dense matrix, LinearOperator), optional] Preconditioner for A. The preconditioner should approximate the inverse of A. gcrotmk is a 'flexible' algorithm and the preconditioner can vary from iteration to iteration. Effective
preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

**callback**  
[function, optional] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

**m**  
[int, optional] Number of inner FGMRES iterations per each outer iteration. Default: 20

**k**  
[int, optional] Number of vectors to carry between inner FGMRES iterations. According to [2], good values are around m. Default: m

**CU**  
[list of tuples, optional] List of tuples (c, u) which contain the columns of the matrices C and U in the GCR(m,k) algorithm. For details, see [2]. The list given and vectors contained in it are modified in-place. If not given, start from empty matrices. The c elements in the tuples can be None, in which case the vectors are recomputed via c = A u on start and orthogonalized as described in [3].

**discard_C**  
[bool, optional] Discard the C-vectors at the end. Useful if recycling Krylov subspaces for different linear systems.

**truncate**  

**Returns**

- **x**  
  [array or matrix] The solution found.
- **info**  
  [int] Provides convergence information:
  - 0 : successful exit
  - >0 : convergence to tolerance not achieved, number of iterations

**References**

[1], [2], [3]

Iterative methods for least-squares problems:

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>lsqr(A, b[, damp, atol, btol, conlim, ...])</code></td>
<td>Find the least-squares solution to a large, sparse, linear system of equations.</td>
</tr>
<tr>
<td><code>lsmr(A, b[, damp, atol, btol, conlim, ...])</code></td>
<td>Iterative solver for least-squares problems.</td>
</tr>
</tbody>
</table>

**scipy.sparse.linalg lsqr**

`scipy.sparse.linalg lsqr(A, b, damp=0.0, atol=1e-08, btol=1e-08, conlim=10000000.0, iter_lim=None, show=False, calc_var=False, x0=None)`

Find the least-squares solution to a large, sparse, linear system of equations.

The function solves \( Ax = b \) or \( \min ||b - Ax||^2 \) or \( \min ||Ax - b||^2 + d^2 \ ||x||^2 \).

The matrix A may be square or rectangular (over-determined or under-determined), and may have any rank.

1. **Unsymmetric equations --**  
   \( \text{solve } A*x = b \)

2. **Linear least squares --**  
   \( \text{solve } A*x = b \)  
   \text{in the least-squares sense}

3. **Damped least squares --**  
   \( \text{solve } (A + \text{damp}I)*x = (b) \)  
   \( \text{in the least-squares sense} \)
Parameters

A  [{sparse matrix, ndarray, LinearOperator}] Representation of an m-by-n matrix. It is required that the linear operator can produce \( Ax \) and \( A^T x \).

b  [array_like, shape (m,)] Right-hand side vector \( b \).

damp  [float] Damping coefficient.

atol, btol  [float, optional] Stopping tolerances. If both are 1.0e-9 (say), the final residual norm should be accurate to about 9 digits. (The final x will usually have fewer correct digits, depending on \( \text{cond}(A) \) and the size of damp.)

conlim  [float, optional] Another stopping tolerance. lsqr terminates if an estimate of \( \text{cond}(A) \) exceeds conlim. For compatible systems \( Ax = b \), conlim could be as large as 1.0e+12 (say). For least-squares problems, conlim should be less than 1.0e+8. Maximum precision can be obtained by setting \( \text{atol} = \text{btol} = \text{conlim} = \text{zero} \), but the number of iterations may then be excessive.

iter_lim  [int, optional] Explicit limitation on number of iterations (for safety).

show  [bool, optional] Display an iteration log.

calc_var  [bool, optional] Whether to estimate diagonals of \((A'A + \text{damp}^2\text{I})^{-1}\).

x0  [array_like, shape (n,), optional] Initial guess of x, if None zeros are used. New in version 1.0.0.

Returns

x  [ndarray of float] The final solution.

istop  [int] Gives the reason for termination. 1 means x is an approximate solution to \( Ax = b \). 2 means x approximately solves the least-squares problem.

itn  [int] Iteration number upon termination.

r1norm  [float] \( \|r\| \), where \( r = b - Ax \).

r2norm  [float] \( \sqrt{\|r\|^2 + \text{damp}^2 \|x\|^2} \). Equal to r1norm if damp == 0.

anorm  [float] Estimate of Frobenius norm of \( Abar = [A; [\text{damp}\times\text{I}]] \).

acond  [float] Estimate of \( \text{cond}(Abar) \).

arnorm  [float] Estimate of \( \|A'A^T r - \text{damp}^2 x\| \).

xnorm  [float] \( \|x\| \).

var  [ndarray of float] If calc_var is True, estimates all diagonals of \((A'A)^{-1}\) (if damp == 0) or more generally \((A'A + \text{damp}^2\text{I})^{-1}\). This is well defined if A has full column rank or damp > 0. (Not sure what var means if rank(A) < n and damp = 0.)

Notes

LSQR uses an iterative method to approximate the solution. The number of iterations required to reach a certain accuracy depends strongly on the scaling of the problem. Poor scaling of the rows or columns of A should therefore be avoided where possible.

For example, in problem 1 the solution is unaltered by row-scaling. If a row of A is very small or large compared to the other rows of A, the corresponding row of ( A b ) should be scaled up or down.

In problems 1 and 2, the solution x is easily recovered following column-scaling. Unless better information is known, the nonzero columns of A should be scaled so that they all have the same Euclidean norm (e.g., 1.0).

In problem 3, there is no freedom to re-scale if damp is nonzero. However, the value of damp should be assigned only after attention has been paid to the scaling of A.

The parameter damp is intended to help regularize ill-conditioned systems, by preventing the true solution from being very large. Another aid to regularization is provided by the parameter acond, which may be used to terminate iterations before the computed solution becomes very large.
If some initial estimate $x_0$ is known and if $\text{damp} == 0$, one could proceed as follows:

1. Compute a residual vector $r_0 = b - A*x_0$.
2. Use LSQR to solve the system $A*\delta x = r_0$.
3. Add the correction $\delta x$ to obtain a final solution $x = x_0 + \delta x$.

This requires that $x_0$ be available before and after the call to LSQR. To judge the benefits, suppose LSQR takes $k_1$ iterations to solve $A*x = b$ and $k_2$ iterations to solve $A*\delta x = r_0$. If $x_0$ is “good”, $\text{norm}(r_0)$ will be smaller than $\text{norm}(b)$. If the same stopping tolerances atol and btol are used for each system, $k_1$ and $k_2$ will be similar, but the final solution $x_0 + \delta x$ should be more accurate. The only way to reduce the total work is to use a larger stopping tolerance for the second system. If some value btol is suitable for $A*x = b$, the larger value $\text{btol}^*\text{norm}(b)/\text{norm}(r_0)$ should be suitable for $A*\delta x = r_0$.

Preconditioning is another way to reduce the number of iterations. If it is possible to solve a related system $M*x = b$ efficiently, where $M$ approximates $A$ in some helpful way (e.g. $M - A$ has low rank or its elements are small relative to those of $A$), LSQR may converge more rapidly on the system $A*M(\text{inverse})*z = b$, after which $x$ can be recovered by solving $M*x = z$.

If $A$ is symmetric, LSQR should not be used! Alternatives are the symmetric conjugate-gradient method (cg) and/or SYMMLQ. SYMMLQ is an implementation of symmetric cg that applies to any symmetric $A$ and will converge more rapidly than LSQR. If $A$ is positive definite, there are other implementations of symmetric cg that require slightly less work per iteration than SYMMLQ (but will take the same number of iterations).

References
[1], [2], [3]

Examples

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import lsqr
>>> A = csc_matrix([[1., 0.], [1., 1.], [0., 1.]], dtype=float)
```

The first example has the trivial solution $[0, 0]$

```python
>>> b = np.array([0., 0., 0.], dtype=float)
>>> x, istop, itn, normr = lsqr(A, b)[:4]
>>> x, istop, itn, normr = lsqr(A, b)[:4]
```

The exact solution is $x = 0$

```python
>>> istop
0
>>> x
array([ 0., 0.])
```

The stopping code $\text{istop}=0$ returned indicates that a vector of zeros was found as a solution. The returned solution $x$ indeed contains $[0., 0.]$. The next example has a non-trivial solution:

```python
>>> b = np.array([1., 0., -1.], dtype=float)
>>> x, istop, itn, r1norm = lsqr(A, b)[:4]
>>> x
array([ 1., -1.])
>>> itn
1
```

(continues on next page)
As indicated by $istop=1$, $lsqr$ found a solution obeying the tolerance limits. The given solution $[1., -1.]$ obviously solves the equation. The remaining return values include information about the number of iterations ($itn=1$) and the remaining difference of left and right side of the solved equation. The final example demonstrates the behavior in the case where there is no solution for the equation:

```python
>>> r1norm
4.440892098500627e-16
```

`istop` indicates that the system is inconsistent and thus $x$ is rather an approximate solution to the corresponding least-squares problem. $r1norm$ contains the norm of the minimal residual that was found.

### scipy.sparse.linalg.lsmr

$lsmr$ solves the system of linear equations $Ax = b$. If the system is inconsistent, it solves the least-squares problem $\min ||b - Ax||_2$ where $A$ is a rectangular matrix of dimension $m$-by-$n$, where all cases are allowed: $m = n$, $m > n$, or $m < n$. $B$ is a vector of length $m$. The matrix $A$ may be dense or sparse (usually sparse).

**Parameters**

- **A**
- **b**
  - [array_like, shape (m,)] Vector $b$ in the linear system.
- **damp**
  - [float] Damping factor for regularized least-squares. $lsmr$ solves the regularized least-squares problem:

$$\min ||(b) - (A)x||_2$$

$$||0|| (damp*I) ||_2$$

where damp is a scalar. If damp is None or 0, the system is solved without regularization.

- **atol**, **btol**
  - [float, optional] Stopping tolerances. $lsmr$ continues iterations until a certain backward error estimate is smaller than some quantity depending on atol and btol. Let $r = b - Ax$ be the residual vector for the current approximate solution $x$. If $Ax = b$ seems to be consistent, $lsmr$ terminates when $\text{norm}(r) <= \text{atol} \times \text{norm}(A) \times \text{norm}(x) + \text{btol} \times \text{norm}(b)$. Otherwise, $lsmr$ terminates when $\text{norm}(A^{\top} r) <= \text{atol} \times \text{norm}(A) \times \text{norm}(r)$. If both tolerances are $1.0e-6$ (say), the final $\text{norm}(r)$ should be accurate to about 6 digits. (The final $x$ will usually have fewer correct digits, depending on $\text{cond}(A)$ and the size of LAMBDA.) If $atol$ or $btol$ is
None, a default value of 1.0e-6 will be used. Ideally, they should be estimates of the relative error in the entries of A and B respectively. For example, if the entries of A have 7 correct digits, set atol = 1e-7. This prevents the algorithm from doing unnecessary work beyond the uncertainty of the input data.

**conlim** [float, optional] *lsmr* terminates if an estimate of \( \text{cond}(A) \) exceeds *conlim*. For compatible systems \( Ax = b \), conlim could be as large as 1.0e+12 (say). For least-squares problems, *conlim* should be less than 1.0e+8. If *conlim* is None, the default value is 1e+8. Maximum precision can be obtained by setting atol = btol = conlim = 0, but the number of iterations may then be excessive.

**maxiter** [int, optional] *lsmr* terminates if the number of iterations reaches *maxiter*. The default is *maxiter* = \( \min(m, n) \). For ill-conditioned systems, a larger value of *maxiter* may be needed.

**show** [bool, optional] Print iterations logs if show=True.

**x0** [array_like, shape (n,), optional] Initial guess of x, if None zeros are used. New in version 1.0.0.

**Returns**

- **x** [ndarray of float] Least-square solution returned.
- **istop** [int] istop gives the reason for stopping:

<table>
<thead>
<tr>
<th>istop</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>x = 0 is a solution. If x0 was given, then x = x0 is a solution.</td>
</tr>
<tr>
<td>1</td>
<td>x is an approximate solution to ( A\times x = b ), according to atol and btol.</td>
</tr>
<tr>
<td>2</td>
<td>x approximately solves the least-squares problem according to atol.</td>
</tr>
<tr>
<td>3</td>
<td>( \text{COND}(A) ) seems to be greater than ( \text{CONLIM} ).</td>
</tr>
<tr>
<td>4</td>
<td>is the same as 1 with atol = btol = eps (machine precision)</td>
</tr>
<tr>
<td>5</td>
<td>is the same as 2 with atol = eps.</td>
</tr>
<tr>
<td>6</td>
<td>is the same as 3 with ( \text{CONLIM} = 1/\text{eps} ).</td>
</tr>
<tr>
<td>7</td>
<td>ITN reached maxiter before the other stopping conditions were satisfied.</td>
</tr>
</tbody>
</table>

- **itn** [int] Number of iterations used.
- **normr** [float] \( \| b - Ax \| \)
- **normar** [float] \( \| A^T (b - Ax) \| \)
- **norma** [float] \( \| A \| \)
- **conda** [float] Condition number of A.
- **normx** [float] \( \| x \| \)

**Notes**

New in version 0.11.0.

**References**

[1], [2]

**Examples**

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import lsqr
>>> A = csc_matrix([[1., 0.], [1., 1.], [0., 1.]], dtype=float)
```

The first example has the trivial solution \([0, 0]^{T}\)
The stopping code `istop=0` returned indicates that a vector of zeros was found as a solution. The returned solution `x` indeed contains `[0., 0.]`. The next example has a non-trivial solution:

```python
>>> b = np.array([1., 0., -1.], dtype=float)
>>> x, istop, itn, normr = lsmr(A, b)[:4]
>>> istop
1
>>> x
array([ 1., -1.])
>>> itn
1
>>> normr
4.40892098500627e-16
```

As indicated by `istop=1`, `lsmr` found a solution obeying the tolerance limits. The given solution `[1., -1.]` obviously solves the equation. The remaining return values include information about the number of iterations (`itn=1`) and the remaining difference of left and right side of the solved equation. The final example demonstrates the behavior in the case where there is no solution for the equation:

```python
>>> b = np.array([1., 0.01, -1.], dtype=float)
>>> x, istop, itn, normr = lsmr(A, b)[:4]
>>> istop
2
>>> x
array([-1.00333333, 0.99666667])
>>> A.dot(x)-b
array([ 1.00333333, -1.00333333, 0.00333333])
>>> normr
0.005773502691896255
```

`istop` indicates that the system is inconsistent and thus `x` is rather an approximate solution to the corresponding least-squares problem. `normr` contains the minimal distance that was found.

### Matrix factorizations

Eigenvalue problems:

- **`eigs(A[, k, M, sigma, which, v0, ncv, ...])`**
  
  Find k eigenvalues and eigenvectors of the square matrix A.

- **`eigsh(A[, k, M, sigma, which, v0, ncv, ...])`**
  
  Find k eigenvalues and eigenvectors of the real symmetric square matrix or complex hermitian matrix A.

- **`lobpcg(A, X[, B, M, Y, tol, maxiter, ...])`**
  
  Locally Optimal Block Preconditioned Conjugate Gradient Method (LOBPCG)
scipy.sparse.linalg.eigs

scipy.sparse.linalg.eigs(A, k=6, M=None, sigma=None, which='LM', v0=None, ncv=None, maxiter=None, tol=0, return_eigenvectors=True, Minv=None, OPinv=None, OPpart=None)

Find k eigenvalues and eigenvectors of the square matrix A.

Solves \( A \cdot x[i] = w[i] \cdot x[i] \), the standard eigenvalue problem for \( w[i] \) eigenvalues with corresponding eigenvectors \( x[i] \).

If M is specified, solves \( A \cdot x[i] = w[i] \cdot M \cdot x[i] \), the generalized eigenvalue problem for \( w[i] \) eigenvalues with corresponding eigenvectors \( x[i] \).

Parameters

- **A**: [ndarray, sparse matrix or LinearOperator] An array, sparse matrix, or LinearOperator representing the operation \( A \cdot x \), where A is a real or complex square matrix.
- **k**: [int, optional] The number of eigenvalues and eigenvectors desired. \( k \) must be smaller than N-1. It is not possible to compute all eigenvectors of a matrix.
- **M**: [ndarray, sparse matrix or LinearOperator, optional] An array, sparse matrix, or LinearOperator representing the operation \( M \cdot x \) for the generalized eigenvalue problem. \( A \cdot x = w \cdot M \cdot x \). M must represent a real, symmetric matrix if A is real, and must represent a complex, hermitian matrix if A is complex. For best results, the data type of M should be the same as that of A. Additionally:
  - If sigma is None, M is positive definite.
  - If sigma is specified, M is positive semi-definite.

If sigma is None, eigs requires an operator to compute the solution of the linear equation \( M \cdot x = b \). This is done internally via a (sparse) LU decomposition for an explicit matrix M, or via an iterative solver for a general linear operator. Alternatively, the user can supply the matrix or operator Minv, which gives \( x = \text{Minv} \cdot b = M^{-1} \cdot b \).

- **sigma**: [real or complex, optional] Find eigenvalues near sigma using shift-invert mode. This requires an operator to compute the solution of the linear system \( [A - sigma \cdot M] \cdot x = b \), where M is the identity matrix if unspecified. This is computed internally via a (sparse) LU decomposition for explicit matrices A & M, or via an iterative solver if either A or M is a general linear operator. Alternatively, the user can supply the matrix or operator OPinv, which gives \( x = \text{OPinv} \cdot b = [A - sigma \cdot M]^{-1} \cdot b \). For a real matrix A, shift-invert can either be done in imaginary mode or real mode, specified by the parameter OPpart (‘r’ or ‘i’). Note that when sigma is specified, the keyword ‘which’ (below) refers to the shifted eigenvalues \( w'[i] \) where:
  - If A is real and OPpart == ‘r’ (default), \( w'[i] = 1/2 \cdot [1/(w[i]-sigma) + 1/(w[i]-\text{conj}(sigma))] \).
  - If A is real and OPpart == ‘i’, \( w'[i] = 1/2i \cdot [1/(w[i]-sigma) - 1/(w[i]-\text{conj}(sigma))] \).
  - If A is complex, \( w'[i] = 1/(w[i]-sigma) \).

- **v0**: [ndarray, optional] Starting vector for iteration. Default: random
- **ncv**: [int, optional] The number of Lanczos vectors generated. \( ncv \) must be greater than \( k \); it is recommended that \( ncv > 2k \). Default: \( \min(n, \max(2k + 1, 20)) \)

- **which**: [str, ‘LM’ | ‘SM’ | ‘LR’ | ‘SR’ | ‘LI’ | ‘SI’], optional] Which \( k \) eigenvectors and eigenvalues to find:
  - ‘LM’: largest magnitude
  - ‘SM’: smallest magnitude

Chapter 6. API Reference
'LR': largest real part
'SR': smallest real part
'LI': largest imaginary part
'SI': smallest imaginary part

When sigma != None, 'which' refers to the shifted eigenvalues w'[i]' (see discussion in 'sigma', above). ARPACK is generally better at finding large values than small values. If small eigenvalues are desired, consider using shift-invert mode for better performance.

maxiter [int, optional] Maximum number of Arnoldi update iterations allowed Default: n*10
tol [float, optional] Relative accuracy for eigenvalues (stopping criterion) The default value of 0 implies machine precision.

return_eigenvectors [bool, optional] Return eigenvectors (True) in addition to eigenvalues

Minv [ndarray, sparse matrix or LinearOperator, optional] See notes in M, above.
OPinv [ndarray, sparse matrix or LinearOperator, optional] See notes in sigma, above.
OPpart ['r' or 'i', optional] See notes in sigma, above

Returns

w [ndarray] Array of k eigenvalues.
v [ndarray] An array of k eigenvectors. v[:, i] is the eigenvector corresponding to the eigenvalue w[i].

Raises

ArpackNoConvergence

When the requested convergence is not obtained. The currently converged eigenvalues and eigenvectors can be found as eigenvalues and eigenvectors attributes of the exception object.

See also:
eigsh
eigenvalues and eigenvectors for symmetric matrix A

svds

singular value decomposition for a matrix A

Notes

This function is a wrapper to the ARPACK [1] SNEUPD, DNEUPD, CNEUPD, ZNEUPD, functions which use the Implicitly Restarted Arnoldi Method to find the eigenvalues and eigenvectors [2].

References

[1], [2]

Examples

Find 6 eigenvectors of the identity matrix:

```python
>>> from scipy.sparse.linalg import eigs
>>> id = np.eye(13)
>>> vals, vecs = eigs(id, k=6)
>>> vals
array([-1.0000, -1.0000, -1.0000, -1.0000, -1.0000, -1.0000])
>>> vecs.shape
(13, 6)
```
Find k eigenvalues and eigenvectors of the real symmetric square matrix or complex hermitian matrix A.

Solves $A \times x[i] = w[i] \times x[i]$, the standard eigenvalue problem for $w[i]$ eigenvalues with corresponding eigenvectors $x[i]$.

If M is specified, solves $A \times x[i] = w[i] \times M \times x[i]$, the generalized eigenvalue problem for $w[i]$ eigenvalues with corresponding eigenvectors $x[i]$.

**Parameters**

- **A** [ndarray, sparse matrix or LinearOperator] A square operator representing the operation $A \times x$, where A is real symmetric or complex hermitian. For buckling mode (see below) A must additionally be positive-definite.
- **k** [int, optional] The number of eigenvalues and eigenvectors desired. k must be smaller than N. It is not possible to compute all eigenvectors of a matrix.

**Returns**

- **w** [array] Array of k eigenvalues.
- **v** [array] An array representing the $k$ eigenvectors. The column $v[:, i]$ is the eigenvector corresponding to the eigenvalue $w[i]$.

**Other Parameters**

- **M** [An N x N matrix, array, sparse matrix, or linear operator representing] the operation $M \times x$ for the generalized eigenvalue problem $A \times x = w \times M \times x$.
  M must represent a real, symmetric matrix if A is real, and must represent a complex, hermitian matrix if A is complex. For best results, the data type of M should be the same as that of A. Additionally:
  - If sigma is None, M is symmetric positive definite.
  - If sigma is specified, M is symmetric positive semi-definite.
  - In buckling mode, M is symmetric indefinite.
  If sigma is None, eigsh requires an operator to compute the solution of the linear equation $M \times x = b$. This is done internally via a (sparse) LU decomposition for an explicit matrix M, or via an iterative solver for a general linear operator. Alternatively, the user can supply the matrix or operator Minv, which gives $x = Minv \times b = M^{-1} \times b$.
- **sigma** [real] Find eigenvalues near sigma using shift-invert mode. This requires an operator to compute the solution of the linear system $[A - sigma \times M] \times x = b$, where M is the identity matrix if unspecified. This is computed internally via a (sparse) LU decomposition for explicit matrices A & M, or via an iterative solver if either A or M is a general linear operator. Alternatively, the user can supply the matrix or operator OPinv, which gives $x = OPinv \times b = [A - sigma \times M]^{-1} \times b$. Note that when sigma is specified, the keyword ‘which’ refers to the shifted eigenvalues $w'[i]$ where:
  - if mode == ‘normal’, $w'[i] = 1 / (w[i] - sigma)$.
  - if mode == ‘cayley’, $w'[i] = (w[i] + sigma) / (w[i] - sigma)$.
  - if mode == ‘buckling’, $w'[i] = w[i] / (w[i] - sigma)$.
  (see further discussion in ‘mode’ below)
- **v0** [ndarray, optional] Starting vector for iteration. Default: random
ncv [int, optional] The number of Lanczos vectors generated ncv must be greater than k and smaller than n; it is recommended that ncv > 2*k. Default: min(n, max(2*k + 1, 20))

which [str [‘LM’ | ‘SM’ | ‘LA’ | ‘SA’ | ‘BE’]] If A is a complex hermitian matrix, ‘BE’ is invalid. Which k eigenvectors and eigenvalues to find:

‘LM’ : Largest (in magnitude) eigenvalues.
‘SM’ : Smallest (in magnitude) eigenvalues.
‘LA’ : Largest (algebraic) eigenvalues.
‘SA’ : Smallest (algebraic) eigenvalues.
‘BE’ : Half (k/2) from each end of the spectrum.
When k is odd, return one more (k/2+1) from the high end. When sigma != None, ‘which’ refers to the shifted eigenvalues w'[i] (see discussion in ‘sigma’, above). ARPACK is generally better at finding large values than small values. If small eigenvalues are desired, consider using shift-invert mode for better performance.

maxiter [int, optional] Maximum number of Arnoldi update iterations allowed. Default: n*10

tol [float] Relative accuracy for eigenvalues (stopping criterion). The default value of 0 implies machine precision.

Minv [N x N matrix, array, sparse matrix, or LinearOperator] See notes in M, above.

OPinv [N x N matrix, array, sparse matrix, or LinearOperator] See notes in sigma, above.

return_eigenvectors [bool] Return eigenvectors (True) in addition to eigenvalues. This value determines the order in which eigenvalues are sorted. The sort order is also dependent on the which variable.

For which = ‘LM’ or ‘SA’:
If return_eigenvectors is True, eigenvalues are sorted by algebraic value.
If return_eigenvectors is False, eigenvalues are sorted by absolute value.

For which = ‘BE’ or ‘LA’:
eigenvalues are always sorted by algebraic value.

For which = ‘SM’:
If return_eigenvectors is True, eigenvalues are sorted by algebraic value.
If return_eigenvectors is False, eigenvalues are sorted by decreasing absolute value.

mode [string [‘normal’ | ‘buckling’ | ‘cayley’]] Specify strategy to use for shift-invert mode. This argument applies only for real-valued A and sigma != None. For shift-invert mode, ARPACK internally solves the eigenvalue problem OP * x'[i] = w'[i] * B * x'[i] and transforms the resulting Ritz vectors x'[i] and Ritz values w'[i] into the desired eigenvectors and eigenvalues of the problem A * x[i] = w[i] * M * x[i]. The modes are as follows:

‘normal’ :
OP = [A - sigma * M]^{-1} @ M, B = M, w'[i] = 1 / (w[i] - sigma)

‘buckling’ :
OP = [A - sigma * M]^{-1} @ A, B = A, w'[i] = w[i] / (w[i] - sigma)

‘cayley’ :
OP = [A - sigma * M]^{-1} @ [A + sigma * M], B = M, w'[i] = (w[i] + sigma) / (w[i] - sigma)

The choice of mode will affect which eigenvalues are selected by the keyword ‘which’, and can also impact the stability of convergence (see [2] for a discussion).

Raises

ArpackNoConvergence
When the requested convergence is not obtained.
The currently converged eigenvalues and eigenvectors can be found as `eigenvalues` and `eigenvectors` attributes of the exception object.

See also:

**eigs**

eigenvalues and eigenvectors for a general (nonsymmetric) matrix A

**svds**

singular value decomposition for a matrix A

Notes

This function is a wrapper to the ARPACK [1] SSEUPD and DSEUPD functions which use the Implicitly Restarted Lanczos Method to find the eigenvalues and eigenvectors [2].

References

[1], [2]

Examples

```python
>>> from scipy.sparse.linalg import eigh
>>> identity = np.eye(13)
>>> eigenvalues, eigenvectors = eigh(identity, k=6)
>>> eigenvalues
array([1., 1., 1., 1., 1., 1.])
>>> eigenvectors.shape
(13, 6)
```

scipy.sparse.linalg.lobpcg

`scipy.sparse.linalg.lobpcg(A, X, B=None, M=None, Y=None, tol=None, maxiter=20, largest=True, verbosityLevel=0, retLambdaHistory=False, retResidualsHistory=False)`

Locally Optimal Block Preconditioned Conjugate Gradient Method (LOBPCG)

LOBPCG is a preconditioned eigensolver for large symmetric positive definite (SPD) generalized eigenproblems.

**Parameters**

- **A** ([sparse matrix, dense matrix, LinearOperator]) The symmetric linear operator of the problem, usually a sparse matrix. Often called the “stiffness matrix”.
- **X** ([array_like]) Initial approximation to the k eigenvectors. If A has shape=(n,n) then X should have shape shape=(n,k).
- **B** ([{dense matrix, sparse matrix, LinearOperator}, optional]) the right hand side operator in a generalized eigenproblem. by default, B = Identity often called the “mass matrix”
- **M** ([{dense matrix, sparse matrix, LinearOperator}, optional]) preconditioner to A; by default M = Identity M should approximate the inverse of A
- **Y** ([array_like, optional]) n-by-sizeY matrix of constraints, sizeY < n The iterations will be performed in the B-orthogonal complement of the column-space of Y. Y must be full rank.

**Returns**

- **w** [array] Array of k eigenvalues
- **v** [array] An array of k eigenvectors. V has the same shape as X.

**Other Parameters**
tol  [scalar, optional] Solver tolerance (stopping criterion) by default: tol=n*sqrt(eps)
maxiter [integer, optional] maximum number of iterations by default: maxiter=min(n,20)
largest [bool, optional] when True, solve for the largest eigenvalues, otherwise the smallest
verbosityLevel [integer, optional] controls solver output. default: verbosityLevel = 0.
retLambdaHistory [boolean, optional] whether to return eigenvalue history
retResidualNormsHistory [boolean, optional] whether to return history of residual norms

Notes
If both retLambdaHistory and retResidualNormsHistory are True, the return tuple has the following format (lambda, V, lambda history, residual norms history).

In the following n denotes the matrix size and m the number of required eigenvalues (smallest or largest).
The LOBPCG code internally solves eigenproblems of the size 3''m'' on every iteration by calling the "standard" dense eigensolver, so if m is not small enough compared to n, it does not make sense to call the LOBPCG code, but rather one should use the "standard" eigensolver, e.g. numpy or scipy function in this case. If one calls the LOBPCG algorithm for 5''m''>''n'', it will most likely break internally, so the code tries to call the standard function instead.

It is not that n should be large for the LOBPCG to work, but rather the ratio n/m should be large. It you call the LOBPCG code with m``=1 and ``n``=10, it should work, though ``n is small. The method is intended for extremely large n/m, see e.g., reference [28] in https://arxiv.org/abs/0705.2626

The convergence speed depends basically on two factors:

1. How well relatively separated the seeking eigenvalues are from the rest of the eigenvalues. One can try to vary m to make this better.

2. How well conditioned the problem is. This can be changed by using proper preconditioning. For example, a rod vibration test problem (under tests directory) is ill-conditioned for large n, so convergence will be slow, unless efficient preconditioning is used. For this specific problem, a good simple preconditioner function would be a linear solve for A, which is easy to code since A is tridiagonal.

Acknowledgements

lobpcg.py code was written by Robert Cimrman. Many thanks belong to Andrew Knyazev, the author of the algorithm, for lots of advice and support.

References
[1], [2], [3]

Examples
Solve A x = lambda B x with constraints and preconditioning.

```python
>>> from scipy.sparse import spdiags, issparse
>>> from scipy.sparse.linalg import lobpcg, LinearOperator
>>> n = 100
>>> vals = [np.arange(n, dtype=np.float64) + 1]
>>> A = spdiags(vals, 0, n, n)
>>> A.toarray()
array([[ 1.,  0.,  0., ...,  0.,  0.,  0.],
       [ 0.,  2.,  0., ...,  0.,  0.,  0.],
       [ 0.,  0.,  3., ...,  0.,  0.,  0.],
       ..., ]
       [ 0.,  0.,  0., ..., 98.,  0.,  0.],
```

(continues on next page)
Constraints.

```python
>>> Y = np.eye(n, 3)
```

Initial guess for eigenvectors, should have linearly independent columns. Column dimension = number of requested eigenvalues.

```python
>>> X = np.random.rand(n, 3)
```

Preconditioner – inverse of A (as an abstract linear operator).

```python
>>> invA = spdiags([1./vals[0]], 0, n, n)
>>> def precond(x):
...     return invA * x
>>> M = LinearOperator(matvec=precond, shape=(n, n), dtype=float)
```

Here, invA could of course have been used directly as a preconditioner. Let us then solve the problem:

```python
>>> eigs, vecs = lobpcg(A, X, Y=Y, M=M, tol=1e-4, maxiter=40, largest=False)
>>> eigs
array([ 4.,  5.,  6.])
```

Note that the vectors passed in Y are the eigenvectors of the 3 smallest eigenvalues. The results returned are orthogonal to those.

Singular values problems:

```python
svds(A[, k, ncv, tol, which, v0, maxiter, ...]) Compute the largest k singular values/vectors for a sparse matrix.
```

**Parameters**

- **A**
  - [[sparse matrix, LinearOperator]] Array to compute the SVD on, of shape (M, N)
- **k**
  - [int, optional] Number of singular values and vectors to compute. Must be 1 <= k < min(A.shape).
- **ncv**
  - [int, optional] The number of Lanczos vectors generated ncv must be greater than k+1 and smaller than n; it is recommended that ncv > 2^k Default: min(n, max(2*k + 1, 20))
- **tol**
- **which**
  - [str, ['LM', 'SM'], optional] Which k singular values to find:
    - ‘LM’ : largest singular values
    - ‘SM’ : smallest singular values
  New in version 0.12.0.
v0 [ndarray, optional] Starting vector for iteration, of length min(A.shape). Should be an (approximate) left singular vector if N > M and a right singular vector otherwise. Default: random
New in version 0.12.0.
maxiter [int, optional] Maximum number of iterations.
New in version 0.12.0.
return_singular_vectors [bool or str, optional]
• True: return singular vectors (True) in addition to singular values.
  New in version 0.12.0.
• “u”: only return the u matrix, without computing vh (if N > M).
• “vh”: only return the vh matrix, without computing u (if N <= M).
  New in version 0.16.0.

Returns
u [ndarray, shape=(M, k)] Unitary matrix having left singular vectors as columns. If return_singular_vectors is “vh”, this variable is not computed, and None is returned instead.
s [ndarray, shape=(k,)] The singular values.
vt [ndarray, shape=(k, N)] Unitary matrix having right singular vectors as rows. If return_singular_vectors is “u”, this variable is not computed, and None is returned instead.

Notes
This is a naive implementation using ARPACK as an eigensolver on A.H * A or A * A.H, depending on which one is more efficient.

Examples
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import svds, eigs
>>> A = csc_matrix([[1, 0, 0], [5, 0, 2], [0, -1, 0], [0, 0, 3]], dtype=float)
>>> u, s, vt = svds(A, k=2)

s
darray([ 2.75193379, 5.6059665 ])

np.sqrt(eigs(A.dot(A.T), k=2)[0]).real
darray([5.6059665, 2.75193379])

Complete or incomplete LU factorizations

splu(A[, permc_spec, diag_pivot_thresh, ...]) Compute the LU decomposition of a sparse, square matrix.
spilu(A[, drop_tol, fill_factor, drop_rule, ...]) Compute an incomplete LU decomposition for a sparse, square matrix.
SuperLU LU factorization of a sparse matrix.

scipy.sparse.linalg.splu
scipy.sparse.linalg.spilu(A[, permc_spec=None, diag_pivot_thresh=None, relax=None, panel_size=None, options={}]) Compute the LU decomposition of a sparse, square matrix.

Parameters
A [sparse matrix] Sparse matrix to factorize. Should be in CSR or CSC format.
permc_spec

6.21. Sparse matrices (scipy.sparse)
[str, optional] How to permute the columns of the matrix for sparsity preservation.
(default: ‘COLAMD’)
• NATURAL: natural ordering.
• MMDATA: minimum degree ordering on the structure of $A^T A$.
• MMD_AT_PLUS_A: minimum degree ordering on the structure of $A^T + A$.
• COLAMD: approximate minimum degree column ordering

**diag_pivot_thresh**
[float, optional] Threshold used for a diagonal entry to be an acceptable pivot. See SuperLU user’s guide for details [1]

**relax**
[int, optional] Expert option for customizing the degree of relaxing supernodes. See SuperLU user’s guide for details [1]

**panel_size**
[int, optional] Expert option for customizing the panel size. See SuperLU user’s guide for details [1]

**options**
[dict, optional] Dictionary containing additional expert options to SuperLU. See SuperLU user guide [1] (section 2.4 on the ‘Options’ argument) for more details. For example, you can specify options=dict(Equil=False, IterRefine='SINGLE')) to turn equilibration off and perform a single iterative refinement.

**Returns**


See also:

**splu**

incomplete LU decomposition

Notes

This function uses the SuperLU library.

References

[1]

Examples

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import splu
>>> A = csc_matrix([[1., 0., 0.], [5., 0., 2.], [0., -1., 0.]], dtype=float)
>>> B = splu(A)
>>> x = np.array([1., 2., 3.], dtype=float)
>>> B.solve(x)
array([ 1. , -3. , -1.5])
>>> A.dot(B.solve(x))
array([ 1., 2., 3.])
>>> B.solve(A.dot(x))
array([ 1., 2., 3.])
```

scipy.sparse.linalg.spilu

```python
scipy.sparse.linalg.spilu(A, drop_tol=None, fill_factor=None, drop_rule=None, permc_spec=None, diag_pivot_thresh=None, relax=None, panel_size=None, options=None)
```

Compute an incomplete LU decomposition for a sparse, square matrix.

The resulting object is an approximation to the inverse of $A$.  

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Prameters

A
(N, N) array_like] Sparse matrix to factorize

drop_tol
[\text{float, optional}] Drop tolerance \(0 \leq \text{tol} \leq 1\) for an incomplete LU decomposition. (default: \(1e^{-4}\))

fill_factor
[\text{float, optional}] Specifies the fill ratio upper bound \((\geq 1.0)\) for ILU. (default: 10)

drop_rule
[\text{str, optional}] Comma-separated string of drop rules to use. Available rules: basic, prows, column, area, secondary, dynamic, interp. (Default: basic, area)
See SuperLU documentation for details.

Remaining other options
Same as for \text{spilu}

Returns

invA_approx
[\text{scipy.sparse.linalg.SuperLU}] Object, which has a \text{solve} method.

See also:

\text{spilu}
complete LU decomposition

Notes
To improve the better approximation to the inverse, you may need to increase \text{fill_factor} AND decrease \text{drop_tol}.

This function uses the SuperLU library.

Examples

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import spilu
>>> A = csc_matrix([[1., 0., 0.], [5., 0., 2.], [0., -1., 0.]], dtype=float)
>>> B = spilu(A)
>>> x = np.array([1., 2., 3.], dtype=float)
>>> B.solve(x)
array([ 1., -3., -1.5])
>>> A.dot(B.solve(x))
array([ 1.,  2.,  3.])
```
Examples

The LU decomposition can be used to solve matrix equations. Consider:

```python
>>> import numpy as np
>>> from scipy.sparse import csc_matrix, linalg as sla
>>> A = csc_matrix([[1, 2, 0, 4], [1, 0, 0, 1], [1, 0, 2, 1], [2, 2, 1, 0]])
```

This can be solved for a given right-hand side:

```python
>>> lu = sla.splu(A)
>>> b = np.array([1, 2, 3, 4])
>>> x = lu.solve(b)
>>> A.dot(x)
array([1., 2., 3., 4.])
```

The `lu` object also contains an explicit representation of the decomposition. The permutations are represented as mappings of indices:

```python
>>> lu.perm_r
array([0, 2, 1, 3], dtype=int32)
>>> lu.perm_c
array([2, 0, 1, 3], dtype=int32)
```

The L and U factors are sparse matrices in CSC format:

```python
>>> lu.L.A
array([[1., 0., 0., 0.],
       [0., 1., 0., 0.],
       [0., 0., 1., 0.],
       [1., 0.5, 0.5, 1.]])
>>> lu.U.A
array([[2., 0., 1., 4.],
       [0., 2., 1., 1.],
       [0., 0., 1., 1.],
       [0., 0., 0., -5.]])
```

The permutation matrices can be constructed:

```python
>>> Pr = csc_matrix((4, 4))
>>> Pr[lu.perm_r, np.arange(4)] = 1
>>> Pc = csc_matrix((4, 4))
>>> Pc[np.arange(4), lu.perm_c] = 1
```

We can reassemble the original matrix:

```python
>>> (Pr.T * (lu.L * lu.U) * Pc.T).A
array([[1., 2., 0., 4.],
       [1., 0., 0., 1.],
       [1., 0., 2., 1.],
       [2., 2., 1., 0.]])
```

Attributes

- **shape**
  Shape of the original matrix as a tuple of ints.
- **nnz**
  Number of nonzero elements in the matrix.
perm_c  Permutation Pc represented as an array of indices.
perm_r  Permutation Pr represented as an array of indices.
L       Lower triangular factor with unit diagonal as a :class:`scipy.sparse.csc_matrix`
U       Upper triangular factor as a :class:`scipy.sparse.csc_matrix`.

Methods

solve(rhs[, trans])  Solves linear system of equations with one or several right-hand sides.

.. currentmodule:: scipy.sparse.linalg

.. autofunction:: SuperLU.solve

**SuperLU.solve**

Solves linear system of equations with one or several right-hand sides.

Parameters

- **rhs**  [ndarray, shape (n,) or (n, k)] Right hand side(s) of equation
- **trans**  [{’N’, ’T’, ’H’}, optional] Type of system to solve:
  - ’N’:  $A \times x = rhs$ (default)
  - ’T’:  $A^T \times x = rhs$
  - ’H’:  $A^H \times x = rhs$

i.e., normal, transposed, and hermitian conjugate.

Returns

- **x**  [ndarray, shape rhs.shape] Solution vector(s)

Exceptions

- **ArpackNoConvergence**  (msg, eigenvalues, ...)  ARPACK iteration did not converge
- **ArpackError**  (info[, infodict])  ARPACK error

.. currentmodule:: scipy.sparse.linalg

**ArpackNoConvergence**  

Exception  :class:`scipy.sparse.linalg.ArpackNoConvergence`

.. currentmodule:: scipy.sparse.linalg

**ArpackNoConvergence**  (msg, eigenvalues, eigenvectors)

ARPACK iteration did not converge

Attributes

- **eigenvalues**  [ndarray] Partial result. Converged eigenvalues.
- **eigenvectors**  [ndarray] Partial result. Converged eigenvectors.
scipy.sparse.linalg.ArpackError

exception scipy.sparse.linalg.ArpackError

scipy.sparse.linalg.ArpackError:

info, infodict={'c': {0: 'Normal exit.', 1: 'Maximum number of iterations taken. All possible eigenvalues of OP has been found. IPARAM(5) returns the number of wanted converged Ritz values.', 2: 'No longer an informational error. Deprecated starting with release 2 of ARPACK.', 3: 'No shifts could be applied during a cycle of the Implicitly restarted Arnoldi iteration. One possibility is to increase the size of NCV relative to NEV.', 4: 'NEV must be positive.', 5: 'NCV-NEV >= 2 and less than or equal to N.', 6: 'The maximum number of Arnoldi update iterations allowed must be greater than zero.', 7: 'Length of private work array WORKL is not sufficient.', 8: 'Error return from LAPACK eigenvalue calculation.', 9: 'Starting vector is zero.', 10: 'IPARAM(7) must be 1, 2, 3.', 11: 'IPARAM(7) = 1 and BMAT = 'G' are incompatible.', 12: 'IPARAM(1) must be equal to 0 or 1.', 13: 'NEV and WHICH = 'BE' are incompatible.', 14: 'Could not build an Arnoldi factorization. IPARAM(5) returns the size of the current Arnoldi factorization. The user is advised to check that enough workspace and array storage has been allocated.'}, 'd': {0: 'Normal exit.', 1: 'Maximum number of iterations taken. All possible eigenvalues of OP has been found. IPARAM(5) returns the number of wanted converged Ritz values.', 2: 'No longer an informational error. Deprecated starting with release 2 of ARPACK.', 3: 'No shifts could be applied during a cycle of the Implicitly restarted Arnoldi iteration. One possibility is to increase the size of NCV relative to NEV.', 4: 'NEV must be positive.', 5: 'NCV-NEV >= 2 and less than or equal to N.', 6: 'The maximum number of Arnoldi update iterations allowed must be greater than zero.', 7: 'Length of private work array WORKL is not sufficient.', 8: 'Error return from LAPACK eigenvalue calculation.', 9: 'Starting vector is zero.', 10: 'IPARAM(7) must be 1, 2, 3.', 11: 'IPARAM(7) = 1 and BMAT = 'G' are incompatible.', 12: 'IPARAM(1) must be equal to 0 or 1.', 13: 'NEV and WHICH = 'BE' are incompatible.', 9999: 'Could not build an Arnoldi factorization. IPARAM(5) returns the size of the current Arnoldi factorization. The user is advised to check that enough workspace and array storage has been allocated.'}, 'i': {0: 'Normal exit.', 1: 'Maximum number of iterations taken. All possible eigenvalues of OP has been found. IPARAM(5) returns the number of wanted converged Ritz values.', 2: 'No longer an informational error. Deprecated starting with release 2 of ARPACK.', 3: 'No shifts could be applied during a cycle of the Implicitly restarted Arnoldi iteration. One possibility is to increase the size of NCV relative to NEV.', 4: 'NEV must be positive.', 5: 'NCV-NEV >= 2 and less than or equal to N.', 6: 'The maximum number of Arnoldi update iterations allowed must be greater than zero.', 7: 'Length of private work array WORKL is not sufficient.', 8: 'Error return from LAPACK eigenvalue calculation.', 9: 'Starting vector is zero.', 10: 'IPARAM(7) must be 1, 2, 3.', 11: 'IPARAM(7) = 1 and BMAT = 'G' are incompatible.', 12: 'IPARAM(1) must be equal to 0 or 1.', 13: 'NEV and WHICH = 'BE' are incompatible.', 9999: 'Could not build an Arnoldi factorization. IPARAM(5) returns the size of the current Arnoldi factorization. The user is advised to check that enough workspace and array storage has been allocated.'}, 's': {0: 'Normal exit.', 1: 'Maximum number of iterations taken. All possible eigenvalues of OP has been found. IPARAM(5) returns the number of wanted converged Ritz values.', 2: 'No longer an informational error. Deprecated starting with release 2 of ARPACK.', 3: 'No shifts could be applied during a cycle of the Implicitly restarted Arnoldi iteration. One possibility is to increase the size of NCV relative to NEV.', 4: 'NEV must be positive.', 5: 'NCV-NEV >= 2 and less than or equal to N.', 6: 'The maximum number of Arnoldi update iterations allowed must be greater than zero.', 7: 'Length of private work array WORKL is not sufficient.', 8: 'Error return from LAPACK eigenvalue calculation.', 9: 'Starting vector is zero.', 10: 'IPARAM(7) must be 1, 2, 3.', 11: 'IPARAM(7) = 1 and BMAT = 'G' are incompatible.', 12: 'IPARAM(1) must be equal to 0 or 1.', 13: 'NEV and WHICH = 'BE' are incompatible.', 9999: 'Could not build an Arnoldi factorization. IPARAM(5) returns the size of the current Arnoldi factorization. The user is advised to check that enough workspace and array storage has been allocated.'}, 'z': {0: 'Normal exit.', 1: 'Maximum number of iterations taken. All possible eigenvalues of OP has been found. IPARAM(5) returns the number of wanted converged Ritz values.', 2: 'No longer an informational error. Deprecated starting with release 2 of ARPACK.', 3: 'No shifts could be applied during a cycle of the Implicitly restarted Arnoldi iteration. One possibility is to increase the size of NCV relative to NEV.', 4: 'NEV must be positive.', 5: 'NCV-NEV >= 2 and less than or equal to N.', 6: 'The maximum number of Arnoldi update iterations allowed must be greater than zero.', 7: 'Length of private work array WORKL is not sufficient.', 8: 'Error return from LAPACK eigenvalue calculation.', 9: 'Starting vector is zero.', 10: 'IPARAM(7) must be 1, 2, 3.', 11: 'IPARAM(7) = 1 and BMAT = 'G' are incompatible.', 12: 'IPARAM(1) must be equal to 0 or 1.', 13: 'NEV and WHICH = 'BE' are incompatible.', 9999: 'Could not build an Arnoldi factorization. IPARAM(5) returns the size of the current Arnoldi factorization. The user is advised to check that enough workspace and array storage has been allocated.'}}
### Exceptions

* `SparseEfficiencyWarning`  
  exception `scipy.sparse.SparseEfficiencyWarning`  
  `scipy.sparse.SparseEfficiencyWarning` exception

* `SparseWarning`  
  exception `scipy.sparse.SparseWarning`  
  `scipy.sparse.SparseWarning` exception

### 6.21.2 Usage information

There are seven available sparse matrix types:

1. `csc_matrix`: Compressed Sparse Column format  
2. `csr_matrix`: Compressed Sparse Row format  
3. `bsr_matrix`: Block Sparse Row format  
4. `lil_matrix`: List of Lists format  
5. `dok_matrix`: Dictionary of Keys format  
6. `coo_matrix`: COOrdinate format (aka IJV, triplet format)  
7. `dia_matrix`: DIAgonal format

To construct a matrix efficiently, use either `dok_matrix` or `lil_matrix`. The `lil_matrix` class supports basic slicing and fancy indexing with a similar syntax to NumPy arrays. As illustrated below, the COO format may also be used to efficiently construct matrices. Despite their similarity to NumPy arrays, it is strongly discouraged to use NumPy functions directly on these matrices because NumPy may not properly convert them for computations, leading to unexpected (and incorrect) results. If you do want to apply a NumPy function to these matrices, first check if SciPy has its own implementation for the given sparse matrix class, or convert the sparse matrix to a NumPy array (e.g. using the `toarray()` method of the class) first before applying the method.

To perform manipulations such as multiplication or inversion, first convert the matrix to either CSC or CSR format. The `lil_matrix` format is row-based, so conversion to CSR is efficient, whereas conversion to CSC is less so.

All conversions among the CSR, CSC, and COO formats are efficient, linear-time operations.

### Matrix vector product

To do a vector product between a sparse matrix and a vector simply use the matrix `dot` method, as described in its docstring:

```python
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

**Warning:** As of NumPy 1.7, `np.dot` is not aware of sparse matrices, therefore using it will result on unexpected results or errors. The corresponding dense array should be obtained first instead:
The CSR format is specially suitable for fast matrix vector products.

## Example 1

Construct a 1000x1000 lil_matrix and add some values to it:

```python
>>> from scipy.sparse import lil_matrix
>>> from scipy.sparse.linalg import spsolve
>>> from numpy.linalg import solve, norm
>>> from numpy.random import rand

>>> A = lil_matrix((1000, 1000))
>>> A[0, :100] = rand(100)
>>> A[1, 100:200] = A[0, :100]
>>> A.setdiag(rand(1000))

Now convert it to CSR format and solve $A \mathbf{x} = \mathbf{b}$ for $\mathbf{x}$:

```python
>>> A = A.tocsr()
>>> b = rand(1000)
>>> x = spsolve(A, b)
```

Convert it to a dense matrix and solve, and check that the result is the same:

```python
>>> x_ = solve(A.toarray(), b)
```

Now we can compute norm of the error with:

```python
>>> err = norm(x-x_)
>>> err < 1e-10
True
```

It should be small :) 

## Example 2

Construct a matrix in COO format:

```python
>>> from scipy import sparse
>>> from numpy import array

>>> I = array([0,3,1,0])
>>> J = array([0,3,1,2])
>>> V = array([4,5,7,9])
>>> A = sparse.coo_matrix((V,(I,J)),shape=(4,4))
```

Notice that the indices do not need to be sorted.

Duplicate (i,j) entries are summed when converting to CSR or CSC.
```python
>>> I = array([0,0,1,3,1,0])
>>> J = array([0,2,1,3,1,0])
>>> V = array([1,1,1,1,1,1])
>>> B = sparse.coo_matrix((V,(I,J)),shape=(4,4)).tocsr()
```

This is useful for constructing finite-element stiffness and mass matrices.

**Further Details**

CSR column indices are not necessarily sorted. Likewise for CSC row indices. Use the .sorted_indices() and .sort_indices() methods when sorted indices are required (e.g. when passing data to other libraries).

### 6.22 Sparse linear algebra (scipy.sparse.linalg)

#### 6.22.1 Abstract linear operators

```python
LinearOperator(dtype, shape)  # Common interface for performing matrix vector products

aslinearoperator(A)  # Return A as a LinearOperator.
```

**scipy.sparse.linalg.LinearOperator**

**class** scipy.sparse.linalg.LinearOperator(dtype, shape)

Common interface for performing matrix vector products

Many iterative methods (e.g. cg, gmres) do not need to know the individual entries of a matrix to solve a linear system $A\cdot x = b$. Such solvers only require the computation of matrix vector products, $A\cdot v$ where $v$ is a dense vector. This class serves as an abstract interface between iterative solvers and matrix-like objects.

To construct a concrete LinearOperator, either pass appropriate callables to the constructor of this class, or subclass it.

A subclass must implement either one of the methods _matvec and _matmat, and the attributes/properties shape (pair of integers) and dtype (may be None). It may call the __init__ on this class to have these attributes validated. Implementing _matvec automatically implements _matmat (using a naive algorithm) and vice-versa.

Optionally, a subclass may implement _rmatvec or _adjoint to implement the Hermitian adjoint (conjugate transpose). As with _matvec and _matmat, implementing either _rmatvec or _adjoint implements the other automatically. Implementing _adjoint is preferable; _rmatvec is mostly there for backwards compatibility.

**Parameters**

- **shape** [tuple] Matrix dimensions (M,N).
- **matvec** [callable f(v)] Returns returns $A \cdot v$.
- **rmatvec** [callable f(v)] Returns $A^\dagger \cdot v$, where $A^\dagger$ is the conjugate transpose of $A$.
- **matmat** [callable f(V)] Returns $A \cdot V$, where $V$ is a dense matrix with dimensions (N,K).
- **dtype** [dtype] Data type of the matrix.

See also:

- aslinearoperator

Construct LinearOperators
Notes
The user-defined matvec() function must properly handle the case where v has shape (N,) as well as
the (N,1) case. The shape of the return type is handled internally by LinearOperator.

LinearOperator instances can also be multiplied, added with each other and exponentiated, all lazily:
the result of these operations is always a new, composite LinearOperator, that defers linear operations
to the original operators and combines the results.

Examples
>>> import numpy as np
>>> from scipy.sparse.linalg import LinearOperator
>>> def mv(v):
...     return np.array([2*v[0], 3*v[1]])
...     
>>> A = LinearOperator((2,2), matvec=mv)
>>> A
<2x2 _CustomLinearOperator with dtype=float64>
>>> A.matvec(np.ones(2))
array([ 2.,  3.])
>>> A * np.ones(2)
array([ 2.,  3.])

Attributes
args [tuple] For linear operators describing products etc. of other linear operators, the
operands of the binary operation.

Methods
__call__(x) Call self as a function.
adjoint() Hermitian adjoint.
dot(x) Matrix-matrix or matrix-vector multiplication.
matmat(X) Matrix-matrix multiplication.
matvec(x) Matrix-vector multiplication.
rmatvec(x) Adjoint matrix-vector multiplication.
transpose() Transpose this linear operator.

scipy.sparse.linalg.LinearOperator.__call__
LinearOperator.__call__(x)
Call self as a function.

scipy.sparse.linalg.LinearOperator.adjoint
LinearOperator.adjoint()
Hermitian adjoint.

Returns

scipy.sparse.linalg.LinearOperator.dot
LinearOperator.dot(x)
Matrix-matrix or matrix-vector multiplication.
Parameters

x  [array_like] 1-d or 2-d array, representing a vector or matrix.

Returns

Ax  [array] 1-d or 2-d array (depending on the shape of x) that represents the result of applying this linear operator on x.

scipy.sparse.linalg.LinearOperator.matmat

LinearOperator.matmat(X)

Matrix-matrix multiplication.

Performs the operation y = A * X where A is an MxN linear operator and X dense N*K matrix or ndarray.

Parameters

X  [{matrix, ndarray}] An array with shape (N,K).

Returns

Y  [{matrix, ndarray}] A matrix or ndarray with shape (M,K) depending on the type of the X argument.

Notes

This matmat wraps any user-specified matmat routine or overridden _matmat method to ensure that y has the correct type.

scipy.sparse.linalg.LinearOperator.matvec

LinearOperator.matvec(x)

Matrix-vector multiplication.

Performs the operation y = A * x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters

x  [{matrix, ndarray}] An array with shape (N,) or (N,1).

Returns

y  [{matrix, ndarray}] A matrix or ndarray with shape (M,) or (M,1) depending on the type and shape of the x argument.

Notes

This matvec wraps the user-specified matvec routine or overridden _matvec method to ensure that y has the correct shape and type.

scipy.sparse.linalg.LinearOperator.rmatvec

LinearOperator.rmatvec(x)

Adjoint matrix-vector multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters

x  [{matrix, ndarray}] An array with shape (M,) or (M,1).

Returns

y  [{matrix, ndarray}] A matrix or ndarray with shape (N,) or (N,1) depending on the type and shape of the x argument.
Notes
This rmatvec wraps the user-specified rmatvec routine or overridden _rmatvec method to ensure that y has the correct shape and type.

scipy.sparse.linalg.LinearOperator.transpose
LinearOperator.transpose()
Transpose this linear operator.
Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

scipy.sparse.linalg.aslinearoperator
scipy.sparse.linalg.aslinearoperator(A)
Return A as a LinearOperator.
‘A’ may be any of the following types:
- ndarray
- matrix
- sparse matrix (e.g. csr_matrix, lil_matrix, etc.)
- LinearOperator
- An object with .shape and .matvec attributes

See the LinearOperator documentation for additional information.

Notes
If ‘A’ has no .dtype attribute, the data type is determined by calling LinearOperator.matvec - set the .dtype attribute to prevent this call upon the linear operator creation.

Examples

```python
>>> from scipy.sparse.linalg import aslinearoperator
>>> M = np.array([[1, 2, 3], [4, 5, 6]], dtype=np.int32)
>>> aslinearoperator(M)
<2x3 MatrixLinearOperator with dtype=int32>
```

6.22.2 Matrix Operations

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>inv(A)</td>
<td>Compute the inverse of a sparse matrix</td>
</tr>
<tr>
<td>expm(A)</td>
<td>Compute the matrix exponential using Pade app-</td>
</tr>
<tr>
<td></td>
<td>roximation.</td>
</tr>
<tr>
<td>expm_multiply(A, B,</td>
<td>Compute the action of the matrix exponential of</td>
</tr>
<tr>
<td>start, stop, num,</td>
<td>A on B.</td>
</tr>
<tr>
<td>endpoint)</td>
<td></td>
</tr>
</tbody>
</table>

scipy.sparse.linalg.inv
scipy.sparse.linalg.inv(A)
Compute the inverse of a sparse matrix

Parameters

- A        [(M,M) ndarray or sparse matrix] square matrix to be inverted

Returns

- Ainv     [(M,M) ndarray or sparse matrix] inverse of A
Notes
This computes the sparse inverse of \( A \). If the inverse of \( A \) is expected to be non-sparse, it will likely be faster to convert \( A \) to dense and use scipy.linalg.inv.

Examples

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import inv
>>> A = csc_matrix([[1., 0.], [1., 2.]])
>>> Ainv = inv(A)
>>> Ainv
<2x2 sparse matrix of type '<class 'numpy.float64'>'
    with 3 stored elements in Compressed Sparse Column format>
>>> A.dot(Ainv)
<2x2 sparse matrix of type '<class 'numpy.float64'>'
    with 2 stored elements in Compressed Sparse Column format>
>>> A.dot(Ainv).todense()
matrix([[ 1., 0.],
        [ 0., 1.]], dtype=float64)
```

New in version 0.12.0.

**scipy.sparse.linalg.expm**

`scipy.sparse.linalg.expm(A)`

Compute the matrix exponential using Pade approximation.

**Parameters**

\( A \)  
[(M,M) array_like or sparse matrix] 2D Array or Matrix (sparse or dense) to be exponentiated

**Returns**

\( expA \)  
[(M,M) ndarray] Matrix exponential of \( A \)

**Notes**

This is algorithm (6.1) which is a simplification of algorithm (5.1).

New in version 0.12.0.

**References**

/[1/]

**Examples**

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import expm
>>> A = csc_matrix([[1, 0, 0], [0, 2, 0], [0, 0, 3]])
>>> A.todense()
matrix([[1, 0, 0],
        [0, 2, 0],
        [0, 0, 3]], dtype=int64)
>>> Aexp = expm(A)
>>> Aexp
<3x3 sparse matrix of type '<class 'numpy.float64'>'
    with 3 stored elements in Compressed Sparse Column format>
>>> Aexp.todense()
matrix([[ 2.71828183, 0. , 0. ],
        [ 0. , 2.71828183, 0. ],
        [ 0. , 0. , 3. ]],
```

(continues on next page)
scipy.sparse.linalg.expm_multiply

scipy.sparse.linalg.expm_multiply(A, B, start=None, stop=None, num=None, endpoint=None)

Compute the action of the matrix exponential of A on B.

Parameters

A     [transposable linear operator] The operator whose exponential is of interest.
B     [ndarray] The matrix or vector to be multiplied by the matrix exponential of A.
start [scalar, optional] The starting time point of the sequence.
stop  [scalar, optional] The end time point of the sequence, unless endpoint is set to False. In that case, the sequence consists of all but the last of num + 1 evenly spaced time points, so that stop is excluded. Note that the step size changes when endpoint is False.
num   [int, optional] Number of time points to use.
endpoint [bool, optional] If True, stop is the last time point. Otherwise, it is not included.

Returns

expm_A_B [ndarray] The result of the action $e^{t_A}B$.

Notes

The optional arguments defining the sequence of evenly spaced time points are compatible with the arguments of numpy.linspace.

The output ndarray shape is somewhat complicated so I explain it here. The ndim of the output could be either 1, 2, or 3. It would be 1 if you are computing the expm action on a single vector at a single time point. It would be 2 if you are computing the expm action on a vector at multiple time points, or if you are computing the expm action on a matrix at a single time point. It would be 3 if you want the action on a matrix with multiple columns at multiple time points. If multiple time points are requested, expm_A_B[0] will always be the action of the expm at the first time point, regardless of whether the action is on a vector or a matrix.

References

[1], [2]

Examples

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import expm, expm_multiply
>>> A = csc_matrix([[1, 0], [0, 1]])
>>> A.todense()
matrix([[1, 0],
        [0, 1]], dtype=int64)
>>> B = np.array([np.exp(-1.), np.exp(-2.)])
>>> B
array([ 0.36787944, 0.13533528])
>>> expm_multiply(A, B, start=1, stop=2, num=3, endpoint=True)
array([[ 1.        , 0.36787944],
       [1.64872127, 0.60653066],
       [2.71828183, 1.        ]])
>>> expm(A).dot(B) # Verify 1st timestep
array([ 1.        , 0.36787944])
```
```python
>>> expm(1.5*A).dot(B)  # Verify 2nd timestep
array([[ 1.64872127,  0.60653066]])
>>> expm(2*A).dot(B)   # Verify 3rd timestep
array([[ 2.71828183,  1. ]])
```

### 6.22.3 Matrix norms

**norm(x, ord, axis)**

Norm of a sparse matrix

**onenormest(A, t, itmax, compute_v, compute_w)**

Compute a lower bound of the 1-norm of a sparse matrix.

#### scipy.sparse.linalg.norm

**scipy.sparse.linalg.norm(x, ord=None, axis=None)**

Norm of a sparse matrix

This function is able to return one of seven different matrix norms, depending on the value of the `ord` parameter.

**Parameters**

- `x` : [a sparse matrix] Input sparse matrix.
- `axis` : [{int, 2-tuple of ints, None}, optional] If `axis` is an integer, it specifies the axis of `x` along which to compute the vector norms. If `axis` is a 2-tuple, it specifies the axes that hold 2-D matrices, and the matrix norms of these matrices are computed. If `axis` is None then either a vector norm (when `x` is 1-D) or a matrix norm (when `x` is 2-D) is returned.

**Returns**

- `n` : [float or ndarray]

#### Notes

Some of the ord are not implemented because some associated functions like, _multi_svd_norm, are not yet available for sparse matrix.

This docstring is modified based on numpy.linalg.norm.  https://github.com/numpy/numpy/blob/master/numpy/linalg/linalg.py

The following norms can be calculated:

<table>
<thead>
<tr>
<th>ord</th>
<th>norm for sparse matrices</th>
</tr>
</thead>
<tbody>
<tr>
<td>None</td>
<td>Frobenius norm</td>
</tr>
<tr>
<td>‘fro’</td>
<td>Frobenius norm</td>
</tr>
<tr>
<td>inf</td>
<td>max(sum(abs(x), axis=1))</td>
</tr>
<tr>
<td>-inf</td>
<td>min(sum(abs(x), axis=1))</td>
</tr>
<tr>
<td>0</td>
<td>abs(x).sum(axis=axis)</td>
</tr>
<tr>
<td>1</td>
<td>max(sum(abs(x), axis=0))</td>
</tr>
<tr>
<td>-1</td>
<td>min(sum(abs(x), axis=0))</td>
</tr>
<tr>
<td>2</td>
<td>Not implemented</td>
</tr>
<tr>
<td>-2</td>
<td>Not implemented</td>
</tr>
<tr>
<td>other</td>
<td>Not implemented</td>
</tr>
</tbody>
</table>
The Frobenius norm is given by [1]:

\[ \|A\|_F = \left( \sum_{i,j} |a_{i,j}|^2 \right)^{1/2} \]

References
[1]

Examples

```python
>>> from scipy.sparse import *
>>> import numpy as np
>>> from scipy.sparse.linalg import norm
>>> a = np.arange(9) - 4
>>> a
array([-4, -3, -2, -1, 0, 1, 2, 3, 4])
>>> b = a.reshape((3, 3))
>>> b
array([[-4, -3, -2],
       [-1,  0,  1],
       [ 2,  3,  4]])

>>> b = csr_matrix(b)
>>> norm(b)
7.745966692414834
>>> norm(b, 'fro')
7.745966692414834
>>> norm(b, np.inf)
9
>>> norm(b, -np.inf)
2
>>> norm(b, 1)
7
>>> norm(b, -1)
6
```

**scipy.sparse.linalg.onenormest**

`scipy.sparse.linalg.onenormest(A, t=2, itmax=5, compute_v=False, compute_w=False)`

Compute a lower bound of the 1-norm of a sparse matrix.

**Parameters**

- **A** [ndarray or other linear operator] A linear operator that can be transposed and that can produce matrix products.
- **t** [int, optional] A positive parameter controlling the tradeoff between accuracy versus time and memory usage. Larger values take longer and use more memory but give more accurate output.
- **itmax** [int, optional] Use at most this many iterations.
- **compute_v** [bool, optional] Request a norm-maximizing linear operator input vector if True.
- **compute_w** [bool, optional] Request a norm-maximizing linear operator output vector if True.

**Returns**

- **est** [float] An underestimate of the 1-norm of the sparse matrix.
v [ndarray, optional] The vector such that \|Av\|_1 = est*\|v\|_1. It can be thought of as an input to the linear operator that gives an output with particularly large norm.

w [ndarray, optional] The vector Av which has relatively large 1-norm. It can be thought of as an output of the linear operator that is relatively large in norm compared to the input.

Notes
This is algorithm 2.4 of [1].

In [2] it is described as follows. “This algorithm typically requires the evaluation of about 4t matrix-vector products and almost invariably produces a norm estimate (which is, in fact, a lower bound on the norm) correct to within a factor 3.”

New in version 0.13.0.

References
[1], [2]

Examples
```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import onenormest
>>> A = csc_matrix([[1., 0., 0.], [5., 8., 2.], [0., -1., 0.]], dtype=float)
>>> A.todense()
matrix([[ 1.,  0.,  0.],
        [ 5.,  8.,  2.],
        [ 0., -1.,  0.]])
>>> onenormest(A)
9.0
>>> np.linalg.norm(A.todense(), ord=1)
9.0
```

### 6.22.4 Solving linear problems

Direct methods for linear equation systems:

- `spsolve(A, b[, permc_spec, use_umfpack])`: Solve the sparse linear system \( Ax=b \), where \( b \) may be a vector or a matrix.

- `spsolve_triangular(A, b[, lower, …])`: Solve the equation \( A \ x = b \) for \( x \), assuming \( A \) is a triangular matrix.

- `factorized(A)`: Return a function for solving a sparse linear system, with \( A \) pre-factorized.

- `MatrixRankWarning`: Use default sparse direct solver to be used.

```
scipy.sparse.linalg.spsolve
```

`scipy.sparse.linalg.spsolve(A, b[, permc_spec=None, use_umfpack=True])`

Solve the sparse linear system \( Ax=b \), where \( b \) may be a vector or a matrix.

**Parameters**

- \( A \) [ndarray or sparse matrix] The square matrix \( A \) will be converted into CSC or CSR form
- \( b \) [ndarray or sparse matrix] The matrix or vector representing the right hand side of the equation. If a vector, \( b \).shape must be \((n,)\) or \((n, 1)\).

```
```

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How to permute the columns of the matrix for sparsity preservation.
(default: ‘COLAMD’)
- NATURAL: natural ordering.
- MMD_ATA: minimum degree ordering on the structure of $A^\top A$.
- MMD_AT_PLUS_A: minimum degree ordering on the structure of $A^\top+ A$.
- COLAMD: approximate minimum degree column ordering

use_umfpack
[bool, optional] if True (default) then use umfpack for the solution. This is only referenced if b is a vector and scikit-umfpack is installed.

Returns
- x [ndarray or sparse matrix] the solution of the sparse linear equation. If b is a vector, then x is a vector of size A.shape[1] If b is a matrix, then x is a matrix of size (A.shape[1], b.shape[1])

Notes
For solving the matrix expression $AX = B$, this solver assumes the resulting matrix X is sparse, as is often the case for very sparse inputs. If the resulting X is dense, the construction of this sparse result will be relatively expensive. In that case, consider converting A to a dense matrix and using scipy.linalg.solve or its variants.

Examples
```python
given code snippet
```
**Raises**

- **LinAlgError**
  - If $A$ is singular or not triangular.
- **ValueError**
  - If shape of $A$ or shape of $b$ do not match the requirements.

**Notes**
New in version 0.19.0.

**Examples**

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.linalg import spsolve_triangular
>>> A = csr_matrix([[3, 0, 0], [1, -1, 0], [2, 0, 1]], dtype=float)
>>> B = np.array([[2, 0], [-1, 0], [2, 0]], dtype=float)
>>> x = spsolve_triangular(A, B)
>>> np.allclose(A.dot(x), B)
True
```

### scipy.sparse.linalg.factorized

**scipy.sparse.linalg.factorized**

`scipy.sparse.linalg.factorized(A)`

Return a function for solving a sparse linear system, with $A$ pre-factorized.

**Parameters**

- **A**
  - [(N, N) array_like] Input.

**Returns**

- **solve**
  - [callable] To solve the linear system of equations given in $A$, the `solve` callable should be passed an ndarray of shape (N,).

**Examples**

```python
>>> from scipy.sparse.linalg import factorized
>>> A = np.array([[3., 2., -1.],
...                [2., -2., 4.],
...                [-1., 0.5, -1.]])
>>> solve = factorized(A)  # Makes LU decomposition.
>>> rhs1 = np.array([1, -2, 0])
>>> solve(rhs1)  # Uses the LU factors.
array([ 1., -2., -2.])
```

### scipy.sparse.linalg.MatrixRankWarning

**exception** `scipy.sparse.linalg.MatrixRankWarning`

### scipy.sparse.linalg.use_solver

**scipy.sparse.linalg.use_solver(**kwargs**)

Select default sparse direct solver to be used.

**Parameters**

- **useUmfpack**
  - [bool, optional] Use UMFPACK over SuperLU. Has effect only if scikits.umfpack is installed. Default: True
assumeSortedIndices
[bool, optional] Allow UMFPACK to skip the step of sorting indices for a CSR/CSC matrix. Has effect only if useUmfpack is True and scikits.umfpack is installed. Default: False

Notes
The default sparse solver is umfpack when available (scikits.umfpack is installed). This can be changed by passing useUmfpack = False, which then causes the always present SuperLU based solver to be used.

Umfpack requires a CSR/CSC matrix to have sorted column/row indices. If sure that the matrix fulfills this, pass assumeSortedIndices=True to gain some speed.

Iterative methods for linear equation systems:

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>bicg</code></td>
<td>Use BIConjugate Gradient iteration to solve ( Ax = b ).</td>
</tr>
<tr>
<td><code>bicgstab</code></td>
<td>Use BIConjugate Gradient STABilized iteration to solve ( Ax = b ).</td>
</tr>
<tr>
<td><code>cg</code></td>
<td>Use Conjugate Gradient iteration to solve ( Ax = b ).</td>
</tr>
<tr>
<td><code>cgs</code></td>
<td>Use Conjugate Gradient Squared iteration to solve ( Ax = b ).</td>
</tr>
<tr>
<td><code>gmres</code></td>
<td>Use Generalized Minimal RESidual iteration to solve ( Ax = b ).</td>
</tr>
<tr>
<td><code>lgmres</code></td>
<td>Solve a matrix equation using the LGMRES algorithm.</td>
</tr>
<tr>
<td><code>minres</code></td>
<td>Use MINimum RESidual iteration to solve ( Ax = b ).</td>
</tr>
<tr>
<td><code>qmr</code></td>
<td>Use Quasi-Minimal Residual iteration to solve ( Ax = b ).</td>
</tr>
<tr>
<td><code>gcrotmk</code></td>
<td>Solve a matrix equation using flexible GCROT(m,k) algorithm.</td>
</tr>
</tbody>
</table>

`scipy.sparse.linalg.bicg`

`scipy.sparse.linalg.bicg(A, b[, x0=None, tol=1e-05, maxiter=None, M=None, callback=None, atol=None])`

Use BIConjugate Gradient iteration to solve \( Ax = b \).

Parameters

- **A** ([sparse matrix, dense matrix, LinearOperator]) The real or complex N-by-N matrix of the linear system. It is required that the linear operator can produce \( Ax \) and \( A^T x \).
- **b** ([array, matrix]) Right hand side of the linear system. Has shape \((N,)\) or \((N,1)\).

Returns

- **x** ([array, matrix]) The converged solution.
- **info** [integer] Provides convergence information:
  - 0 : successful exit
  - >0 : convergence to tolerance not achieved, number of iterations
  - <0 : illegal input or breakdown

Other Parameters

- **x0** ([array, matrix]) Starting guess for the solution.
- **tol, atol** [float, optional] Tolerances for convergence, \( \text{norm(residual)} \leq \max(\text{tol}\cdot\text{norm}(b), \text{atol}) \). The default for \( \text{atol} \) is ‘legacy’, which emulates a different legacy behavior.
Warning: The default value for `atol` will be changed in a future release. For future compatibility, specify `atol` explicitly.

maxiter [integer] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M [{sparse matrix, dense matrix, LinearOperator}] Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback [function] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

scipy.sparse.linalg.bicgstab

scipy.sparse.linalg.bicgstab(A, b, x0=None, tol=1e-05, maxiter=None, M=None, callback=None, atol=None)

Use BIConjugate Gradient STABilized iteration to solve $Ax = b$.

Parameters

A [{sparse matrix, dense matrix, LinearOperator}] The real or complex N-by-N matrix of the linear system.

b [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x [{array, matrix}] The converged solution.

info [integer]

Provides convergence information:

- 0 : successful exit
- >0 : convergence to tolerance not achieved, number of iterations
- <0 : illegal input or breakdown

Other Parameters

x0 [{array, matrix}] Starting guess for the solution.

tol, atol [float, optional] Tolerances for convergence, $\text{norm(residual)} \leq \max(\text{tol} \cdot \text{norm(b)}, \text{atol})$. The default for `atol` is 'legacy', which emulates a different legacy behavior.

Warning: The default value for `atol` will be changed in a future release. For future compatibility, specify `atol` explicitly.

maxiter [integer] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M [{sparse matrix, dense matrix, LinearOperator}] Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback [function] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

scipy.sparse.linalg.cg

scipy.sparse.linalg.cg(A, b, x0=None, tol=1e-05, maxiter=None, M=None, callback=None, atol=None)

Use Conjugate Gradient iteration to solve $Ax = b$. 

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Parameters

A  [{sparse matrix, dense matrix, LinearOperator}] The real or complex N-by-N matrix of the linear system. A must represent a hermitian, positive definite matrix.

b  [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x  [{array, matrix}] The converged solution.

info  [integer]

Provides convergence information:

0 : successful exit
>0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0  [{array, matrix}] Starting guess for the solution.

tol, atol  [float, optional] Tolerances for convergence, \( \text{norm(residual)} \leq \max(\text{tol}\cdot\text{norm(b)}, \text{atol}) \). The default for atol is 'legacy', which emulates a different legacy behavior.

maxiter  [integer] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M  [{sparse matrix, dense matrix, LinearOperator}] Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback  [function] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

scipy.sparse.linalg.cgs

scipy.sparse.linalg.cgs(A, b, x0=None, tol=1e-05, maxiter=None, M=None, callback=None, atol=None)

Use Conjugate Gradient Squared iteration to solve \( Ax = b \).

Parameters

A  [{sparse matrix, dense matrix, LinearOperator}] The real-valued N-by-N matrix of the linear system.

b  [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x  [{array, matrix}] The converged solution.

info  [integer]

Provides convergence information:

0 : successful exit
>0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0  [{array, matrix}] Starting guess for the solution.

tol, atol  [float, optional] Tolerances for convergence, \( \text{norm(residual)} \leq \max(\text{tol}\cdot\text{norm(b)}, \text{atol}) \). The default for atol is 'legacy', which emulates a different legacy behavior.
**Warning:** The default value for `atol` will be changed in a future release. For future compatibility, specify `atol` explicitly.

maxiter [integer] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M [{sparse matrix, dense matrix, LinearOperator}] Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback [function] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

**scipy.sparse.linalg.gmres**

`scipy.sparse.linalg.gmres(A, b, x0=None, tol=1e-05, restart=None, maxiter=None, M=None, callback=None, restrt=None, atol=None)`

Use Generalized Minimal RESidual iteration to solve \(Ax = b\).

**Parameters**

A [{sparse matrix, dense matrix, LinearOperator}] The real or complex N-by-N matrix of the linear system.

b [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

**Returns**

x [{array, matrix}] The converged solution.

info [int] Provides convergence information:

- 0 : successful exit
- >0 : convergence to tolerance not achieved, number of iterations
- <0 : illegal input or breakdown

**Other Parameters**

x0 [{array, matrix}] Starting guess for the solution (a vector of zeros by default).

tol, atol [float, optional] Tolerances for convergence, \(\text{norm(residual)} \leq \max(tol*\text{norm(b)}, atol)\). The default for `atol` is 'legacy', which emulates a different legacy behavior.

**Warning:** The default value for `atol` will be changed in a future release. For future compatibility, specify `atol` explicitly.

restart [int, optional] Number of iterations between restarts. Larger values increase iteration cost, but may be necessary for convergence. Default is 20.

maxiter [int, optional] Maximum number of iterations (restart cycles). Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M [{sparse matrix, dense matrix, LinearOperator}] Inverse of the preconditioner of A. M should approximate the inverse of A and be easy to solve for (see Notes). Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance. By default, no preconditioner is used.

callback [function] User-supplied function to call after each iteration. It is called as callback(rk), where rk is the current residual vector.

restrt [int, optional] DEPRECATED - use `restart` instead.
See also:

LinearOperator

Notes
A preconditioner, P, is chosen such that P is close to A but easy to solve for. The preconditioner parameter required by this routine is \( M = P^{-1} \). The inverse should preferably not be calculated explicitly. Rather, use the following template to produce M:

```python
# Construct a linear operator that computes P^-1 * x.
import scipy.sparse.linalg as spla
M_x = lambda x: spla.spsolve(P, x)
M = spla.LinearOperator((n, n), M_x)
```

Examples
```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import gmres
>>> A = csc_matrix([[3, 2, 0], [1, -1, 0], [0, 5, 1]], dtype=float)
>>> b = np.array([2, 4, -1], dtype=float)
>>> x, exitCode = gmres(A, b)
>>> print(exitCode)  # 0 indicates successful convergence
0
>>> np.allclose(A.dot(x), b)
True
```

scipy.sparse.linalg.lgmres

Solve a matrix equation using the LGMRES algorithm.

The LGMRES algorithm \([1] \) \([2] \) is designed to avoid some problems in the convergence in restarted GMRES, and often converges in fewer iterations.

**Parameters**

\( A \)  
[[sparse matrix, dense matrix, LinearOperator]]  The real or complex N-by-N matrix of the linear system.

\( b \)  
[[array, matrix]]  Right hand side of the linear system. Has shape (N,) or (N,1).

\( x0 \)  
[[array, matrix]]  Starting guess for the solution.

\( tol, atol \)  
[float, optional]  Tolerances for convergence, \( \text{norm(residual)} \leq \text{max(tol*\text{norm(b)}, \text{atol})} \). The default for \( atol \) is \( tol \).

**Warning:**  The default value for \( atol \) will be changed in a future release. For future compatibility, specify \( atol \) explicitly.

\( \text{maxiter} \)  
[int, optional]  Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

\( M \)  
[[sparse matrix, dense matrix, LinearOperator], optional]  Preconditioner for \( A \). The preconditioner should approximate the inverse of \( A \). Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

\( \text{callback} \)  
[function, optional]  User-supplied function to call after each iteration. It is called as \( \text{callback}(\text{xk}) \), where \( \text{xk} \) is the current solution vector.

\( \text{inner_m} \)  
[int, optional]  Number of inner GMRES iterations per each outer iteration.
outer_k [int, optional] Number of vectors to carry between inner GMRES iterations. According to [1], good values are in the range of 1...3. However, note that if you want to use the additional vectors to accelerate solving multiple similar problems, larger values may be beneficial.

outer_v [list of tuples, optional] List containing tuples ($v, Av$) of vectors and corresponding matrix-vector products, used to augment the Krylov subspace, and carried between inner GMRES iterations. The element $Av$ can be None if the matrix-vector product should be re-evaluated. This parameter is modified in-place by lgmres, and can be used to pass “guess” vectors in and out of the algorithm when solving similar problems.

store_outer_Av [bool, optional] Whether LGMRES should store also $A*v$ in addition to vectors $v$ in the outer_v list. Default is True.


Returns

x [array or matrix] The converged solution.

info [int] Provides convergence information:

- 0 : successful exit
- >0 : convergence to tolerance not achieved, number of iterations
- <0 : illegal input or breakdown

Notes

The LGMRES algorithm [1]/[2] is designed to avoid the slowing of convergence in restarted GMRES, due to alternating residual vectors. Typically, it often outperforms GMRES(m) of comparable memory requirements by some measure, or at least is not much worse.

Another advantage in this algorithm is that you can supply it with ‘guess’ vectors in the outer_v argument that augment the Krylov subspace. If the solution lies close to the span of these vectors, the algorithm converges faster. This can be useful if several very similar matrices need to be inverted one after another, such as in Newton-Krylov iteration where the Jacobian matrix often changes little in the nonlinear steps.

References

[1], [2]

Examples

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import lgmres
>>> A = csc_matrix([[3, 2, 0], [1, -1, 0], [0, 5, 1]], dtype=float)
>>> b = np.array([2, 4, -1], dtype=float)
>>> x, exitCode = lgmres(A, b)
>>> print(exitCode)  # 0 indicates successful convergence
0
>>> np.allclose(A.dot(x), b)
True
```

scipy.sparse.linalg.minres

scipy.sparse.linalg.minres($A, b, x0=None, shift=0.0, tol=1e-05, maxiter=None, M=None, callback=None, show=False, check=False$)

Use MINimum RESidual iteration to solve $Ax=b$

MINRES minimizes $\|A^*x - b\|$ for a real symmetric matrix $A$. Unlike the Conjugate Gradient method, $A$ can be indefinite or singular.
If shift != 0 then the method solves (A - shift*I)x = b

**Parameters**

- **A**: \( \text{[sparse matrix, dense matrix, LinearOperator]} \) The real symmetric N-by-N matrix of the linear system.
- **b**: \( \text{[array, matrix]} \) Right hand side of the linear system. Has shape (N,) or (N,1).

**Returns**

- **x**: \( \text{[array, matrix]} \) The converged solution.
- **info**: \( \text{[integer]} \) Provides convergence information:
  - 0 : successful exit
  - >0 : convergence to tolerance not achieved, number of iterations
  - <0 : illegal input or breakdown

**Other Parameters**

- **x0**: \( \text{[array, matrix]} \) Starting guess for the solution.
- **tol**: \( \text{[float]} \) Tolerance to achieve. The algorithm terminates when the relative residual is below \( \text{tol} \).
- **maxiter**: \( \text{[integer]} \) Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.
- **M**: \( \text{[sparse matrix, dense matrix, LinearOperator]} \) Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.
- **callback**: \( \text{[function]} \) User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

**References**

*Solution of sparse indefinite systems of linear equations,*


This file is a translation of the following MATLAB implementation:

https://web.stanford.edu/group/SOL/software/minres/minres-matlab.zip

scipy.sparse.linalg.qmr

**scipy.sparse.linalg.qmr**(A, b, x0=None, tol=1e-05, maxiter=None, M1=None, M2=None, callback=None, atol=None)

Use Quasi-Minimal Residual iteration to solve \( Ax = b \).

**Parameters**

- **A**: \( \text{[sparse matrix, dense matrix, LinearOperator]} \) The real-valued N-by-N matrix of the linear system. It is required that the linear operator can produce \( Ax \) and \( A^T x \).
- **b**: \( \text{[array, matrix]} \) Right hand side of the linear system. Has shape (N,) or (N,1).

**Returns**

- **x**: \( \text{[array, matrix]} \) The converged solution.
- **info**: \( \text{[integer]} \) Provides convergence information:
  - 0 : successful exit
  - >0 : convergence to tolerance not achieved, number of iterations
  - <0 : illegal input or breakdown

**Other Parameters**
SciPy Reference Guide, Release 1.2.0

x0  [{array, matrix}] Starting guess for the solution.
tol, atol [float, optional] Tolerances for convergence, \( \text{norm}(\text{residual}) \leq \max(\text{tol} \times \text{norm}(b), \text{atol}) \). The default for atol is 'legacy', which emulates a different legacy behavior.

**Warning:** The default value for atol will be changed in a future release. For future compatibility, specify atol explicitly.

maxiter [integer] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M1 [{sparse matrix, dense matrix, LinearOperator}] Left preconditioner for A.
M2 [{sparse matrix, dense matrix, LinearOperator}] Right preconditioner for A. Used together with the left preconditioner M1. The matrix M1*A*M2 should have better conditioned than A alone.
callback [function] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

See also:

* LinearOperator

**Examples**

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import qmr
>>> A = csc_matrix([[3, 2, 0],[1, -1, 0],[0, 5, 1]], dtype=float)
>>> b = np.array([2, 4, -1], dtype=float)
>>> x, exitCode = qmr(A, b)
>>> print(exitCode)  # 0 indicates successful convergence
0
>>> np.allclose(A.dot(x), b)
True
```

scipy.sparse.linalg.gcrotmk

scipy.sparse.linalg.gcrotmk(A, b, x0=None, tol=1e-05, maxiter=1000, M=None, callback=None, m=20, k=None, CU=None, discard_C=False, truncate='oldest', atol=None)

Solve a matrix equation using flexible GCROT(m,k) algorithm.

**Parameters**

A [{sparse matrix, dense matrix, LinearOperator}] The real or complex N-by-N matrix of the linear system.
b [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).
x0 [{array, matrix}] Starting guess for the solution.
tol, atol [float, optional] Tolerances for convergence, \( \text{norm}(\text{residual}) \leq \max(\text{tol} \times \text{norm}(b), \text{atol}) \). The default for atol is tol.

**Warning:** The default value for atol will be changed in a future release. For future compatibility, specify atol explicitly.

maxiter [int, optional] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M [{sparse matrix, dense matrix, LinearOperator}, optional] Preconditioner for A. The preconditioner should approximate the inverse of A. gcrotmk is a 'flexible' algorithm and the preconditioner can vary from iteration to iteration. Effective
preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

**callback**  
[function, optional] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

**m**  
[int, optional] Number of inner FGMRES iterations per each outer iteration. Default: 20

**k**  
[int, optional] Number of vectors to carry between inner FGMRES iterations. According to [2], good values are around m. Default: m

**CU**  
[list of tuples, optional] List of tuples (c, u) which contain the columns of the matrices C and U in the GCROT(m,k) algorithm. For details, see [2]. The list given and vectors contained in it are modified in-place. If not given, start from empty matrices. The c elements in the tuples can be None, in which case the vectors are recomputed via c = A u on start and orthogonalized as described in [3].

**discard_C**  
[bool, optional] Discard the C-vectors at the end. Useful if recycling Krylov subspaces for different linear systems.

**truncation**  

**Returns**

- **x** [array or matrix] The solution found.
- **info** [int] Provides convergence information:
  - 0 : successful exit
  - >0 : convergence to tolerance not achieved, number of iterations

**References**

[1], [2], [3]

Iterative methods for least-squares problems:

```python
lsq(A, b[, damp, atol, btol, conlim, ...]) Find the least-squares solution to a large, sparse, linear system of equations.
lsmer(A, b[, damp, atol, btol, conlim, ...]) Iterative solver for least-squares problems.
```

**scipy.sparse.linalg.lsqr**

```python
scipy.sparse.linalg.lsqr(A, b, damp=0.0, atol=1e-08, btol=1e-08, conlim=100000000.0, iter_lim=None, show=False, calc_var=False, x0=None) Find the least-squares solution to a large, sparse, linear system of equations.
The function solves Ax = b or \( \min ||b - Ax||^2 \) or \( \min ||Ax - b||^2 + d^2 \ ||x||^2 \).
The matrix A may be square or rectangular (over-determined or under-determined), and may have any rank.

1. Unsymmetric equations -- solve \( A\cdot x = b \)
2. Linear least squares -- solve \( A\cdot x = b \)  
in the least-squares sense
3. Damped least squares -- solve \( ( A + \text{damp}\cdot I )\cdot x = ( b ) \)  
in the least-squares sense
```

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\textbf{Parameters}

\begin{itemize}
\item \textbf{A} \hspace{1cm} ([sparse matrix, ndarray, LinearOperator]) Representation of an m-by-n matrix. It is required that the linear operator can produce \( Ax \) and \( A^T x \).
\item \textbf{b} \hspace{1cm} [array_like, shape (m,)] Right-hand side vector \( b \).
\item \textbf{damp} \hspace{1cm} [float] Damping coefficient.
\item \textbf{atol}, \textbf{btol} \hspace{1cm} [float, optional] Stopping tolerances. If both are 1.0e-9 (say), the final residual norm should be accurate to about 9 digits. (The final x will usually have fewer correct digits, depending on \( \text{cond}(A) \) and the size of damp.)
\item \textbf{conlim} \hspace{1cm} [float, optional] Another stopping tolerance. \text{lsqr} terminates if an estimate of \( \text{cond}(A) \) exceeds \text{conlim}. For compatible systems \( Ax = b \), \text{conlim} could be as large as 1.0e+12 (say). For least-squares problems, \text{conlim} should be less than 1.0e+8. Maximum precision can be obtained by setting \( \text{atol} = \text{btol} = \text{conlim} = \text{zero} \), but the number of iterations may then be excessive.
\item \textbf{iter\_lim} \hspace{1cm} [int, optional] Explicit limitation on number of iterations (for safety).
\item \textbf{show} \hspace{1cm} [bool, optional] Display an iteration log.
\item \textbf{calc\_var} \hspace{1cm} [bool, optional] Whether to estimate diagonals of \( (A'A + \text{damp}^2I)^{-1} \). New in version 1.0.0.
\item \textbf{x0} \hspace{1cm} [array_like, shape (n,), optional] Initial guess of \( x \), if None zeros are used.
\end{itemize}

\textbf{Returns}

\begin{itemize}
\item \textbf{x} \hspace{1cm} [ndarray of float] The final solution.
\item \textbf{istop} \hspace{1cm} [int] Gives the reason for termination. 1 means \( x \) is an approximate solution to \( Ax = b \). 2 means \( x \) approximately solves the least-squares problem.
\item \textbf{itn} \hspace{1cm} [int] Iteration number upon termination.
\item \textbf{r1norm} \hspace{1cm} [float] \( \text{norm}(r) \), where \( r = b - Ax \).
\item \textbf{r2norm} \hspace{1cm} [float] \( \sqrt{\text{norm}(r)^2 + \text{damp}^2 \cdot \text{norm}(x)^2} \). Equal to \( r1norm \) if \( \text{damp} = 0 \).
\item \textbf{anorm} \hspace{1cm} [float] Estimate of Frobenius norm of \( Abar = [[A]; [\text{damp}\cdot I]] \).
\item \textbf{acond} \hspace{1cm} [float] Estimate of \( \text{cond}(Abar) \).
\item \textbf{arnorm} \hspace{1cm} [float] Estimate of \( \text{norm}(A'\cdot r - \text{damp}^2\cdot x) \).
\item \textbf{xnorm} \hspace{1cm} [float] \( \text{norm}(x) \)
\item \textbf{var} \hspace{1cm} [ndarray of float] If \text{calc\_var} is True, estimates all diagonals of \( (A'A)^{-1} \) (if \( \text{damp} = 0 \)) or more generally \( (A'A + \text{damp}^2I)^{-1} \). This is well defined if \( A \) has full column rank or \( \text{damp} > 0 \). (Not sure what \text{var} means if \( \text{rank}(A) < n \) and \( \text{damp} = 0 \).)
\end{itemize}

\textbf{Notes}

\text{LSQR} uses an iterative method to approximate the solution. The number of iterations required to reach a certain accuracy depends strongly on the scaling of the problem. Poor scaling of the rows or columns of \( A \) should therefore be avoided where possible.

For example, in problem 1 the solution is unaltered by row-scaling. If a row of \( A \) is very small or large compared to the other rows of \( A \), the corresponding row of \( (A \ b) \) should be scaled up or down.

In problems 1 and 2, the solution \( x \) is easily recovered following column-scaling. Unless better information is known, the nonzero columns of \( A \) should be scaled so that they all have the same Euclidean norm (e.g., 1.0).

In problem 3, there is no freedom to re-scale if \( \text{damp} \) is nonzero. However, the value of \( \text{damp} \) should be assigned only after attention has been paid to the scaling of \( A \).

The parameter \( \text{damp} \) is intended to help regularize ill-conditioned systems, by preventing the true solution from being very large. Another aid to regularization is provided by the parameter \( \text{acond} \), which may be used to terminate iterations before the computed solution becomes very large.

\section*{6.22. Sparse linear algebra (scipy.sparse.linalg)}
If some initial estimate \( x_0 \) is known and if \( \text{damp} == 0 \), one could proceed as follows:

1. Compute a residual vector \( r_0 = b - A \times x_0 \).
2. Use LSQR to solve the system \( A \times dx = r_0 \).
3. Add the correction \( dx \) to obtain a final solution \( x = x_0 + dx \).

This requires that \( x_0 \) be available before and after the call to LSQR. To judge the benefits, suppose LSQR takes \( k_1 \) iterations to solve \( A \times x = b \) and \( k_2 \) iterations to solve \( A \times dx = r_0 \). If \( x_0 \) is “good”, \( \text{norm}(r_0) \) will be smaller than \( \text{norm}(b) \). If the same stopping tolerances \( \text{atol} \) and \( \text{btol} \) are used for each system, \( k_1 \) and \( k_2 \) will be similar, but the final solution \( x_0 + dx \) should be more accurate. The only way to reduce the total work is to use a larger stopping tolerance for the second system. If some value \( \text{btol} \) is suitable for \( A \times x = b \), the larger value \( \text{btol} \times \text{norm}(b) / \text{norm}(r_0) \) should be suitable for \( A \times dx = r_0 \).

Preconditioning is another way to reduce the number of iterations. If it is possible to solve a related system \( M \times x = b \) efficiently, where \( M \) approximates \( A \) in some helpful way (e.g. \( M - A \) has low rank or its elements are small relative to those of \( A \)), LSQR may converge more rapidly on the system \( A \times M^{-1} \times z = b \), after which \( x \) can be recovered by solving \( M \times x = z \).

If \( A \) is symmetric, LSQR should not be used!

Alternatives are the symmetric conjugate-gradient method (cg) and/or SYMMLQ. SYMMLQ is an implementation of symmetric cg that applies to any symmetric \( A \) and will converge more rapidly than LSQR. If \( A \) is positive definite, there are other implementations of symmetric cg that require slightly less work per iteration than SYMMLQ (but will take the same number of iterations).

References
[1], [2], [3]

Examples

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import lsqr
>>> A = csc_matrix([[1., 0.], [1., 1.], [0., 1.]], dtype=float)
```

The first example has the trivial solution \([0, 0]\)

```python
>>> b = np.array([0., 0., 0.], dtype=float)
>>> x, istop, itn, normr = lsqr(A, b)[:4]
>>> istop
0
>>> x
array([ 0., 0.])
```

The stopping code \( \text{istop}=0 \) returned indicates that a vector of zeros was found as a solution. The returned solution \( x \) indeed contains \([0, 0]\). The next example has a non-trivial solution:

```python
>>> b = np.array([1., 0., -1.], dtype=float)
>>> x, istop, itn, r1norm = lsqr(A, b)[:4]
>>> istop
1
>>> x
array([ 1., -1.])
>>> itn
1
```

(continues on next page)
As indicated by `istop=1`, `lsqr` found a solution obeying the tolerance limits. The given solution `[1., -1.]` obviously solves the equation. The remaining return values include information about the number of iterations (`itn=1`) and the remaining difference of left and right side of the solved equation. The final example demonstrates the behavior in the case where there is no solution for the equation:

```python
>>> b = np.array([1., 0.01, -1.], dtype=float)
>>> x, istop, itn, r1norm = lsqr(A, b)[4]
>>> istop
2
>>> x
array([ 1.00333333, -0.99666667])
>>> A.dot(x) - b
array([ 0.00333333, -0.00333333, 0.00333333])
>>> r1norm
0.005773502691896255
```

`istop` indicates that the system is inconsistent and thus `x` is rather an approximate solution to the corresponding least-squares problem. `r1norm` contains the norm of the minimal residual that was found.

**scipy.sparse.linalg.lsmr**

Iterative solver for least-squares problems. `lsmr` solves the system of linear equations $Ax = b$. If the system is inconsistent, it solves the least-squares problem $\min ||b - Ax||_2$. A is a rectangular matrix of dimension m-by-n, where all cases are allowed: $m = n$, $m > n$, or $m < n$. B is a vector of length m. The matrix A may be dense or sparse (usually sparse).

**Parameters**

- **A**
  - ([matrix, sparse matrix, ndarray, LinearOperator]) Matrix A in the linear system.
- **b**
  - ([array_like, shape (m,)]) Vector b in the linear system.
- **damp**
  - (float) Damping factor for regularized least-squares. `lsmr` solves the regularized least-squares problem:
    \[
    \min ||(b) - (A)x||_2
    \]
    where damp is a scalar. If damp is None or 0, the system is solved without regularization.
- **atol, btol**
  - ([float, optional]) Stopping tolerances. `lsmr` continues iterations until a certain backward error estimate is smaller than some quantity depending on atol and btol. Let $r = b - Ax$ be the residual vector for the current approximate solution $x$. If $Ax = b$ seems to be consistent, `lsmr` terminates when $\text{norm}(r) \leq \text{atol} \cdot \text{norm}(A) + \text{btol} \cdot \text{norm}(b)$. Otherwise, lsqr terminates when $\text{norm}(A^T r) \leq \text{atol} \cdot \text{norm}(A) \cdot \text{norm}(r)$. If both tolerances are $1.0e-6$ (say), the final `norm(r)` should be accurate to about 6 digits. (The final x will usually have fewer correct digits, depending on \text{cond}(A) and the size of LAMBDA.) If atol or btol is
None, a default value of 1.0e-6 will be used. Ideally, they should be estimates of the relative error in the entries of A and B respectively. For example, if the entries of A have 7 correct digits, set atol = 1e-7. This prevents the algorithm from doing unnecessary work beyond the uncertainty of the input data.

**conlim**  
[float, optional] *lsmr* terminates if an estimate of \( \text{cond}(A) \) exceeds conlim. For compatible systems \( Ax = b \), conlim could be as large as 1.0e+12 (say). For least-squares problems, conlim should be less than 1.0e+8. If conlim is None, the default value is 1e+8. Maximum precision can be obtained by setting atol = btol = conlim = 0, but the number of iterations may then be excessive.

**maxiter**  
[int, optional] *lsmr* terminates if the number of iterations reaches maxiter. The default is maxiter = \( \min(m, n) \). For ill-conditioned systems, a larger value of maxiter may be needed.

**show**  
[bool, optional] Print iterations logs if show=True.

**x0**  
[array_like, shape (n,), optional] Initial guess of x, if None zeros are used. New in version 1.0.0.

**Returns**  

| **x** | [ndarray of float] Least-square solution returned. |
| **istop** | [int] istop gives the reason for stopping: |

- istop = 0 means x=0 is a solution. If x0 was given, then x=x0 is a solution.
- istop = 1 means x is an approximate solution to A*x = B, according to atol and btol.
- istop = 2 means x approximately solves the least-squares problem according to atol.
- istop = 3 means \( \text{COND}(A) \) seems to be greater than CONLIM.
- istop = 4 is the same as 1 with atol = btol = eps (machine precision)
- istop = 5 is the same as 2 with atol = eps.
- istop = 6 is the same as 3 with CONLIM = 1/eps.
- istop = 7 means ITN reached maxiter before the other stopping conditions were satisfied.

**Notes**  
New in version 0.11.0.

**References**  
[1], [2]

**Examples**

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import lsmr
>>> A = csc_matrix([[1., 0.], [1., 1.], [0., 1.]], dtype=float)
```

The first example has the trivial solution [0, 0]
>>> b = np.array([0., 0., 0.], dtype=float)
>>> x, istop, itn, normr = lsmr(A, b)[:4]
>>> istop
0
>>> x
array([ 0.,  0.])

The stopping code $istop=0$ returned indicates that a vector of zeros was found as a solution. The returned solution $x$ indeed contains $[0., 0.]$. The next example has a non-trivial solution:

```python
>>> b = np.array([1., 0., -1.], dtype=float)
>>> x, istop, itn, normr = lsmr(A, b)[:4]
>>> istop
1
>>> x
array([ 1., -1.])
>>> itn
1
>>> normr
4.40892098500627e-16
```

As indicated by $istop=1$, $lsmr$ found a solution obeying the tolerance limits. The given solution $[1., -1.]$ obviously solves the equation. The remaining return values include information about the number of iterations ($itn=1$) and the remaining difference of left and right side of the solved equation. The final example demonstrates the behavior in the case where there is no solution for the equation:

```python
>>> b = np.array([1., 0.01, -1.], dtype=float)
>>> x, istop, itn, normr = lsmr(A, b)[:4]
>>> istop
2
>>> x
array([ 1.00333333, -0.99666667])
>>> A.dot(x)-b
array([ 0.00333333, -0.00333333,  0.00333333])
>>> normr
0.006773502691896255
```

$istop$ indicates that the system is inconsistent and thus $x$ is rather an approximate solution to the corresponding least-squares problem. $normr$ contains the minimal distance that was found.

### 6.22.5 Matrix factorizations

Eigenvalue problems:

- **eigs(A[, k, M, sigma, which, v0, ncv, ...])** Find k eigenvalues and eigenvectors of the square matrix $A$.
- **eigsh(A[, k, M, sigma, which, v0, ncv, ...])** Find k eigenvalues and eigenvectors of the real symmetric square matrix or complex hermitian matrix $A$.
- **lobpcg(A, X[, B, M, Y, tol, maxiter, ...])** Locally Optimal Block Preconditioned Conjugate Gradient Method (LOBPCG)
scipy.sparse.linalg.eigs

scipy.sparse.linalg.eigs(A, k=6, M=None, sigma=None, which='LM', v0=None, ncv=None, maxiter=None, tol=0, return_eigenvectors=True, Minv=None, OPinv=None, OPpart=None)

Find k eigenvalues and eigenvectors of the square matrix A.

Solves $A * x[i] = w[i] * x[i]$, the standard eigenvalue problem for $w[i]$ eigenvalues with corresponding eigenvectors $x[i]$.

If M is specified, solves $A * x[i] = w[i] * M * x[i]$, the generalized eigenvalue problem for $w[i]$ eigenvalues with corresponding eigenvectors $x[i]$.

Parameters

- **A** [ndarray, sparse matrix or LinearOperator] An array, sparse matrix, or LinearOperator representing the operation $A * x$, where $A$ is a real or complex square matrix.
- **k** [int, optional] The number of eigenvalues and eigenvectors desired. $k$ must be smaller than $N-1$. It is not possible to compute all eigenvectors of a matrix.
- **M** [ndarray, sparse matrix or LinearOperator, optional] An array, sparse matrix, or LinearOperator representing the operation $M*x$ for the generalized eigenvalue problem $A * x = w * M * x$.
  - M must represent a real, symmetric matrix if $A$ is real, and must represent a complex, hermitian matrix if $A$ is complex. For best results, the data type of $M$ should be the same as that of $A$. Additionally:
    - If $sigma$ is None, $M$ is positive definite.
    - If $sigma$ is specified, $M$ is positive semi-definite.
  - If $sigma$ is None, eigs requires an operator to compute the solution of the linear equation $M * x = b$. This is done internally via a (sparse) LU decomposition for an explicit matrix $M$, or via an iterative solver for a general linear operator. Alternatively, the user can supply the matrix or operator Minv, which gives $x = Minv * b = M^{-1} * b$.
- **sigma** [real or complex, optional] Find eigenvalues near sigma using shift-invert mode. This requires an operator to compute the solution of the linear system $[A - sigma * M] * x = b$, where $M$ is the identity matrix if unspecified. This is computed internally via a (sparse) LU decomposition for explicit matrices $A$ & $M$, or via an iterative solver if either $A$ or $M$ is a general linear operator. Alternatively, the user can supply the matrix or operator OPinv, which gives $x = OPinv * b = (A - sigma * M)^{-1} * b$. For a real matrix $A$, shift-invert can either be done in imaginary mode or real mode, specified by the parameter OPpart (‘r’ or ‘i’). Note that when $sigma$ is specified, the keyword ‘which’ (below) refers to the shifted eigenvalues $w'[i]$ where:
    - If $A$ is real and OPpart == ‘r’ (default), $w'[i] = 1/2 * [1/(w[i]-sigma) + 1/(w[i]-conj(sigma))].$
    - If $A$ is real and OPpart == ‘i’, $w'[i] = 1/2i * [1/(w[i]-sigma) - 1/(w[i]-conj(sigma))].$
    - If $A$ is complex, $w'[i] = 1/(w[i]-sigma)$.
- **v0** [ndarray, optional] Starting vector for iteration. Default: random.
- **ncv** [int, optional] The number of Lanczos vectors generated $ncv$ must be greater than $k$; it is recommended that $ncv > 2k$. Default: $\min(n, \max(2k + 1, 20))$.
- **which** [str, ['LM' | 'SM' | 'LR' | 'SR' | 'LI' | 'SI'], optional] Which $k$ eigenvectors and eigenvalues to find:
    - ‘LM’ : largest magnitude
    - ‘SM’ : smallest magnitude
‘LR’ : largest real part
‘SR’ : smallest real part
‘LI’ : largest imaginary part
‘SI’ : smallest imaginary part

When sigma != None, ‘which’ refers to the shifted eigenvalues w’[i] (see discussion in ‘sigma’, above). ARPACK is generally better at finding large values than small values. If small eigenvalues are desired, consider using shift-invert mode for better performance.

maxiter : [int, optional]  Maximum number of Arnoldi update iterations allowed
Default: n*10

tol : [float, optional]  Relative accuracy for eigenvalues (stopping criterion)
The default value of 0 implies machine precision.

return_eigenvectors : [bool, optional]  Return eigenvectors (True) in addition to eigenvalues

Minv : [ndarray, sparse matrix or LinearOperator, optional]  See notes in M, above.

OPinv : [ndarray, sparse matrix or LinearOperator, optional]  See notes in sigma, above.

OPpart : [{‘r’ or ‘i’}, optional]  See notes in sigma, above

Returns

w : [ndarray]  Array of k eigenvalues.

v : [ndarray]  An array of k eigenvectors. v[:, i] is the eigenvector corresponding to the eigenvalue w[i].

Raises

ArpackNoConvergence
When the requested convergence is not obtained. The currently converged eigenvalues and eigenvectors can be found as eigenvalues and eigenvectors attributes of the exception object.

See also:

eigsh

eigenvalues and eigenvectors for symmetric matrix A

svds

singular value decomposition for a matrix A

Notes

This function is a wrapper to the ARPACK [1] SNEUPD, DNEUPD, CNEUPD, ZNEUPD, functions which use the Implicitly Restarted Arnoldi Method to find the eigenvalues and eigenvectors [2].

References

[1], [2]

Examples

Find 6 eigenvectors of the identity matrix:

```python
>>> from scipy.sparse.linalg import eigs
>>> id = np.eye(13)
>>> vals, vecs = eigs(id, k=6)
>>> vals
array([ 1.+0.j, 1.+0.j, 1.+0.j, 1.+0.j, 1.+0.j, 1.+0.j])
>>> vecs.shape
(13, 6)
```
scipy.sparse.linalg.eigsh

scipy.sparse.linalg.eigsh(A, k=6, M=None, sigma=None, which='LM', v0=None, ncv=None, maxiter=None, tol=0, return_eigenvectors=True, Minv=None, OPinv=None, mode='normal')

Find k eigenvalues and eigenvectors of the real symmetric square matrix or complex hermitian matrix A.

Solves \( A \times x[i] = w[i] \times x[i] \), the standard eigenvalue problem for \( w[i] \) eigenvalues with corresponding eigenvectors \( x[i] \).

If M is specified, solves \( A \times x[i] = w[i] \times M \times x[i] \), the generalized eigenvalue problem for \( w[i] \) eigenvalues with corresponding eigenvectors \( x[i] \).

**Parameters**

- **A** [ndarray, sparse matrix or LinearOperator] A square operator representing the operation \( A \times x \), where \( A \) is real symmetric or complex hermitian. For buckling mode (see below) \( A \) must additionally be positive-definite.
- **k** [int, optional] The number of eigenvalues and eigenvectors desired. \( k \) must be smaller than \( N \). It is not possible to compute all eigenvectors of a matrix.

**Returns**

- **w** [array] Array of \( k \) eigenvalues.
- **v** [array] An array representing the \( k \) eigenvectors. The column \( v[:, i] \) is the eigenvector corresponding to the eigenvalue \( w[i] \).

**Other Parameters**

- **M** [An \( N \times N \) matrix, array, sparse matrix, or linear operator representing] the operation \( M \times x \) for the generalized eigenvalue problem \( A \times x = w \times M \times x \).

  \( M \) must represent a real, symmetric matrix if \( A \) is real, and must represent a complex, hermitian matrix if \( A \) is complex. For best results, the data type of \( M \) should be the same as that of \( A \). Additionally:
  - If \( \sigma \) is None, \( M \) is symmetric positive definite.
  - If \( \sigma \) is specified, \( M \) is symmetric positive semi-definite.
  - In buckling mode, \( M \) is symmetric indefinite.

  If \( \sigma \) is None, eigsh requires an operator to compute the solution of the linear equation \( M \times x = b \). This is done internally via a (sparse) LU decomposition for an explicit matrix \( M \), or via an iterative solver for a general linear operator. Alternatively, the user can supply the matrix or operator \( M \), which gives \( x = M^{-1} \times b \).

- **sigma** [real] Find eigenvalues near \( \sigma \) using shift-invert mode. This requires an operator to compute the solution of the linear system \( (A - \sigma \times M) \times x = b \), where \( M \) is the identity matrix if unspecified. This is computed internally via a (sparse) LU decomposition for explicit matrices \( A \) & \( M \), or via an iterative solver if either \( A \) or \( M \) is a general linear operator. Alternatively, the user can supply the matrix or operator \( OPinv \), which gives \( x = OPinv \times b = (A - \sigma \times M)^{-1} \times b \). Note that when \( \sigma \) is specified, the keyword ‘which’ refers to the shifted eigenvalues \( w'[i] \) where:
  - if mode == ‘normal’, \( w'[i] = 1 / (w[i] - \sigma) \).
  - if mode == ‘cayley’, \( w'[i] = (w[i] + \sigma) / (w[i] - \sigma) \).
  - if mode == ‘buckling’, \( w'[i] = w[i] / (w[i] - \sigma) \).

(see further discussion in ‘mode’ below)

- **v0** [ndarray, optional] Starting vector for iteration. Default: random
ncv [int, optional] The number of Lanczos vectors generated ncv must be greater than k and smaller than n; it is recommended that ncv > 2*k. Default: min(n, max(2*k + 1, 20))

which [str ['LM' | 'SM' | 'LA' | 'SA' | 'BE']] If A is a complex hermitian matrix, ‘BE’ is invalid. Which k eigenvectors and eigenvalues to find:

‘LM’ : Largest (in magnitude) eigenvalues.
‘SM’ : Smallest (in magnitude) eigenvalues.
‘LA’ : Largest (algebraic) eigenvalues.
‘SA’ : Smallest (algebraic) eigenvalues.
‘BE’ : Half (k/2) from each end of the spectrum.
When k is odd, return one more (k/2+1) from the high end. When sigma != None, ‘which’ refers to the shifted eigenvalues w'[i] (see discussion in ‘sigma’, above).
ARPACK is generally better at finding large values than small values. If small eigenvalues are desired, consider using shift-invert mode for better performance.

maxiter [int, optional] Maximum number of Arnoldi update iterations allowed. Default: n*10

tol [float] Relative accuracy for eigenvalues (stopping criterion). The default value of 0 implies machine precision.

Minv [N x N matrix, array, sparse matrix, or LinearOperator] See notes in M, above.

OPinv [N x N matrix, array, sparse matrix, or LinearOperator] See notes in sigma, above.

return_eigenvectors [bool] Return eigenvectors (True) in addition to eigenvalues. This value determines the order in which eigenvalues are sorted. The sort order is also dependent on the which variable.

   For which = ‘LM’ or ‘SA’:
      If return_eigenvectors is True, eigenvalues are sorted by algebraic value.
      If return_eigenvectors is False, eigenvalues are sorted by absolute value.

   For which = ‘BE’ or ‘LA’:
      eigenvalues are always sorted by algebraic value.

   For which = ‘SM’:
      If return_eigenvectors is True, eigenvalues are sorted by algebraic value.
      If return_eigenvectors is False, eigenvalues are sorted by decreasing absolute value.

mode [string ['normal' | 'buckling' | 'cayley']] Specify strategy to use for shift-invert mode. This argument applies only for real-valued A and sigma != None. For shift-invert mode, ARPACK internally solves the eigenvalue problem OP * x'[i] = w'[i] * B * x'[i] and transforms the resulting Ritz vectors x'[i] and Ritz values w'[i] into the desired eigenvectors and eigenvalues of the problem A * x[i] = w[i] * M * x[i]. The modes are as follows:

‘normal’ :
    OP = [A - sigma * M]^-1 @ M, B = M, w'[i] = 1 / (w[i] - sigma)

‘buckling’ :
    OP = [A - sigma * M]^-1 @ A, B = A, w'[i] = w[i] / (w[i] - sigma)

‘cayley’ :
    OP = [A - sigma * M]^-1 @ [A + sigma * M], B = M, w'[i] = (w[i] + sigma) / (w[i] - sigma)

The choice of mode will affect which eigenvalues are selected by the keyword ‘which’, and can also impact the stability of convergence (see [2] for a discussion).

Raises

ArpackNoConvergence
When the requested convergence is not obtained.

6.22. Sparse linear algebra (scipy.sparse.linalg) 1761
The currently converged eigenvalues and eigenvectors can be found as `eigenvalues` and `eigenvectors` attributes of the exception object.

See also:

- **eigs**
  - eigenvalues and eigenvectors for a general (nonsymmetric) matrix A
- **svds**
  - singular value decomposition for a matrix A

Notes
This function is a wrapper to the ARPACK [1] SSEUPD and DSEUPD functions which use the Implicitly Restarted Lanczos Method to find the eigenvalues and eigenvectors [2].

References
[1], [2]

Examples
```python
>>> from scipy.sparse.linalg import eigsh
>>> identity = np.eye(13)
>>> eigenvalues, eigenvectors = eigsh(identity, k=6)
>>> eigenvalues
array([1., 1., 1., 1., 1., 1.])
>>> eigenvectors.shape
(13, 6)
```

**scipy.sparse.linalg.lobpcg**

`scipy.sparse.linalg.lobpcg(A, X, B=None, M=None, Y=None, tol=None, maxiter=20, largest=True, verbosityLevel=0, retLambdaHistory=False, retResidualNormsHistory=False)`

Locally Optimal Block Preconditioned Conjugate Gradient Method (LOBPCG)

LOBPCG is a preconditioned eigensolver for large symmetric positive definite (SPD) generalized eigenproblems.

**Parameters**
- **A** ([sparse matrix, dense matrix, LinearOperator]) The symmetric linear operator of the problem, usually a sparse matrix. Often called the “stiffness matrix”.
- **X** ([array_like]) Initial approximation to the k eigenvectors. If A has shape=(n,n) then X should have shape=(n,k).
- **B** ([dense matrix, sparse matrix, LinearOperator], optional) the right hand side operator in a generalized eigenproblem. by default, B = Identity often called the “mass matrix”
- **M** ([dense matrix, sparse matrix, LinearOperator], optional) preconditioner to A; by default M = Identity M should approximate the inverse of A
- **Y** ([array_like, optional]) n-by-sizeY matrix of constraints, sizeY < n The iterations will be performed in the B-orthogonal complement of the column-space of Y. Y must be full rank.

**Returns**
- **w** [array] Array of k eigenvalues
- **v** [array] An array of k eigenvectors. V has the same shape as X.

**Other Parameters**
tol [scalar, optional] Solver tolerance (stopping criterion) by default: tol=n*sqrt(eps)

maxiter [integer, optional] maximum number of iterations by default: maxiter=min(n,20)

largest [bool, optional] when True, solve for the largest eigenvalues, otherwise the smallest

verbosityLevel [integer, optional] controls solver output. default: verbosityLevel = 0.

retLambdaHistory [boolean, optional] whether to return eigenvalue history

retResidualNormsHistory [boolean, optional] whether to return history of residual norms

Notes

If both retLambdaHistory and retResidualNormsHistory are True, the return tuple has the following format (lambda, V, lambda history, residual norms history).

In the following n denotes the matrix size and m the number of required eigenvalues (smallest or largest).

The LOBPCG code internally solves eigenproblems of the size 3``m`` on every iteration by calling the “standard” dense eigensolver, so if m is not small enough compared to n, it does not make sense to call the LOBPCG code, but rather one should use the “standard” eigensolver, e.g. numpy or scipy function in this case. If one calls the LOBPCG algorithm for 5``m``>“n”, it will most likely break internally, so the code tries to call the standard function instead.

It is not that n should be large for the LOBPCG to work, but rather the ratio n/m should be large. It you call the LOBPCG code with m``=1 and n``=10, it should work, though n is small. The method is intended for extremely large n/m, see e.g., reference [28] in https://arxiv.org/abs/0705.2626

The convergence speed depends basically on two factors:

1. How well relatively separated the seeking eigenvalues are from the rest of the eigenvalues. One can try to vary m to make this better.

2. How well conditioned the problem is. This can be changed by using proper preconditioning. For example, a rod vibration test problem (under tests directory) is ill-conditioned for large n, so convergence will be slow, unless efficient preconditioning is used. For this specific problem, a good simple preconditioner function would be a linear solve for A, which is easy to code since A is tridiagonal.

Acknowledgements

lobpcg.py code was written by Robert Cimrman. Many thanks belong to Andrew Knyazev, the author of the algorithm, for lots of advice and support.

References

[1], [2], [3]

Examples

Solve A x = lambda B x with constraints and preconditioning.

```python
>>> from scipy.sparse import spdiags, issparse
>>> from scipy.sparse.linalg import lobpcg, LinearOperator
>>> n = 100
>>> vals = [np.arange(n, dtype=np.float64) + 1]
>>> A = spdiags(vals, 0, n, n)
>>> A.toarray()
array([[ 1.,  0.,  0., ...,  0.,  0.,  0.],
       [ 0.,  2.,  0., ...,  0.,  0.,  0.],
       [ 0.,  0.,  3., ...,  0.,  0.,  0.],
       ..., 
       [ 0.,  0.,  0., ...,  98.,  0.,  0.],
       [ 0.,  0.,  0., ...,  98.,  0.,  0.],
       [ 0.,  0.,  0., ...,  98.,  0.,  0.]],
       [continues on next page])```
Constraints.

```python
>>> Y = np.eye(n, 3)
```

Initial guess for eigenvectors, should have linearly independent columns. Column dimension = number of requested eigenvalues.

```python
>>> X = np.random.rand(n, 3)
```

Preconditioner – inverse of A (as an abstract linear operator).

```python
>>> invA = spdiags([1./vals[0]], 0, n, n)
>>> def precond(x):
...     return invA * x
>>> M = LinearOperator(matvec=precond, shape=(n, n), dtype=float)
```

Here, `invA` could of course have been used directly as a preconditioner. Let us then solve the problem:

```python
>>> eigs, vecs = lobpcg(A, X, Y=Y, M=M, tol=1e-4, maxiter=40, largest=False)
```

Note that the vectors passed in Y are the eigenvectors of the 3 smallest eigenvalues. The results returned are orthogonal to those.

Singular values problems:

```python
svds(A[, k, ncv, tol, which, v0, maxiter, ...]) Compute the largest k singular values/vectors for a sparse matrix.
```

```python
scipy.sparse.linalg.svds
```

```python
scipy.sparse.linalg.svds(A, k=6, ncv=None, tol=0, which='LM', v0=None, maxiter=None, return_singular_vectors=True)
```

Compute the largest k singular values/vectors for a sparse matrix.

**Parameters**

- `A` ([sparse matrix, LinearOperator]) Array to compute the SVD on, of shape (M, N)
- `k` [int, optional] Number of singular values and vectors to compute. Must be 1 <= k < min(A.shape).
- `ncv` [int, optional] The number of Lanczos vectors generated ncv must be greater than k+1 and smaller than n; it is recommended that ncv > 2*k Default: min(n, max(2*k + 1, 20))
- `which` [str, ['LM' | 'SM'], optional] Which k singular values to find:
  - ‘LM’ : largest singular values
  - ‘SM’ : smallest singular values
  New in version 0.12.0.
- `v0` [ndarray, optional] Starting vector for iteration, of length min(A.shape). Should
be an (approximate) left singular vector if \( N > M \) and a right singular vector otherwise. Default: random

New in version 0.12.0.

**maxiter**  
[int, optional] Maximum number of iterations.  
New in version 0.12.0.

**return_singular_vectors**  
[bool or str, optional]  
- True: return singular vectors (True) in addition to singular values.  
  New in version 0.12.0.  
- “u”: only return the u matrix, without computing vh (if \( N > M \)).  
- “vh”: only return the vh matrix, without computing u (if \( N \leq M \)).  
  New in version 0.16.0.

Returns  
- \( u \) [ndarray, shape=(M, k)] Unitary matrix having left singular vectors as columns. If return_singular_vectors is “vh”, this variable is not computed, and None is returned instead.
- \( s \) [ndarray, shape=(k,)] The singular values.
- \( vt \) [ndarray, shape=(k, N)] Unitary matrix having right singular vectors as rows. If return_singular_vectors is “u”, this variable is not computed, and None is returned instead.

Notes  
This is a naive implementation using ARPACK as an eigensolver on \( A^H A \) or \( A A^H \), depending on which one is more efficient.

Examples

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import svds, eigs
>>> A = csc_matrix([[1, 0, 0], [5, 0, 2], [0, -1, 0], [0, 0, 3]], dtype=float)
>>> u, s, vt = svds(A, k=2)
>>> s
array([ 2.75193379, 5.60596652])
>>> np.sqrt(eigs(A.dot(A.T), k=2)[0]).real
array([ 5.60596652 , 2.75193379])
```

Complete or incomplete LU factorizations

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>splu(A[, permc_spec, diag_pivot_thresh, ...])</td>
<td>Compute the LU decomposition of a sparse, square matrix.</td>
</tr>
<tr>
<td>spilu(A[, drop_tol, fill_factor, drop_rule, ...])</td>
<td>Compute an incomplete LU decomposition for a sparse, square matrix.</td>
</tr>
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**SuperLU**  
LU factorization of a sparse matrix.

**scipy.sparse.linalg.splu**  
**scipy.sparse.linalg.spilu**  
**scipy.sparse.linalg.splu**(A[, permc_spec=None, diag_pivot_thresh=None, relax=None, panel_size=None, options={}])  
Compute the LU decomposition of a sparse, square matrix.

**Parameters**  
- A [sparse matrix] Sparse matrix to factorize. Should be in CSR or CSC format.
- permc_spec [str, optional] How to permute the columns of the matrix for sparsity preservation.
(default: ‘COLAMD’)

- NATURAL: natural ordering.
- MMD_ATA: minimum degree ordering on the structure of A^T A.
- MMD_AT_PLUS_A: minimum degree ordering on the structure of A^T+A.
- COLAMD: approximate minimum degree column ordering

**diag_pivot_thresh**

[float, optional] Threshold used for a diagonal entry to be an acceptable pivot. See SuperLU user’s guide for details [1]

**relax**

[int, optional] Expert option for customizing the degree of relaxing supernodes. See SuperLU user’s guide for details [1]

**panel_size**

[int, optional] Expert option for customizing the panel size. See SuperLU user’s guide for details [1]

**options**

[dict, optional] Dictionary containing additional expert options to SuperLU. See SuperLU user guide [1] (section 2.4 on the ‘Options’ argument) for more details. For example, you can specify `options=dict(Equil=False, IterRefine='SINGLE'))` to turn equilibration off and perform a single iterative refinement.

**Returns**


See also:

- `spilu`
  incomplete LU decomposition

**Notes**

This function uses the SuperLU library.

**References**

[1]

**Examples**

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import splu
>>> A = csc_matrix([[1., 0., 0.], [5., 0., 2.], [0., -1., 0.]], dtype=float)
>>> B = splu(A)
>>> x = np.array([1., 2., 3.], dtype=float)
>>> B.solve(x)
array([ 1. , -3. , -1.5])
>>> A.dot(B.solve(x))
array([ 1., 2., 3.])
>>> B.solve(A.dot(x))
array([ 1., 2., 3.])
```

**scipy.sparse.linalg.spilu**

- `scipy.sparse.linalg.spilu(A, drop_tol=None, fill_factor=None, drop_rule=None, permc_spec=None, diag_pivot_thresh=None, relax=None, panel_size=None, options=None)`

  Compute an incomplete LU decomposition for a sparse, square matrix.

  The resulting object is an approximation to the inverse of A.

  **Parameters**
A     [(N, N) array_like] Sparse matrix to factorize

drop_tol
    [float, optional] Drop tolerance (0 <= tol <= 1) for an incomplete LU decom-
    position. (default: 1e-4)

fill_factor
    [float, optional] Specifies the fill ratio upper bound (>= 1.0) for ILU. (default: 10)

drop_rule
    [str, optional] Comma-separated string of drop rules to use. Available rules: basic,
    prows, column, area, secondary, dynamic, interp. (Default: basic,area)
    See SuperLU documentation for details.

Remaining other options
    Same as for splu

Returns

invA_approx
    [scipy.sparse.linalg.SuperLU] Object, which has a solve method.

See also:

splu
    complete LU decomposition

Notes
To improve the better approximation to the inverse, you may need to increase fill_factor AND decrease
drop_tol.

This function uses the SuperLU library.

Examples

```python
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import spilu
>>> A = csc_matrix([[1., 0., 0.], [5., 0., 2.], [0., -1., 0.]], dtype=float)
>>> B = spilu(A)
>>> x = np.array([1., 2., 3.], dtype=float)
>>> B.solve(x)
array([-1. ,  2.5, -1.5])
>>> A.dot(B.solve(x))
array([ 1.,  2.,  3.])
>>> B.solve(A.dot(x))
array([ 1.,  2.,  3.])
```

**scipy.sparse.linalg.SuperLU**

class scipy.sparse.linalg.SuperLU
LU factorization of a sparse matrix.

Factorization is represented as:

```
Pr * A * Pc = L * U
```

To construct these SuperLU objects, call the splu and spilu functions.

Notes
New in version 0.14.0.
Examples
The LU decomposition can be used to solve matrix equations. Consider:

```python
>>> import numpy as np
>>> from scipy.sparse import csc_matrix, linalg as sla
>>> A = csc_matrix([[1, 2, 0, 4], [1, 0, 0, 1], [1, 0, 2, 1], [2, 2, 1, 0]])
```

This can be solved for a given right-hand side:

```python
>>> lu = sla.splu(A)
>>> b = np.array([1, 2, 3, 4])
>>> x = lu.solve(b)
>>> A.dot(x)
array([1., 2., 3., 4.])
```

The `lu` object also contains an explicit representation of the decomposition. The permutations are represented as mappings of indices:

```python
>>> lu.perm_r
array([0, 2, 1, 3], dtype=int32)
>>> lu.perm_c
array([2, 0, 1, 3], dtype=int32)
```

The L and U factors are sparse matrices in CSC format:

```python
>>> lu.L.A
array([[1., 0., 0., 0.],
       [0., 1., 0., 0.],
       [0., 0., 1., 0.],
       [1., 0.5, 0.5, 1.]])
>>> lu.U.A
array([[2., 0., 1., 4.],
       [0., 2., 1., 1.],
       [0., 0., 1., 1.],
       [0., 0., 0., -5.]])
```

The permutation matrices can be constructed:

```python
>>> Pr = csc_matrix((4, 4))
>>> Pr[lu.perm_r, np.arange(4)] = 1
>>> Pc = csc_matrix((4, 4))
>>> Pc[np.arange(4), lu.perm_c] = 1
```

We can reassemble the original matrix:

```python
>>> (Pr.T * (lu.L * lu.U) * Pc.T).A
array([[1., 2., 0., 4.],
       [1., 0., 0., 1.],
       [1., 0., 2., 1.],
       [2., 2., 1., 0.]])
```

Attributes
- **shape**: Shape of the original matrix as a tuple of ints.
- **nnz**: Number of nonzero elements in the matrix.
perm_c  Permutation Pc represented as an array of indices.
perm_r  Permutation Pr represented as an array of indices.
L      Lower triangular factor with unit diagonal as a \texttt{scipy.sparse.csc_matrix}.
U      Upper triangular factor as a \texttt{scipy.sparse.csc_matrix}.

Methods

\texttt{solve(rhs[, trans])}  Solves linear system of equations with one or several right-hand sides.

\texttt{scipy.sparse.linalg.SuperLU.solve}
\texttt{SuperLU.solve(rhs[, trans])}  Solves linear system of equations with one or several right-hand sides.

**Parameters**

- \texttt{rhs}  [ndarray, shape (n,) or (n, k)] Right hand side(s) of equation
- \texttt{trans}  [{‘N’, ‘T’, ‘H’}, optional] Type of system to solve:

  - ‘N’: \(A \times x = rhs\)  (default)
  - ‘T’: \(A^T \times x = rhs\)
  - ‘H’: \(A^H \times x = rhs\)

  i.e., normal, transposed, and hermitian conjugate.

**Returns**

- \texttt{x}  [ndarray, shape \texttt{rhs.shape}] Solution vector(s)

6.22.6 Exceptions

- \texttt{ArpackNoConvergence(msg, eigenvalues, ...)}  ARPACK iteration did not converge
- \texttt{ArpackError(info[, infodict])}  ARPACK error

\texttt{scipy.sparse.linalg.ArpackNoConvergence}

\texttt{exception scipy.sparse.linalg.ArpackNoConvergence(msg, eigenvalues, eigenvectors)}  ARPACK iteration did not converge

**Attributes**

- \texttt{eigenvalues}  [ndarray] Partial result. Converged eigenvalues.
- \texttt{eigenvectors}  [ndarray] Partial result. Converged eigenvectors.

6.22. Sparse linear algebra (\texttt{scipy.sparse.linalg})
scipy.sparse.linalg.ArpackError

exception scipy.sparse.linalg.ArpackError

(info, infodict={'c': {0: 'Normal exit.', 1: 'Maximum number of iterations taken. All possible eigenvalues of OP has been found. IPARAM(5) returns the number of wanted converged Ritz values.', 2: 'No longer an informational error. Deprecated starting with release 2 of ARPACK.', 3: 'No shifts could be applied during a cycle of the Implicitly restarted Arnoldi iteration. One possibility is to increase the size of NCV relative to NEV. ', -1: 'N must be positive.', -2: 'NEV must be positive.', -3: 'NCV-NEV >= 2 and less than or equal to N.', -4: 'The maximum number of Arnoldi update iterations allowed must be greater than zero.', -5: ' WHICH must be one of '}, 'd': {0: 'Normal exit.', 1: 'Maximum number of iterations taken. All possible eigenvalues of OP has been found. IPARAM(5) returns the number of wanted converged Ritz values.', 2: 'No longer an informational error. 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6.23 Compressed Sparse Graph Routines (scipy.sparse.csgraph)

Fast graph algorithms based on sparse matrix representations.

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scipy.sparse.csgraph.connected_components

scipy.sparse.csgraph.connected_components(csgraph, directed=True, connection='weak', return_labels=True)

Analyze the connected components of a sparse graph

New in version 0.11.0.

Parameters

- **csgraph** [array_like or sparse matrix] The N x N matrix representing the compressed sparse graph. The input csgraph will be converted to csr format for the calculation.
- **directed** [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].
- **connection** [str, optional] ['weak'|'strong']. For directed graphs, the type of connection to use.
Nodes i and j are strongly connected if a path exists both from i to j and from j to i. Nodes i and j are weakly connected if only one of these paths exists. If directed == False, this keyword is not referenced.

return_labels
[bool, optional] If True (default), then return the labels for each of the connected components.

Returns

n_components: int
The number of connected components.

labels: ndarray
The length-N array of labels of the connected components.

References

[1]

Examples

>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import connected_components

>>> graph = [
... [0, 1, 1, 0, 0],
... [0, 0, 1, 0, 0],
... [0, 0, 0, 0, 0],
... [0, 0, 0, 0, 1],
... [0, 0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 1
(1, 2) 1
(3, 4) 1

>>> n_components, labels = connected_components(csgraph=graph, directed=False,
... return_labels=True)
>>> n_components
2
>>> labels
array([0, 0, 1, 1], dtype=int32)

scipy.sparse.csgraph.laplacian

scipy.sparse.csgraph.laplacian(csgraph, normed=False, return_diag=False, use_out_degree=False)

Return the Laplacian matrix of a directed graph.

Parameters

csgraph [array_like or sparse matrix, 2 dimensions] compressed-sparse graph, with shape (N, N).
normed [bool, optional] If True, then compute normalized Laplacian.
return_diag [bool, optional] If True, then also return an array related to vertex degrees.
use_out_degree

[bool, optional] If True, then use out-degree instead of in-degree. This distinction matters only if the graph is asymmetric. Default: False.

Returns

lap [ndarray or sparse matrix] The N x N laplacian matrix of csgraph. It will be a numpy array (dense) if the input was dense, or a sparse matrix otherwise.
diag [ndarray, optional] The length-N diagonal of the Laplacian matrix. For the normalized Laplacian, this is the array of square roots of vertex degrees or 1 if the degree is zero.

Notes

The Laplacian matrix of a graph is sometimes referred to as the “Kirchoff matrix” or the “admittance matrix”, and is useful in many parts of spectral graph theory. In particular, the eigen-decomposition of the laplacian matrix can give insight into many properties of the graph.

Examples

```python
>>> from scipy.sparse import csgraph
>>> G = np.arange(5) * np.arange(5)[np.newaxis]
>>> G
array([[ 0,  0,  0,  0,  0],
       [ 0,  1,  2,  3,  4],
       [ 0,  2,  4,  6,  8],
       [ 0,  3,  6,  9, 12],
       [ 0,  4,  8, 12, 16]])
>>> csgraph.laplacian(G, normed=False)
array([[ 0,   0,   0,   0,   0],
       [ 0,   9, -2, -3, -4],
       [ 0,  -2, 16, -6, -8],
       [ 0,  -3, -6, 21, -12],
       [ 0,  -4, -8, -12, 24]])
```

scipy.sparse.csgraph.shortest_path

```python
scipy.sparse.csgraph.shortest_path(csgraph, method='auto', directed=True, return_predecessors=False, unweighted=False, overwrite=False, indices=None)
```

Perform a shortest-path graph search on a positive directed or undirected graph.

New in version 0.11.0.

Parameters

- **csgraph** [array, matrix, or sparse matrix, 2 dimensions] The N x N array of distances representing the input graph.
- **method** [string ['auto','FW','D'], optional] Algorithm to use for shortest paths. Options are:
  - ‘FW’ – **Floyd-Warshall algorithm. Computational cost is** approximately $O[N^3]$. The input csgraph will be converted to a dense representation.
  - ‘D’ – **Dijkstra’s algorithm with Fibonacci heaps. Computational cost is approximately $O(N*(N*k + N*log(N)))$**, where $k$ is the average number of connected edges per node. The input csgraph will be converted to a csr representation.
‘BF’ – Bellman-Ford algorithm. This algorithm can be used when weights are negative. If a negative cycle is encountered, an error will be raised. Computational cost is approximately \(O(N(N^2 N_k))\), where \(N_k\) is the average number of connected edges per node. The input csgraph will be converted to a csr representation.

‘J’ – Johnson’s algorithm. Like the Bellman-Ford algorithm, Johnson’s algorithm is designed for use when the weights are negative. It combines the Bellman-Ford algorithm with Dijkstra’s algorithm for faster computation.

directed [bool, optional] If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]

return_predecessors [bool, optional] If True, return the size (N, N) predecessor matrix

unweighted [bool, optional] If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

overwrite [bool, optional] If True, overwrite csgraph with the result. This applies only if method == ‘FW’ and csgraph is a dense, c-ordered array with dtype=float64.

indices [array_like or int, optional] If specified, only compute the paths for the points at the given indices. Incompatible with method == ‘FW’.

Returns

dist_matrix [ndarray] The N x N matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.

predecessors [ndarray] Returned only if return_predecessors == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Raises

NegativeCycleError: if there are negative cycles in the graph

Notes

As currently implemented, Dijkstra’s algorithm and Johnson’s algorithm do not work for graphs with direction-dependent distances when directed == False. i.e., if csgraph[i,j] and csgraph[j,i] are non-equal edges, method=’D’ may yield an incorrect result.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import shortest_path

>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [2, 0, 0, 3],
... [0, 0, 0, 0]
] (continues on next page)
```
...]

```python
>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 3) 1
(2, 0) 2
(2, 3) 3
```

```python
>>> dist_matrix, predecessors = shortest_path(csgraph=graph, directed=False,
                                          indices=0, return_predecessors=True)
>>> dist_matrix
array([ 0., 1., 2., 2.])
>>> predecessors
array([-9999,  0,  0,  1], dtype=int32)
```

**scipy.sparse.csgraph.dijkstra**

New in version 0.11.0.

**Parameters**

- `csgraph` [array, matrix, or sparse matrix, 2 dimensions] The N x N array of non-negative distances representing the input graph.
- `directed` [bool, optional] If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j] and from point j to i along paths csgraph[j, i]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j or j to i along either csgraph[i, j] or csgraph[j, i].
- `indices` [array_like or int, optional] if specified, only compute the paths for the points at the given indices.
- `return_predecessors` [bool, optional] If True, return the size (N, N) predecessor matrix.
- `unweighted` [bool, optional] If True, return the size (N, N) predecessor matrix.
- `unweighted` [bool, optional] If True, return the size (N, N) predecessor matrix.
- `limit` [float, optional] The maximum distance to calculate, must be >= 0. Using a smaller limit will decrease computation time by aborting calculations between pairs that are separated by a distance > limit. For such pairs, the distance will be equal to `np.inf` (i.e., not connected).

**Returns**

- `dist_matrix` [ndarray] The matrix of distances between graph nodes. `dist_matrix[i,j]` gives the shortest distance from point i to point j along the graph.
- `predecessors` [ndarray] Returned only if `return_predecessors == True`. The matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor
matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Notes
As currently implemented, Dijkstra’s algorithm does not work for graphs with direction-dependent distances when directed == False. i.e., if csgraph[i,j] and csgraph[j,i] are not equal and both are nonzero, setting directed=False will not yield the correct result.

Also, this routine does not work for graphs with negative distances. Negative distances can lead to infinite cycles that must be handled by specialized algorithms such as Bellman-Ford’s algorithm or Johnson’s algorithm.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import dijkstra

>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 3) 1
(2, 3) 3

>>> dist_matrix, predecessors = dijkstra(csgraph=graph, directed=False, indices=0,
... return_predecessors=True)
>>> dist_matrix
array([ 0., 1., 2., 2.])
>>> predecessors
array([-9999, 0, 0, 1], dtype=int32)
```

scipy.sparse.csgraph.floyd_warshall

Compute the shortest path lengths using the Floyd-Warshall algorithm

New in version 0.11.0.

Parameters

- **csgraph** [array, matrix, or sparse matrix, 2 dimensions] The N x N array of distances representing the input graph.
- **directed** [bool, optional] If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]
- **return_predecessors** [bool, optional] If True, return the size (N, N) predecessor matrix
- **unweighted** [bool, optional] If True, return the size (N, N) predecessor matrix
[bool, optional] If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

overwrite
[bool, optional] If True, overwrite csgraph with the result. This applies only if csgraph is a dense, c-ordered array with dtype=float64.

Returns

dist_matrix
[ndarray] The N x N matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.

predecessors
[ndarray] Returned only if return_predecessors == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Raises

NegativeCycleError:
if there are negative cycles in the graph

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import floyd_warshall

>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [2, 0, 0, 3],
... [0, 0, 0, 0]
... ]

>>> graph = csr_matrix(graph)

>>> print(graph

(0, 1) 1
(0, 2) 2
(1, 3) 1
(2, 0) 2
(2, 3) 3

>>> dist_matrix, predecessors = floyd_warshall(csgraph=graph, directed=False,
... return_predecessors=True)

>>> dist_matrix

array([[ 0., 1., 2., 2.],
       [ 1., 0., 3., 1.],
       [ 2., 3., 0., 3.],
       [ 2., 1., 3., 0.]]

>>> predecessors
array([[-9999, 0, 0, 1],
       [ 1, -9999, 0, 1],
       [ 2, 0, -9999, 2],
       [ 1, 3, 3, -9999]], dtype=int32)
```
scipy.sparse.csgraph.bellman_ford

`scipy.sparse.csgraph.bellman_ford(csgraph, directed=True, indices=None, return_predecessors=False, unweighted=False)`

Compute the shortest path lengths using the Bellman-Ford algorithm.

The Bellman-ford algorithm can robustly deal with graphs with negative weights. If a negative cycle is detected, an error is raised. For graphs without negative edge weights, Dijkstra’s algorithm may be faster.

New in version 0.11.0.

Parameters

- `csgraph` [array, matrix, or sparse matrix, 2 dimensions] The N x N array of distances representing the input graph.
- `directed` [bool, optional] If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths `csgraph[i, j]`. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along `csgraph[i, j]` or `csgraph[j, i]`.
- `indices` [array_like or int, optional] If specified, only compute the paths for the points at the given indices.
- `return_predecessors` [bool, optional] If True, return the size (N, N) predecessor matrix.
- `unweighted` [bool, optional] If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

Returns

- `dist_matrix` [ndarray] The N x N matrix of distances between graph nodes. `dist_matrix[i,j]` gives the shortest distance from point i to point j along the graph.
- `predecessors` [ndarray] Returned only if `return_predecessors` == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry `predecessors[i, j]` gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then `predecessors[i, j]` = -9999.

Raises

- `NegativeCycleError`: if there are negative cycles in the graph.

Notes

This routine is specially designed for graphs with negative edge weights. If all edge weights are positive, then Dijkstra’s algorithm is a better choice.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import bellman_ford

>>> graph = [
    ... [0, 1, 2, 0],
    ... [0, 0, 0, 1],
    ... [2, 0, 0, 3],
]  
(continues on next page)```
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 3) 1
(2, 0) 2
(2, 3) 3

>>> dist_matrix, predecessors = bellman_ford(csgraph=graph, directed=False, indices=0, return_predecessors=True)
>>> dist_matrix
array([ 0., 1., 2., 2.])
>>> predecessors
array([-9999, 0, 0, 1], dtype=int32)

scipy.sparse.csgraph.johnson

scipy.sparse.csgraph.johnson(csgraph, directed=True, indices=None, return_predecessors=False, unweighted=False)

Compute the shortest path lengths using Johnson’s algorithm.

Johnson’s algorithm combines the Bellman-Ford algorithm and Dijkstra’s algorithm to quickly find shortest paths in a way that is robust to the presence of negative cycles. If a negative cycle is detected, an error is raised. For graphs without negative edge weights, dijkstra() may be faster.

New in version 0.11.0.

Parameters

csgraph [array, matrix, or sparse matrix, 2 dimensions] The N x N array of distances representing the input graph.
directed [bool, optional] If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]
directed [array_like or int, optional] If specified, only compute the paths for the points at the given indices.
return_predecessors [bool, optional] If True, return the size (N, N) predecessor matrix
unweighted [bool, optional] If True, return the size (N, N) predecessor matrix

Returns

dist_matrix [ndarray] The N x N matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.
predecessors [ndarray] Returned only if return_predecessors == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each
entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

**Raises**

**NegativeCycleError:**
if there are negative cycles in the graph

**Notes**
This routine is specially designed for graphs with negative edge weights. If all edge weights are positive, then Dijkstra’s algorithm is a better choice.

**Examples**

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import johnson

>>> graph = [
    ... [0, 1, 2, 0],
    ... [0, 0, 1],
    ... [2, 0, 3],
    ... [0, 0, 0]
    ... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 3) 1
(2, 0) 2
(2, 3) 3

>>> dist_matrix, predecessors = johnson(csgraph=graph, directed=False, indices=0,
    ... return_predecessors=True)
>>> dist_matrix
array([ 0., 1., 2., 2.])
>>> predecessors
array([-9999, 0, 0, 1], dtype=int32)
```

**scipy.sparse.csgraph.breadth_first_order**

`scipy.sparse.csgraph.breadth_first_order(csgraph, i_start, directed=True, return_predecessors=True)`

Return a breadth-first ordering starting with specified node.

Note that a breadth-first order is not unique, but the tree which it generates is unique.

New in version 0.11.0.

**Parameters**

- **csgraph** [array_like or sparse matrix] The N x N compressed sparse graph. The input csgraph will be converted to csr format for the calculation.
- **i_start** [int] The index of starting node.
- **directed** [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].
return_predecessors

[bool, optional] If True (default), then return the predecessor array (see below).

Returns

node_array

[ndarray, one dimension] The breadth-first list of nodes, starting with specified node. The length of node_array is the number of nodes reachable from the specified node.

predecessors

[ndarray, one dimension] Returned only if return_predecessors is True. The length-N list of predecessors of each node in a breadth-first tree. If node i is in the tree, then its parent is given by predecessors[i]. If node i is not in the tree (and for the parent node) then predecessors[i] = -9999.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import breadth_first_order

>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [2, 0, 0, 3],
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 3) 1
(2, 0) 2
(2, 3) 3

>>> breadth_first_order(graph, 0)
(array([0, 1, 2, 3], dtype=int32), array([1, 0, 0, 1], dtype=int32))
```

scipy.sparse.csgraph.depth_first_order

scipy.sparse.csgraph.depth_first_order(csgraph, i_start, directed=True, return_predecessors=True)

Return a depth-first ordering starting with specified node.

Note that a depth-first order is not unique. Furthermore, for graphs with cycles, the tree generated by a depth-first search is not unique either.

New in version 0.11.0.

Parameters

- csgraph [array_like or sparse matrix] The N x N compressed sparse graph. The input csgraph will be converted to csr format for the calculation.
- i_start [int] The index of starting node.
- directed [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

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return_predecessors

[bool, optional] If True (default), then return the predecessor array (see below).

Returns

node_array

[ndarray, one dimension] The depth-first list of nodes, starting with specified node. The length of node_array is the number of nodes reachable from the specified node.

predecessors

[ndarray, one dimension] Returned only if return_predecessors is True. The length-N list of predecessors of each node in a depth-first tree. If node i is in the tree, then its parent is given by predecessors[i]. If node i is not in the tree (and for the parent node) then predecessors[i] = -9999.

Examples

```python
from scipy.sparse import csr_matrix
from scipy.sparse.csgraph import depth_first_order

>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 1, 0],
... [2, 0, 0, 3],
... [0, 0, 0, 0],
...]
>>> graph = csr_matrix(graph)
>>> depth_first_order(graph, 0)
(array([0, 1, 3, 2], dtype=int32), array([-9999, 0, 0, 1], dtype=int32))
```

scipy.sparse.csgraph.breadth_first_tree

scipy.sparse.csgraph.breadth_first_tree(csgraph, i_start, directed=True)

Return the tree generated by a breadth-first search

Note that a breadth-first tree from a specified node is unique.

New in version 0.11.0.

Parameters

csgraph [array_like or sparse matrix] The N x N matrix representing the compressed sparse graph. The input csgraph will be converted to csr format for the calculation.
i_start [int] The index of starting node.
directed [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

Returns
cstree  [csr matrix] The N x N directed compressed-sparse representation of the breadth-first tree drawn from csgraph, starting at the specified node.

Examples
The following example shows the computation of a depth-first tree over a simple four-component graph, starting at node 0:

```
input graph       breadth first tree from (0)

(0)                 (0)
/ \                 / \     \
3 8 3 8             3 8     \
/ \    / \           / \       (3)---5---(1)     (3) (1)
\  /    / \          / /        \       \  \
6 2 2 6 2           2 6 2     \       (2) (2)
\ /    /             /         \ 
(2)                 (2)
```

In compressed sparse representation, the solution looks like this:

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import breadth_first_tree
>>> X = csr_matrix([[0, 8, 0, 3],
...                 [0, 0, 2, 5],
...                 [0, 0, 0, 6],
...                 [0, 0, 0, 0]])
>>> Tcsr = breadth_first_tree(X, 0, directed=False)
>>> Tcsr.toarray().astype(int)
array([[0, 8, 0, 3],
       [0, 0, 2, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]])
```

Note that the resulting graph is a Directed Acyclic Graph which spans the graph. A breadth-first tree from a given node is unique.

scipy.sparse.csgraph.depth_first_tree

scipy.sparse.csgraph.depth_first_tree(csgraph, i_start, directed=True)

Return a tree generated by a depth-first search.

Note that a tree generated by a depth-first search is not unique: it depends on the order that the children of each node are searched.

New in version 0.11.0.

Parameters

- csgraph  [array_like or sparse matrix] The N x N matrix representing the compressed sparse graph. The input csgraph will be converted to csr format for the calculation.
- i_start  [int] The index of starting node.
- directed  [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

Returns
cstree  [csr matrix] The N x N directed compressed-sparse representation of the depth-first tree drawn from csgraph, starting at the specified node.

Examples
The following example shows the computation of a depth-first tree over a simple four-component graph, starting at node 0:

\[
\begin{array}{ccc}
(0) & (0) & (3) \\
/ \quad / & \quad (3) & \quad (1) \\
3 \quad 8 & \quad 8 & \quad 5 \\
/ \quad / \quad / \\
(3) & (1) & (0) \\
/ \quad / \quad / \\
6 \quad 2 & \quad 6 \quad 2 \\
/ \quad / \quad / \\
(2) & (2) & (3)
\end{array}
\]

In compressed sparse representation, the solution looks like this:

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import depth_first_tree
>>> X = csr_matrix([[0, 8, 0, 3],
...                  [0, 0, 2, 5],
...                  [0, 0, 0, 6],
...                  [0, 0, 0, 0]])
>>> Tcsr = depth_first_tree(X, 0, directed=False)
>>> Tcsr.toarray().astype(int)
array([[0, 8, 0, 0],
       [0, 0, 2, 0],
       [0, 0, 0, 6],
       [0, 0, 0, 0]])
```

Note that the resulting graph is a Directed Acyclic Graph which spans the graph. Unlike a breadth-first tree, a depth-first tree of a given graph is not unique if the graph contains cycles. If the above solution had begun with the edge connecting nodes 0 and 3, the result would have been different.

scipy.sparse.csgraph.minimum_spanning_tree

scipy.sparse.csgraph.minimum_spanning_tree(csgraph, overwrite=False)

Return a minimum spanning tree of an undirected graph

A minimum spanning tree is a graph consisting of the subset of edges which together connect all connected nodes, while minimizing the total sum of weights on the edges. This is computed using the Kruskal algorithm.

New in version 0.11.0.

Parameters

csgraph  [array_like or sparse matrix, 2 dimensions] The N x N matrix representing an undirected graph over N nodes (see notes below).

overwrite  [bool, optional] if true, then parts of the input graph will be overwritten for efficiency.

Returns
span_tree

 csr matrix  The N x N compressed-sparse representation of the undirected minimum spanning tree over the input (see notes below).

Notes

This routine uses undirected graphs as input and output. That is, if graph[i, j] and graph[j, i] are both zero, then nodes i and j do not have an edge connecting them. If either is nonzero, then the two are connected by the minimum nonzero value of the two.

Examples

The following example shows the computation of a minimum spanning tree over a simple four-component graph:

<table>
<thead>
<tr>
<th>input graph</th>
<th>minimum spanning tree</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>(0)</td>
</tr>
<tr>
<td></td>
<td>/</td>
</tr>
<tr>
<td></td>
<td>/ \</td>
</tr>
<tr>
<td></td>
<td>3 8   3</td>
</tr>
<tr>
<td></td>
<td>/ \</td>
</tr>
<tr>
<td></td>
<td>(3)---5---(1)</td>
</tr>
<tr>
<td></td>
<td>\ /</td>
</tr>
<tr>
<td></td>
<td>6 2   2</td>
</tr>
<tr>
<td></td>
<td>\ /</td>
</tr>
<tr>
<td></td>
<td>(2)</td>
</tr>
<tr>
<td></td>
<td>(2)</td>
</tr>
</tbody>
</table>

It is easy to see from inspection that the minimum spanning tree involves removing the edges with weights 8 and 6. In compressed sparse representation, the solution looks like this:

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import minimum_spanning_tree
>>> X = csr_matrix([[0, 8, 0, 3],
                  [0, 0, 2, 5],
                  [0, 0, 0, 6],
                  [0, 0, 0, 0]])
>>> Tcsr = minimum_spanning_tree(X)
>>> Tcsr.toarray().astype(int)
array([[0, 0, 2, 5],
      [0, 0, 0, 0],
      [0, 0, 0, 0]])
```

scipy.sparse.csgraph.reverse_cuthill_mckee

scipy.sparse.csgraph.reverse_cuthill_mckee(graph, symmetric_mode=False)

Returns the permutation array that orders a sparse CSR or CSC matrix in Reverse-Cuthill McKee ordering.

It is assumed by default, symmetric_mode=False, that the input matrix is not symmetric and works on the matrix A+A.T. If you are guaranteed that the matrix is symmetric in structure (values of matrix elements do not matter) then set symmetric_mode=True.

Parameters

- graph  [sparse matrix] Input sparse in CSC or CSR sparse matrix format.
- symmetric_mode  [bool, optional] Is input matrix guaranteed to be symmetric.
**Returns**

perm  [ndarray] Array of permuted row and column indices.

**Notes**

New in version 0.15.0.

**References**


**Examples**

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import reverse_cuthill_mckee

>>> graph = [
...    [0, 1, 2, 0],
...    [0, 0, 1, 0],
...    [2, 0, 0, 3],
...    [0, 0, 0, 0]
...]
>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 3) 1
(2, 0) 2
(2, 3) 3

>>> reverse_cuthill_mckee(graph)
array([3, 2, 1, 0], dtype=int32)
```

`scipy.sparse.csgraph.maximum_bipartite_matching`

**scipy.sparse.csgraph.maximum_bipartite_matching**

`scipy.sparse.csgraph.maximum_bipartite_matching(graph, perm_type='row')`

Returns an array of row or column permutations that makes the diagonal of a nonsingular square CSC sparse matrix zero free.

Such a permutation is always possible provided that the matrix is nonsingular. This function looks at the structure of the matrix only. The input matrix will be converted to CSC matrix format if necessary.

**Parameters**

- **graph**  [sparse matrix] Input sparse in CSC format
- **perm_type**  [str, {'row', 'column'}] Type of permutation to generate.

**Returns**

- **perm**  [ndarray] Array of row or column permutations.

**Notes**

This function relies on a maximum cardinality bipartite matching algorithm based on a breadth-first search (BFS) of the underlying graph.

New in version 0.15.0.

**References**

**Examples**

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import maximum_bipartite_matching

>>> graph = [
... [0, 1, 2, 0],
... [1, 0, 0, 1],
... [2, 0, 0, 3],
... [0, 1, 3, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 0) 1
(1, 3) 1
(2, 0) 2
(2, 3) 3
(3, 1) 1
(3, 2) 3

>>> maximum_bipartite_matching(graph, perm_type='row')
array([1, 0, 3, 2], dtype=int32)
```

**scipy.sparse.csgraph.structural_rank**

`scipy.sparse.csgraph.structural_rank(graph)`

Compute the structural rank of a graph (matrix) with a given sparsity pattern.

The structural rank of a matrix is the number of entries in the maximum transversal of the corresponding bipartite graph, and is an upper bound on the numerical rank of the matrix. A graph has full structural rank if it is possible to permute the elements to make the diagonal zero-free.

New in version 0.19.0.

**Parameters**

- `graph` (sparse matrix) Input sparse matrix.

**Returns**

- `rank` (int) The structural rank of the sparse graph.

**References**

[1], [2]

**Examples**

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import structural_rank

>>> graph = [
... [0, 1, 2, 0],
... [1, 0, 0, 1],
... [2, 0, 0, 3],
... [0, 1, 3, 0]
... ]
```

(continues on next page)
```python
>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 0) 1
(1, 3) 1
(2, 0) 2
(2, 3) 3
(3, 1) 1
(3, 2) 3
```
```python
>>> structural_rank(graph)
4
```

scipy.sparse.csgraph.NegativeCycleError

exception scipy.sparse.csgraph.NegativeCycleError

scipy.sparse.csgraph.construct_dist_matrix

\[ \text{construct_dist_matrix}(\text{graph}, \text{predecessors}, \ldots) \] Construct distance matrix from a predecessor matrix

scipy.sparse.csgraph.construct_dist_matrix

\[ \text{csgraph.from_dense}(\text{graph}, \text{null_value}, \ldots) \] Construct a CSR-format sparse graph from a dense matrix.

scipy.sparse.csgraph.construct_dist_matrix

\[ \text{csgraph.from_masked}(\text{graph}) \] Construct a CSR-format graph from a masked array.

scipy.sparse.csgraph.construct_dist_matrix

\[ \text{csgraph.masked_from_dense}(\text{graph}, \ldots) \] Construct a masked array graph representation from a dense matrix.

scipy.sparse.csgraph.construct_dist_matrix

\[ \text{csgraph.to_dense}(\text{csgraph}, \text{null_value}) \] Convert a sparse graph representation to a dense representation

scipy.sparse.csgraph.construct_dist_matrix

\[ \text{csgraph.to_masked}(\text{csgraph}) \] Convert a sparse graph representation to a masked array representation

scipy.sparse.csgraph.construct_dist_matrix

\[ \text{reconstruct_path}(\text{csgraph}, \text{predecessors}, \ldots) \] Construct a tree from a graph and a predecessor list.

Parameters

- **graph** [array_like or sparse] The N x N matrix representation of a directed or undirected graph. If dense, then non-edges are indicated by zeros or infinities.
- **predecessors** [array_like] The N x N matrix of predecessors of each node (see Notes below).
- **directed** [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then operate on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].
- **null_value**
[bool, optional] value to use for distances between unconnected nodes. Default is np.inf

Returns
dist_matrix
[ndarray] The N x N matrix of distances between nodes along the path specified by the predecessor matrix. If no path exists, the distance is zero.

Notes
The predecessor matrix is of the form returned by graph_shortest_path. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Examples
```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import construct_dist_matrix

>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
(0, 1) 1
(0, 2) 2
(1, 3) 1
(2, 3) 3

>>> pred = np.array([[9999, 0, 0, 2],
... [1, 9999, 0, 1],
... [2, 0, 9999, 2],
... [1, 3, 3, 9999]], dtype=np.int32)

>>> construct_dist_matrix(graph=graph, predecessors=pred, directed=False)
array([[ 0.,  1.,  2.,  5.],
[ 1.,  0.,  3.,  1.],
[ 2.,  3.,  0.,  3.],
[ 2.,  1.,  3.,  0.]])
```

scipy.sparse.csgraph.csgraph_from_dense

scipy.sparse.csgraph.csgraph_from_dense(graph, null_value=0, nan_null=True, infinity_null=True)
Construct a CSR-format sparse graph from a dense matrix.
New in version 0.11.0.

Parameters
graph [array_like] Input graph. Shape should be (n_nodes, n_nodes).
null_value [float or None (optional)] Value that denotes non-edges in the graph. Default is zero.
infinity_null
[bool] If True (default), then infinite entries (both positive and negative) are treated as null edges.

nan_null
[bool] If True (default), then NaN entries are treated as non-edges

Returns

csgraph  [csr_matrix] Compressed sparse representation of graph,

Examples

```python
>>> from scipy.sparse.csgraph import csgraph_from_dense

>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [0, 0, 3],
... [0, 0, 0]
... ]

>>> csgraph_from_dense(graph)
<4x4 sparse matrix of type '<class 'numpy.float64'>'
with 4 stored elements in Compressed Sparse Row format>
```

scipy.sparse.csgraph.csgraph_from_masked

`scipy.sparse.csgraph.csgraph_from_masked(graph)`

Construct a CSR-format graph from a masked array.

New in version 0.11.0.

Parameters

graph  [MaskedArray] Input graph. Shape should be `(n_nodes, n_nodes)`.

Returns

csgraph  [csr_matrix] Compressed sparse representation of graph,

Examples

```python
>>> import numpy as np

>>> from scipy.sparse.csgraph import csgraph_from_masked

>>> graph_masked = np.ma.masked_array(data =[
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [0, 0, 3],
... [0, 0, 0]
... ],
... mask=[[ True, False, False, True],
... [ True, True, False, False],
... [ True, True, False, True],
... [ True, True, True, False]],
... fill_value = 0)
```
csgraph_from_masked(graph_masked)

A 4x4 sparse matrix of type '<class 'numpy.float64'>'
with 4 stored elements in Compressed Sparse Row format.

scipy.sparse.csgraph.csgraph_masked_from_dense

scipy.sparse.csgraph.csgraph_masked_from_dense(graph, null_value=0, nan_null=True, infinity_null=True, copy=True)

Construct a masked array graph representation from a dense matrix.
New in version 0.11.0.

Parameters

- graph: [array_like] Input graph. Shape should be (n_nodes, n_nodes).
- null_value: [float or None (optional)] Value that denotes non-edges in the graph. Default is zero.
- infinity_null: [bool] If True (default), then infinite entries (both positive and negative) are treated as null edges.
- nan_null: [bool] If True (default), then NaN entries are treated as non-edges

Returns

- csgraph: [MaskedArray] masked array representation of graph

Examples

```python
cigraph_masked_from_dense(graph)
```

```python
graph = [
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... ]
```

```python
cigraph_masked_from_dense(graph)
masked_array(
    data=[[-- , 1, 2, --],
          [-- , --, --, 1]],
          [-- , --, --, 3]],
          [-- , --, --, --]],
    mask=[[ True, False, False, True],
          [ True, True, True, False],
          [ True, True, True, False],
          [ True, True, True, True]],
    fill_value=0)
```

### scipy.sparse.csgraph.csgraph_to_dense

scipy.sparse.csgraph.csgraph_to_dense(csgraph, null_value=0)

Convert a sparse graph representation to a dense representation

New in version 0.11.0.
Parameters

csgraph  [csr_matrix, csc_matrix, or lil_matrix] Sparse representation of a graph.
null_value  [float, optional] The value used to indicate null edges in the dense representation. Default is 0.

Returns

graph  [ndarray] The dense representation of the sparse graph.

Notes
For normal sparse graph representations, calling csgraph_to_dense with null_value=0 produces an equivalent result to using dense format conversions in the main sparse package. When the sparse representations have repeated values, however, the results will differ. The tools in scipy.sparse will add repeating values to obtain a final value. This function will select the minimum among repeating values to obtain a final value. For example, here we'll create a two-node directed sparse graph with multiple edges from node 0 to node 1, of weights 2 and 3. This illustrates the difference in behavior:

```python
>>> from scipy.sparse import csr_matrix, csgraph
data = np.array([2, 3])
indices = np.array([1, 1])
indptr = np.array([0, 2, 2])
M = csr_matrix((data, indices, indptr), shape=(2, 2))
M.toarray()
array([[0, 5],
       [0, 0]])
>>> csgraph.csgraph_to_dense(M)
array([[0., 2.],
       [0., 0.]])
```

The reason for this difference is to allow a compressed sparse graph to represent multiple edges between any two nodes. As most sparse graph algorithms are concerned with the single lowest-cost edge between any two nodes, the default scipy.sparse behavior of summing multiple weights does not make sense in this context.

The other reason for using this routine is to allow for graphs with zero-weight edges. Let’s look at the example of a two-node directed graph, connected by an edge of weight zero:

```python
>>> from scipy.sparse import csr_matrix, csgraph
data = np.array([0.0])
indices = np.array([1])
indptr = np.array([0, 1, 1])
M = csr_matrix((data, indices, indptr), shape=(2, 2))
M.toarray()
array([[0, 0],
       [0, 0]])
>>> csgraph.csgraph_to_dense(M, np.inf)
array([[inf, 0.],
       [inf, inf]])
```

In the first case, the zero-weight edge gets lost in the dense representation. In the second case, we can choose a different null value and see the true form of the graph.

Examples

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import csgraph_to_dense
```
```
>>> graph = csr_matrix( 
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... )

>>> graph
<4x4 sparse matrix of type '<class 'numpy.int64'>'
with 4 stored elements in Compressed Sparse Row format>
```

```
>>> csgraph_to_dense(graph)
array([[0., 1., 2., 0.],
       [0., 0., 0., 1.],
       [0., 0., 0., 3.],
       [0., 0., 0., 0.]])
```

`scipy.sparse.csgraph.csgraph_to_masked`

`scipy.sparse.csgraph.csgraph_to_masked(csgraph)`

Convert a sparse graph representation to a masked array representation

New in version 0.11.0.

**Parameters**

csgraph : [csr_matrix, csc_matrix, or lil_matrix] Sparse representation of a graph.

**Returns**

graph : [MaskedArray] The masked dense representation of the sparse graph.

**Examples**

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import csgraph_to_masked
```

```
>>> graph = csr_matrix( 
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... )

>>> graph
<4x4 sparse matrix of type '<class 'numpy.int64'>'
with 4 stored elements in Compressed Sparse Row format>
```

```
>>> csgraph_to_masked(graph)
masked_array(

data=[[--, 1.0, 2.0, --],
      [--, --, --, 1.0],
      [--, --, --, 3.0],
      [--, --, --, --]],

mask=[[ True, False, False, True],
      [ True, True, True, False],
      [ True, True, True, False],
      [ True, True, True, False]],
```

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scipy.sparse.csgraph.reconstruct_path

**scipy.sparse.csgraph.reconstruct_path(csgraph, predecessors, directed=True)**

Construct a tree from a graph and a predecessor list.

New in version 0.11.0.

**Parameters**

- `csgraph` [array_like or sparse matrix] The N x N matrix representing the directed or undirected graph from which the predecessors are drawn.
- `predecessors` [array_like, one dimension] The length-N array of indices of predecessors for the tree. The index of the parent of node i is given by predecessors[i].
- `directed` [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then operate on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

**Returns**

- `cstree` [csr matrix] The N x N directed compressed-sparse representation of the tree drawn from csgraph which is encoded by the predecessor list.

**Examples**

```python
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import reconstruct_path

>>> graph = [
    ... [0, 1, 2, 0],
    ... [0, 0, 0, 1],
    ... [0, 0, 0, 3],
    ... [0, 0, 0, 0]
    ... ]
>>> graph = csr_matrix(graph)
>>> print(csr_matrix(graph))
    (0, 1) 1
    (0, 2) 2
    (1, 3) 1
    (2, 3) 3

>>> pred = np.array([-9999, 0, 0, 1], dtype=np.int32)

>>> cstree = reconstruct_path(csgraph=graph, predecessors=pred, directed=False)
>>> cstree.todense()
matrix([[ 0.,  1.,  2.,  0.],
        [ 0.,  0.,  0.,  1.],
        [ 0.,  0.,  0.,  0.],
        [ 0.,  0.,  0.,  0.]])
```
6.23.2 Graph Representations

This module uses graphs which are stored in a matrix format. A graph with \(N\) nodes can be represented by an \((N \times N)\) adjacency matrix \(G\). If there is a connection from node \(i\) to node \(j\), then \(G[i, j] = w\), where \(w\) is the weight of the connection. For nodes \(i\) and \(j\) which are not connected, the value depends on the representation:

- for dense array representations, non-edges are represented by \(G[i, j] = 0\), infinity, or NaN.
- for dense masked representations (of type \(np.ma.MaskedArray\)), non-edges are represented by masked values. This can be useful when graphs with zero-weight edges are desired.
- for sparse array representations, non-edges are represented by non-entries in the matrix. This sort of sparse representation also allows for edges with zero weights.

As a concrete example, imagine that you would like to represent the following undirected graph:

```
G

(0)
/ \  
1 2
/ \  
(2)  (1)
```

This graph has three nodes, where node 0 and 1 are connected by an edge of weight 2, and nodes 0 and 2 are connected by an edge of weight 1. We can construct the dense, masked, and sparse representations as follows, keeping in mind that an undirected graph is represented by a symmetric matrix:

```python
>>> G_dense = np.array(
    [[0, 2, 1],
     [2, 0, 0],
     [1, 0, 0]])
>>> G_masked = np.ma.masked_values(G_dense, 0)
>>> from scipy.sparse import csr_matrix
>>> G_sparse = csr_matrix(G_dense)
```

This becomes more difficult when zero edges are significant. For example, consider the situation when we slightly modify the above graph:

```
G2

(0)
/ \  
0 2
/ \  
(2)  (1)
```

This is identical to the previous graph, except nodes 0 and 2 are connected by an edge of zero weight. In this case, the dense representation above leads to ambiguities: how can non-edges be represented if zero is a meaningful value? In this case, either a masked or sparse representation must be used to eliminate the ambiguity:

```python
>>> G2_data = np.array(
    [[np.inf, 2, 0],
     [2, np.inf, np.inf],
     [0, np.inf, np.inf]])
>>> G2_masked = np.ma.masked_invalid(G2_data)
```

(continues on next page)
Here we have used a utility routine from the csgraph submodule in order to convert the dense representation to a sparse representation which can be understood by the algorithms in submodule. By viewing the data array, we can see that the zero values are explicitly encoded in the graph.

**Directed vs. Undirected**

Matrices may represent either directed or undirected graphs. This is specified throughout the csgraph module by a boolean keyword. Graphs are assumed to be directed by default. In a directed graph, traversal from node \(i\) to node \(j\) can be accomplished over the edge \(G[i, j]\), but not the edge \(G[j, i]\). Consider the following dense graph:

```python
>>> G_dense = np.array([[0, 1, 0],
                      ... [2, 0, 3],
                      ... [0, 4, 0]])
```

When `directed=True` we get the graph:

```
-+-1---> ---3-->
(0)    (1)   (2)
<--2--- <--4---
```

In a non-directed graph, traversal from node \(i\) to node \(j\) can be accomplished over either \(G[i, j]\) or \(G[j, i]\). If both edges are not null, and the two have unequal weights, then the smaller of the two is used.

So for the same graph, when `directed=False` we get the graph:

```
(0)--1--(1)--2--(2)
```

Note that a symmetric matrix will represent an undirected graph, regardless of whether the ‘directed’ keyword is set to True or False. In this case, using `directed=True` generally leads to more efficient computation.

The routines in this module accept as input either scipy.sparse representations (csr, csc, or lil format), masked representations, or dense representations with non-edges indicated by zeros, infinities, and NaN entries.

### 6.24 Spatial algorithms and data structures (scipy.spatial)

#### 6.24.1 Spatial Transformations

Contained in the `scipy.spatial.transform` submodule.

#### 6.24.2 Nearest-neighbor Queries

- `KDTree(data[, leafsize])`  
  kd-tree for quick nearest-neighbor lookup
- `cKDTree(data[, leafsize, compact_nodes, ...])`  
  kd-tree for quick nearest-neighbor lookup
- `Rectangle(maxes, mins)`  
  Hyperrectangle class.
scipy.spatial.KDTree

class scipy.spatial.KDTree(data, leafsize=10)

kd-tree for quick nearest-neighbor lookup

This class provides an index into a set of k-dimensional points which can be used to rapidly look up the nearest neighbors of any point.

**Parameters**

- **data** [(N,K) array_like] The data points to be indexed. This array is not copied, and so modifying this data will result in bogus results.
- **leafsize** [int, optional] The number of points at which the algorithm switches over to brute-force. Has to be positive.

**Raises**

- **RuntimeError** The maximum recursion limit can be exceeded for large data sets. If this happens, either increase the value for the leafsize parameter or increase the recursion limit by:

  ```
  >>> import sys
  >>> sys.setrecursionlimit(10000)
  ```

**See also:**

cKDTree

Implementation of KDTree in Cython

**Notes**

The algorithm used is described in Maneewongvatana and Mount 1999. The general idea is that the kd-tree is a binary tree, each of whose nodes represents an axis-aligned hyperrectangle. Each node specifies an axis and splits the set of points based on whether their coordinate along that axis is greater than or less than a particular value.

During construction, the axis and splitting point are chosen by the “sliding midpoint” rule, which ensures that the cells do not all become long and thin.

The tree can be queried for the r closest neighbors of any given point (optionally returning only those within some maximum distance of the point). It can also be queried, with a substantial gain in efficiency, for the r approximate closest neighbors.

For large dimensions (20 is already large) do not expect this to run significantly faster than brute force. High-dimensional nearest-neighbor queries are a substantial open problem in computer science.

The tree also supports all-neighbors queries, both with arrays of points and with other kd-trees. These do use a reasonably efficient algorithm, but the kd-tree is not necessarily the best data structure for this sort of calculation.

**Methods**

- **count_neighbors**(other, r[, p]) Count how many nearby pairs can be formed.
- **query**(x[, k, eps, p, distance_upper_bound]) Query the kd-tree for nearest neighbors
- **query_ball_point**(x, r[, p, eps]) Find all points within distance r of point(s) x.
- **query_ball_tree**(other, r[, p, eps]) Find all pairs of points whose distance is at most r
- **query_pairs**(r[, p, eps]) Find all pairs of points within a distance.

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**scipy.spatial.KDTree.count_neighbors**

`KDTree.count_neighbors(other, r, p=2.0)`

Count how many nearby pairs can be formed.

Count the number of pairs \((x_1, x_2)\) can be formed, with \(x_1\) drawn from self and \(x_2\) drawn from `other`, and where \(\text{distance}(x_1, x_2, \ p) \leq r\). This is the “two-point correlation” described in Gray and Moore 2000, “N-body problems in statistical learning”, and the code here is based on their algorithm.

**Parameters**

- `other` [KDTree instance] The other tree to draw points from.
- `r` [float or one-dimensional array of floats] The radius to produce a count for. Multiple radii are searched with a single tree traversal.
- `p` [float, \(1 \leq p \leq \infty\), optional] Which Minkowski p-norm to use

**Returns**

- `result` [int or 1-D array of ints] The number of pairs. Note that this is internally stored in a numpy int, and so may overflow if very large (2e9).

**scipy.spatial.KDTree.query**

`KDTree.query(x, k=1, eps=0, p=2, distance_upper_bound=\infty)`

Query the kd-tree for nearest neighbors

**Parameters**

- `x` [array_like, last dimension self.m] An array of points to query.
- `k` [int, optional] The number of nearest neighbors to return.
- `eps` [nonnegative float, optional] Return approximate nearest neighbors; the kth returned value is guaranteed to be no further than \((1+\text{eps})\) times the distance to the real kth nearest neighbor.
- `p` [float, \(1 \leq p \leq \infty\), optional] Which Minkowski p-norm to use. 1 is the sum-of-absolute-values “Manhattan” distance 2 is the usual Euclidean distance infinity is the maximum-coordinate-difference distance
- `distance_upper_bound` [nonnegative float, optional] Return only neighbors within this distance. This is used to prune tree searches, so if you are doing a series of nearest-neighbor queries, it may help to supply the distance to the nearest neighbor of the most recent point.

**Returns**

- `d` [float or array of floats] The distances to the nearest neighbors. If \(x\) has shape tuple+\((\text{self.m},)\), then \(d\) has shape tuple if \(k\) is one, or tuple+(\(k,)\) if \(k\) is larger than one. Missing neighbors (e.g. when \(k > n\) or `distance_upper_bound` is given) are indicated with infinite distances. If \(k\) is None, then \(d\) is an object array of shape tuple, containing lists of distances. In either case the hits are sorted by distance (nearest first).
- `i` [integer or array of integers] The locations of the neighbors in `self.data`. \(i\) is the same shape as \(d\).

**Examples**
```python
>>> from scipy import spatial
>>> x, y = np.mgrid[0:5, 2:8]
>>> tree = spatial.KDTree(list(zip(x.ravel(), y.ravel())))
>>> tree.data
array([[0, 2],
        [0, 3],
        [0, 4],
        [0, 5],
        [0, 6],
        [0, 7],
        [1, 2],
        [1, 3],
        [1, 4],
        [1, 5],
        [1, 6],
        [1, 7],
        [2, 2],
        [2, 3],
        [2, 4],
        [2, 5],
        [2, 6],
        [2, 7],
        [3, 2],
        [3, 3],
        [3, 4],
        [3, 5],
        [3, 6],
        [3, 7],
        [4, 2],
        [4, 3],
        [4, 4],
        [4, 5],
        [4, 6],
        [4, 7]])
>>> pts = np.array([[0, 0], [2.1, 2.9]])
>>> tree.query(pts)
(array([ 2. , 0.14142136]), array([ 0, 13]))
>>> tree.query(pts[0])
(2.0, 0)
```

**scipy.spatial.KDTree.query_ball_point**

KDTree.query_ball_point(x, r, p=2.0, eps=0)

Find all points within distance r of point(s) x.

**Parameters**

- **x**: [array_like, shape tuple + (self.m,)] The point or points to search for neighbors of.
- **r**: [positive float] The radius of points to return.
- **p**: [float, optional] Which Minkowski p-norm to use. Should be in the range [1, inf].
- **eps**: [nonnegative float, optional] Approximate search. Branches of the tree are not explored if their nearest points are further than \( r / (1 + \text{eps}) \), and branches are added in bulk if their furthest points are nearer than \( r * (1 + \text{eps}) \).

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**Returns**

results [list or array of lists] If \( x \) is a single point, returns a list of the indices of the neighbors of \( x \). If \( x \) is an array of points, returns an object array of shape tuple containing lists of neighbors.

**Notes**

If you have many points whose neighbors you want to find, you may save substantial amounts of time by putting them in a KDTree and using `query_ball_tree`.

**Examples**

```python
>>> from scipy import spatial
>>> x, y = np.mgrid[0:5, 0:5]
>>> points = np.c_[x.ravel(), y.ravel()]
>>> tree = spatial.KDTree(points)
>>> tree.query_ball_point([[2, 0]], 1)  # indices of all points within distance 1
[5, 10, 11, 15]

Query multiple points and plot the results:

```python
>>> import matplotlib.pyplot as plt
>>> points = np.asarray(points)
>>> plt.plot(points[:,0], points[:,1], '.')
>>> for results in tree.query_ball_point([[2, 0], [3, 3]], 1):
...       nearby_points = points[results]
...       plt.plot(nearby_points[:,0], nearby_points[:,1], 'o')
>>> plt.margins(0.1, 0.1)
>>> plt.show()
```

![Plot of query results](image.png)

`scipy.spatial.KDTree.query_ball_tree`

`KDTree.query_ball_tree(other, r, p=2.0, eps=0)`

Find all pairs of points whose distance is at most \( r \)

**Parameters**

- **other** [KDTree instance] The tree containing points to search against.
- **r** [float] The maximum distance, has to be positive.
p [float, optional] Which Minkowski norm to use. \( p \) has to meet the condition \( 1 \leq p \leq \infty \).

eps [float, optional] Approximate search. Branches of the tree are not explored if their nearest points are further than \( r/(1+\text{eps}) \), and branches are added in bulk if their furthest points are nearer than \( r \times (1+\text{eps}) \). \( \text{eps} \) has to be non-negative.

Returns

results [list of lists] For each element \( \text{self.data}[i] \) of this tree, \( \text{results}[i] \) is a list of the indices of its neighbors in \( \text{other.data} \).

scipy.spatial.KDTree.query_pairs

KDTree.query_pairs\( (r, p=2.0, \text{eps}=0) \)

Find all pairs of points within a distance.

Parameters

r [positive float] The maximum distance.
p [float, optional] Which Minkowski norm to use. \( p \) has to meet the condition \( 1 \leq p \leq \infty \).

eps [float, optional] Approximate search. Branches of the tree are not explored if their nearest points are further than \( r/(1+\text{eps}) \), and branches are added in bulk if their furthest points are nearer than \( r \times (1+\text{eps}) \). \( \text{eps} \) has to be non-negative.

Returns

results [set] Set of pairs \( (i,j) \), with \( i < j \), for which the corresponding positions are close.

scipy.spatial.KDTree.sparse_distance_matrix

KDTree.sparse_distance_matrix\( (\text{other}, \text{max\_distance}, p=2.0) \)

Compute a sparse distance matrix

Computes a distance matrix between two KDTrees, leaving as zero any distance greater than \( \text{max\_distance} \).

Parameters

other [KDTree]

max\_distance [positive float]

p [float, optional]

Returns

result [dok_matrix] Sparse matrix representing the results in “dictionary of keys” format.

scipy.spatial.cKDTree

class scipy.spatial.cKDTree\( (\text{data}, \text{leafsize}=16, \text{compact\_nodes}=\text{True}, \text{copy\_data}=\text{False}, \text{balanced\_tree}=\text{True}) \)

kd-tree for quick nearest-neighbor lookup
This class provides an index into a set of k-dimensional points which can be used to rapidly look up the nearest neighbors of any point.

The algorithm used is described in Maneewongvatana and Mount 1999. The general idea is that the kd-tree is a binary trie, each of whose nodes represents an axis-aligned hyperrectangle. Each node specifies an axis and splits the set of points based on whether their coordinate along that axis is greater than or less than a particular value.

During construction, the axis and splitting point are chosen by the “sliding midpoint” rule, which ensures that the cells do not all become long and thin.

The tree can be queried for the r closest neighbors of any given point (optionally returning only those within some maximum distance of the point). It can also be queried, with a substantial gain in efficiency, for the r approximate closest neighbors.

For large dimensions (20 is already large) do not expect this to run significantly faster than brute force. High-dimensional nearest-neighbor queries are a substantial open problem in computer science.

**Parameters**

- `data` [array_like, shape (n,m)] The n data points of dimension m to be indexed. This array is not copied unless this is necessary to produce a contiguous array of doubles, and so modifying this data will result in bogus results. The data are also copied if the kd-tree is built with `copy_data=True`.

- `leafsize` [positive int, optional] The number of points at which the algorithm switches over to brute-force. Default: 16.

- `compact_nodes` [bool, optional] If True, the kd-tree is built to shrink the hyperrectangles to the actual data range. This usually gives a more compact tree that is robust against degenerated input data and gives faster queries at the expense of longer build time. Default: True.

- `copy_data` [bool, optional] If True the data is always copied to protect the kd-tree against data corruption. Default: False.

- `balanced_tree` [bool, optional] If True, the median is used to split the hyperrectangles instead of the midpoint. This usually gives a more compact tree and faster queries at the expense of longer build time. Default: True.

- `boxsize` [array_like or scalar, optional] Apply a m-d toroidal topology to the KDTree. The topology is generated by $x_i + n_i L_i$ where $n_i$ are integers and $L_i$ is the boxsize along i-th dimension. The input data shall be wrapped into $[0, L_i)$. A ValueError is raised if any of the data is outside of this bound.

**See also:**

- **KDTree**
  Implementation of `cKDTree` in pure Python

**Attributes**

- `data` [ndarray, shape (n,m)] The n data points of dimension m to be indexed. This array is not copied unless this is necessary to produce a contiguous array of doubles. The data are also copied if the kd-tree is built with `copy_data=True`.

- `leafsize` [positive int] The number of points at which the algorithm switches over to brute-force.

- `m` [int] The dimension of a single data-point.

- `n` [int] The number of data points.
maxes [ndarray, shape (m,)] The maximum value in each dimension of the n data points.
mins [ndarray, shape (m,)] The minimum value in each dimension of the n data points.
tree [object, class cKDTreeNode] This class exposes a Python view of the root node in the cKDTree object.
size [int] The number of nodes in the tree.

Methods

count_neighbors(self, other, r[, p, ...]) Count how many nearby pairs can be formed.
query(self, x[, k, p, ...]) Query the kd-tree for nearest neighbors
query_ball_point(self, x, r[, p, eps]) Find all points within distance r of point(s) x.
query_ball_tree(self, other, r[, p, eps]) Find all pairs of points whose distance is at most r.
query_pairs(self, r[, p, eps]) Find all pairs of points whose distance is at most r.
sparse_distance_matrix(self, other, max_distance) Compute a sparse distance matrix

scipy.spatial.cKDTree.count_neighbors
cKDTree.count_neighbors(self, other, r=2., weights=None, cumulative=True)
Count how many nearby pairs can be formed. (pair-counting)

Count the number of pairs (x1,x2) can be formed, with x1 drawn from self and x2 drawn from other, and where \( \text{distance}(x1, x2, p) \leq r \).

Data points on self and other are optionally weighted by the weights argument. (See below)

The algorithm we implement here is based on [1]. See notes for further discussion.

Parameters

other [cKDTree instance] The other tree to draw points from, can be the same tree as self.
r [float or one-dimensional array of floats] The radius to produce a count for. Multiple radii are searched with a single tree traversal. If the count is non-cumulative(cumulative=False), r defines the edges of the bins, and must be non-decreasing.
p [float, optional] \( 1 \leq p \leq \infty \). Which Minkowski p-norm to use. Default 2.0.
weights [tuple, array_like, or None, optional] If None, the pair-counting is unweighted. If given as a tuple, weights[0] is the weights of points in self, and weights[1] is the weights of points in other; either can be None to indicate the points are unweighted. If given as an array_like, weights is the weights of points in self and other. For this to make sense, self and other must be the same tree. If self and other are two different trees, a ValueError is raised. Default: None

cumulative [bool, optional] Whether the returned counts are cumulative. When cumulative is set to False the algorithm is optimized to work with a large number of bins (>10) specified by r. When cumulative is set to True, the algorithm is optimized to work with a small number of r. Default: True

Returns

result [scalar or 1-D array] The number of pairs. For unweighted counts, the result is integer. For weighted counts, the result is float. If cumulative is False, result[i] contains the counts with \( (-\infty \text{ if } i == 0 \text{ else } r[i-1]) < R \leq r[i] \)
Notes
Pair-counting is the basic operation used to calculate the two point correlation functions from a data set composed of position of objects.

Two point correlation function measures the clustering of objects and is widely used in cosmology to quantify the large scale structure in our Universe, but it may be useful for data analysis in other fields where self-similar assembly of objects also occur.

The Landy-Szalay estimator for the two point correlation function of D measures the clustering signal in D. [2]

For example, given the position of two sets of objects,
- objects D (data) contains the clustering signal, and
- objects R (random) that contains no signal,

$$\xi(r) = \frac{<D,D> - 2f <D,R> + f^2 <R,R>}{f^2 <R,R>},$$

where the brackets represents counting pairs between two data sets in a finite bin around r (distance), corresponding to setting cumulative=False, and $f = \frac{\text{float(len(D))}}{\text{float(len(R))}}$ is the ratio between number of objects from data and random.

The algorithm implemented here is loosely based on the dual-tree algorithm described in [1]. We switch between two different pair-cumulation scheme depending on the setting of cumulative. The computing time of the method we use when for cumulative == False does not scale with the total number of bins. The algorithm for cumulative == True scales linearly with the number of bins, though it is slightly faster when only 1 or 2 bins are used. [5].

As an extension to the naive pair-counting, weighted pair-counting counts the product of weights instead of number of pairs. Weighted pair-counting is used to estimate marked correlation functions ([3], section 2.2), or to properly calculate the average of data per distance bin (e.g. [4], section 2.1 on redshift).

scipy.spatial.cKDTree.query
cKDTree.query(self, x, k=1, eps=0, p=2, distance_upper_bound=np.inf, n_jobs=1)
Query the kd-tree for nearest neighbors

Parameters
- x  [array_like, last dimension self.m] An array of points to query.
- k  [list of integer or integer] The list of k-th nearest neighbors to return. If k is an integer it is treated as a list of [1, ..., k] (range(1, k+1)). Note that the counting starts from 1.
- eps [non-negative float] Return approximate nearest neighbors; the k-th returned value is guaranteed to be no further than (1+eps) times the distance to the real k-th nearest neighbor.
- p  [float, 1<=p<=infinity] Which Minkowski p-norm to use. 1 is the sum-of-absolute-values “Manhattan” distance 2 is the usual Euclidean distance infinity is the maximum-coordinate-difference distance
- distance_upper_bound [nonnegative float] Return only neighbors within this distance. This is used to prune tree searches, so if you are doing a series of nearest-neighbor queries, it may help to supply the distance to the nearest neighbor of the most recent point.
- n_jobs [int, optional] Number of jobs to schedule for parallel processing. If -1 is given all processors are used. Default: 1.

Returns

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| d | [array of floats] The distances to the nearest neighbors. If x has shape `tuple+(self.m,)`, then d has shape `tuple+(k,)`. When k == 1, the last dimension of the output is squeezed. Missing neighbors are indicated with infinite distances. |
| i | [ndarray of ints] The locations of the neighbors in `self.data`. If x has shape `tuple+(self.m,)`, then i has shape `tuple+(k,)`. When k == 1, the last dimension of the output is squeezed. Missing neighbors are indicated with `self.n`. |

**Notes**

If the KD-Tree is periodic, the position x is wrapped into the box.

When the input k is a list, a query for `arange(max(k))` is performed, but only columns that store the requested values of k are preserved. This is implemented in a manner that reduces memory usage.

**Examples**

```python
>>> import numpy as np
>>> from scipy.spatial import cKDTree
>>> x, y = np.mgrid[0:5, 2:8]
>>> tree = cKDTree(np.c_[x.ravel(), y.ravel()])
```

To query the nearest neighbours and return squeezed result, use

```python
>>> dd, ii = tree.query([[0, 0], [2.1, 2.9]], k=1)
>>> print(dd, ii)
[2. 0.14142136] [ 0 13]
```

To query the nearest neighbours and return unsqueezed result, use

```python
>>> dd, ii = tree.query([[0, 0], [2.1, 2.9]], k=[1])
>>> print(dd, ii)
[[2. ]
 [0.14142136]] [[ 0]
 [13]]
```

To query the second nearest neighbours and return unsqueezed result, use

```python
>>> dd, ii = tree.query([[0, 0], [2.1, 2.9]], k=2)
>>> print(dd, ii)
[[2.23606798]
 [0.90553851]] [[ 6]
 [12]]
```

To query the first and second nearest neighbours, use

```python
>>> dd, ii = tree.query([[0, 0], [2.1, 2.9]], k=2)
>>> print(dd, ii)
[[2. 2.23606798]
 [0.14142136 0.90553851]] [[ 0  6]
 [13 12]]
```

or, be more specific

```python
>>> dd, ii = tree.query([[0, 0], [2.1, 2.9]], k=[1, 2])
>>> print(dd, ii)
```

(continues on next page)
scipy.spatial.cKDTree.query_ball_point

cKDTree.query_ball_point(self, x, r, p=2., eps=0)
Find all points within distance r of point(s) x.

Parameters

- **x**: array_like, shape tuple + (self.m,) The point or points to search for neighbors of.
- **r**: positive float] The radius of points to return.
- **p**: float, optional] Which Minkowski p-norm to use. Should be in the range [1, inf].
- **eps**: nonnegative float, optional] Approximate search. Branches of the tree are not explored if their nearest points are further than \( r / (1 + eps) \), and branches are added in bulk if their furthest points are nearer than \( r * (1 + eps) \).
- **n_jobs**: int, optional] Number of jobs to schedule for parallel processing. If -1 is given all processors are used. Default: 1.
- **return_sorted**: bool, optional] Sorts returned indices if True and does not sort them if False. If None, does not sort single point queries, but does sort multi-point queries which was the behavior before this option was added. New in version 1.2.0.

Returns

- **results**: list or array of lists] If x is a single point, returns a list of the indices of the neighbors of x. If x is an array of points, returns an object array of shape tuple containing lists of neighbors.

Notes

If you have many points whose neighbors you want to find, you may save substantial amounts of time by putting them in a cKDTree and using query_ball_tree.

Examples

```python
>>> from scipy import spatial
>>> x, y = np.mgrid[0:4, 0:4]
>>> points = np.c_[x.ravel(), y.ravel()]
>>> tree = spatial.cKDTree(points)
>>> tree.query_ball_point([2, 0], 1)
[4, 8, 9, 12]
```

scipy.spatial.cKDTree.query_ball_tree

cKDTree.query_ball_tree(self, other, r, p=2., eps=0)
Find all pairs of points whose distance is at most r

Parameters

- **other**: cKDTree instance] The tree containing points to search against.
- **r**: float] The maximum distance, has to be positive.
- **p**: float, optional] Which Minkowski norm to use. p has to meet the condition \( 1 \leq p \leq \infty \).
- **eps**: float, optional] Approximate search. Branches of the tree are not explored if their nearest points are further than \( r/(1+eps) \), and branches are added
in bulk if their furthest points are nearer than $r \times (1+\text{eps})$. $\text{eps}$ has to be non-negative.

**Returns**

`results` [list of lists] For each element `self.data[i]` of this tree, `results[i]` is a list of the indices of its neighbors in `other.data`.

`scipy.spatial.cKDTree.query_pairs`  
`cKDTree.query_pairs(self, r, p=2., eps=0)`  
Find all pairs of points whose distance is at most $r$.

**Parameters**

- `r` [positive float] The maximum distance.
- `p` [float, optional] Which Minkowski norm to use. $p$ has to meet the condition $1 \leq p \leq \infty$.
- `eps` [float, optional] Approximate search. Branches of the tree are not explored if their nearest points are further than $r/(1+\text{eps})$, and branches are added in bulk if their furthest points are nearer than $r \times (1+\text{eps})$. $\text{eps}$ has to be non-negative.
- `output_type` [string, optional] Choose the output container, ‘set’ or ‘ndarray’. Default: ‘set’

**Returns**

`results` [set or ndarray] Set of pairs $(i,j)$, with $i < j$, for which the corresponding positions are close. If `output_type` is ‘ndarray’, an ndarray is returned instead of a set.

`scipy.spatial.cKDTree.sparse_distance_matrix`  
`cKDTree.sparse_distance_matrix(self, other, max_distance, p=2.)`  
Compute a sparse distance matrix

Computes a distance matrix between two cKDTrees, leaving as zero any distance greater than `max_distance`.

**Parameters**

- `other` [cKDTree]  
- `max_distance` [positive float]  
- `p` [float, $1 \leq p \leq \infty$] Which Minkowski p-norm to use.

**Returns**

`result` [dok_matrix, coo_matrix, dict or ndarray] Sparse matrix representing the results in “dictionary of keys” format. If a dict is returned the keys are $(i,j)$ tuples of indices. If `output_type` is ‘ndarray’ a record array with fields ‘i’, ‘j’, and ‘k’ is returned.

`scipy.spatial.Rectangle`  
`class scipy.spatial.Rectangle(maxes, mins)`  
Hyperrectangle class.

Represents a Cartesian product of intervals.

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Methods

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**scipy.spatial.Rectangle.max_distance_point**

`Rectangle.max_distance_point(x, p=2.0)`

Return the maximum distance between input and points in the hyperrectangle.

**Parameters**

- `x` [array_like] Input array.
- `p` [float, optional] Input.

**scipy.spatial.Rectangle.max_distance_rectangle**

`Rectangle.max_distance_rectangle(other, p=2.0)`

Compute the maximum distance between points in the two hyperrectangles.

**Parameters**

- `other` [hyperrectangle] Input.
- `p` [float, optional] Input.

**scipy.spatial.Rectangle.min_distance_point**

`Rectangle.min_distance_point(x, p=2.0)`

Return the minimum distance between input and points in the hyperrectangle.

**Parameters**

- `x` [array_like] Input.
- `p` [float, optional] Input.

**scipy.spatial.Rectangle.min_distance_rectangle**

`Rectangle.min_distance_rectangle(other, p=2.0)`

Compute the minimum distance between points in the two hyperrectangles.

**Parameters**

- `other` [hyperrectangle] Input.
- `p` [float] Input.

**scipy.spatial.Rectangle.split**

`Rectangle.split(d, split)`

Produce two hyperrectangles by splitting.

In general, if you need to compute maximum and minimum distances to the children, it can be done more efficiently by updating the maximum and minimum distances to the parent.

**Parameters**

- `d` [int] Axis to split hyperrectangle along.
- `split` [float] Position along axis `d` to split at.
Distance metrics are contained in the `scipy.spatial.distance` submodule.

### 6.24.3 Delaunay Triangulation, Convex Hulls and Voronoi Diagrams

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**scipy.spatial.Delaunay**

```python
class scipy.spatial.Delaunay(points, furthest_site=False, incremental=False, qhull_options=None)
```

Delaunay tessellation in N dimensions.

New in version 0.9.

**Parameters**

- `points` [ndarray of floats, shape (npoints, ndim)] Coordinates of points to triangulate
- `furthest_site` [bool, optional] Whether to compute a furthest-site Delaunay triangulation. Default: False
- `incremental` [bool, optional] Allow adding new points incrementally. This takes up some additional resources.
- `qhull_options` [str, optional] Additional options to pass to Qhull. See Qhull manual for details. Option “Qt” is always enabled. Default: “Qbb Qc Qz Qx Q12” for ndim > 4 and “Qbb Qc Qz Q12” otherwise. Incremental mode omits “Qz”. New in version 0.12.0.

**Raises**

- `QhullError` Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.
- `ValueError` Raised if an incompatible array is given as input.

**Notes**

The tessellation is computed using the Qhull library [Qhull library](https://www.qhull.org/).

**Note:** Unless you pass in the Qhull option “QJ”, Qhull does not guarantee that each input point appears as a vertex in the Delaunay triangulation. Omitted points are listed in the `coplanar` attribute.

**Examples**

Triangulation of a set of points:
```python
>>> points = np.array([[0, 0], [0, 1.1], [1, 0], [1, 1]])
>>> from scipy.spatial import Delaunay
>>> tri = Delaunay(points)

We can plot it:

```python
>>> import matplotlib.pyplot as plt
>>> plt.triplot(points[:,0], points[:,1], tri.simplices)
>>> plt.plot(points[:,0], points[:,1], 'o')
>>> plt.show()
```

![Plot of triangulation](image)

Point indices and coordinates for the two triangles forming the triangulation:

```python
>>> tri.simplices
array([[2, 3, 0], # may vary
        [3, 1, 0]], dtype=int32)
```

Note that depending on how rounding errors go, the simplices may be in a different order than above.

```python
>>> points[tri.simplices]
array([[ 1. , 0. ], # may vary
        [ 1. , 1. ],
        [ 0. , 0. ]],
       [[ 1. , 1. ],
        [ 0. , 1.1],
        [ 0. , 0. ]]])
```

Triangle 0 is the only neighbor of triangle 1, and it’s opposite to vertex 1 of triangle 1:

```python
>>> tri.neighbors[1]
array([-1,  0, -1], dtype=int32)
>>> points[tri.simplices[1,1]]
array([ 0. ,  1.1])
```

We can find out which triangle points are in:
```python
>>> p = np.array([(0.1, 0.2), (1.5, 0.5), (0.5, 1.05)])
>>> tri.find_simplex(p)
array([ 1, -1,  1], dtype=int32)
```

The returned integers in the array are the indices of the simplex the corresponding point is in. If -1 is returned, the point is in no simplex. Be aware that the shortcut in the following example only works correctly for valid points as invalid points result in -1 which is itself a valid index for the last simplex in the list.

```python
>>> p_valids = np.array([(0.1, 0.2), (0.5, 1.05)])
>>> tri.simplices[tri.find_simplex(p_valids)]
array([[3, 1, 0], # may vary
       [3, 1, 0]], dtype=int32)
```

We can also compute barycentric coordinates in triangle 1 for these points:

```python
>>> b = tri.transform[1, :2].dot(np.linalg.inv(p - tri.transform[1, :2]))
>>> np.c_[np.linalg.inv(b), 1 - b.sum(axis=0)]
array([[ 0.1 , 0.09090909, 0.80909091],
       [ 1.5 , -0.90909091, 0.40909091],
       [ 0.5 , 0.5 , 0. ]])
```

The coordinates for the first point are all positive, meaning it is indeed inside the triangle. The third point is on a vertex, hence its null third coordinate.

**Attributes**

- **points** [ndarray of double, shape (npoints, ndim)] Coordinates of input points.
- **simplices** [ndarray of ints, shape (nsimplex, ndim+1)] Indices of the points forming the simplices in the triangulation. For 2-D, the points are oriented counterclockwise.
- **neighbors** [ndarray of ints, shape (nsimplex, ndim+1)] Indices of neighbor simplices for each simplex. The kth neighbor is opposite to the kth vertex. For simplices at the boundary, -1 denotes no neighbor.
- **equations** [ndarray of double, shape (nsimplex, ndim+2)] [normal, offset] forming the hyperplane equation of the facet on the paraboloid (see Qhull documentation for more).
- **paraboloid_scale**, **paraboloid_shift** [float] Scale and shift for the extra paraboloid dimension (see Qhull documentation for more).
- **transform** [ndarray of double, shape (nsimplex, ndim+1, ndim)] Affine transform from x to the barycentric coordinates c.
- **vertex_to_simplex** [ndarray of int, shape (npoints,)] Lookup array, from a vertex, to some simplex which it is a part of.
- **convex_hull** [ndarray of int, shape (nfaces, ndim)] Vertices of facets forming the convex hull of the point set.
- **coplanar** [ndarray of int, shape (ncoplanar, 3)] Indices of coplanar points and the corresponding indices of the nearest facet and the nearest vertex. Coplanar points are input points which were not included in the triangulation due to numerical precision issues. If option “Qc” is not specified, this list is not computed. New in version 0.12.0.
vertices  Same as simplices, but deprecated.
vertex_neighbor_vertices
[tuple of two ndarrays of int; (indptr, indices)] Neighboring vertices of vertices.

Methods

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<td>Find the simplices containing the given points.</td>
</tr>
<tr>
<td>lift_points(self, x)</td>
<td>Lift points to the Qhull paraboloid.</td>
</tr>
<tr>
<td>plane_distance(self, xi)</td>
<td>Compute hyperplane distances to the point $x_i$ from all simplices.</td>
</tr>
</tbody>
</table>

scipy.spatial.Delaunay.add_points
Delaunay.add_points(points, restart=False)
Process a set of additional new points.

Parameters

- points  [ndarray] New points to add. The dimensionality should match that of the initial points.
- restart  [bool, optional] Whether to restart processing from scratch, rather than adding points incrementally.

Raises

QhullError
Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.

See also:

close

Notes
You need to specify incremental=True when constructing the object to be able to add points incrementally. Incremental addition of points is also not possible after close has been called.

scipy.spatial.Delaunay.close
Delaunay.close
Finish incremental processing.

Call this to free resources taken up by Qhull, when using the incremental mode. After calling this, adding more points is no longer possible.

scipy.spatial.Delaunay.find_simplex
Delaunay.find_simplex(self, xi[, bruteforce=False, tol=None])
Find the simplices containing the given points.

Parameters

- tri  [DelaunayInfo] Delaunay triangulation
- xi  [ndarray of double, shape (…, ndim)] Points to locate
- bruteforce  [bool, optional] Whether to only perform a brute-force search
- tol  [float, optional] Tolerance allowed in the inside-triangle check. Default is 100*eps.

Returns

- i  [ndarray of int, same shape as xi] Indices of simplices containing each point. Points outside the triangulation get the value -1.
Notes
This uses an algorithm adapted from Qhull’s `qh_findbestfacet`, which makes use of the connection between a convex hull and a Delaunay triangulation. After finding the simplex closest to the point in N+1 dimensions, the algorithm falls back to directed search in N dimensions.

**scipy.spatial.Delaunay.lift_points**

Delaunay.lift_points(self, x)

Lift points to the Qhull paraboloid.

**scipy.spatial.Delaunay.plane_distance**

Delaunay.plane_distance(self, xi)

Compute hyperplane distances to the point `xi` from all simplices.

**scipy.spatial.ConvexHull**

class scipy.spatial.ConvexHull(points, incremental=False, qhull_options=None)

Convex hulls in N dimensions.

New in version 0.12.0.

**Parameters**

points [ndarray of floats, shape (npoints, ndim)] Coordinates of points to construct a convex hull from

incremental [bool, optional] Allow adding new points incrementally. This takes up some additional resources.

qhull_options [str, optional] Additional options to pass to Qhull. See Qhull manual for details. (Default: “Qx” for ndim > 4 and “” otherwise) Option “Qt” is always enabled.

**Raises**

**QhullError**
Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.

**ValueError**
Raised if an incompatible array is given as input.

Notes
The convex hull is computed using the Qhull library.

References
[Qhull]

Examples
Convex hull of a random set of points:

```python
>>> from scipy.spatial import ConvexHull
>>> points = np.random.rand(30, 2)  # 30 random points in 2-D
>>> hull = ConvexHull(points)
```

Plot it:

```python
>>> import matplotlib.pyplot as plt
>>> plt.plot(points[:,0], points[:,1], 'o')
>>> for simplex in hull.simplices:
...     plt.plot(points[simplex, 0], points[simplex, 1], 'k-')
```
We could also have directly used the vertices of the hull, which for 2-D are guaranteed to be in counterclockwise order:

```python
>>> plt.plot(points[hull.vertices,0], points[hull.vertices,1], 'r--', lw=2)
>>> plt.plot(points[hull.vertices[0,0], points[hull.vertices[0,1], 'ro'])
>>> plt.show()
```

### Attributes

- **points** [ndarray of double, shape (npoints, ndim)] Coordinates of input points.
- **vertices** [ndarray of ints, shape (nvertices,)] Indices of points forming the vertices of the convex hull. For 2-D convex hulls, the vertices are in counterclockwise order. For other dimensions, they are in input order.
- **simplices** [ndarray of ints, shape (nfacet, ndim)] Indices of points forming the simplical facets of the convex hull.
- **neighbors** [ndarray of ints, shape (nfacet, ndim)] Indices of neighbor facets for each facet. The kth neighbor is opposite to the kth vertex. -1 denotes no neighbor.
- **equations** [ndarray of double, shape (nfacet, ndim+1)] [normal, offset] forming the hyperplane equation of the facet (see Qhull documentation for more).
- **coplanar** [ndarray of int, shape (ncoplanar, 3)] Indices of coplanar points and the corresponding indices of the nearest facets and nearest vertex indices. Coplanar points are input points which were not included in the triangulation due to numerical precision issues.
  If option “Qc” is not specified, this list is not computed.
- **area** [float] Area of the convex hull.
  New in version 0.17.0.
- **volume** [float] Volume of the convex hull.
  New in version 0.17.0.

### Methods

- **add_points**(points[, restart]) Process a set of additional new points.
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**close()**

Finish incremental processing.

### scipy.spatial.ConvexHull.add_points

**ConvexHull.add_points(points, restart=False)**

Process a set of additional new points.

**Parameters**

- **points** [ndarray] New points to add. The dimensionality should match that of the initial points.
- **restart** [bool, optional] Whether to restart processing from scratch, rather than adding points incrementally.

**Raises**

- **QhullError** Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.

**See also:**

- close

**Notes**

You need to specify `incremental=True` when constructing the object to be able to add points incrementally. Incremental addition of points is also not possible after `close` has been called.

### scipy.spatial.ConvexHull.close

**ConvexHull.close**

Finish incremental processing.

Call this to free resources taken up by Qhull, when using the incremental mode. After calling this, adding more points is no longer possible.

### scipy.spatial.Voronoi

**class scipy.spatial.Voronoi(points, furthest_site=False, incremental=False, qhull_options=None)**

Voronoi diagrams in N dimensions.

New in version 0.12.0.

**Parameters**

- **points** [ndarray of floats, shape (npoints, ndim)] Coordinates of points to construct a convex hull from
- **furthest_site** [bool, optional] Whether to compute a furthest-site Voronoi diagram. Default: False
- **incremental** [bool, optional] Allow adding new points incrementally. This takes up some additional resources.
- **qhull_options** [str, optional] Additional options to pass to Qhull. See Qhull manual for details. (Default: “Qbb Qc Qz Qx” for ndim > 4 and “Qbb Qc Qz” otherwise. Incremental mode omits “Qz”)

**Raises**
QhullError
Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.

ValueError
Raised if an incompatible array is given as input.

Notes
The Voronoi diagram is computed using the Qhull library.

Examples
Voronoi diagram for a set of point:

```python
>>> points = np.array([[0, 0], [0, 1], [0, 2], [1, 0], [1, 1], [1, 2],
                     [2, 0], [2, 1], [2, 2]])
>>> from scipy.spatial import Voronoi, voronoi_plot_2d
>>> vor = Voronoi(points)

Plot it:

```python
>>> import matplotlib.pyplot as plt
>>> fig = voronoi_plot_2d(vor)
>>> plt.show()
```

The Voronoi vertices:

```python
>>> vor.vertices
array([[ 0.5, 0.5],
       [ 1.5, 0.5],
       [ 0.5, 1.5],
       [ 1.5, 1.5]])
```

There is a single finite Voronoi region, and four finite Voronoi ridges:

```python
>>> vor.regions
[[1, -1, 0], [-1, 1], [1, -1, 0], [3, -1, 2], [-1, 3], [-1, 2], [3, 2, 0, 1], [2, -
  -1, 0], [3, -1, 1]]
```
The ridges are perpendicular between lines drawn between the following input points:

```python
>>> vor.ridge_points
array([[0, 1],
       [0, 3],
       [6, 3],
       [6, 7],
       [3, 4],
       [5, 8],
       [5, 2],
       [5, 4],
       [8, 7],
       [2, 1],
       [4, 1],
       [4, 7]], dtype=int32)
```

**Attributes**

- **points**
  - ndarray of double, shape (npoints, ndim) Coordinates of input points.
- **vertices**
  - ndarray of double, shape (nvertices, ndim) Coordinates of the Voronoi vertices.
- **ridge_points**
  - ndarray of ints, shape (nridges, 2) Indices of the points between which each Voronoi ridge lies.
- **ridge_vertices**
  - list of list of ints, shape (nridges, *) Indices of the Voronoi vertices forming each Voronoi ridge.
- **regions**
  - list of list of ints, shape (nregions, *) Indices of the Voronoi vertices forming each Voronoi region. -1 indicates vertex outside the Voronoi diagram.
- **point_region**
  - list of ints, shape (npoints) Index of the Voronoi region for each input point. If qhull option “Qc” was not specified, the list will contain -1 for points that are not associated with a Voronoi region.

**Methods**

- **add_points(points[, restart])**
  - Process a set of additional new points.
- **close()**
  - Finish incremental processing.

**scipy.spatial.Voronoi.add_points**

```
Voronoi.add_points(points, restart=False)
```

Process a set of additional new points.

**Parameters**

- **points**
  - ndarray New points to add. The dimensionality should match that of the initial points.
- **restart**
  - bool, optional Whether to restart processing from scratch, rather than adding points incrementally.

**Raises**
SciPy Reference Guide, Release 1.2.0

QhullError
Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.

See also:
close

Notes
You need to specify incremental=True when constructing the object to be able to add points incrementally. Incremental addition of points is also not possible after close has been called.

scipy.spatial.Voronoi.close
Voronoi.close
Finish incremental processing.
Call this to free resources taken up by Qhull, when using the incremental mode. After calling this, adding more points is no longer possible.

scipy.spatial.SphericalVoronoi
class scipy.spatial.SphericalVoronoi(points, radius=None, center=None, threshold=1e-06)
Voronoi diagrams on the surface of a sphere.
New in version 0.18.0.

Parameters
points [ndarray of floats, shape (npoints, 3)] Coordinates of points to construct a spherical Voronoi diagram from
radius [float, optional] Radius of the sphere (Default: 1)
center [ndarray of floats, shape (3,)] Center of sphere (Default: origin)
threshold [float] Threshold for detecting duplicate points and mismatches between points and sphere parameters. (Default: 1e-06)

Raises
ValueError
If there are duplicates in points. If the provided radius is not consistent with points.

See also:
Voronoi
Conventional Voronoi diagrams in N dimensions.

Notes
The spherical Voronoi diagram algorithm proceeds as follows. The Convex Hull of the input points (generators) is calculated, and is equivalent to their Delaunay triangulation on the surface of the sphere [Caroli]. A 3D Delaunay tetrahedralization is obtained by including the origin of the coordinate system as the fourth vertex of each simplex of the Convex Hull. The circumcenters of all tetrahedra in the system are calculated and projected to the surface of the sphere, producing the Voronoi vertices. The Delaunay tetrahedralization neighbour information is then used to order the Voronoi region vertices around each generator. The latter approach is substantially less sensitive to floating point issues than angle-based methods of Voronoi region vertex sorting.

The surface area of spherical polygons is calculated by decomposing them into triangles and using L'Huilier's Theorem to calculate the spherical excess of each triangle [Weisstein]. The sum of the spherical excesses is multiplied by the square of the sphere radius to obtain the surface area of the
spherical polygon. For nearly-degenerate spherical polygons an area of approximately 0 is returned by default, rather than attempting the unstable calculation.

Empirical assessment of spherical Voronoi algorithm performance suggests quadratic time complexity (loglinear is optimal, but algorithms are more challenging to implement). The reconstitution of the surface area of the sphere, measured as the sum of the surface areas of all Voronoi regions, is closest to 100 % for larger (>> 10) numbers of generators.

References
[Caroli], [Weisstein]

Examples

```python
>>> from matplotlib import colors
>>> from mpl_toolkits.mplot3d.art3d import Poly3DCollection
>>> from mpl_toolkits.mplot3d import proj3d
>>> import matplotlib.pyplot as plt
>>> from scipy.spatial import SphericalVoronoi
>>> # set input data
>>> points = np.array([[0, 0, 1], [0, 0, -1], [1, 0, 0], [0, 1, 0], [0, -1, 0], [-1, 0, 0], ...])
>>> center = np.array([0, 0, 0])
>>> radius = 1
>>> # calculate spherical Voronoi diagram
>>> sv = SphericalVoronoi(points, radius, center)
>>> # sort vertices (optional, helpful for plotting)
>>> sv.sort_vertices_of_regions()
>>> # generate plot
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111, projection='3d')
>>> # plot the unit sphere for reference (optional)
>>> u = np.linspace(0, 2 * np.pi, 100)
>>> v = np.linspace(0, np.pi, 100)
>>> x = np.outer(np.cos(u), np.sin(v))
>>> y = np.outer(np.sin(u), np.sin(v))
>>> z = np.outer(np.ones(np.size(u)), np.cos(v))
>>> ax.plot_surface(x, y, z, color='y', alpha=0.1)
>>> # plot generator points
>>> ax.scatter(points[:, 0], points[:, 1], points[:, 2], c='b')
>>> # plot Voronoi vertices
>>> ax.scatter(sv.vertices[:, 0], sv.vertices[:, 1], sv.vertices[:, 2], c='g')
>>> # indicate Voronoi regions (as Euclidean polygons)
>>> for region in sv.regions:
...     random_color = colors.rgb2hex(np.random.rand(3))
...     polygon = Poly3DCollection([sv.vertices[region]], alpha=1.0)
...     polygon.set_color(random_color)
...     ax.add_collection3d(polygon)
>>> plt.show()
```

Attributes

points [double array of shape (npoints, 3)] the points in 3D to generate the Voronoi diagram from
radius [double] radius of the sphere Default: None (forces estimation, which is less precise)
center [double array of shape (3,)] center of the sphere Default: None (assumes sphere is
vertices [double array of shape (nvertices, 3)] Voronoi vertices corresponding to points centered at origin.
regions [list of list of integers of shape (npoints, _)] the n-th entry is a list consisting of the indices of the vertices belonging to the n-th point in points

Methods

scipy.spatial.SphericalVoronoi.sort_vertices_of_regions()
For each region in regions, it sorts the indices of the Voronoi vertices such that the resulting points are in a clockwise or counterclockwise order around the generator point.

scipy.spatial.HalfspaceIntersection
class scipy.spatial.HalfspaceIntersection(halfspaces, interior_point, incremental=False, qhull_options=None)
Halfspace intersections in N dimensions.
New in version 0.19.0.

Parameters

halfspaces [ndarray of floats, shape (nineq, ndim+1)] Stacked Inequalities of the form $Ax + b <= 0$ in format $[A; b]$
iinterior_point [ndarray of floats, shape (ndim,)]} Point clearly inside the region defined by halfspaces. Also called a feasible point, it can be obtained by linear programming.
iincremental [bool, optional] Allow adding new halfspaces incrementally. This takes up some additional resources.

qhull_options [str, optional] Additional options to pass to Qhull. See Qhull manual for details. (Default: "Qx" for ndim > 4 and "" otherwise) Option "H" is always enabled.

Raises

QhullError Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.
ValueError Raised if an incompatible array is given as input.
**Notes**
The intersections are computed using the Qhull library. This reproduces the “qhalf” functionality of Qhull.

**References**
[Qhull], [1]

**Examples**
Halfspace intersection of planes forming some polygon

```python
>>> from scipy.spatial import HalfspaceIntersection
>>> halfspaces = np.array([[1, 0., 0.],
                        [0., -1., 0.],
                        [2., 1., -4.],
                        [-0.5, 1., -2.]])
>>> feasible_point = np.array([0.5, 0.5])
>>> hs = HalfspaceIntersection(halfspaces, feasible_point)
```

Plot halfspaces as filled regions and intersection points:

```python
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> ax = fig.add_subplot('111', aspect='equal')
>>> xlim, ylim = (-1, 3), (-1, 3)
>>> ax.set_xlim(xlim)
>>> ax.set_ylim(ylim)
>>> x = np.linspace(xlim[sign], -h[2]/h[0], 100)
>>> ax.fill_between(x, ylim[sign], y, **fmt)
>>> ax.plot(x, (-h[2]-h[0]*x)/h[1], label='{}x+{}y+{}=0'.format(*hlist))
>>> ax.fill_between(x, (-h[2]-h[0]*y)/h[1], ylim[sign], **fmt)
```

By default, qhull does not provide with a way to compute an interior point. This can easily be computed using linear programming. Considering halfspaces of the form $Ax + b \leq 0$, solving the linear program:

\[
\begin{align*}
\max & \quad y \\
\text{s.t.} & \quad Ax + y||A_i|| \leq -b
\end{align*}
\]

With $A_i$ being the rows of $A$, i.e. the normals to each plane.

Will yield a point $x$ that is furthest inside the convex polyhedron. To be precise, it is the center of the largest hypersphere of radius $y$ inscribed in the polyhedron. This point is called the Chebyshev center of the polyhedron (see [1] 4.3.1, pp148-149). The equations outputted by Qhull are always normalized.
```python
>>> from scipy.optimize import linprog
>>> from matplotlib.patches import Circle

>>> norm_vector = np.reshape(np.linalg.norm(halfspaces[:, :-1], axis=1),
                           (halfspaces.shape[0], 1))
>>> c = np.zeros((halfspaces.shape[1],))
>>> c[-1] = -1
>>> A = np.hstack((halfspaces[:, :-1], norm_vector))
>>> b = -halfspaces[:, -1:]
>>> res = linprog(c, A_ub=A, b_ub=b)
>>> x = res.x[:-1]
>>> y = res.x[-1]
>>> circle = Circle(x, radius=y, alpha=0.3)
>>> ax.add_patch(circle)
>>> plt.legend(bbox_to_anchor=(1.6, 1.0))
>>> plt.show()
```

Attributes

**halflspaces**
- ndarray of double, shape (nineq, ndim+1) Input halflspaces.

**interior_point**
- ndarray of floats, shape (ndim,) Input interior point.

**intersections**
- ndarray of double, shape (ninter, ndim) Intersections of all halflspaces.

**dual_points**
- ndarray of double, shape (nineq, ndim) Dual points of the input halflspaces.

**dual_facets**
- list of lists of ints Indices of points forming the (non necessarily simplicial) facets of the dual convex hull.

**dual_vertices**
- ndarray of ints, shape (nvertices,) Indices of halflspaces forming the vertices of the dual convex hull. For 2-D convex hulls, the vertices are in counterclockwise order. For other dimensions, they are in input order.
dual_equations
   [ndarray of double, shape (nfacet, ndim+1)] [normal, offset] forming the hyperplane
equation of the dual facet (see Qhull documentation for more).

dual_area
   [float] Area of the dual convex hull

dual_volume
   [float] Volume of the dual convex hull

Methods

add_halfspaces(halfspaces[, restart]) Process a set of additional new halfspaces.
close() Finish incremental processing.

scipy.spatial.HalfspaceIntersection.add_halfspaces
HalfspaceIntersection.add_halfspaces(halfspaces, restart=False)
   Process a set of additional new halfspaces.

   Parameters
   halfspaces  [ndarray] New halfspaces to add. The dimensionality should match that of the
   initial halfspaces.
   restart  [bool, optional] Whether to restart processing from scratch, rather than adding
   halfspaces incrementally.

   Raises
   QhullError
   Raised when Qhull encounters an error condition, such as geometrical degen-
   eracy when options to resolve are not enabled.

   See also:
   close

   Notes
   You need to specify incremental=True when constructing the object to be able to add halfspaces
   incrementally. Incremental addition of halfspaces is also not possible after close has been called.

scipy.spatial.HalfspaceIntersection.close
HalfspaceIntersection.close
   Finish incremental processing.

   Call this to free resources taken up by Qhull, when using the incremental mode. After calling
   this, adding more points is no longer possible.

6.24.4 Plotting Helpers

delaunay_plot_2d(tri[, ax]) Plot the given Delaunay triangulation in 2-D
convex_hull_plot_2d(hull[, ax]) Plot the given convex hull diagram in 2-D
voronoi_plot_2d(vor[, ax]) Plot the given Voronoi diagram in 2-D

scipy.spatial.delaunay_plot_2d
scipy.spatial.delaunay_plot_2d(tri, ax=None)
   Plot the given Delaunay triangulation in 2-D

   Parameters
tri [scipy.spatial.Delaunay instance] Triangulation to plot
ax [matplotlib.axes.Axes instance, optional] Axes to plot on

Returns
fig [matplotlib.figure.Figure instance] Figure for the plot

See also:
Delaunay, matplotlib.pyplot.triplot

Notes
Requires Matplotlib.

Examples
>>> import matplotlib.pyplot as plt
>>> from scipy.spatial import Delaunay, delaunay_plot_2d

The Delaunay triangulation of a set of random points:

>>> points = np.random.rand(30, 2)
>>> tri = Delaunay(points)

Plot it:

>>> _ = delaunay_plot_2d(tri)
>>> plt.show()
**fig**  [matplotlib.figure.Figure instance] Figure for the plot

See also:

*ConvexHull*

**Notes**
Requires Matplotlib.

**Examples**

```python
>>> import matplotlib.pyplot as plt
>>> from scipy.spatial import ConvexHull, convex_hull_plot_2d

The convex hull of a random set of points:

```python
>>> points = np.random.rand(30, 2)
>>> hull = ConvexHull(points)
```

Plot it:

```python
>>> _ = convex_hull_plot_2d(hull)
>>> plt.show()
```

---

**scipy.spatial.voronoï_plot_2d**

`scipy.spatial.voronoï_plot_2d(vor, ax=None, **kw)`

Plot the given Voronoï diagram in 2-D

**Parameters**

- `vor`  [scipy.spatial.Voronoi instance] Diagram to plot
- `ax`  [matplotlib.axes.Axes instance, optional] Axes to plot on
- `show_points`: bool, optional  
  Add the Voronoï points to the plot.
- `show_vertices`  [bool, optional]  Add the Voronoï vertices to the plot.
- `line_colors`  [string, optional] Specifies the line color for polygon boundaries
line_width
  [float, optional] Specifies the line width for polygon boundaries

line_alpha: float, optional
  Specifies the line alpha for polygon boundaries

point_size: float, optional
  Specifies the size of points

Returns

fig
  [matplotlib.figure.Figure instance] Figure for the plot

See also:

Voronoi

Notes
Requires Matplotlib.

Examples
Set of point:

```python
>>> import matplotlib.pyplot as plt
>>> points = np.random.rand(10, 2)  # random
```

Voronoi diagram of the points:

```python
>>> from scipy.spatial import Voronoi, voronoi_plot_2d
>>> vor = Voronoi(points)
```

using `voronoi_plot_2d` for visualisation:

```python
>>> fig = voronoi_plot_2d(vor)
```

using `voronoi_plot_2d` for visualisation with enhancements:

```python
>>> fig = voronoi_plot_2d(vor, show_vertices=False, line_colors='orange', ...
... line_width=2, line_alpha=0.6, point_size=2)
>>> plt.show()
```
See also:

Tutorial

6.24.5 Simplex representation

The simplices (triangles, tetrahedra, ...) appearing in the Delaunay tessellation (N-dim simplices), convex hull facets, and Voronoi ridges (N-1 dim simplices) are represented in the following scheme:

```python
tess = Delaunay(points)
hull = ConvexHull(points)
voro = Voronoi(points)

# coordinates of the j-th vertex of the i-th simplex
tess.points[tess.simplices[i, j], :]  # tessellation element
hull.points[hull.simplices[i, j], :]  # convex hull facet
voro.vertices[voro.ridge_vertices[i, j], :]  # ridge between Voronoi cells
```

For Delaunay triangulations and convex hulls, the neighborhood structure of the simplices satisfies the condition:

```
tess.neighbors[i, j] is the neighboring simplex of the i-th simplex, opposite to the j-vertex. It is -1 in case of no neighbor.
```

Convex hull facets also define a hyperplane equation:

```
(hull.equations[i, :-1] * coord).sum() + hull.equations[i, -1] == 0
```

Similar hyperplane equations for the Delaunay triangulation correspond to the convex hull facets on the corresponding N+1 dimensional paraboloid.

The Delaunay triangulation objects offer a method for locating the simplex containing a given point, and barycentric coordinate computations.

Functions
### scipy.spatial.tsearch

Find simplices containing the given points.

This function does the same thing as Delaunay.find_simplex.

New in version 0.9.

See also:

Delaunay.find_simplex

#### Examples

```python
g = import numpy as np
g = import matplotlib.pyplot as plt
g = from scipy.spatial import Delaunay, delaunay_plot_2d, tsearch

The Delaunay triangulation of a set of random points:

```python
g = pts = np.random.rand(20, 2)
g = tri = Delaunay(pts)
g = _ = delaunay_plot_2d(tri)

Find the simplices containing a given set of points:

```python
g = loc = np.random.uniform(0.2, 0.8, (5, 2))
g = s = tsearch(tri, loc)
g = plt.triplot(pts[:, 0], pts[:, 1], tri.simplices[s], 'b-', mask=s==1)
g = plt.scatter(loc[:, 0], loc[:, 1], c='r', marker='x')
g = plt.show()
```

### scipy.spatial.distance_matrix

Compute the distance matrix.

Returns the matrix of all pair-wise distances.

#### Parameters

- **x** ([M, K] array_like) Matrix of M vectors in K dimensions.
- **p** (float, 1 <= p <= infinity) Which Minkowski p-norm to use.
- **threshold** (positive int) If M * N * K > threshold, algorithm uses a Python loop instead of large temporary arrays.

#### Returns

- **result** ([M, N] ndarray) Matrix containing the distance from every vector in x to every vector in y.
Examples

```python
>>> from scipy.spatial import distance_matrix
>>> distance_matrix([[0,0],[0,1]], [[1,0],[1,1]])
array([[ 1. , 1.41421356],
       [ 1.41421356, 1. ]])
```

`scipy.spatial.minkowski_distance`

Compute the $L^p$ distance between two arrays.

**Parameters**

- `x` : [(M, K) array_like] Input array.
- `y` : [(N, K) array_like] Input array.
- `p` : float, $1 \leq p \leq \infty$ Which Minkowski p-norm to use.

**Examples**

```python
>>> from scipy.spatial import minkowski_distance
>>> minkowski_distance([[0,0],[0,0]], [[1,1],[0,1]])
array([ 1.41421356, 1. ])
```

`scipy.spatial.minkowski_distance_p`

Compute the $p$-th power of the $L^p$ distance between two arrays.

For efficiency, this function computes the $L^p$ distance but does not extract the pth root. If $p$ is 1 or infinity, this is equal to the actual $L^p$ distance.

**Parameters**

- `x` : [(M, K) array_like] Input array.
- `y` : [(N, K) array_like] Input array.
- `p` : float, $1 \leq p \leq \infty$ Which Minkowski p-norm to use.

**Examples**

```python
```
```python
>>> from scipy.spatial import minkowski_distance_p
>>> minkowski_distance_p([[0, 0], [0, 0]], [[1, 1], [0, 1]])
array([2, 1])
```

**scipy.spatial.procrustes**

```
scipy.spatial.procrustes(data1, data2)
```

Procrustes analysis, a similarity test for two data sets.

Each input matrix is a set of points or vectors (the rows of the matrix). The dimension of the space is the number of columns of each matrix. Given two identically sized matrices, procrustes standardizes both such that:

- $\text{tr}(AA^T) = 1$.
- Both sets of points are centered around the origin.

Procrustes ([1], [2]) then applies the optimal transform to the second matrix (including scaling/dilation, rotations, and reflections) to minimize $M^2 = \sum (data1 - data2)^2$, or the sum of the squares of the pointwise differences between the two input datasets.

This function was not designed to handle datasets with different numbers of datapoints (rows). If two data sets have different dimensionality (different number of columns), simply add columns of zeros to the smaller of the two.

**Parameters**

- `data1` [array_like] Matrix, n rows represent points in k (columns) space. Data1 is the reference data, after it is standardised, the data from `data2` will be transformed to fit the pattern in `data1` (must have >1 unique points).
- `data2` [array_like] n rows of data in k space to be fit to `data1`. Must be the same shape (numrows, numcols) as data1 (must have >1 unique points).

**Returns**

- `mtx1` [array_like] A standardized version of `data1`.
- `mtx2` [array_like] The orientation of `data2` that best fits `data1`. Centered, but not necessarily $\text{tr}(AA^T) = 1$.
- `disparity` [float] $M^2$ as defined above.

**Raises**

- `ValueError` If the input arrays are not two-dimensional. If the shape of the input arrays is different. If the input arrays have zero columns or zero rows.

**See also:**

- `scipy.linalg.orthogonal_procrustes`
- `scipy.spatial.distance.directed_hausdorff`

Another similarity test for two data sets

**Notes**

- The disparity should not depend on the order of the input matrices, but the output matrices will, as only the first output matrix is guaranteed to be scaled such that $\text{tr}(AA^T) = 1$.
- Duplicate data points are generally ok, duplicating a data point will increase its effect on the procrustes fit.
- The disparity scales as the number of points per input matrix.
References
[1], [2]

Examples

```python
>>> from scipy.spatial import procrustes
```

The matrix \( b \) is a rotated, shifted, scaled and mirrored version of \( a \) here:

```python
>>> a = np.array([[1, 3], [1, 2], [1, 1], [2, 1]], 'd')
>>> b = np.array([[4, -2], [4, -4], [4, -6], [2, -6]], 'd')
>>> mtx1, mtx2, disparity = procrustes(a, b)
```

```plaintext
>>> round(disparity)
0.0
```

## 6.25 Distance computations (scipy.spatial.distance)

### 6.25.1 Function Reference

Distance matrix computation from a collection of raw observation vectors stored in a rectangular array.

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>pdist(X[, metric])</code></td>
<td>Pairwise distances between observations in n-dimensional space.</td>
</tr>
<tr>
<td><code>cdist(XA, XB[, metric])</code></td>
<td>Compute distance between each pair of the two collections of inputs.</td>
</tr>
<tr>
<td><code>squareform(X[, force, checks])</code></td>
<td>Convert a vector-form distance vector to a square-form distance matrix, and vice-versa.</td>
</tr>
<tr>
<td><code>directed_hausdorff(u, v[, seed])</code></td>
<td>Compute the directed Hausdorff distance between two N-D arrays.</td>
</tr>
</tbody>
</table>

**scipy.spatial.distance.pdist**

```python
scipy.spatial.distance.pdist(X, metric='euclidean', *args, **kwargs)
```

Pairwise distances between observations in n-dimensional space.

See Notes for common calling conventions.

**Parameters**

- **X** [ndarray] An \( m \) by \( n \) array of \( m \) original observations in an \( n \)-dimensional space.
- ***args** [tuple. Deprecated.] Additional arguments should be passed as keyword arguments
- ****kwargs** [dict, optional] Extra arguments to `metric`: refer to each metric documentation for a list of all possible arguments. Some possible arguments:
  - \( p \) : scalar The \( p \)-norm to apply for Minkowski, weighted and unweighted. Default: 2.
  - \( w \) : ndarray The weight vector for metrics that support weights (e.g., Minkowski).
  - \( V \) : ndarray The variance vector for standardized Euclidean. Default: \( \text{var}(X, axis=0, ddof=1) \)
VI : ndarray The inverse of the covariance matrix for Mahalanobis. Default: \( \text{inv(cov(X.T)).T} \)

out : ndarray. The output array If not None, condensed distance matrix \( Y \) is stored in this array. Note: metric independent, it will become a regular keyword arg in a future scipy version

**Returns**

\( Y \) [ndarray] Returns a condensed distance matrix \( Y \). For each \( i \) and \( j \) (where \( i < j < m \)), where \( m \) is the number of original observations. The metric \( \text{dist}(u=X[i], v=X[j]) \) is computed and stored in entry \( ij \).

See also:

squareform

converts between condensed distance matrices and square distance matrices.

**Notes**

See squareform for information on how to calculate the index of this entry or to convert the condensed distance matrix to a redundant square matrix.

The following are common calling conventions.

1. \( Y = \text{pdist}(X, \text{‘euclidean’}) \)

   Computes the distance between \( m \) points using Euclidean distance (2-norm) as the distance metric between the points. The points are arranged as \( m \) \( n \)-dimensional row vectors in the matrix \( X \).

2. \( Y = \text{pdist}(X, \text{‘minkowski’, p=2.}) \)

   Computes the distances using the Minkowski distance \( ||u - v||_p \) (p-norm) where \( p \geq 1 \).

3. \( Y = \text{pdist}(X, \text{‘cityblock’}) \)

   Computes the city block or Manhattan distance between the points.

4. \( Y = \text{pdist}(X, \text{‘seuclidean’, V=None}) \)

   Computes the standardized Euclidean distance. The standardized Euclidean distance between two \( n \)-vectors \( u \) and \( v \) is

   \[
   \sqrt{\sum (u_i - v_i)^2 / V[x_i]}
   \]

   \( V \) is the variance vector; \( V[i] \) is the variance computed over all the \( i \)'th components of the points. If not passed, it is automatically computed.

5. \( Y = \text{pdist}(X, \text{‘sqeuclidean’}) \)

   Computes the squared Euclidean distance \( ||u - v||_2^2 \) between the vectors.

6. \( Y = \text{pdist}(X, \text{‘cosine’}) \)

   Computes the cosine distance between vectors \( u \) and \( v \),

   \[
   1 - \frac{u \cdot v}{||u||_2||v||_2}
   \]

   where \( || \cdot ||_2 \) is the 2-norm of its argument \( \cdot \), and \( u \cdot v \) is the dot product of \( u \) and \( v \).

7. \( Y = \text{pdist}(X, \text{‘correlation’}) \)

   Computes the correlation distance between vectors \( u \) and \( v \). This is

   \[
   1 - \frac{(u - \bar{u}) \cdot (v - \bar{v})}{||(u - \bar{u})||_2||(v - \bar{v})||_2}
   \]
where $\bar{v}$ is the mean of the elements of vector $v$, and $x \cdot y$ is the dot product of $x$ and $y$.

8. $Y = \text{pdist}(X, \ 'hamming')$

Computes the normalized Hamming distance, or the proportion of those vector elements between two n-vectors $u$ and $v$ which disagree. To save memory, the matrix $X$ can be of type boolean.

9. $Y = \text{pdist}(X, \ 'jaccard')$

Computes the Jaccard distance between the points. Given two vectors, $u$ and $v$, the Jaccard distance is the proportion of those elements $u[i]$ and $v[i]$ that disagree.

10. $Y = \text{pdist}(X, \ 'chebyshev')$

Computes the Chebyshev distance between the points. The Chebyshev distance between two n-vectors $u$ and $v$ is the maximum norm-1 distance between their respective elements. More precisely, the distance is given by

$$d(u, v) = \max_{i} |u_i - v_i|$$

11. $Y = \text{pdist}(X, \ 'canberra')$

Computes the Canberra distance between the points. The Canberra distance between two points $u$ and $v$ is

$$d(u, v) = \sum_{i} \frac{|u_i - v_i|}{|u_i| + |v_i|}$$

12. $Y = \text{pdist}(X, \ 'braycurtis')$

Computes the Bray-Curtis distance between the points. The Bray-Curtis distance between two points $u$ and $v$ is

$$d(u, v) = \frac{\sum_{i} |u_i - v_i|}{\sum_{i} |u_i + v_i|}$$

13. $Y = \text{pdist}(X, \ 'mahalanobis', VI=None)$

Computes the Mahalanobis distance between the points. The Mahalanobis distance between two points $u$ and $v$ is $\sqrt{(u - v)(1/V)(u - v)^T}$ where $(1/V)$ (the VI variable) is the inverse covariance. If VI is not None, VI will be used as the inverse covariance matrix.

14. $Y = \text{pdist}(X, \ 'yule')$

Computes the Yule distance between each pair of boolean vectors. (see yule function documentation)

15. $Y = \text{pdist}(X, \ 'matching')$

Synonym for 'hamming'.

16. $Y = \text{pdist}(X, \ 'dice')$

Computes the Dice distance between each pair of boolean vectors. (see dice function documentation)

17. $Y = \text{pdist}(X, \ 'kulsinski')$
18. \[ Y = \text{pdist}(X, \text{'rogerstanimoto'}) \]

Computes the Rogers-Tanimoto distance between each pair of boolean vectors. (see rogerstanimoto function documentation)

19. \[ Y = \text{pdist}(X, \text{'russellrao'}) \]

Computes the Russell-Rao distance between each pair of boolean vectors. (see russellrao function documentation)

20. \[ Y = \text{pdist}(X, \text{'sokalmichener'}) \]

Computes the Sokal-Michener distance between each pair of boolean vectors. (see sokalmichener function documentation)

21. \[ Y = \text{pdist}(X, \text{'sokalsneath'}) \]

Computes the Sokal-Sneath distance between each pair of boolean vectors. (see sokalsneath function documentation)

22. \[ Y = \text{pdist}(X, \text{'wminkowski'}, p=2, w=w) \]

Computes the weighted Minkowski distance between each pair of vectors. (see wminkowski function documentation)

23. \[ Y = \text{pdist}(X, f) \]

Computes the distance between all pairs of vectors in \( X \) using the user supplied 2-arity function \( f \). For example, Euclidean distance between the vectors could be computed as follows:

```python
dm = \text{pdist}(X, \lambda u, v: \text{np.sqrt}(((u-v)**2).sum()))
```

Note that you should avoid passing a reference to one of the distance functions defined in this library. For example:

```python
dm = \text{pdist}(X, \text{'sokalsneath'})
```

would calculate the pair-wise distances between the vectors in \( X \) using the Python function sokalsneath. This would result in sokalsneath being called \( \binom{n}{2} \) times, which is inefficient. Instead, the optimized C version is more efficient, and we call it using the following syntax:

```python
dm = \text{pdist}(X, \text{'sokalsneath'})
```

### scipy.spatial.distance.cdist

**scipy.spatial.distance.cdist**

\( \text{scipy.spatial.distance.cdist}(XA, XB, metric='euclidean', *args, **kwargs) \)

Compute distance between each pair of the two collections of inputs.

See Notes for common calling conventions.

**Parameters**

- **XA** [ndarray] An \( m_A \) by \( n \) array of \( m_A \) original observations in an \( n \)-dimensional space. Inputs are converted to float type.
 XB: [ndarray] An \( m_B \) by \( n \) array of \( m_B \) original observations in an \( n \)-dimensional space. Inputs are converted to float type.

 metric: [str or callable, optional] The distance metric to use. If a string, the distance function can be `braycurtis`, `canberra`, `chebyshev`, `cityblock`, `correlation`, `cosine`, `dice`, `euclidean`, `hamming`, `jaccard`, `jensenshannon`, `kulsinski`, `mahalanobis`, `matching`, `minkowski`, `rogerstanimoto`, `russellrao`, `seuclidean`, `sokalmichener`, `sokalsneath`, `sqeuclidean`, `wminkowski`, `yule`.

 *args: [tuple, Deprecated.] Additional arguments should be passed as keyword arguments.

 **kwargs: [dict, optional] Extra arguments to metric: refer to each metric documentation for a list of all possible arguments. Some possible arguments:

 p: scalar The \( p \)-norm to apply for Minkowski, weighted and unweighted. Default: 2.

 w: ndarray The weight vector for metrics that support weights (e.g., Minkowski).

 V: ndarray The variance vector for standardized Euclidean. Default: \( \text{var}(\text{vstack}([XA, XB]), \text{axis}=0, \text{ddof}=1) \)

 VI: ndarray The inverse of the covariance matrix for Mahalanobis. Default: \( \text{inv}(\text{cov}(\text{vstack}([XA, XB].T))).T \)

 out: ndarray The output array. If not None, the distance matrix \( Y \) is stored in this array. Note: metric independent, it will become a regular keyword arg in a future scipy version.

 Returns:

 \( Y \): [ndarray] A \( m_A \) by \( m_B \) distance matrix is returned. For each \( i \) and \( j \), the metric \( \text{dist}(u=XA[i], v=XB[j]) \) is computed and stored in the \( ij \)th entry.

 Raises:

 ValueError: An exception is thrown if \( XA \) and \( XB \) do not have the same number of columns.

 Notes:

 The following are common calling conventions:

 1. \( Y = \text{cdist}(XA, XB, '\text{euclidean}') \)

 Computes the distance between \( m \) points using Euclidean distance (2-norm) as the distance metric between the points. The points are arranged as \( m \) \( n \)-dimensional row vectors in the matrix \( X \).

 2. \( Y = \text{cdist}(XA, XB, '\text{minkowski}', p=2.) \)

 Computes the distances using the Minkowski distance \( ||u - v||_p \) (\( p \)-norm) where \( p \geq 1 \).

 3. \( Y = \text{cdist}(XA, XB, '\text{cityblock}') \)

 Computes the city block or Manhattan distance between the points.

 4. \( Y = \text{cdist}(XA, XB, '\text{seuclidean}', V=None) \)

 Computes the standardized Euclidean distance. The standardized Euclidean distance between two \( n \)-vectors \( u \) and \( v \) is

 \[
 \sqrt{\sum \frac{(u_i - v_i)^2}{V[i]} / V[i]}.
 \]

 \( V \) is the variance vector; \( V[i] \) is the variance computed over all the \( i \)th components of the points. If not passed, it is automatically computed.

 5. \( Y = \text{cdist}(XA, XB, '\text{sqeuclidean}') \)

 Computes the squared Euclidean distance \( ||u - v||_2^2 \) between the vectors.
6. \( Y = \text{cdist}(XA, XB, 'cosine') \)

Computes the cosine distance between vectors \( u \) and \( v \),

\[
1 - \frac{u \cdot v}{\|u\|_2 \|v\|_2}
\]

where \( \| \cdot \|_2 \) is the 2-norm of its argument \( \cdot \), and \( u \cdot v \) is the dot product of \( u \) and \( v \).

7. \( Y = \text{cdist}(XA, XB, 'correlation') \)

Computes the correlation distance between vectors \( u \) and \( v \). This is

\[
1 - \frac{(u - \bar{u}) \cdot (v - \bar{v})}{\| (u - \bar{u}) \|_2 \| (v - \bar{v}) \|_2}
\]

where \( \bar{v} \) is the mean of the elements of vector \( v \), and \( x \cdot y \) is the dot product of \( x \) and \( y \).

8. \( Y = \text{cdist}(XA, XB, 'hamming') \)

Computes the normalized Hamming distance, or the proportion of those vector elements between two \( n \)-vectors \( u \) and \( v \) which disagree. To save memory, the matrix \( X \) can be of type boolean.

9. \( Y = \text{cdist}(XA, XB, 'jaccard') \)

Computes the Jaccard distance between the points. Given two vectors, \( u \) and \( v \), the Jaccard distance is the proportion of those elements \( u[i] \) and \( v[i] \) that disagree where at least one of them is non-zero.

10. \( Y = \text{cdist}(XA, XB, 'chebyshev') \)

Computes the Chebyshev distance between the points. The Chebyshev distance between two \( n \)-vectors \( u \) and \( v \) is the maximum norm-1 distance between their respective elements. More precisely, the distance is given by

\[
d(u, v) = \max_i |u_i - v_i|.
\]

11. \( Y = \text{cdist}(XA, XB, 'canberra') \)

Computes the Canberra distance between the points. The Canberra distance between two points \( u \) and \( v \) is

\[
d(u, v) = \sum_i \frac{|u_i - v_i|}{|u_i| + |v_i|}.
\]

12. \( Y = \text{cdist}(XA, XB, 'braycurtis') \)

Computes the Bray-Curtis distance between the points. The Bray-Curtis distance between two points \( u \) and \( v \) is

\[
d(u, v) = \frac{\sum_i (|u_i - v_i|)}{\sum_i (|u_i + v_i|)}.
\]

13. \( Y = \text{cdist}(XA, XB, 'mahalanobis', VI=None) \)

Computes the Mahalanobis distance between the points. The Mahalanobis distance between two points \( u \) and \( v \) is \( \sqrt{(u - v)(1/V)(u - v)^T} \) where \((1/V)\) (the VI variable) is the inverse covariance. If \( VI \) is not None, \( VI \) will be used as the inverse covariance matrix.

14. \( Y = \text{cdist}(XA, XB, 'yule') \)
Computes the Yule distance between the boolean vectors. (see \textit{yule} function documentation)

15. $Y = \text{cdist}(XA, XB, \text{'}matching\text{')}$

   Synonym for ‘hamming’.

16. $Y = \text{cdist}(XA, XB, \text{'}dice\text{')}$

   Computes the Dice distance between the boolean vectors. (see \textit{dice} function documentation)

17. $Y = \text{cdist}(XA, XB, \text{'}kulsinski\text{')}$

   Computes the Kulsinski distance between the boolean vectors. (see \textit{kulsinski} function documentation)

18. $Y = \text{cdist}(XA, XB, \text{'}rogerstanimoto\text{')}$

   Computes the Rogers-Tanimoto distance between the boolean vectors. (see \textit{rogerstanimoto} function documentation)

19. $Y = \text{cdist}(XA, XB, \text{'}russellrao\text{')}$

   Computes the Russell-Rao distance between the boolean vectors. (see \textit{russellrao} function documentation)

20. $Y = \text{cdist}(XA, XB, \text{'}sokalmichener\text{')}$

   Computes the Sokal-Michener distance between the boolean vectors. (see \textit{sokalmichener} function documentation)

21. $Y = \text{cdist}(XA, XB, \text{'}sokalsneath\text{')}$

   Computes the Sokal-Sneath distance between the vectors. (see \textit{sokalsneath} function documentation)

22. $Y = \text{cdist}(XA, XB, \text{'}wminkowski\text{'}, p=2., w=w)$

   Computes the weighted Minkowski distance between the vectors. (see \textit{wminkowski} function documentation)

23. $Y = \text{cdist}(XA, XB, f)$

   Computes the distance between all pairs of vectors in X using the user supplied 2-arity function \textit{f}. For example, Euclidean distance between the vectors could be computed as follows:

   \begin{verbatim}
   dm = cdist(XA, XB, lambda u, v: np.sqrt(((u-v)**2).sum()))
   \end{verbatim}

   Note that you should avoid passing a reference to one of the distance functions defined in this library. For example:

   \begin{verbatim}
   dm = cdist(XA, XB, sokalsneath)
   \end{verbatim}

   would calculate the pair-wise distances between the vectors in X using the Python function \textit{sokalsneath}. This would result in sokalsneath being called $n(n-1)/2$ times, which is inefficient. Instead, the optimized C version is more efficient, and we call it using the following syntax:
Examples
Find the Euclidean distances between four 2-D coordinates:

```python
from scipy.spatial import distance
coords = [(35.0456, -85.2672),
          (35.1174, -89.9711),
          (35.9728, -83.9422),
          (36.1667, -86.7833)]
distance.cdist(coords, coords, 'euclidean')
array([[ 0. , 4.7044, 1.6172, 1.8856],
       [ 4.7044, 0. , 6.0893, 3.3561],
       [ 1.6172, 6.0893, 0. , 2.8477],
       [ 1.8856, 3.3561, 2.8477, 0. ]])
```

Find the Manhattan distance from a 3-D point to the corners of the unit cube:

```python
a = np.array([[0, 0, 0],
              [0, 0, 1],
              [0, 1, 0],
              [0, 1, 1],
              [1, 0, 0],
              [1, 0, 1],
              [1, 1, 0],
              [1, 1, 1]])
b = np.array([[0.1, 0.2, 0.4]])
distance.cdist(a, b, 'cityblock')
array([[ 0.7],
       [ 0.9],
       [ 1.3],
       [ 1.5],
       [ 1.5],
       [ 1.7],
       [ 2.1],
       [ 2.3]])
```

`scipy.spatial.distance.squareform`

`scipy.spatial.distance.squareform(X, force='no', checks=True)`

Convert a vector-form distance vector to a square-form distance matrix, and vice-versa.

Parameters

- **X** [ndarray] Either a condensed or redundant distance matrix.
- **force** [str, optional] As with MATLAB(TM), if force is equal to 'tovector' or 'tomatrix', the input will be treated as a distance matrix or distance vector respectively.
- **checks** [bool, optional] If set to False, no checks will be made for matrix symmetry nor zero diagonals. This is useful if it is known that $X - X.T1$ is small and `diag(X)` is close to zero. These values are ignored any way so they do not disrupt the squareform transformation.

Returns
Y  [ndarray] If a condensed distance matrix is passed, a redundant one is returned, or if a redundant one is passed, a condensed distance matrix is returned.

Notes
1. v = squareform(X)
   Given a square d-by-d symmetric distance matrix X, v = squareform(X) returns a \( d \times (d-1)/2 \) sized vector v.
   \( v[[n^2 - (n-i) + (j-i-1)] \) is the distance between points i and j. If X is non-square or asymmetric, an error is returned.

2. X = squareform(v)
   Given a \( d \times (d-1)/2 \) sized v for some integer \( d \geq 2 \) encoding distances as described, X = squareform(v) returns a d by d distance matrix X. The X[i, j] and X[j, i] values are set to \( v[[n^2 - (n-i) + (j-i-1)] \) and all diagonal elements are zero.

In Scipy 0.19.0, squareform stopped casting all input types to float64, and started returning arrays of the same dtype as the input.

scipy.spatial.distance.directed_hausdorff

scipy.spatial.distance.directed_hausdorff(u, v, seed=0)
Compute the directed Hausdorff distance between two N-D arrays.
Distances between pairs are calculated using a Euclidean metric.

Parameters
- u  [(M, N) ndarray] Input array.
- v  [(O, N) ndarray] Input array.
- seed  [int or None] Local np.random.RandomState seed. Default is 0, a random shuffling of u and v that guarantees reproducibility.

Returns
- d  [double] The directed Hausdorff distance between arrays u and v,
- index_1  [int] index of point contributing to Hausdorff pair in u
- index_2  [int] index of point contributing to Hausdorff pair in v

See also:

scipy.spatial.procrustes
Another similarity test for two data sets

Notes
Uses the early break technique and the random sampling approach described by [1]. Although worst-case performance is \( O(m \times o) \) (as with the brute force algorithm), this is unlikely in practice as the input data would have to require the algorithm to explore every single point interaction, and after the algorithm shuffles the input points at that. The best case performance is \( O(m) \), which is satisfied by selecting an inner loop distance that is less than cmax and leads to an early break as often as possible. The authors have formally shown that the average runtime is closer to \( O(m) \).

New in version 0.19.0.

References
[1]
Examples
Find the directed Hausdorff distance between two 2-D arrays of coordinates:

```python
>>> from scipy.spatial.distance import directed_hausdorff
>>> u = np.array(((1.0, 0.0),
    ... (-1.0, 0.0),
    ... (0.0, -1.0)))
>>> v = np.array(((2.0, 0.0),
    ... (0.0, 2.0),
    ... (-2.0, 0.0),
    ... (0.0, -4.0)))
```

```python
>>> directed_hausdorff(u, v)[0]
2.23606797749979
>>> directed_hausdorff(v, u)[0]
3.0
```

Find the general (symmetric) Hausdorff distance between two 2-D arrays of coordinates:

```python
>>> max(directed_hausdorff(u, v)[0], directed_hausdorff(v, u)[0])
3.0
```

Find the indices of the points that generate the Hausdorff distance (the Hausdorff pair):

```python
>>> directed_hausdorff(v, u)[1:]
(3, 3)
```

Predicates for checking the validity of distance matrices, both condensed and redundant. Also contained in this module are functions for computing the number of observations in a distance matrix.

**scipy.spatial.distance.is_valid_dm**

```python
scipy.spatial.distance.is_valid_dm(D, tol=0.0, throw=False, name='D', warning=False)
```

Return True if input array is a valid distance matrix.

Distance matrices must be 2-dimensional numpy arrays. They must have a zero-diagonal, and they must be symmetric.
name [str, optional] The name of the variable to checked. This is useful if throw is set to True so the offending variable can be identified in the exception message when an exception is thrown.

warning [bool, optional] Instead of throwing an exception, a warning message is raised.

Returns valid [bool] True if the variable \( D \) passed is a valid distance matrix.

Notes Small numerical differences in \( D \) and \( D.T \) and non-zeroness of the diagonal are ignored if they are within the tolerance specified by \( tol \).

scipy.spatial.distance.is_valid_y

scipy.spatial.distance.is_valid_y(\( y \), warning=False, throw=False, name=None)

Return True if the input array is a valid condensed distance matrix.

Condensed distance matrices must be 1-dimensional numpy arrays. Their length must be a binomial coefficient \( \binom{n}{2} \) for some positive integer \( n \).

Parameters y [ndarray] The condensed distance matrix.

warning [bool, optional] Invokes a warning if the variable passed is not a valid condensed distance matrix. The warning message explains why the distance matrix is not valid. name is used when referencing the offending variable.

throw [bool, optional] Throws an exception if the variable passed is not a valid condensed distance matrix.

name [bool, optional] Used when referencing the offending variable in the warning or exception message.

scipy.spatial.distance.num_obs_dm

scipy.spatial.distance.num_obs_dm(\( d \))

Return the number of original observations that correspond to a square, redundant distance matrix.

Parameters d [ndarray] The target distance matrix.

Returns

num_obs_dm [int] The number of observations in the redundant distance matrix.

scipy.spatial.distance.num_obs_y

scipy.spatial.distance.num_obs_y(\( Y \))

Return the number of original observations that correspond to a condensed distance matrix.

Parameters Y [ndarray] Condensed distance matrix.

Returns

n [int] The number of observations in the condensed distance matrix \( Y \).

Distance functions between two numeric vectors \( u \) and \( v \). Computing distances over a large collection of vectors is inefficient for these functions. Use \texttt{pdist} for this purpose.
**braycurtis**

**braycurtis**(u, v[, w])

Compute the Bray-Curtis distance between two 1-D arrays.

Bray-Curtis distance is defined as

\[ \sum |u_i - v_i| / \sum |u_i + v_i| \]

The Bray-Curtis distance is in the range \([0, 1]\) if all coordinates are positive, and is undefined if the inputs are of length zero.

**Parameters**

- **u** [(N,) array_like] Input array.
- **v** [(N,) array_like] Input array.
- **w** [(N,) array_like, optional] The weights for each value in u and v. Default is None, which gives each value a weight of 1.0

**Returns**

- **braycurtis** [double] The Bray-Curtis distance between 1-D arrays u and v.

**Examples**

```python
>>> from scipy.spatial import distance
>>> distance.braycurtis([1, 0, 0], [0, 1, 0])
1.0
>>> distance.braycurtis([1, 1, 0], [0, 1, 0])
0.33333333333333331
```
scipy.spatial.distance.canberra

scipy.spatial.distance.canberra(u, v, w=None)

Compute the Canberra distance between two 1-D arrays.

The Canberra distance is defined as

\[ d(u, v) = \sum_i \frac{|u_i - v_i|}{|u_i| + |v_i|}. \]

Parameters

- **u** [(N, ) array_like] Input array.
- **v** [(N, ) array_like] Input array.
- **w** [(N, ) array_like, optional] The weights for each value in u and v. Default is None, which gives each value a weight of 1.0

Returns

- **canberra** [double] The Canberra distance between vectors u and v.

Notes

When \( u[i] \) and \( v[i] \) are 0 for given i, then the fraction 0/0 = 0 is used in the calculation.

Examples

```python
>>> from scipy.spatial import distance
>>> distance.canberra([1, 0, 0], [0, 1, 0])
2.0
>>> distance.canberra([1, 1, 0], [0, 1, 0])
1.0
```

scipy.spatial.distance.chebyshev

scipy.spatial.distance.chebyshev(u, v, w=None)

Compute the Chebyshev distance.

Computes the Chebyshev distance between two 1-D arrays u and v, which is defined as

\[ \max_i |u_i - v_i|. \]

Parameters

- **u** [(N, ) array_like] Input vector.
- **v** [(N, ) array_like] Input vector.
- **w** [(N, ) array_like, optional] The weights for each value in u and v. Default is None, which gives each value a weight of 1.0

Returns

- **chebyshev** [double] The Chebyshev distance between vectors u and v.

Examples

```python
>>> from scipy.spatial import distance
>>> distance.chebyshev([1, 0, 0], [0, 1, 0])
1
>>> distance.chebyshev([1, 1, 0], [0, 1, 0])
1
```
scipy.spatial.distance.cityblock

`scipy.spatial.distance.cityblock(u, v, w=None)`

Compute the City Block (Manhattan) distance.

Computes the Manhattan distance between two 1-D arrays `u` and `v`, which is defined as

\[ \sum_{i} |u_i - v_i|. \]

**Parameters**

- `u` : [(N,) array_like] Input array.
- `v` : [(N,) array_like] Input array.
- `w` : [(N,) array_like, optional] The weights for each value in `u` and `v`. Default is None, which gives each value a weight of 1.0

**Returns**

- `cityblock` : [double] The City Block (Manhattan) distance between vectors `u` and `v`.

**Examples**

```python
>>> from scipy.spatial import distance
>>> distance.cityblock([1, 0, 0], [0, 1, 0])
2
>>> distance.cityblock([1, 0, 0], [0, 2, 0])
3
>>> distance.cityblock([1, 0, 0], [1, 1, 0])
1
```

scipy.spatial.distance.correlation

`scipy.spatial.distance.correlation(u, v, w=None, centered=True)`

Compute the correlation distance between two 1-D arrays.

The correlation distance between `u` and `v`, is defined as

\[ 1 - \frac{(u - \bar{u}) \cdot (v - \bar{v})}{\|u - \bar{u}\|_2 \|v - \bar{v}\|_2} \]

where \( \bar{u} \) is the mean of the elements of `u` and \( x \cdot y \) is the dot product of `x` and `y`.

**Parameters**

- `u` : [(N,) array_like] Input array.
- `v` : [(N,) array_like] Input array.
- `w` : [(N,) array_like, optional] The weights for each value in `u` and `v`. Default is None, which gives each value a weight of 1.0

**Returns**

- `correlation` : [double] The correlation distance between 1-D array `u` and `v`.
scipy.spatial.distance.cosine

scipy.spatial.distance.cosine(u, v, w=None)

Compute the Cosine distance between 1-D arrays.

The Cosine distance between $u$ and $v$, is defined as

$$1 - \frac{u \cdot v}{\|u\|_2 \|v\|_2},$$

where $u \cdot v$ is the dot product of $u$ and $v$.

**Parameters**

- **u** : [(N,) array_like] Input array.
- **v** : [(N,) array_like] Input array.
- **w** : [(N,) array_like, optional] The weights for each value in $u$ and $v$. Default is None, which gives each value a weight of 1.0

**Returns**

- **cosine** : [double] The Cosine distance between vectors $u$ and $v$.

**Examples**

```python
>>> from scipy.spatial import distance
>>> distance.cosine([1, 0, 0], [0, 1, 0])
1.0
>>> distance.cosine([100, 0, 0], [0, 1, 0])
1.0
>>> distance.cosine([1, 1, 0], [0, 1, 0])
0.29289321881345254
```

scipy.spatial.distance.euclidean

scipy.spatial.distance.euclidean(u, v, w=None)

Computes the Euclidean distance between two 1-D arrays.

The Euclidean distance between 1-D arrays $u$ and $v$, is defined as

$$\|u - v\|_2 = \left( \sum (w_i |(u_i - v_i)|^2) \right)^{1/2}$$

**Parameters**

- **u** : [(N,) array_like] Input array.
- **v** : [(N,) array_like] Input array.
- **w** : [(N,) array_like, optional] The weights for each value in $u$ and $v$. Default is None, which gives each value a weight of 1.0

**Returns**

- **euclidean** : [double] The Euclidean distance between vectors $u$ and $v$.

**Examples**

```python
>>> from scipy.spatial import distance
>>> distance.euclidean([1, 0, 0], [0, 1, 0])
1.4142135623730951
>>> distance.euclidean([1, 1, 0], [0, 1, 0])
1.0
```
scipy.spatial.distance.jensenshannon

**scipy.spatial.distance.jensenshannon(p, q, base=None)**

Compute the Jensen-Shannon distance (metric) between two 1-D probability arrays. This is the square root of the Jensen-Shannon divergence.

The Jensen-Shannon distance between two probability vectors \( p \) and \( q \) is defined as,

\[
\sqrt{\frac{D(p \parallel m) + D(q \parallel m)}{2}}
\]

where \( m \) is the pointwise mean of \( p \) and \( q \) and \( D \) is the Kullback-Leibler divergence.

This routine will normalize \( p \) and \( q \) if they don’t sum to 1.0.

**Parameters**

- **p** [(N,) array_like] left probability vector
- **q** [(N,) array_like] right probability vector
- **base** [double, optional] the base of the logarithm used to compute the output if not given, then the routine uses the default base of scipy.stats.entropy.

**Returns**

- **js** [double] The Jensen-Shannon distance between \( p \) and \( q \)

.. versionadded:: 1.2.0

**Examples**

```python
>>> from scipy.spatial import distance
>>> distance.jensenshannon([1.0, 0.0, 0.0], [0.0, 1.0, 0.0], 2.0)
1.0
>>> distance.jensenshannon([1.0, 0.0], [0.5, 0.5])
0.46450140402245893
>>> distance.jensenshannon([1.0, 0.0, 0.0], [1.0, 0.0, 0.0])
0.0
```

scipy.spatial.distance.mahalanobis

**scipy.spatial.distance.mahalanobis(u, v, VI)**

Compute the Mahalanobis distance between two 1-D arrays.

The Mahalanobis distance between 1-D arrays \( u \) and \( v \), is defined as

\[
\sqrt{(u - v)V^{-1}(u - v)^T}
\]

where \( V \) is the covariance matrix. Note that the argument \( VI \) is the inverse of \( V \).

**Parameters**

- **u** [(N,) array_like] Input array.
- **v** [(N,) array_like] Input array.
- **VI** [ndarray] The inverse of the covariance matrix.

**Returns**

- **mahalanobis** [double] The Mahalanobis distance between vectors \( u \) and \( v \).

**Examples**
>>> from scipy.spatial import distance
>>> iv = [[1, 0.5, 0.5], [0.5, 1, 0.5], [0.5, 0.5, 1]]
>>> distance.mahalanobis([1, 0, 0], [0, 1, 0], iv)
1.0
>>> distance.mahalanobis([0, 2, 0], [0, 1, 0], iv)
1.0
>>> distance.mahalanobis([2, 0, 0], [0, 1, 0], iv)
1.7320508075688772

scipy.spatial.distance.minkowski

scipy.spatial.distance.minkowski(u, v, p=2, w=None)
Compute the Minkowski distance between two 1-D arrays.

The Minkowski distance between 1-D arrays u and v, is defined as

$$||u - v||_p = \left( \sum |u_i - v_i|^p \right)^{1/p}.$$  

Parameters

- u [(N,) array_like] Input array.
- v [(N,) array_like] Input array.
- p [int] The order of the norm of the difference ||u - v||_p.
- w [(N,) array_like, optional] The weights for each value in u and v. Default is None, which gives each value a weight of 1.0

Returns

minkowski [double] The Minkowski distance between vectors u and v.

Examples

>>> from scipy.spatial import distance
>>> distance.minkowski([1, 0, 0], [0, 1, 0], 1)
2.0
>>> distance.minkowski([1, 0, 0], [0, 1, 0], 2)
1.4142135623706951
>>> distance.minkowski([1, 0, 0], [0, 1, 0], 3)
1.2599210498001046
>>> distance.minkowski([1, 1, 0], [0, 1, 0], 1)
1.0
>>> distance.minkowski([1, 1, 0], [0, 1, 0], 2)
1.0
>>> distance.minkowski([1, 1, 0], [0, 1, 0], 3)
1.0

scipy.spatial.distance.seuclidean

scipy.spatial.distance.seuclidean(u, v, V)
Return the standardized Euclidean distance between two 1-D arrays.

The standardized Euclidean distance between u and v.

Parameters
u  [(N,) array_like] Input array.
v  [(N,) array_like] Input array.
V  [(N,) array_like] V is an 1-D array of component variances. It is usually computed among a larger collection vectors.

Returns

seuclidean  [double] The standardized Euclidean distance between vectors u and v.

Examples

```python
>>> from scipy.spatial import distance
>>> distance.seuclidean([1, 0, 0, 0], [0, 1, 0, 0.1])
4.4721359549995796
>>> distance.seuclidean([1, 0, 0], [0, 1, 0], [1, 0.1, 0.1])
3.3166247903553998
>>> distance.seuclidean([1, 0, 0], [0, 1, 0], [10, 0.1, 0.1])
3.1780497164141406
```

scipy.spatial.distance.sqeuclidean

scipy.spatial.distance.sqeuclidean(u, v, w=None)
Compute the squared Euclidean distance between two 1-D arrays.

The squared Euclidean distance between u and v is defined as

\[ \sqrt{\sum w_i (u_i - v_i)^2} \]

Parameters

u  [(N,) array_like] Input array.
v  [(N,) array_like] Input array.
w  [(N,) array_like, optional] The weights for each value in u and v. Default is None, which gives each value a weight of 1.0

Returns

sqeuclidean  [double] The squared Euclidean distance between vectors u and v.

Examples

```python
>>> from scipy.spatial import distance
>>> distance.sqeuclidean([1, 0, 0], [0, 1, 0])
2.0
>>> distance.sqeuclidean([1, 1, 0], [0, 1, 0])
1.0
```

scipy.spatial.distance.wminkowski

scipy.spatial.distance.wminkowski(u, v, p, w)
Compute the weighted Minkowski distance between two 1-D arrays.

The weighted Minkowski distance between u and v, defined as

\[ \left( \sum w_i (|u_i - v_i|^p) \right)^{1/p} \]
Parameters

- **u**: [(N,) array_like] Input array.
- **v**: [(N,) array_like] Input array.
- **p**: [int] The order of the norm of the difference \( \|u - v\|_p \).
- **w**: [(N,) array_like] The weight vector.

Returns

- **wminkowski**: [double] The weighted Minkowski distance between vectors u and v.

Notes

*wminkowski* is DEPRECATED. It implements a definition where weights are powered. It is recommended to use the weighted version of *minkowski* instead. This function will be removed in a future version of scipy.

Examples

```python
>>> from scipy.spatial import distance
>>> distance.wminkowski([1, 0, 0], [0, 1, 0], 1, np.ones(3))
2.0
>>> distance.wminkowski([1, 0, 0], [0, 1, 0], 2, np.ones(3))
1.4142135623730951
>>> distance.wminkowski([1, 0, 0], [0, 1, 0], 3, np.ones(3))
1.2599210498948732
>>> distance.wminkowski([1, 1, 0], [0, 1, 0], 1, np.ones(3))
1.0
>>> distance.wminkowski([1, 1, 0], [0, 1, 0], 2, np.ones(3))
1.0
>>> distance.wminkowski([1, 1, 0], [0, 1, 0], 3, np.ones(3))
1.0
```

Distance functions between two boolean vectors (representing sets) u and v. As in the case of numerical vectors, *pdist* is more efficient for computing the distances between all pairs.

- **dice(u, v[, w])** Compute the Dice dissimilarity between two boolean 1-D arrays.
- **hamming(u, v[, w])** Compute the Hamming distance between two 1-D arrays.
- **jaccard(u, v[, w])** Compute the Jaccard-Needham dissimilarity between two boolean 1-D arrays.
- **kulsinski(u, v[, w])** Compute the Kulsinski dissimilarity between two boolean 1-D arrays.
- **rogerstanimoto(u, v[, w])** Compute the Rogers-Tanimoto dissimilarity between two boolean 1-D arrays.
- **russellrao(u, v[, w])** Compute the Russell-Rao dissimilarity between two boolean 1-D arrays.
- **sokalmichener(u, v[, w])** Compute the Sokal-Michener dissimilarity between two boolean 1-D arrays.
- **sokalsneath(u, v[, w])** Compute the Sokal-Sneath dissimilarity between two boolean 1-D arrays.
- **yule(u, v[, w])** Compute the Yule dissimilarity between two boolean 1-D arrays.
**scipy.spatial.distance.dice**

**scipy.spatial.distance.dice**\((u, v, w=None)\)

Compute the Dice dissimilarity between two boolean 1-D arrays.

The Dice dissimilarity between \(u\) and \(v\), is

\[
\frac{c_{TF} + c_{FT}}{2c_{TT} + c_{FT} + c_{TF}}
\]

where \(c_{ij}\) is the number of occurrences of \(u[k] = i\) and \(v[k] = j\) for \(k < n\).

**Parameters**

- **u**: \([N,] \text{ndarray, bool}\) Input 1-D array.
- **v**: \([N,] \text{ndarray, bool}\) Input 1-D array.
- **w**: \([N,] \text{array_like, optional}\) The weights for each value in \(u\) and \(v\). Default is None, which gives each value a weight of 1.0

**Returns**

- **dice**: [double] The Dice dissimilarity between 1-D arrays \(u\) and \(v\).

**Examples**

```python
>>> from scipy.spatial import distance
>>> distance.dice([1, 0, 0], [0, 1, 0])
1.0
>>> distance.dice([1, 0, 0], [1, 1, 0])
0.3333333333333333
>>> distance.dice([1, 0, 0], [2, 0, 0])
-0.3333333333333333
```

**scipy.spatial.distance.hamming**

**scipy.spatial.distance.hamming**\((u, v, w=None)\)

Compute the Hamming distance between two 1-D arrays.

The Hamming distance between 1-D arrays \(u\) and \(v\), is simply the proportion of disagreeing components in \(u\) and \(v\). If \(u\) and \(v\) are boolean vectors, the Hamming distance is

\[
\frac{c_{01} + c_{10}}{n}
\]

where \(c_{ij}\) is the number of occurrences of \(u[k] = i\) and \(v[k] = j\) for \(k < n\).

**Parameters**

- **u**: \([N,] \text{array_like}\) Input array.
- **v**: \([N,] \text{array_like}\) Input array.
- **w**: \([N,] \text{array_like, optional}\) The weights for each value in \(u\) and \(v\). Default is None, which gives each value a weight of 1.0

**Returns**

- **hamming**: [double] The Hamming distance between vectors \(u\) and \(v\).

**Examples**

```python
>>> from scipy.spatial import distance
>>> distance.hamming([1, 0, 0], [0, 1, 0])
1.0
>>> distance.hamming([1, 0, 0], [1, 1, 0])
0.3333333333333333
>>> distance.hamming([1, 0, 0], [2, 0, 0])
-0.3333333333333333
```
scipy.spatial.distance.jaccard

scipy.spatial.distance.jaccard(u, v, w=None)

Compute the Jaccard-Needham dissimilarity between two boolean 1-D arrays.

The Jaccard-Needham dissimilarity between 1-D boolean arrays \( u \) and \( v \), is defined as

\[
\frac{c_{TF} + c_{FT}}{c_{TT} + c_{FT} + c_{TF}}
\]

where \( c_{ij} \) is the number of occurrences of \( u[k] = i \) and \( v[k] = j \) for \( k < n \).

Parameters
- **u** [(N,) array_like, bool] Input array.
- **v** [(N,) array_like, bool] Input array.
- **w** [(N,) array_like, optional] The weights for each value in \( u \) and \( v \). Default is None, which gives each value a weight of 1.0

Returns
- **jaccard** [double] The Jaccard distance between vectors \( u \) and \( v \).

Notes
When both \( u \) and \( v \) lead to a 0/0 division i.e. there is no overlap between the items in the vectors the returned distance is 0. See the Wikipedia page on the Jaccard index [1], and this paper [2].

Changed in version 1.2.0: Previously, when \( u \) and \( v \) lead to a 0/0 division, the function would return NaN. This was changed to return 0 instead.

References
[1], [2]

Examples

```python
>>> from scipy.spatial import distance
>>> distance.jaccard([1, 0, 0], [0, 1, 0])
1.0
>>> distance.jaccard([1, 0, 0], [1, 1, 0])
0.5
>>> distance.jaccard([1, 0, 0], [1, 2, 0])
0.5
>>> distance.jaccard([1, 0, 0], [1, 1, 1])
0.6666666666666666
```

scipy.spatial.distance.kulsinski

scipy.spatial.distance.kulsinski(u, v, w=None)

Compute the Kulsinski dissimilarity between two boolean 1-D arrays.
The Kulsinski dissimilarity between two boolean 1-D arrays $u$ and $v$, is defined as
\[
\frac{c_{TF} + c_{FT} - c_{TT} + n}{c_{FT} + c_{TF} + n}
\]
where $c_{ij}$ is the number of occurrences of $u[k] = i$ and $v[k] = j$ for $k < n$.

**Parameters**
- $u$ [(N,) array_like, bool] Input array.
- $v$ [(N,) array_like, bool] Input array.
- $w$ [(N,) array_like, optional] The weights for each value in $u$ and $v$. Default is None, which gives each value a weight of 1.0

**Returns**
- kulsinski [double] The Kulsinski distance between vectors $u$ and $v$.

**Examples**
```python
>>> from scipy.spatial import distance
>>> distance.kulsinski([1, 0, 0], [0, 1, 0])
1.0
>>> distance.kulsinski([1, 0, 0], [1, 1, 0])
0.75
>>> distance.kulsinski([1, 0, 0], [2, 1, 0])
0.33333333333333331
>>> distance.kulsinski([1, 0, 0], [3, 1, 0])
-0.5
```

scipy.spatial.distance.rogerstanimoto

**scipy.spatial.distance.rogerstanimoto**($u$, $v$, $w=None$)

Compute the Rogers-Tanimoto dissimilarity between two boolean 1-D arrays.

The Rogers-Tanimoto dissimilarity between two boolean 1-D arrays $u$ and $v$, is defined as
\[
R = \frac{2(c_{TF} + c_{FT})}{c_{TT} + c_{FF}}
\]
where $c_{ij}$ is the number of occurrences of $u[k] = i$ and $v[k] = j$ for $k < n$ and $R = 2(c_{TF} + c_{FT})$.

**Parameters**
- $u$ [(N,) array_like, bool] Input array.
- $v$ [(N,) array_like, bool] Input array.
- $w$ [(N,) array_like, optional] The weights for each value in $u$ and $v$. Default is None, which gives each value a weight of 1.0

**Returns**
- rogerstanimoto [double] The Rogers-Tanimoto dissimilarity between vectors $u$ and $v$.

**Examples**
```python
>>> from scipy.spatial import distance
>>> distance.rogerstanimoto([1, 0, 0], [0, 1, 0])
0.8
>>> distance.rogerstanimoto([1, 0, 0], [1, 1, 0])
0.5
>>> distance.rogerstanimoto([1, 0, 0], [2, 0, 0])
-1.0
```
scipy.spatial.distance.russellrao

scipy.spatial.distance.russellrao(u, v, w=None)

Compute the Russell-Rao dissimilarity between two boolean 1-D arrays.

The Russell-Rao dissimilarity between two boolean 1-D arrays, $u$ and $v$, is defined as

$$\frac{n - c_{TT}}{n}$$

where $c_{ij}$ is the number of occurrences of $u[k] = i$ and $v[k] = j$ for $k < n$.

Parameters

- **u**: [(N, ) array_like, bool] Input array.
- **v**: [(N, ) array_like, bool] Input array.
- **w**: [(N, ) array_like, optional] The weights for each value in $u$ and $v$. Default is None, which gives each value a weight of 1.0

Returns

- **russellrao**: [double] The Russell-Rao dissimilarity between vectors $u$ and $v$.

Examples

```python
>>> from scipy.spatial import distance
>>> distance.russellrao([1, 0, 0], [0, 1, 0])
1.0
>>> distance.russellrao([1, 0, 0], [1, 1, 0])
0.6666666666666666
>>> distance.russellrao([1, 0, 0], [2, 0, 0])
0.3333333333333333
```

scipy.spatial.distance.sokalmichener

scipy.spatial.distance.sokalmichener(u, v, w=None)

Compute the Sokal-Michener dissimilarity between two boolean 1-D arrays.

The Sokal-Michener dissimilarity between boolean 1-D arrays $u$ and $v$, is defined as

$$\frac{R}{S + R}$$

where $c_{ij}$ is the number of occurrences of $u[k] = i$ and $v[k] = j$ for $k < n$, $R = 2 * (c_{TF} + c_{FT})$ and $S = c_{FF} + c_{TT}$.

Parameters

- **u**: [(N, ) array_like, bool] Input array.
- **v**: [(N, ) array_like, bool] Input array.
- **w**: [(N, ) array_like, optional] The weights for each value in $u$ and $v$. Default is None, which gives each value a weight of 1.0

Returns

- **sokalmichener**: [double] The Sokal-Michener dissimilarity between vectors $u$ and $v$.

Examples
```python
>>> from scipy.spatial import distance
dlance.sokalmichener([1, 0, 0], [0, 1, 0])
0.8
>>> distance.sokalmichener([1, 0, 0], [1, 1, 0])
0.5
>>> distance.sokalmichener([1, 0, 0], [2, 0, 0])
-1.0
```

**scipy.spatial.distance.sokalsneath**

`scipy.spatial.distance.sokalsneath(u, v, w=None)`

Compute the Sokal-Sneath dissimilarity between two boolean 1-D arrays.

The Sokal-Sneath dissimilarity between \(u\) and \(v\),

\[
\frac{R}{c_{TT} + R}
\]

where \(c_{ij}\) is the number of occurrences of \(u[k] = i\) and \(v[k] = j\) for \(k < n\) and \(R = 2(c_{TF} + c_{FT})\).

**Parameters**

- **u** [(N,) array_like, bool] Input array.
- **v** [(N,) array_like, bool] Input array.
- **w** [(N,) array_like, optional] The weights for each value in \(u\) and \(v\). Default is None, which gives each value a weight of 1.0

**Returns**

- **sokalsneath** [double] The Sokal-Sneath dissimilarity between vectors \(u\) and \(v\).

**Examples**

```python
>>> from scipy.spatial import distance
dlance.sokalsneath([1, 0, 0], [0, 1, 0])
1.0
>>> distance.sokalsneath([1, 0, 0], [1, 1, 0])
0.6666666666666666
>>> distance.sokalsneath([1, 0, 0], [2, 1, 0])
0.0
>>> distance.sokalsneath([1, 0, 0], [3, 1, 0])
-2.0
```

**scipy.spatial.distance.yule**

`scipy.spatial.distance.yule(u, v, w=None)`

Compute the Yule dissimilarity between two boolean 1-D arrays.

The Yule dissimilarity is defined as

\[
\frac{R}{c_{TT} + R}
\]

where \(c_{ij}\) is the number of occurrences of \(u[k] = i\) and \(v[k] = j\) for \(k < n\) and \(R = 2 * c_{TF} * c_{FT}\).

**Parameters**

- **u** [(N,) array_like, bool] Input array.
v  [(N,) array_like, bool] Input array.
w  [(N,) array_like, optional] The weights for each value in u and v. Default is None, which gives each value a weight of 1.0

Returns
yule  [double] The Yule dissimilarity between vectors u and v.

Examples
```python
>>> from scipy.spatial import distance
>>> distance.yule([1, 0, 0], [0, 1, 0])
2.0
>>> distance.yule([1, 1, 0], [0, 1, 0])
0.0
```

`hamming` also operates over discrete numerical vectors.

## 6.26 Special functions (scipy.special)

Nearly all of the functions below are universal functions and follow broadcasting and automatic array-looping rules. Exceptions are noted.

See also:

- `scipy.special.cython_special` — Typed Cython versions of special functions

### 6.26.1 Error handling

Errors are handled by returning NaNs or other appropriate values. Some of the special function routines can emit warnings or raise exceptions when an error occurs. By default this is disabled; to query and control the current error handling state the following functions are provided.

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<td>Get the current way of handling special-function errors.</td>
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<td>Set how special-function errors are handled.</td>
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<td><code>errstate</code></td>
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<td><code>SpecialFunctionWarning</code></td>
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</tr>
<tr>
<td><code>SpecialFunctionError</code></td>
<td>Exception that can be raised by special functions.</td>
</tr>
</tbody>
</table>

```python
def geterr():
    # Get the current way of handling special-function errors.

def seterr(**kwargs):
    # Set how special-function errors are handled.
```

### scipy.special.geterr

- `scipy.special.geterr()`
  - Get the current way of handling special-function errors.

  Returns
  - `err`  [dict] A dictionary with keys “singular”, “underflow”, “overflow”, “slow”, “loss”, “no_result”, “domain”, “arg”, and “other”, whose values are from the strings “ignore”, “warn”, and “raise”. The keys represent possible special-function errors, and the values define how these errors are handled.

  See also:

  - `seterr`
    - set how special-function errors are handled
errstate
context manager for special-function error handling

numpy.geterr
similar numpy function for floating-point errors

Notes
For complete documentation of the types of special-function errors and treatment options, see seterr.

Examples
By default all errors are ignored.

```python
>>> import scipy.special as sc
>>> for key, value in sorted(sc.geterr().items()):
...     print("{}: {}".format(key, value))
... arg: ignore
domain: ignore
loss: ignore
no_result: ignore
other: ignore
overflow: ignore
singular: ignore
slow: ignore
underflow: ignore
```

scipy.special.seterr

scipy.special.seterr()
Set how special-function errors are handled.

Parameters

- **all**
  [{‘ignore’, ‘warn’, ‘raise’}, optional] Set treatment for all type of special-function errors at once. The options are:
  - ‘ignore’ Take no action when the error occurs
  - ‘warn’ Print a SpecialFunctionWarning when the error occurs (via the Python warnings module)
  - ‘raise’ Raise a SpecialFunctionError when the error occurs.
  The default is to not change the current behavior. If behaviors for additional categories of special-function errors are specified, then all is applied first, followed by the additional categories.

- **singular**

- **underflow**

- **overflow**

- **slow**

- **loss**

- **no_result**
  [{‘ignore’, ‘warn’, ‘raise’}, optional] Treatment for failing to find a result.

- **domain**

- **arg**

- **other**
Returns

olderr  [dict] Dictionary containing the old settings.

See also:

geterr

get the current way of handling special-function errors

errstate

class manager for special-function error handling

numpy.seterr

similar numpy function for floating-point errors

Examples

```python
>>> import scipy.special as sc
>>> from pytest import raises
>>> sc.gammaln(0)
inf
>>> olderr = sc.seterr(singular='raise')
>>> with raises(sc.SpecialFunctionError):
...    sc.gammaln(0)
...    sc.gammaln(0)
...    sc.gammaln(0)
>>> _ = sc.seterr(**olderr)

We can also raise for every category except one.

```python
>>> olderr = sc.seterr(all='raise', singular='ignore')
>>> sc.gammaln(0)
in
>>> with raises(sc.SpecialFunctionError):
...    sc.spence(-1)
...    sc.spence(-1)
...    sc.spence(-1)
>>> _ = sc.seterr(**olderr)
```

scipy.special.errstate

class scipy.special.errstate

Context manager for special-function error handling.

Using an instance of errstate as a context manager allows statements in that context to execute with a known error handling behavior. Upon entering the context the error handling is set with seterr, and upon exiting it is restored to what it was before.

Parameters

kwarg  [{all, singular, underflow, overflow, slow, loss, no_result, domain, arg, other}]

Keyword arguments. The valid keywords are possible special-function errors. Each keyword should have a string value that defines the treatement for the particular type of error. Values must be ‘ignore’, ‘warn’, or ‘other’. See seterr for details.

See also:

geterr

get the current way of handling special-function errors
seterr
set how special-function errors are handled

numpy.errstate
similar numpy function for floating-point errors

Examples

```python
>>> import scipy.special as sc
>>> from pytest import raises
>>> sc.gammaln(0)
inf
>>> with sc.errstate(singular='raise'):
    ...    with raises(sc.SpecialFunctionError):
    ...        sc.gammaln(0)
...    ...
>>> sc.gammaln(0)
in
```

We can also raise on every category except one.

```python
>>> with sc.errstate(all='raise', singular='ignore'):
...    sc.gammaln(0)
...    with raises(sc.SpecialFunctionError):
...        sc.spence(-1)
...    ...
...    inf
```

scipy.special.SpecialFunctionWarning

exception scipy.special.SpecialFunctionWarning
Warning that can be emitted by special functions.

scipy.special.SpecialFunctionError

exception scipy.special.SpecialFunctionError
Exception that can be raised by special functions.

6.26.2 Available functions

Airy functions

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scipy.special.airy
scipy.special.airy(z) = <ufunc 'airy'>
Airy functions and their derivatives.
Parameters

\(z\) [array_like] Real or complex argument.

Returns

\(\text{Ai, Aip, Bi, Bip}\) [ndarrays] Airy functions \(\text{Ai}\) and \(\text{Bi}\), and their derivatives \(\text{Aip}\) and \(\text{Bip}\).

See also:

\text{airy}

exponentially scaled Airy functions.

Notes

The Airy functions \(\text{Ai}\) and \(\text{Bi}\) are two independent solutions of

\[
y''(x) = xy(x).
\]

For real \(z\) in \([-10, 10]\), the computation is carried out by calling the Cephes [1] \text{airy} routine, which uses power series summation for small \(z\) and rational minimax approximations for large \(z\).

Outside this range, the AMOS [2] \text{zairy} and \text{zbiry} routines are employed. They are computed using power series for \(|z| < 1\) and the following relations to modified Bessel functions for larger \(z\) (where \(t \equiv 2z^{3/2}/3\)):

\[
\begin{align*}
\text{Ai}(z) &= \frac{1}{\pi^{1/3}} K_{1/3}(t) \\
\text{Ai}'(z) &= -\frac{z}{\pi^{1/3}} K_{2/3}(t) \\
\text{Bi}(z) &= \sqrt{\frac{z}{3}} (I_{-1/3}(t) + I_{1/3}(t)) \\
\text{Bi}'(z) &= \frac{z}{\sqrt{3}} (I_{-2/3}(t) + I_{2/3}(t))
\end{align*}
\]

References

[1], [2]

Examples

Compute the Airy functions on the interval \([-15, 5]\).

```python
>>> from scipy import special
>>> x = np.linspace(-15, 5, 201)
>>> ai, aip, bi, bip = special.airy(x)
```

Plot \(\text{Ai}(x)\) and \(\text{Bi}(x)\).

```python
>>> import matplotlib.pyplot as plt
>>> plt.plot(x, ai, 'r', label='\(\text{Ai}(x)\)')
>>> plt.plot(x, bi, 'b--', label='\(\text{Bi}(x)\)')
>>> plt.ylim(-0.5, 1.0)
>>> plt.grid()
>>> plt.legend(loc='upper left')
>>> plt.show()
```
scipy.special.aiye
scipy.special.aiye(z) = <ufunc 'aiye'>
Exponentially scaled Airy functions and their derivatives.

Scaling:

\[
\begin{align*}
eAi &= Ai \times \exp\left(\frac{2}{3} \times z \times \sqrt{z}\right) \\
eAip &= Aip \times \exp\left(\frac{2}{3} \times z \times \sqrt{z}\right) \\
eBi &= Bi \times \exp\left(-\text{abs}\left(\frac{2}{3} \times (z \times \sqrt{z})\right)\right) \\text{.real} \\
eBip &= Bip \times \exp\left(-\text{abs}\left(\frac{2}{3} \times (z \times \sqrt{z})\right)\right) \\text{.real}
\end{align*}
\]

Parameters

- z [array_like] Real or complex argument.

Returns
eAi, eAip, eBi, eBip [array_like] Airy functions Ai and Bi, and their derivatives Aip and Bip

See also:
airy

Notes
Wrapper for the AMOS [1] routines zairy and zbiry.

References
[1]

scipy.special.ai_zeros
scipy.special.ai_zeros(nt)
Compute nt zeros and values of the Airy function Ai and its derivative.

Computes the first nt zeros, a, of the Airy function Ai(x); first nt zeros, ap, of the derivative of the Airy function Ai'(x); the corresponding values Ai(a'); and the corresponding values Ai'(a).

Parameters

- nt [int] Number of zeros to compute
Returns
- \( a \) [ndarray] First \( nt \) zeros of \( \text{Ai}(x) \)
- \( ap \) [ndarray] First \( nt \) zeros of \( \text{Ai}'(x) \)
- \( ai \) [ndarray] Values of \( \text{Ai}(x) \) evaluated at first \( nt \) zeros of \( \text{Ai}'(x) \)
- \( aip \) [ndarray] Values of \( \text{Ai}'(x) \) evaluated at first \( nt \) zeros of \( \text{Ai}(x) \)

References
[1]

scipy.special.bi_zeros
scipy.special.bi_zeros\((nt)\)

Compute \( nt \) zeros and values of the Airy function \( \text{Bi} \) and its derivative.

Computes the first \( nt \) zeros, \( b \), of the Airy function \( \text{Bi}(x) \); first \( nt \) zeros, \( b' \), of the derivative of the Airy function \( \text{Bi}'(x) \); the corresponding values \( \text{Bi}(b') \); and the corresponding values \( \text{Bi}'(b) \).

Parameters
- \( nt \) [int] Number of zeros to compute

Returns
- \( b \) [ndarray] First \( nt \) zeros of \( \text{Bi}(x) \)
- \( bp \) [ndarray] First \( nt \) zeros of \( \text{Bi}'(x) \)
- \( bi \) [ndarray] Values of \( \text{Bi}(x) \) evaluated at first \( nt \) zeros of \( \text{Bi}'(x) \)
- \( bip \) [ndarray] Values of \( \text{Bi}'(x) \) evaluated at first \( nt \) zeros of \( \text{Bi}(x) \)

References
[1]

scipy.special.itairy
scipy.special.itairy\((x)\) = <ufunc 'itairy'>

Integrals of Airy functions

Calculates the integrals of Airy functions from 0 to \( x \).

Parameters
- \( x \) : array_like
  Upper limit of integration (float).

Returns
- \( A_{pt} \) Integral of \( \text{Ai}(t) \) from 0 to \( x \).
- \( B_{pt} \) Integral of \( \text{Bi}(t) \) from 0 to \( x \).
- \( A_{nt} \) Integral of \( \text{Ai}(-t) \) from 0 to \( x \).
- \( B_{nt} \) Integral of \( \text{Bi}(-t) \) from 0 to \( x \).

Notes
Wrapper for a Fortran routine created by Shanjie Zhang and Jianming Jin [1].

References
[1]

Elliptic Functions and Integrals

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**scipy.special.ellipj**

scipy.special.ellipj(u, m) = <ufunc 'ellipj'>

Jacobian elliptic functions

Calculates the Jacobian elliptic functions of parameter \( m \) between 0 and 1, and real argument \( u \).

**Parameters**

- \( m \) [array_like] Parameter.
- \( u \) [array_like] Argument.

**Returns**

- \( sn \), \( cn \), \( dn \), \( ph \) [ndarrays] The returned functions:
  - \( sn(u|m) \)
  - \( cn(u|m) \)
  - \( dn(u|m) \)

The value \( ph \) is such that if \( u = ellipk(ph, m) \), then
  - \( sn(u|m) = \sin(ph) \)
  - \( cn(u|m) = \cos(ph) \).

See also:

**ellipk**

Complete elliptic integral of the first kind.

**Notes**

Wrapper for the Cephes [1] routine *ellipj*.

These functions are periodic, with quarter-period on the real axis equal to the complete elliptic integral \( ellipk(m) \).

Relation to incomplete elliptic integral: If \( u = ellipk(phi,m) \), then \( sn(u|m) = \sin(phi) \) and \( cn(u|m) = \cos(phi) \). The \( phi \) is called the amplitude of \( u \).

Computation is by means of the arithmetic-geometric mean algorithm, except when \( m \) is within 1e-9 of 0 or 1. In the latter case with \( m \) close to 1, the approximation applies only for \( phi < pi/2 \).

**References**

[1]

**scipy.special.ellipk**

scipy.special.ellipk(m)

Complete elliptic integral of the first kind.

This function is defined as

\[
K(m) = \int_0^{\pi/2} \frac{1}{\sqrt{1 - m \sin(t)^2}} dt
\]

**Parameters**

- \( m \) [array_like] The parameter of the elliptic integral.

**Returns**

- \( K \) [array_like] Value of the elliptic integral.

See also:
ellipkm1

Complete elliptic integral of the first kind around m = 1

ellipkinc

Incomplete elliptic integral of the first kind

ellipe

Complete elliptic integral of the second kind

ellipeinc

Incomplete elliptic integral of the second kind

Notes
For more precision around point m = 1, use ellipkm1, which this function calls.

The parameterization in terms of m follows that of section 17.2 in [1]. Other parameterizations in terms of the complementary parameter 1 - m, modular angle \( \sin^2(\alpha) = m \), or modulus \( k^2 = m \) are also used, so be careful that you choose the correct parameter.

References
[1]

scipy.special.ellipkm1

scipy.special.ellipkm1(p) = <ufunc 'ellipkm1'>

Complete elliptic integral of the first kind around m = 1

This function is defined as

\[
K(p) = \int_0^{\pi/2} [1 - m \sin(t)^2]^{-1/2} dt
\]

where m = 1 - p.

Parameters

p [array_like] Defines the parameter of the elliptic integral as m = 1 - p.

Returns

K [ndarray] Value of the elliptic integral.

See also:

ellip

Complete elliptic integral of the first kind

ellipkinc

Incomplete elliptic integral of the first kind

ellipe

Complete elliptic integral of the second kind

ellipeinc

Incomplete elliptic integral of the second kind
Notes

For $p \leq 1$, computation uses the approximation,

$$K(p) \approx P(p) - \log(p)Q(p),$$

where $P$ and $Q$ are tenth-order polynomials. The argument $p$ is used internally rather than $m$ so that the logarithmic singularity at $m = 1$ will be shifted to the origin; this preserves maximum accuracy. For $p > 1$, the identity

$$K(p) = K(1/p)/\sqrt{p}$$

is used.

References
[1]

scipy.special.ellipkinc

scipy.special.ellipkinc(\phi, m) = <ufunc 'ellipkinc'>

Incomplete elliptic integral of the first kind

This function is defined as

$$K(\phi, m) = \int_0^\phi \frac{1 - m \sin^2(t)}{1 - 2m \sin^2(t)} \, dt$$

This function is also called $F(\phi, m)$.

Parameters

phi
[array_like] amplitude of the elliptic integral

m
[array_like] parameter of the elliptic integral

Returns

K
[ndarray] Value of the elliptic integral

See also:

ellipkm1

Complete elliptic integral of the first kind, near $m = 1$

ellip

Complete elliptic integral of the first kind

ellipe

Complete elliptic integral of the second kind

ellipeinc

Incomplete elliptic integral of the second kind

Notes
Wrapper for the Cephes [1] routine ellik. The computation is carried out using the arithmetic-geometric mean algorithm.

The parameterization in terms of $m$ follows that of section 17.2 in [2]. Other parameterizations in terms of the complementary parameter $1 - m$, modular angle $\sin^2(\alpha) = m$, or modulus $k^2 = m$ are also used, so be careful that you choose the correct parameter.
The complete elliptic integral of the second kind is defined as
\[ E(m) = \int_0^{\pi/2} [1 - m \sin^2(t)]^{1/2} dt \]

**Parameters**
- \( m \) [array_like] Defines the parameter of the elliptic integral.

**Returns**
- \( E \) [ndarray] Value of the elliptic integral.

**See also:**
- \texttt{ellipkm1}
- \texttt{ellipk}
- \texttt{ellipkinc}
- \texttt{ellipeinc}

**Notes**
Wrapper for the Cephes \[1\] routine \texttt{ellpe}.

For \( m > 0 \) the computation uses the approximation,
\[ E(m) \approx P(1 - m) - (1 - m) \log(1 - m)Q(1 - m), \]
where \( P \) and \( Q \) are tenth-order polynomials. For \( m < 0 \), the relation
\[ E(m) = E(m/(m - 1)) \sqrt{1 - m} \]
is used.

The parameterization in terms of \( m \) follows that of section 17.2 in \[2\]. Other parameterizations in terms of the complementary parameter \( 1 - m \), modular angle \( \sin^2(\alpha) = m \), or modulus \( k^2 = m \) are also used, so be careful that you choose the correct parameter.

**References**
\[1\], \[2\]

The incomplete elliptic integral of the second kind is defined as
\[ E(\phi, m) = \int_0^\phi [1 - m \sin(t)^2]^{1/2} dt \]
Parameters

phi [array_like] amplitude of the elliptic integral.
m [array_like] parameter of the elliptic integral.

Returns

E [ndarray] Value of the elliptic integral.

See also:

ellipkm1
Complete elliptic integral of the first kind, near \( m = 1 \)
ellipk
Complete elliptic integral of the first kind
ellipkinc
Incomplete elliptic integral of the first kind
ellipe
Complete elliptic integral of the second kind

Notes
Computation uses arithmetic-geometric means algorithm.
The parameterization in terms of \( m \) follows that of section 17.2 in [2]. Other parameterizations in terms of the complementary parameter \( 1 - m \), modular angle \( \sin^2(\alpha) = m \), or modulus \( k^2 = m \) are also used, so be careful that you choose the correct parameter.

References
[1], [2]

Bessel Functions

\( j_v(v, z) \) Bessel function of the first kind of real order and complex argument.
\( j_ve(v, z) \) Exponentially scaled Bessel function of order \( v \).
\( y_n(n, x) \) Bessel function of the second kind of integer order and real argument.
\( y_v(v, z) \) Bessel function of the second kind of real order and complex argument.
\( y_ve(v, z) \) Exponentially scaled Bessel function of the second kind of real order.
\( k_n(n, x) \) Modified Bessel function of the second kind of integer order \( n \)
\( k_v(v, z) \) Modified Bessel function of the second kind of real order \( v \)
\( k_ve(v, z) \) Exponentially scaled modified Bessel function of the second kind.
\( i_v(v, z) \) Modified Bessel function of the first kind of real order.

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<td><code>hankel2e(v, z)</code></td>
<td>Exponentially scaled Hankel function of the second kind</td>
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</table>

**scipy.special.jv**

`scipy.special.jv(v, z) = <ufunc 'jv'>`

Bessel function of the first kind of real order and complex argument.

**Parameters**

- `v` [array_like] Order (float).
- `z` [array_like] Argument (float or complex).

**Returns**

- `J` [ndarray] Value of the Bessel function, $J_v(z)$.

**See also:**

- `jve` $J_v$ with leading exponential behavior stripped off.
- `spherical_jn` spherical Bessel functions.

**Notes**

For positive $v$ values, the computation is carried out using the AMOS [1] `zbesh` routine, which exploits the connection to the modified Bessel function $I_v$,

$J_v(z) = \exp(v\pi i/2)I_v(-iz)$ \hspace{1cm} (3z > 0)

$J_v(z) = \exp(-v\pi i/2)I_v(iz)$ \hspace{1cm} (3z < 0)

For negative $v$ values the formula,

$J_{-v}(z) = J_v(z)\cos(\pi v) - Y_v(z)\sin(\pi v)$

is used, where $Y_v(z)$ is the Bessel function of the second kind, computed using the AMOS routine `zbesy`. Note that the second term is exactly zero for integer $v$; to improve accuracy the second term is explicitly omitted for $v$ values such that $v = \text{floor}(v)$.

Not to be confused with the spherical Bessel functions (see `spherical_jn`).

**References**

[1]

**scipy.special.jve**

`scipy.special.jve(v, z) = <ufunc 'jve'>`

Exponentially scaled Bessel function of order $v$.

Defined as:
\[ jve(v, z) = jv(v, z) \times \exp(-\text{abs}(z \text{. imag})) \]

**Parameters**

- `v` [array_like] Order (float).
- `z` [array_like] Argument (float or complex).

**Returns**

- `J` [ndarray] Value of the exponentially scaled Bessel function.

**Notes**

For positive `v` values, the computation is carried out using the AMOS [1] `zbesj` routine, which exploits the connection to the modified Bessel function \( I_v \),

\[
J_v(z) = \exp(v\pi i/2)I_v(-iz) \quad (3z > 0)
\]

\[
J_v(z) = \exp(-v\pi i/2)I_v(iz) \quad (3z < 0)
\]

For negative `v` values the formula,

\[
J_{-v}(z) = J_v(z) \cos(\pi v) - Y_v(z) \sin(\pi v)
\]

is used, where \( Y_v(z) \) is the Bessel function of the second kind, computed using the AMOS routine `zbesy`. Note that the second term is exactly zero for integer `v`; to improve accuracy the second term is explicitly omitted for `v` values such that `v = \text{floor}(v)`.

**References**

[1]

scipy.special.yn

scipy.special.yn(n, x) = <ufunc 'yn'>

Bessel function of the second kind of integer order and real argument.

**Parameters**

- `n` [array_like] Order (integer).
- `z` [array_like] Argument (float).

**Returns**

- `Y` [ndarray] Value of the Bessel function, \( Y_n(x) \).

**See also:**

`yv`

For real order and real or complex argument.

**Notes**


The function is evaluated by forward recurrence on `n`, starting with values computed by the Cephes routines `y0` and `y1`. If `n = 0` or `1`, the routine for `y0` or `y1` is called directly.

**References**

[1]
scipy.special.yv

**scipy.special.yv(v, z) = <ufunc 'yv'>**

Bessel function of the second kind of real order and complex argument.

**Parameters**

v  
[array_like] Order (float).

z  
[array_like] Argument (float or complex).

**Returns**

Y  
[ndarray] Value of the Bessel function of the second kind, \( Y_v(x) \).

**See also:**

yve

\( Y_v \) with leading exponential behavior stripped off.

**Notes**

For positive \( v \) values, the computation is carried out using the AMOS [1] `zbesy` routine, which exploits the connection to the Hankel Bessel functions \( H^{(1)}_v \) and \( H^{(2)}_v \),

\[
Y_v(z) = \frac{1}{2i}(H^{(1)}_v - H^{(2)}_v).
\]

For negative \( v \) values the formula,

\[
Y_{-v}(z) = Y_v(z) \cos(\pi v) + J_v(z) \sin(\pi v)
\]

is used, where \( J_v(z) \) is the Bessel function of the first kind, computed using the AMOS routine `zbesi`. Note that the second term is exactly zero for integer \( v \); to improve accuracy the second term is explicitly omitted for \( v \) values such that \( v = \text{floor}(v) \).

**References**

[1]

scipy.special.yve

**scipy.special.yve(v, z) = <ufunc 'yve'>**

Exponentially scaled Bessel function of the second kind of real order.

Returns the exponentially scaled Bessel function of the second kind of real order \( v \) at complex \( z \):

\[
yve(v, z) = yv(v, z) \ast \exp(-\text{abs}(z.imag))
\]

**Parameters**

v  
[array_like] Order (float).

z  
[array_like] Argument (float or complex).

**Returns**

Y  
[ndarray] Value of the exponentially scaled Bessel function.

**Notes**

For positive \( v \) values, the computation is carried out using the AMOS [1] `zbesy` routine, which exploits the connection to the Hankel Bessel functions \( H^{(1)}_v \) and \( H^{(2)}_v \),

\[
Y_v(z) = \frac{1}{2i}(H^{(1)}_v - H^{(2)}_v).
\]
For negative $v$ values the formula,

$$Y_{-v}(z) = Y_v(z) \cos(\pi v) + J_v(z) \sin(\pi v)$$

is used, where $J_v(z)$ is the Bessel function of the first kind, computed using the AMOS routine _zbesj_. Note that the second term is exactly zero for integer $v$; to improve accuracy the second term is explicitly omitted for $v$ values such that $v = \text{floor}(v)$.

**References**

[1] scipy.special.kn

| scipy.special.kn(n, x) | = <ufunc ’kn’> |

Modified Bessel function of the second kind of integer order $n$

Returns the modified Bessel function of the second kind for integer order $n$ at real $z$.

These are also sometimes called functions of the third kind, Basset functions, or Macdonald functions.

**Parameters**

- **n** [array_like of int] Order of Bessel functions (floats will truncate with a warning)
- **z** [array_like of float] Argument at which to evaluate the Bessel functions

**Returns**

- **out** [ndarray] The results

**See also:**

- **kv**
  
  Same function, but accepts real order and complex argument

- **kvp**
  
  Derivative of this function

**Notes**


**References**

[1], [2]

**Examples**

Plot the function of several orders for real input:

```python
>>> from scipy.special import kn
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(0, 5, 1000)
>>> for N in range(6):
...     plt.plot(x, kn(N, x), label='$K_{%d}(x)$'.format(N))
>>> plt.ylim(0, 10)
>>> plt.legend()
>>> plt.title(r'Modified Bessel function of the second kind $K_n(x)$')
>>> plt.show()
```

Calculate for a single value at multiple orders:

```python
>>> kn([4, 5, 6], 1)
array([ 44.23241585, 360.9605896 , 3653.83831186])
```
scipy.special.kv

scipy.special.kv(v, z) = <ufunc 'kv'>

Modified Bessel function of the second kind of real order \( v \)

Returns the modified Bessel function of the second kind for real order \( v \) at complex \( z \).

These are also sometimes called functions of the third kind, Basset functions, or Macdonald functions. They are defined as those solutions of the modified Bessel equation for which,

\[
K_v(x) \sim \sqrt{\pi/(2x)} \exp(-x)
\]

as \( x \to \infty \) [3].

**Parameters**

- **v** [array_like of float] Order of Bessel functions
- **z** [array_like of complex] Argument at which to evaluate the Bessel functions

**Returns**

- **out** [ndarray] The results. Note that input must be of complex type to get complex output, e.g. \( \text{kv}(3, -2+0j) \) instead of \( \text{kv}(3, -2) \).

**See also:**

- **kve**
  This function with leading exponential behavior stripped off.

- **kvp**
  Derivative of this function

**Notes**


**References**

[1], [2], [3]
### Examples
Plot the function of several orders for real input:

```python
>>> from scipy.special import kv
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(0, 5, 1000)
>>> for N in np.linspace(0, 6, 5):
...     plt.plot(x, kv(N, x), label='$K_{{}\{}}} (x)$'.format(N))
>>> plt.ylim(0, 10)
>>> plt.legend()
>>> plt.title(r'Modified Bessel function of the second kind $K_{\nu}(x)$')
>>> plt.show()
```

![Modified Bessel function of the second kind](image)

Calculate for a single value at multiple orders:

```python
>>> kv([4, 4.5, 5], 1+2j)
array([ 0.1992+2.3892j, 2.3493+3.6j , 7.2827+3.8104j])
```

`scipy.special.kve`

`scipy.special.kve(v, z) = <ufunc 'kve'>`

Exponentially scaled modified Bessel function of the second kind.

Returns the exponentially scaled, modified Bessel function of the second kind (sometimes called the third kind) for real order \( \nu \) at complex \( z \):

\[
\text{kve}(v, z) = \text{kv}(v, z) \times \exp(z)
\]

**Parameters**

- **v** [array_like of float] Order of Bessel functions
- **z** [array_like of complex] Argument at which to evaluate the Bessel functions

**Returns**

- **out** [ndarray] The exponentially scaled modified Bessel function of the second kind.
Notes

References
[1], [2]

scipy.special.iv
scipy.special.iv(v, z) = <ufunc 'iv'>
Modified Bessel function of the first kind of real order.

Parameters
v [array_like] Order. If z is of real type and negative, v must be integer valued.
z [array_like of float or complex] Argument.

Returns
out [ndarray] Values of the modified Bessel function.

See also:
kve
This function with leading exponential behavior stripped off.

Notes
For real $z$ and $v \in [-50, 50]$, the evaluation is carried out using Temme’s method [1]. For larger orders, uniform asymptotic expansions are applied.

For complex $z$ and positive $v$, the AMOS [2] zbesi routine is called. It uses a power series for small $z$, the asymptotic expansion for large $\text{abs}(z)$, the Miller algorithm normalized by the Wronskian and a Neumann series for intermediate magnitudes, and the uniform asymptotic expansions for $I_v(z)$ and $J_v(z)$ for large orders. Backward recurrence is used to generate sequences or reduce orders when necessary.

The calculations above are done in the right half plane and continued into the left half plane by the formula,

$$I_v(z \exp(\pm i\pi)) = \exp(\pm \pi v) I_v(z)$$

(valid when the real part of $z$ is positive). For negative $v$, the formula

$$I_{-v}(z) = I_v(z) + \frac{2}{\pi} \sin(\pi v) K_v(z)$$

is used, where $K_v(z)$ is the modified Bessel function of the second kind, evaluated using the AMOS routine zbesk.

References
[1], [2]

scipy.special.ive
scipy.special.ive(v, z) = <ufunc 'ive'>
Exponentially scaled modified Bessel function of the first kind

Defined as:

$$\text{ive}(v, z) = \text{iv}(v, z) * \exp(-\text{abs}(z.\text{real}))$$

Parameters
v [array_like of float] Order.
z \text{ [array_like of float or complex] Argument.}

Returns

out \text{ [ndarray] Values of the exponentially scaled modified Bessel function.}

Notes
For positive $v$, the AMOS \cite{1} \texttt{zbesi} routine is called. It uses a power series for small $z$, the asymptotic expansion for large $\text{abs}(z)$, the Miller algorithm normalized by the Wronskian and a Neumann series for intermediate magnitudes, and the uniform asymptotic expansions for $I_v(z)$ and $J_v(z)$ for large orders. Backward recurrence is used to generate sequences or reduce orders when necessary.

The calculations above are done in the right half plane and continued into the left half plane by the formula,

$$I_v(z \exp(\pm \text{i}\pi)) = \exp(\pm \text{i}\pi v) I_v(z)$$

(valid when the real part of $z$ is positive). For negative $v$, the formula

$$I_{-v}(z) = I_v(z) + \frac{2}{\pi} \sin(\pi v) K_v(z)$$

is used, where $K_v(z)$ is the modified Bessel function of the second kind, evaluated using the AMOS routine \texttt{zbesk}.

References
\cite{1}

scipy.special.hankel1

\texttt{scipy.special.hankel1}(v, z) = <ufunc 'hankel1'>

Hankel function of the first kind

Parameters

\begin{itemize}
  \item \texttt{v} \text{ [array_like] Order (float).}
  \item \texttt{z} \text{ [array_like] Argument (float or complex).}
\end{itemize}

Returns

out \text{ [Values of the Hankel function of the first kind.]}

See also:

\texttt{hankel1e}

this function with leading exponential behavior stripped off.

Notes
A wrapper for the AMOS \cite{1} routine \texttt{zbesh}, which carries out the computation using the relation,

$$H^{(1)}_v(z) = \frac{2}{\text{i}\pi} \exp(-\text{i}\pi v/2) K_v(z \exp(-\text{i}\pi/2))$$

where $K_v$ is the modified Bessel function of the second kind. For negative orders, the relation

$$H^{(1)}_{-v}(z) = H^{(1)}_v(z) \exp(\text{i}\pi v)$$

is used.

References
\cite{1}
scipy.special.hankel1e
scipy.special.hankel1e(v, z) = <ufunc 'hankel1e'>
Exponentially scaled Hankel function of the first kind
Defined as:
\[ hankel1e(v, z) = hankel1(v, z) * \exp(-1j * z) \]

**Parameters**
- **v** [array_like] Order (float).
- **z** [array_like] Argument (float or complex).

**Returns**
- **out** [Values of the exponentially scaled Hankel function.]

**Notes**
A wrapper for the AMOS /1/ routine zbesh, which carries out the computation using the relation,
\[ H^{(1)}_v(z) = \frac{2}{\imath \pi} \exp(-\imath \pi v/2) K_v(z \exp(-\imath \pi/2)) \]
where \( K_v \) is the modified Bessel function of the second kind. For negative orders, the relation
\[ H^{(1)}_{-v}(z) = H^{(1)}_v(z) \exp(\imath \pi v) \]
is used.

**References**
/1/

scipy.special.hankel2
scipy.special.hankel2(v, z) = <ufunc 'hankel2'>
Hankel function of the second kind

**Parameters**
- **v** [array_like] Order (float).
- **z** [array_like] Argument (float or complex).

**Returns**
- **out** [Values of the Hankel function of the second kind.]

**See also:**

hankel2e
this function with leading exponential behavior stripped off.

**Notes**
A wrapper for the AMOS /1/ routine zbesh, which carries out the computation using the relation,
\[ H^{(2)}_v(z) = -\frac{2}{\imath \pi} \exp(\imath \pi v/2) K_v(z \exp(\imath \pi/2)) \]
where \( K_v \) is the modified Bessel function of the second kind. For negative orders, the relation
\[ H^{(2)}_{-v}(z) = H^{(2)}_v(z) \exp(-\imath \pi v) \]
is used.
References

[1]

scipy.special.hankel2e

scipy.special.hankel2e(v, z) = <ufunc 'hankel2e'>

Exponentially scaled Hankel function of the second kind

Defined as:

\[ hankel2e(v, z) = hankel2(v, z) \times \exp(1j \times z) \]

Parameters

\( v \) [array_like] Order (float).
\( z \) [array_like] Argument (float or complex).

Returns

\( out \) [Values of the exponentially scaled Hankel function of the second kind.]

Notes

A wrapper for the AMOS [1] routine zbesh, which carries out the computation using the relation,

\[ H^{(2)}_v(z) = -\frac{2}{i\pi} \exp(\frac{i\pi v}{2}) K_v(z\exp(\frac{i\pi}{2})) \]

where \( K_v \) is the modified Bessel function of the second kind. For negative orders, the relation

\[ H^{(2)}_{-v}(z) = H^{(2)}_v(z) \exp(-i\pi v) \]

is used.

References

[1]

The following is not an universal function:

\[ \lambda \] Jahnke-Emden Lambda function, Lambdav(x).

scipy.special.lmbda

scipy.special.lmbda(v, x)

Jahnke-Emden Lambda function, Lambdav(x).

This function is defined as [2],

\[ \Lambda_v(x) = \Gamma(v+1) \frac{J_v(x)}{(x/2)^v}, \]

where \( \Gamma \) is the gamma function and \( J_v \) is the Bessel function of the first kind.

Parameters

\( v \) [float] Order of the Lambda function
\( x \) [float] Value at which to evaluate the function and derivatives

Returns

\( vl \) [ndarray] Values of Lambda_vi(x), for \( vi=v-int(v) \), \( vi=1+v-int(v) \), ..., \( vi=v \).
\( dl \) [ndarray] Derivatives Lambda_vi'(x), for \( vi=v-int(v) \), \( vi=1+v-int(v) \), ..., \( vi=v \).

References

[1], [2]
**Zeros of Bessel Functions**

These are not universal functions:

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<tr>
<td><code>jyn_zeros(n, nt)</code></td>
<td>Compute nt zeros of Bessel functions J_n(x), J'_n(x), Y_n(x), and Y'_n(x).</td>
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<tr>
<td><code>jn_zeros(n, nt)</code></td>
<td>Compute zeros of integer-order Bessel function J_n(x).</td>
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</tr>
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<td><code>y1_zeros(nt[, complex])</code></td>
<td>Compute nt zeros of Bessel function Y_1(z), and derivative at each zero.</td>
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<td><code>y1p_zeros(nt[, complex])</code></td>
<td>Compute nt zeros of Bessel derivative Y'_1(z), and value at each zero.</td>
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</table>

**scipy.special.jnjnp_zeros**

`scipy.special.jnjnp_zeros(nt)`

Compute zeros of integer-order Bessel functions J_n and J'_n.

Results are arranged in order of the magnitudes of the zeros.

**Parameters**

- `nt` : [int] Number (<=1200) of zeros to compute

**Returns**

- `zo[l-1]` : [ndarray] Value of the lth zero of J_n(x) and J'_n(x). Of length `nt`.
- `n[l-1]` : [ndarray] Order of the J_n(x) or J'_n(x) associated with lth zero. Of length `nt`.
- `m[l-1]` : [ndarray] Serial number of the zeros of J_n(x) or J'_n(x) associated with lth zero. Of length `nt`.
- `t[l-1]` : [ndarray] 0 if lth zero in zo is zero of J_n(x), 1 if it is a zero of J'_n(x). Of length `nt`.

**See also:**

`jn_zeros, jnp_zeros`

**References**

[1]

**scipy.special.jyn_zeros**

`scipy.special.jyn_zeros(n, nt)`

Compute nt zeros of Bessel functions J_n(x), J'_n(x), Y_n(x), and Y'_n(x).

Returns 4 arrays of length `nt`, corresponding to the first `nt` zeros of J_n(x), J'_n(x), Y_n(x), and Y'_n(x), respectively.

**Parameters**

- `n` : [int] Order of the Bessel functions
SciPy Reference Guide, Release 1.2.0

```python
nt  [int] Number (<=1200) of zeros to compute

See jn_zeros, jnp_zeros, yn_zeros, ynp_zeros to get separate arrays.

References
[1]
```

```python
scipy.special.jn_zeros

scipy.special.jn_zeros(n, nt)
  Compute zeros of integer-order Bessel function Jn(x).

  Parameters
  n  [int] Order of Bessel function
  nt [int] Number of zeros to return

  References
  [1]
```

```python
scipy.special.jnp_zeros

scipy.special.jnp_zeros(n, nt)
  Compute zeros of integer-order Bessel function derivative Jn'(x).

  Parameters
  n  [int] Order of Bessel function
  nt [int] Number of zeros to return

  References
  [1]
```

```python
scipy.special.yn_zeros

scipy.special.yn_zeros(n, nt)
  Compute zeros of integer-order Bessel function Yn(x).

  Parameters
  n  [int] Order of Bessel function
  nt [int] Number of zeros to return

  References
  [1]
```

```python
scipy.special.ynp_zeros

scipy.special.ynp_zeros(n, nt)
  Compute zeros of integer-order Bessel function derivative Yn'(x).

  Parameters
  n  [int] Order of Bessel function
  nt [int] Number of zeros to return

  References
  [1]
```
scipy.special.y0_zeros

**scipy.special.y0_zeros**(nt, complex=False)
Compute nt zeros of Bessel function $Y_0(z)$, and derivative at each zero.

The derivatives are given by $Y_0'(z_0) = -Y_1(z_0)$ at each zero $z_0$.

**Parameters**

- nt: [int] Number of zeros to return
- complex: [bool, default False] Set to False to return only the real zeros; set to True to return only the complex zeros with negative real part and positive imaginary part. Note that the complex conjugates of the latter are also zeros of the function, but are not returned by this routine.

**Returns**

- z0n: [ndarray] Location of nth zero of $Y_0(z)$
- y0pz0n: [ndarray] Value of derivative $Y_0'(z_0)$ for nth zero

**References**

[1]

scipy.special.y1_zeros

**scipy.special.y1_zeros**(nt, complex=False)
Compute nt zeros of Bessel function $Y_1(z)$, and derivative at each zero.

The derivatives are given by $Y_1'(z_1) = Y_0(z_1)$ at each zero $z_1$.

**Parameters**

- nt: [int] Number of zeros to return
- complex: [bool, default False] Set to False to return only the real zeros; set to True to return only the complex zeros with negative real part and positive imaginary part. Note that the complex conjugates of the latter are also zeros of the function, but are not returned by this routine.

**Returns**

- z1n: [ndarray] Location of nth zero of $Y_1(z)$
- y1pz1n: [ndarray] Value of derivative $Y_1'(z_1)$ for nth zero

**References**

[1]

scipy.special.y1p_zeros

**scipy.special.y1p_zeros**(nt, complex=False)
Compute nt zeros of Bessel derivative $Y_1'(z)$, and value at each zero.

The values are given by $Y_1(z_1)$ at each $z_1$ where $Y_1'(z_1)=0$.

**Parameters**

- nt: [int] Number of zeros to return
- complex: [bool, default False] Set to False to return only the real zeros; set to True to return only the complex zeros with negative real part and positive imaginary part. Note that the complex conjugates of the latter are also zeros of the function, but are not returned by this routine.

**Returns**

- z1p: [ndarray] Location of nth zero of $Y_1(z)$
- y1pz1p: [ndarray] Value of derivative $Y_1'(z_1)$ for nth zero

**References**

[1]
### z1pn
- ndarray: Location of nth zero of Y1'(z)

### y1z1pn
- ndarray: Value of derivative Y1(z1) for nth zero

### References

[1]

### Faster versions of common Bessel Functions

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### scipy.special.j0

The function `scipy.special.j0(x)` returns the Bessel function of the first kind of order 0.

#### Parameters

- `x`: array_like Argument (float).

#### Returns

- `J`: ndarray Value of the Bessel function of the first kind of order 0 at `x`.

#### See also:

- jv: Bessel function of real order and complex argument.
- spherical_jn: spherical Bessel functions.

#### Notes

The domain is divided into the intervals [0, 5] and (5, infinity). In the first interval the following rational approximation is used:

\[
J_0(x) \approx (w - r_1^2)(w - r_2^2) \frac{P_3(w)}{Q_8(w)},
\]

where $w = x^2$ and $r_1, r_2$ are the zeros of $J_0$, and $P_3$ and $Q_8$ are polynomials of degrees 3 and 8, respectively.
In the second interval, the Hankel asymptotic expansion is employed with two rational functions of degree 6/6 and 7/7.

This function is a wrapper for the Cephes [1] routine j0. It should not be confused with the spherical Bessel functions (see spherical_jn).

References
[1]

scipy.special.j1

scipy.special.j1(x) = <ufunc 'j1'>
Bessel function of the first kind of order 1.

Parameters
x [array_like] Argument (float).

Returns
J [ndarray] Value of the Bessel function of the first kind of order 1 at x.

See also:

jv

spherical_jn

spherical Bessel functions.

Notes
The domain is divided into the intervals [0, 8] and (8, infinity). In the first interval a 24 term Chebyshev expansion is used. In the second, the asymptotic trigonometric representation is employed using two rational functions of degree 5/5.

This function is a wrapper for the Cephes [1] routine j1. It should not be confused with the spherical Bessel functions (see spherical_jn).

References
[1]

scipy.special.y0

scipy.special.y0(x) = <ufunc 'y0'>
Bessel function of the second kind of order 0.

Parameters
x [array_like] Argument (float).

Returns
Y [ndarray] Value of the Bessel function of the second kind of order 0 at x.

See also:

j0, jv

Notes
The domain is divided into the intervals [0, 5] and (5, infinity). In the first interval a rational approximation $R(x)$ is employed to compute,

$$
Y_0(x) = R(x) + \frac{2\log(x)J_0(x)}{\pi},
$$
where $J_0$ is the Bessel function of the first kind of order 0.

In the second interval, the Hankel asymptotic expansion is employed with two rational functions of degree 6/6 and 7/7.

This function is a wrapper for the Cephes \[1\] routine $y0$.

**References**

\[1\]

**scipy.special.y1**

```python
scipy.special.y1(x) = <ufunc 'y1'>
```

Bessel function of the second kind of order 1.

**Parameters**

- $x$ [array_like] Argument (float).

**Returns**

- $Y$ [ndarray] Value of the Bessel function of the second kind of order 1 at $x$.

**See also:**

`j1`, `yn`, `yv`

**Notes**

The domain is divided into the intervals $[0, 8]$ and $(8, \infty)$. In the first interval a 25 term Chebyshev expansion is used, and computing $J_1$ (the Bessel function of the first kind) is required. In the second, the asymptotic trigonometric representation is employed using two rational functions of degree 5/5.

This function is a wrapper for the Cephes \[1\] routine $y1$.

**References**

\[1\]

**scipy.special.i0**

```python
scipy.special.i0(x) = <ufunc 'i0'>
```

Modified Bessel function of order 0.

Defined as,

$$I_0(x) = \sum_{k=0}^{\infty} \frac{(x^2/4)^k}{(k!)^2} = J_0(1x),$$

where $J_0$ is the Bessel function of the first kind of order 0.

**Parameters**

- $x$ [array_like] Argument (float)

**Returns**

- $I$ [ndarray] Value of the modified Bessel function of order 0 at $x$.

**See also:**

`iv`, `i0e`

**Notes**

The range is partitioned into the two intervals $[0, 8]$ and $(8, \infty)$. Chebyshev polynomial expansions are employed in each interval.

This function is a wrapper for the Cephes \[1\] routine $i0$. 
References
[1]

scipy.special.i0e

scipy.special.i0e(x) = <ufunc 'i0e'>
Exponentially scaled modified Bessel function of order 0.
Defined as:
\[ i0e(x) = \exp(-\text{abs}(x)) \times i0(x). \]

Parameters
- x [array_like] Argument (float)

Returns
- I [ndarray] Value of the exponentially scaled modified Bessel function of order 0 at x.

See also:
i0, i0

Notes
The range is partitioned into the two intervals [0, 8] and (8, infinity). Chebyshev polynomial expansions are employed in each interval. The polynomial expansions used are the same as those in i0, but they are not multiplied by the dominant exponential factor.

This function is a wrapper for the Cephes [1] routine i0e.

References
[1]

scipy.special.i1

scipy.special.i1(x) = <ufunc 'i1'>
Modified Bessel function of order 1.
Defined as,
\[ I_1(x) = \frac{1}{2} \sum_{k=0}^{\infty} \frac{(x^2/4)^k}{k!(k+1)!} = -iJ_1(ix), \]
where \( J_1 \) is the Bessel function of the first kind of order 1.

Parameters
- x [array_like] Argument (float)

Returns
- I [ndarray] Value of the modified Bessel function of order 1 at x.

See also:
i0, i0e
Notes
The range is partitioned into the two intervals [0, 8] and (8, infinity). Chebyshev polynomial expansions are employed in each interval.

This function is a wrapper for the Cephes \[1\] routine i1.

References
[1]

\texttt{scipy.special.i1e}

\texttt{scipy.special.i1e(x) = <ufunc 'i1e'>}

Exponentially scaled modified Bessel function of order 1.

Defined as:

\[
i1e(x) = \exp(-\text{abs}(x)) \times i1(x)
\]

Parameters
\[x\] [array_like] Argument (float)

Returns
\[I\] [ndarray] Value of the exponentially scaled modified Bessel function of order 1 at \[x\].

See also:
\texttt{i0}, \texttt{i1}

Notes
The range is partitioned into the two intervals [0, 8] and (8, infinity). Chebyshev polynomial expansions are employed in each interval. The polynomial expansions used are the same as those in \texttt{i1}, but they are not multiplied by the dominant exponential factor.

This function is a wrapper for the Cephes \[1\] routine \texttt{i1e}.

References
[1]

\texttt{scipy.special.k0}

\texttt{scipy.special.k0(x) = <ufunc 'k0'>}

Modified Bessel function of the second kind of order 0, \(K_0\).

This function is also sometimes referred to as the modified Bessel function of the third kind of order 0.

Parameters
\[x\] [array_like] Argument (float).

Returns
\[K\] [ndarray] Value of the modified Bessel function \(K_0\) at \(x\).

See also:
\texttt{kv}, \texttt{k0e}
Notes
The range is partitioned into the two intervals [0, 2] and (2, infinity). Chebyshev polynomial expansions are employed in each interval.

This function is a wrapper for the Cephes [1] routine $k0$.

References
[1]

scipy.special.k0e

scipy.special.k0e(x) = <ufunc 'k0e'>
Exponentially scaled modified Bessel function $K$ of order 0

Defined as:

\[ k0e(x) = \exp(x) \times k0(x). \]

Parameters
x [array_like] Argument (float)

Returns
K [ndarray] Value of the exponentially scaled modified Bessel function $K$ of order 0 at $x$.

See also:
$kv$, $k0$

Notes
The range is partitioned into the two intervals [0, 2] and (2, infinity). Chebyshev polynomial expansions are employed in each interval.

This function is a wrapper for the Cephes [1] routine $k0e$.

References
[1]

scipy.special.k1

scipy.special.k1(x) = <ufunc 'k1'>
Modified Bessel function of the second kind of order 1, $K_1(x)$.

Parameters
x [array_like] Argument (float)

Returns
K [ndarray] Value of the modified Bessel function $K$ of order 1 at $x$.

See also:
$kv$, $k1e$

Notes
The range is partitioned into the two intervals [0, 2] and (2, infinity). Chebyshev polynomial expansions are employed in each interval.

This function is a wrapper for the Cephes [1] routine $k1$. 
References
[1]

**scipy.special.k1e**

**scipy.special.k1e(x) = <ufunc 'k1e'>**
Exponentially scaled modified Bessel function K of order 1

Defined as:

\[ k1e(x) = \exp(x) \ast k1(x) \]

**Parameters**

- **x** [array_like] Argument (float)

**Returns**

- **K** [ndarray] Value of the exponentially scaled modified Bessel function K of order 1 at x.

**See also:**

- kv, k1

**Notes**
The range is partitioned into the two intervals \([0, 2]\) and \((2, \infty)\). Chebyshev polynomial expansions are employed in each interval.

This function is a wrapper for the Cephes [1] routine k1e.

**References**
[1]

**Integrals of Bessel Functions**

<table>
<thead>
<tr>
<th>itj0y0(x)</th>
<th>Integrals of Bessel functions of order 0</th>
</tr>
</thead>
<tbody>
<tr>
<td>it2j0y0(x)</td>
<td>Integrals related to Bessel functions of order 0</td>
</tr>
<tr>
<td>iti0k0(x)</td>
<td>Integrals of modified Bessel functions of order 0</td>
</tr>
<tr>
<td>it2i0k0(x)</td>
<td>Integrals related to modified Bessel functions of order 0</td>
</tr>
<tr>
<td>besselpoly(a, lmb, nu)</td>
<td>Weighted integral of a Bessel function.</td>
</tr>
</tbody>
</table>

**scipy.special.itj0y0**

**scipy.special.itj0y0(x) = <ufunc 'itj0y0'>**
Integrals of Bessel functions of order 0

Returns simple integrals from 0 to \(x\) of the zeroth order Bessel functions \(j0\) and \(y0\).

**Returns**

- ij0, iy0

**scipy.special.it2j0y0**

**scipy.special.it2j0y0(x) = <ufunc 'it2j0y0'>**
Integrals related to Bessel functions of order 0

**Returns**
\[
\text{ij0} \quad \int \frac{(1-j_0(t))}{t} \, dt, \quad t=0..x \\
\text{iy0} \quad \int \frac{y_0(t)}{t} \, dt, \quad t=x..\infty
\]

**scipy.special.iti0k0**

**scipy.special.iti0k0**(x) = <ufunc 'iti0k0'>

Integrals of modified Bessel functions of order 0

Returns simple integrals from 0 to \( x \) of the zeroth order modified Bessel functions \( i_0 \) and \( k_0 \).

Returns

\( ii0, ik0 \)

**scipy.special.it2i0k0**

**scipy.special.it2i0k0**(x) = <ufunc 'it2i0k0'>

Integrals related to modified Bessel functions of order 0

Returns

\( ii0 \quad \int \frac{(i_0(t)-1)}{t} \, dt, \quad t=0..x \\
\text{ik0} \quad \int \frac{k_0(t)}{t} \, dt, \quad t=x..\infty
\]

**scipy.special.besselpoly**

**scipy.special.besselpoly**(a, lmb, nu) = <ufunc 'besselpoly'>

Weighted integral of a Bessel function.

\[
\int_0^1 x^\lambda J_\nu(2ax) \, dx
\]

where \( J_\nu \) is a Bessel function and \( \lambda = lmb, \nu = nu \).

**Derivatives of Bessel Functions**

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>\text{jvp} ( v, z, n )</td>
<td>Compute nth derivative of Bessel function ( J_v(z) ) with respect to ( z ).</td>
</tr>
<tr>
<td>\text{yvp} ( v, z, n )</td>
<td>Compute nth derivative of Bessel function ( Y_v(z) ) with respect to ( z ).</td>
</tr>
<tr>
<td>\text{kvp} ( v, z, n )</td>
<td>Compute nth derivative of real-order modified Bessel function ( K_v(z) ).</td>
</tr>
<tr>
<td>\text{ivp} ( v, z, n )</td>
<td>Compute nth derivative of modified Bessel function ( I_v(z) ) with respect to ( z ).</td>
</tr>
<tr>
<td>\text{h1vp} ( v, z, n )</td>
<td>Compute nth derivative of Hankel function ( H_{1v}(z) ) with respect to ( z ).</td>
</tr>
<tr>
<td>\text{h2vp} ( v, z, n )</td>
<td>Compute nth derivative of Hankel function ( H_{2v}(z) ) with respect to ( z ).</td>
</tr>
</tbody>
</table>

**scipy.special.jvp**

**scipy.special.jvp** \( (v, z, n=1) \)

Compute nth derivative of Bessel function \( J_v(z) \) with respect to \( z \).

**Parameters**

\( v \quad \text{[float]} \) Order of Bessel function
\( z \quad \text{[complex]} \) Argument at which to evaluate the derivative

6.26. Special functions (scipy.special) 1887
n [int, default 1] Order of derivative

Notes
The derivative is computed using the relation DLFM 10.6.7 [2].

References
[1], [2]

scipy.special.yvp

scipy.special.yvp(v, z, n=1)
Compute nth derivative of Bessel function Yv(z) with respect to z.

Parameters
v [float] Order of Bessel function
z [complex] Argument at which to evaluate the derivative
n [int, default 1] Order of derivative

Notes
The derivative is computed using the relation DLFM 10.6.7 [2].

References
[1], [2]

scipy.special.kvp

scipy.special.kvp(v, z, n=1)
Compute nth derivative of real-order modified Bessel function Kv(z)

Kv(z) is the modified Bessel function of the second kind. Derivative is calculated with respect to z.

Parameters
v [array_like of float] Order of Bessel function
z [array_like of complex] Argument at which to evaluate the derivative
n [int] Order of derivative. Default is first derivative.

Returns
out [ndarray] The results

Notes
The derivative is computed using the relation DLFM 10.29.5 [2].

References
[1], [2]

Examples
Calculate multiple values at order 5:

```python
>>> from scipy.special import kvp
>>> kvp(5, (1, 2, 3+5j))
array([-1.84903536+0.j , -2.57735387+0.j , -3.06627741+0.08750845j])
```

Calculate for a single value at multiple orders:

```python
>>> kvp((4, 4.5, 5), 1)
array([ 184.0309,  -568.9585,  -1849.0354])
```
scipy.special.ivp

scipy.special.ivp(v, z, n=1)
Compute nth derivative of modified Bessel function Iv(z) with respect to z.

Parameters
- v : array_like of float
  Order of Bessel function
- z : array_like of complex
  Argument at which to evaluate the derivative
- n : int, default 1
  Order of derivative

Notes
The derivative is computed using the relation DLFM 10.29.5 [2].

References
[1], [2]

scipy.special.h1vp

scipy.special.h1vp(v, z, n=1)
Compute nth derivative of Hankel function H1v(z) with respect to z.

Parameters
- v : float
  Order of Hankel function
- z : complex
  Argument at which to evaluate the derivative
- n : int, default 1
  Order of derivative

Notes
The derivative is computed using the relation DLFM 10.6.7 [2].

References
[1], [2]

scipy.special.h2vp

scipy.special.h2vp(v, z, n=1)
Compute nth derivative of Hankel function H2v(z) with respect to z.

Parameters
- v : float
  Order of Hankel function
- z : complex
  Argument at which to evaluate the derivative
- n : int, default 1
  Order of derivative

Notes
The derivative is computed using the relation DLFM 10.6.7 [2].

References
[1], [2]

Spherical Bessel Functions

- spherical_jn(n, z[, derivative])
  Spherical Bessel function of the first kind or its derivative.
- spherical_yn(n, z[, derivative])
  Spherical Bessel function of the second kind or its derivative.
- spherical_in(n, z[, derivative])
  Modified spherical Bessel function of the first kind or its derivative.
- spherical_kn(n, z[, derivative])
  Modified spherical Bessel function of the second kind or its derivative.
scipy.special.spherical_jn

scipy.special.spherical_jn(n, z, derivative=False)
Spherical Bessel function of the first kind or its derivative.

Defined as [1],

\[ j_n(z) = \sqrt{\frac{\pi}{2z}} J_{n+1/2}(z), \]

where \( J_n \) is the Bessel function of the first kind.

Parameters

- **n** [int, array_like] Order of the Bessel function (\( n \geq 0 \)).
- **z** [complex or float, array_like] Argument of the Bessel function.
- **derivative** [bool, optional] If True, the value of the derivative (rather than the function itself) is returned.

Returns

- **jn** [ndarray]

Notes

For real arguments greater than the order, the function is computed using the ascending recurrence [2]. For small real or complex arguments, the definitional relation to the cylindrical Bessel function of the first kind is used.

The derivative is computed using the relations [3],

\[ j'_n(z) = j_{n-1}(z) - \frac{n + 1}{z} j_n(z). \]
\[ j'_0(z) = -j_1(z) \]

New in version 0.18.0.

References

[1], [2], [3]

scipy.special.spherical_yn

scipy.special.spherical_yn(n, z, derivative=False)
Spherical Bessel function of the second kind or its derivative.

Defined as [1],

\[ y_n(z) = \sqrt{\frac{\pi}{2z}} Y_{n+1/2}(z), \]

where \( Y_n \) is the Bessel function of the second kind.

Parameters

- **n** [int, array_like] Order of the Bessel function (\( n \geq 0 \)).
- **z** [complex or float, array_like] Argument of the Bessel function.
- **derivative** [bool, optional] If True, the value of the derivative (rather than the function itself) is returned.

Returns

- **yn** [ndarray]
Notes
For real arguments, the function is computed using the ascending recurrence [2]. For complex arguments, the definitional relation to the cylindrical Bessel function of the second kind is used.

The derivative is computed using the relations [3],

\[ y'_n = y_{n-1} - \frac{n+1}{z} y_n. \]
\[ y'_0 = -y_1 \]

New in version 0.18.0.

References
[1], [2], [3]

scipy.special.spherical_in

scipy.special.spherical_in(n, z, derivative=False)
Modified spherical Bessel function of the first kind or its derivative.

Defined as [1],

\[ i_n(z) = \sqrt{\frac{\pi}{2z}} I_{n+1/2}(z), \]

where \( I_n \) is the modified Bessel function of the first kind.

Parameters
n [int, array_like] Order of the Bessel function (n >= 0).
z [complex or float, array_like] Argument of the Bessel function.
derivative [bool, optional] If True, the value of the derivative (rather than the function itself) is returned.

Returns
in [ndarray]

Notes
The function is computed using its definitional relation to the modified cylindrical Bessel function of the first kind.

The derivative is computed using the relations [2],

\[ i'_n = i_{n-1} - \frac{n+1}{z} i_n. \]
\[ i'_0 = i_0 \]

New in version 0.18.0.

References
[1], [2]

scipy.special.spherical_kn

scipy.special.spherical_kn(n, z, derivative=False)
Modified spherical Bessel function of the second kind or its derivative.

Defined as [1],

\[ k_n(z) = \sqrt{\frac{\pi}{2z}} K_{n+1/2}(z), \]
where \( K_n \) is the modified Bessel function of the second kind.

**Parameters**

- \( n \) [int, array_like] Order of the Bessel function (\( n \geq 0 \)).
- \( z \) [complex or float, array_like] Argument of the Bessel function.
- \texttt{derivative} [bool, optional] If True, the value of the derivative (rather than the function itself) is returned.

**Returns**

- \( kn \) [ndarray]

**Notes**

The function is computed using its definitional relation to the modified cylindrical Bessel function of the second kind.

The derivative is computed using the relations [2],

\[
\frac{d}{dz}k_n = k_{n-1} - \frac{n+1}{z}k_n.
\]

\( k'_0 = -k_1 \)

New in version 0.18.0.

**References**

[1], [2]

**Riccati-Bessel Functions**

These are not universal functions:

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>\texttt{riccati_jn}(n, x)</td>
<td>Compute Ricatti-Bessel function of the first kind and its derivative.</td>
</tr>
<tr>
<td>\texttt{riccati_yn}(n, x)</td>
<td>Compute Ricatti-Bessel function of the second kind and its derivative.</td>
</tr>
</tbody>
</table>

**scipy.special.riccati_jn**

\texttt{scipy.special.riccati_jn}(n, x)

Compute Ricatti-Bessel function of the first kind and its derivative.

The Ricatti-Bessel function of the first kind is defined as \( xj_n(x) \), where \( j_n \) is the spherical Bessel function of the first kind of order \( n \).

This function computes the value and first derivative of the Ricatti-Bessel function for all orders up to and including \( n \).

**Parameters**

- \( n \) [int] Maximum order of function to compute
- \( x \) [float] Argument at which to evaluate

**Returns**

- \( jn \) [ndarray] Value of \( j_0(x) \), …, \( j_n(x) \)
- \( jnp \) [ndarray] First derivative \( j'_0(x) \), …, \( j'_n(x) \)

**Notes**

The computation is carried out via backward recurrence, using the relation DLMF 10.51.1 [2].

Wrapper for a Fortran routine created by Shanjie Zhang and Jianming Jin [1].
scipy.special.riccati_yn

scipy.special.riccati_yn(n, x)

Compute Ricatti-Bessel function of the second kind and its derivative.

The Ricatti-Bessel function of the second kind is defined as $xy_n(x)$, where $y_n$ is the spherical Bessel function of the second kind of order $n$.

This function computes the value and first derivative of the function for all orders up to and including $n$.

Parameters

- n [int] Maximum order of function to compute
- x [float] Argument at which to evaluate

Returns

- yn [ndarray] Value of $y_0(x)$, ..., $y_n(x)$
- ynp [ndarray] First derivative $y_0'(x)$, ..., $y_n'(x)$

Notes

The computation is carried out via ascending recurrence, using the relation DLMF 10.51.1 [2].

Wrapper for a Fortran routine created by Shanjie Zhang and Jianming Jin [1].

References

[1], [2]

Struve Functions

- struve(v, x) Struve function.
- modstruve(v, x) Modified Struve function.
- itstruve0(x) Integral of the Struve function of order 0.
- it2struve0(x) Integral related to the Struve function of order 0.
- itmodstruve0(x) Integral of the modified Struve function of order 0.

scipy.special.struve

scipy.special.struve(v, x) = <ufunc 'struve'>

Struve function.

Return the value of the Struve function of order $v$ at $x$. The Struve function is defined as,

$$H_v(x) = (z/2)^{v+1} \sum_{n=0}^\infty \frac{(-1)^n(z/2)^{2n}}{\Gamma(n+\frac{3}{2})\Gamma(n+v+\frac{3}{2})},$$

where $\Gamma$ is the gamma function.

Parameters

- v [array_like] Order of the Struve function (float).
- x [array_like] Argument of the Struve function (float; must be positive unless $v$ is an integer).

Returns

- H [ndarray] Value of the Struve function of order $v$ at $x$. 
See also:

modstruve

Notes

Three methods discussed in [1] are used to evaluate the Struve function:

- power series
- expansion in Bessel functions (if $|z| < |v| + 20$)
- asymptotic large-$z$ expansion (if $z \geq 0.7v + 12$

Rounding errors are estimated based on the largest terms in the sums, and the result associated with the smallest error is returned.

References

[1] scipy.special.itstruve0

scipy.special.itstruve0(x) = <ufunc 'itstruve0'>

Integral of the Struve function of order 0.

\[ I = \int_0^x H_0(t) \, dt \]
\( x \quad \) [array_like] Upper limit of integration (float).

**Returns**

\( I \quad \) [ndarray] The integral of \( H_0 \) from 0 to \( x \).

**See also:**

struve

**Notes**

Wrapper for a Fortran routine created by Shanjie Zhang and Jianming Jin [1].

**References**

[1]

scipy.special.it2struve0

scipy.special.it2struve0(x) = <ufunc 'it2struve0'>

Integral related to the Struve function of order 0.

Returns the integral,

\[
\int_x^\infty \frac{H_0(t)}{t} \, dt
\]

where \( H_0 \) is the Struve function of order 0.

**Parameters**

\( x \quad \) [array_like] Lower limit of integration.

**Returns**

\( I \quad \) [ndarray] The value of the integral.

**See also:**

struve

**Notes**

Wrapper for a Fortran routine created by Shanjie Zhang and Jianming Jin [1].

**References**

[1]

scipy.special.itmodstruve0

scipy.special.itmodstruve0(x) = <ufunc 'itmodstruve0'>

Integral of the modified Struve function of order 0.

\[
I = \int_0^x L_0(t) \, dt
\]

**Parameters**

\( x \quad \) [array_like] Upper limit of integration (float).

**Returns**

\( I \quad \) [ndarray] The integral of \( L_0 \) from 0 to \( x \).

**Notes**

Wrapper for a Fortran routine created by Shanjie Zhang and Jianming Jin [1].

**References**

[1]
### Raw Statistical Functions

See also:

```python
scipy.stats`: Friendly versions of these functions.
```

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<tr>
<th>Function</th>
<th>Description</th>
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<tbody>
<tr>
<td><code>bdtr(k, n, p)</code></td>
<td>Binomial distribution cumulative distribution function.</td>
</tr>
<tr>
<td><code>bdtrc(k, n, p)</code></td>
<td>Binomial distribution survival function.</td>
</tr>
<tr>
<td><code>bdtrik(y, n, p)</code></td>
<td>Inverse function to <code>bdtr</code> with respect to <code>p</code>.</td>
</tr>
<tr>
<td><code>bdtrin(k, y, p)</code></td>
<td>Inverse function to <code>bdtr</code> with respect to <code>n</code>.</td>
</tr>
<tr>
<td><code>btdtr(a, b, x)</code></td>
<td>Cumulative density function of the beta distribution.</td>
</tr>
<tr>
<td><code>btdtri(a, b, p)</code></td>
<td>The $p$-th quantile of the beta distribution.</td>
</tr>
<tr>
<td><code>btdtrib(a, p, x)</code></td>
<td>Inverse of <code>btdtr</code> with respect to <code>a</code>.</td>
</tr>
<tr>
<td><code>btdtria(p, b, x)</code></td>
<td>Inverse of <code>btdtr</code> with respect to <code>b</code>.</td>
</tr>
<tr>
<td><code>fdtr(dfn, dfd, x)</code></td>
<td>F cumulative distribution function.</td>
</tr>
<tr>
<td><code>fdtrc(dfn, dfd, x)</code></td>
<td>F survival function.</td>
</tr>
<tr>
<td><code>fdtridfd(dfn, p, x)</code></td>
<td>Inverse to <code>fdtr</code> vs <code>dfd</code>.</td>
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<tr>
<td><code>fdtrib(a, p, x)</code></td>
<td>Gamma distribution cumulative density function.</td>
</tr>
<tr>
<td><code>fdtria(p, b, x)</code></td>
<td>Gamma distribution survival function.</td>
</tr>
<tr>
<td><code>gdtr(a, b, x)</code></td>
<td>Inverse of <code>gdtr</code> vs <code>a</code>.</td>
</tr>
<tr>
<td><code>gdtrc(a, b, x)</code></td>
<td>Inverse of <code>gdtr</code> vs <code>b</code>.</td>
</tr>
<tr>
<td><code>nbdtr(k, n, p)</code></td>
<td>Negative binomial cumulative distribution function.</td>
</tr>
<tr>
<td><code>nbdtrc(k, n, p)</code></td>
<td>Negative binomial survival function.</td>
</tr>
<tr>
<td><code>nbdtrik(y, n, p)</code></td>
<td>Inverse of <code>nbdtr</code> vs <code>p</code>.</td>
</tr>
<tr>
<td><code>nbdtrin(k, y, p)</code></td>
<td>Inverse of <code>nbdtr</code> vs <code>n</code>.</td>
</tr>
<tr>
<td><code>ncfdtr(dfn, dfd, nc, f)</code></td>
<td>Cumulative distribution function of the non-central F distribution.</td>
</tr>
<tr>
<td><code>ncfdtridfd(dfn, p, nc, f)</code></td>
<td>Calculate degrees of freedom (denominator) for the noncentral F-distribution.</td>
</tr>
<tr>
<td><code>ncfdtridfn(p, dfd, nc, f)</code></td>
<td>Calculate degrees of freedom (numerator) for the noncentral F-distribution.</td>
</tr>
<tr>
<td><code>ncfdtri(dfn, dfd, nc, f)</code></td>
<td>Inverse with respect to $f$ of the CDF of the noncentral F distribution.</td>
</tr>
<tr>
<td><code>ncftrinc(dfn, dfd, nc, p)</code></td>
<td>Calculate non-centrality parameter for non-central F distribution.</td>
</tr>
<tr>
<td><code>ncdttr(df, nc, t)</code></td>
<td>Cumulative distribution function of the non-central t distribution.</td>
</tr>
<tr>
<td><code>ncdttridf(p, nc, t)</code></td>
<td>Calculate degrees of freedom for non-central t distribution.</td>
</tr>
<tr>
<td><code>ncdttrist(df, nc, p)</code></td>
<td>Inverse cumulative distribution function of the noncentral t distribution.</td>
</tr>
<tr>
<td><code>ncdttrinc(df, p, t)</code></td>
<td>Calculate non-centrality parameter for non-central t distribution.</td>
</tr>
<tr>
<td><code>nrdtrins(p, x, std)</code></td>
<td>Calculate mean of normal distribution given other params.</td>
</tr>
</tbody>
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<th>Description</th>
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<tbody>
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<td>( \text{nrdtrisd}(p, x, mn) )</td>
<td>Calculate standard deviation of normal distribution given other params.</td>
</tr>
<tr>
<td>( \text{pdtr}(k, m) )</td>
<td>Poisson cumulative distribution function</td>
</tr>
<tr>
<td>( \text{pdtrc}(k, m) )</td>
<td>Poisson survival function</td>
</tr>
<tr>
<td>( \text{pdtri}(k, y) )</td>
<td>Inverse to ( \text{pdtr} ) vs ( m )</td>
</tr>
<tr>
<td>( \text{pdtr}(k, m) )</td>
<td>Inverse to ( \text{pdtr} ) vs ( k )</td>
</tr>
<tr>
<td>( \text{stdtr}(df, t) )</td>
<td>Student t distribution cumulative density function</td>
</tr>
<tr>
<td>( \text{stdtridf}(p, t) )</td>
<td>Inverse of ( \text{stdtr} ) vs ( df )</td>
</tr>
<tr>
<td>( \text{stdtr}(df, p) )</td>
<td>Inverse of ( \text{stdtr} ) vs ( t )</td>
</tr>
<tr>
<td>( \text{chdtr}(v, x) )</td>
<td>Chi square cumulative distribution function</td>
</tr>
<tr>
<td>( \text{chdtr}(v, x) )</td>
<td>Chi square survival function</td>
</tr>
<tr>
<td>( \text{chdtri}(v, p) )</td>
<td>Inverse to ( \text{chdtrc} )</td>
</tr>
<tr>
<td>( \text{chdtr}(v, p) )</td>
<td>Inverse to ( \text{chdtr} ) vs ( v )</td>
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**scipy.special.bdtr**

\[
\text{scipy.special.bdtr}(k, n, p) = \text{ufunc 'bdtr'}
\]

Binomial distribution cumulative distribution function.

Sum of the terms 0 through \( k \) of the Binomial probability density.

\[
\text{bdtr}(k, n, p) = \sum_{j=0}^{k} \binom{n}{j} p^j (1-p)^{n-j}
\]

**Parameters**

- \( k \) [array_like] Number of successes (int).
- \( n \) [array_like] Number of events (int).
p  [array_like] Probability of success in a single event (float).

Returns
y  [ndarray] Probability of $k$ or fewer successes in $n$ independent events with success probabilities of $p$.

Notes
The terms are not summed directly; instead the regularized incomplete beta function is employed, according to the formula,

$$bdtr(k, n, p) = I_{1-p}(n - k, k + 1).$$


References
[1]

**scipy.special.bdtrc**

scipy.special.bdtrc(k, n, p) = <ufunc 'bdtrc'>

Binomial distribution survival function.

Sum of the terms $k + 1$ through $n$ of the binomial probability density,

$$bdtrc(k, n, p) = \sum_{j=k+1}^{n} \binom{n}{j} p^j (1 - p)^{n-j}$$

Parameters
k  [array_like] Number of successes (int).

n  [array_like] Number of events (int).

p  [array_like] Probability of success in a single event.

Returns
y  [ndarray] Probability of $k + 1$ or more successes in $n$ independent events with success probabilities of $p$.

See also:
$bdtr$, $betainc$

Notes
The terms are not summed directly; instead the regularized incomplete beta function is employed, according to the formula,

$$bdtrc(k, n, p) = I_p(k + 1, n - k).$$


References
[1]

**scipy.special.bdtri**

scipy.special.bdtri(k, n, y) = <ufunc 'bdtri'>

Inverse function to $bdtr$ with respect to $p$.

Finds the event probability $p$ such that the sum of the terms 0 through $k$ of the binomial probability density is equal to the given cumulative probability $y$.

Parameters
k  [array_like] Number of successes (float).

n  [array_like] Number of events (float)
**returns**

$y$  
[array_like] Cumulative probability (probability of $k$ or fewer successes in $n$ events).

**returns**

$p$  
[ndarray] The event probability such that $bdtr(k, n, p) = y$.

**see also:**

$bdtr$, $betaincinv$

**notes**

The computation is carried out using the inverse beta integral function and the relation:

$$1 - p = betaincinv(n - k, k + 1, y).$$


**references**

[1]

scipy.special.bdtrik

scipy.special.bdtrik($y$, $n$, $p$) = <ufunc 'bdtrik'>

Inverse function to $bdtr$ with respect to $k$.

Finds the number of successes $k$ such that the sum of the terms 0 through $k$ of the Binomial probability density for $n$ events with probability $p$ is equal to the given cumulative probability $y$.

**parameters**

$y$  
[array_like] Cumulative probability (probability of $k$ or fewer successes in $n$ events).

$n$  
[array_like] Number of events (float).

$p$  
[array_like] Success probability (float).

**returns**

$k$  
[ndarray] The number of successes $k$ such that $bdtr(k, n, p) = y$.

**see also:**

$bdtr$

**notes**

Formula 26.5.24 of [1] is used to reduce the binomial distribution to the cumulative incomplete beta distribution.

Computation of $k$ involves a search for a value that produces the desired value of $y$. The search relies on the monotonicity of $y$ with $k$.


**references**

[1], [2]

scipy.special.bdtrin

scipy.special.bdtrin($k$, $y$, $p$) = <ufunc 'bdtrin'>

Inverse function to $bdtr$ with respect to $n$.

Finds the number of events $n$ such that the sum of the terms 0 through $k$ of the Binomial probability density for events with probability $p$ is equal to the given cumulative probability $y$.

**parameters**

$k$  
[array_like] Number of successes (float).

$y$  
[array_like] Cumulative probability (probability of $k$ or fewer successes in $n$ events).

$p$  
[array_like] Success probability (float).
Returns

\( n \) [ndarray] The number of events \( n \) such that \( \text{bdtr}(k, n, p) = y \).

See also:

\texttt{bdtr}

Notes

Formula 26.5.24 of [1] is used to reduce the binomial distribution to the cumulative incomplete beta distribution.

Computation of \( n \) involves a search for a value that produces the desired value of \( y \). The search relies on the monotonicity of \( y \) with \( n \).

Wrapper for the CDFLIB [2] Fortran routine \texttt{cdfbin}.

References

[1], [2]

\texttt{scipy.special.btdtr}

\texttt{scipy.special.btdtr}(a, b, x) = \<ufunc ‘btdtr’>

Cumulative density function of the beta distribution.

Returns the integral from zero to \( x \) of the beta probability density function,

\[
I = \int_0^x \frac{\Gamma(a + b)}{\Gamma(a)\Gamma(b)} t^{a-1}(1 - t)^{b-1} dt
\]

where \( \Gamma \) is the gamma function.

Parameters

\( a \) [array_like] Shape parameter (\( a > 0 \)).
\( b \) [array_like] Shape parameter (\( b > 0 \)).
\( x \) [array_like] Upper limit of integration, in [0, 1].

Returns

\( I \) [ndarray] Cumulative density function of the beta distribution with parameters \( a \) and \( b \) at \( x \).

See also:

\texttt{betainc}

Notes

This function is identical to the incomplete beta integral function \texttt{betainc}.

Wrapper for the Cephes [1] routine \texttt{btdtr}.

References

[1]

\texttt{scipy.special.btdtri}

\texttt{scipy.special.btdtri}(a, b, p) = \<ufunc ‘btdtri’>

\( p \)-th quantile of the beta distribution.

This function is the inverse of the beta cumulative distribution function, \texttt{btdtr}, returning the value of \( x \) for which \( \text{btdtr}(a, b, x) = p \), or

\[
p = \int_0^x \frac{\Gamma(a + b)}{\Gamma(a)\Gamma(b)} t^{a-1}(1 - t)^{b-1} dt
\]

Parameters

\( a \) [array_like] Shape parameter (\( a > 0 \)).
b  [array_like] Shape parameter \((b > 0)\).

p  [array_like] Cumulative probability, in \([0, 1]\).

**Returns**

x  [ndarray] The quantile corresponding to \(p\).

**See also:**

`betaincinv`, `bttdtr`

**Notes**

The value of \(x\) is found by interval halving or Newton iterations.

Wrapper for the Cephes [1] routine `incbi`, which solves the equivalent problem of finding the inverse of the incomplete beta integral.

**References**

[1] scipy.special.btdtria

scipy.special.btdtria(p, b, x) = <ufunc 'btdtria'>

Inverse of `bttdtr` with respect to \(a\).

This is the inverse of the beta cumulative distribution function, `bttdtr`, considered as a function of \(a\), returning the value of \(a\) for which `bttdtr(a, b, x) = p`, or

\[
p = \int_0^x \frac{\Gamma(a + b)}{\Gamma(a)\Gamma(b)} t^{a-1}(1 - t)^{b-1} dt
\]

**Parameters**

p  [array_like] Cumulative probability, in \([0, 1]\).

b  [array_like] Shape parameter \((b > 0)\).

x  [array_like] The quantile, in \([0, 1]\).

**Returns**

a  [ndarray] The value of the shape parameter \(a\) such that `bttdtr(a, b, x) = p`.

**See also:**

`bttdtr`

Cumulative density function of the beta distribution.

`bttdtri`

Inverse with respect to \(x\).

`bttdtrib`

Inverse with respect to \(b\).

**Notes**


The cumulative distribution function \(p\) is computed using a routine by DiDinato and Morris [2]. Computation of \(a\) involves a search for a value that produces the desired value of \(p\). The search relies on the monotonicity of \(p\) with \(a\).

**References**

[1], [2]
scipy.special.btdtrib

scipy.special.btdtrib(a, p, x) = <ufunc 'btdtrib'>

Inverse of \( btdtr \) with respect to \( b \).

This is the inverse of the beta cumulative distribution function, \( btdtr \), considered as a function of \( b \), returning the value of \( b \) for which \( btdtr(a, b, x) = p \), or

\[
p = \int_0^x \frac{\Gamma(a + b)}{\Gamma(a)\Gamma(b)} t^{a-1}(1 - t)^{b-1} \, dt
\]

Parameters

- **a** [array_like] Shape parameter \((a > 0)\).
- **p** [array_like] Cumulative probability, in \([0, 1]\).
- **x** [array_like] The quantile, in \([0, 1]\).

Returns

**b** [ndarray] The value of the shape parameter \( b \) such that \( btdtr(a, b, x) = p \).

See also:

- **btdtr**
  - Cumulative density function of the beta distribution.
- **btdtri**
  - Inverse with respect to \( x \).
- **btdtria**
  - Inverse with respect to \( a \).

Notes


The cumulative distribution function \( p \) is computed using a routine by DiDinato and Morris [2]. Computation of \( b \) involves a search for a value that produces the desired value of \( p \). The search relies on the monotonicity of \( p \) with \( b \).

References

[1], [2]

scipy.special.fdtr

scipy.special.fdtr(dfn,dfd,x) = <ufunc 'fdtr'>

F cumulative distribution function.

Returns the value of the cumulative density function of the F-distribution, also known as Snedecor’s F-distribution or the Fisher-Snedecor distribution.

The F-distribution with parameters \( d_n \) and \( d_d \) is the distribution of the random variable,

\[
X = \frac{U_n/d_n}{U_d/d_d},
\]

where \( U_n \) and \( U_d \) are random variables distributed \( \chi^2 \), with \( d_n \) and \( d_d \) degrees of freedom, respectively.

Parameters

- **dfn** [array_like] First parameter (positive float).
- **dfd** [array_like] Second parameter (positive float).
- **x** [array_like] Argument (nonnegative float).
Returns

y [ndarray] The CDF of the F-distribution with parameters dfn anddfd at x.

Notes
The regularized incomplete beta function is used, according to the formula,

\[ F(d_n, d_d; x) = I_{x d_n/(d_d + x d_n)}(d_n/2, d_d/2). \]

Wrapper for the Cephes [1] routine \texttt{fdtr}.

References
[1]
scipy.special.fdtrc
scipy.special.fdtrc(dfn, dfd, x) = \texttt{<ufunc 'fdtrc'>}
F survival function.

Returns the complemented F-distribution function (the integral of the density from x to infinity).

Parameters

dfn [array_like] First parameter (positive float).
dfd [array_like] Second parameter (positive float).
x [array_like] Argument (nonnegative float).

Returns

y [ndarray] The complemented F-distribution function with parameters dfn and dfd at x.

See also:
\texttt{fdtr}

Notes
The regularized incomplete beta function is used, according to the formula,

\[ F(d_n, d_d; x) = I_{d_d/(d_d + x d_n)}(d_n/2, d_d/2). \]

Wrapper for the Cephes [1] routine \texttt{fdtrc}.

References
[1]
scipy.special.fdtri
scipy.special.fdtri(dfn, dfd, p) = \texttt{<ufunc 'fdtri'>}
The p-th quantile of the F-distribution.

This function is the inverse of the F-distribution CDF, \texttt{fdtr}, returning the x such that \texttt{fdtr(dfn, dfd, x) = p}.

Parameters

dfn [array_like] First parameter (positive float).
dfd [array_like] Second parameter (positive float).
p [array_like] Cumulative probability, in [0, 1].

Returns

x [ndarray] The quantile corresponding to p.
Notes
The computation is carried out using the relation to the inverse regularized beta function, $I_x^{-1}(a, b)$. Let $z = I_p^{-1}(d_d/2, d_n/2)$. Then,

$$x = \frac{d_d(1-z)}{d_n z}.$$ 

If $p$ is such that $x < 0.5$, the following relation is used instead for improved stability: let $z' = I_{1-p}^{-1}(d_n/2, d_d/2)$. Then,

$$x = \frac{d_d z'}{d_n (1-z')}.$$ 


References
[1]
scipy.special.fdtridfd
scipy.special.fdtridfd$(dfn, p, x) = \langle\text{ufunc} 'fdtridfd'\rangle$
Inverse to $fdtr$ vs dfd
Finds the F density argument dfd such that $fdtr(dfn, dfd, x) == p$.

scipy.special.gdtr
scipy.special.gdtr$(a, b, x) = \langle\text{ufunc} 'gdtr'\rangle$
Gamma distribution cumulative density function.

Returns the integral from zero to $x$ of the gamma probability density function,

$$F = \int_0^x a^b t^{b-1} e^{-at} dt,$$

where $\Gamma$ is the gamma function.

Parameters
a [array_like] The rate parameter of the gamma distribution, sometimes denoted $\beta$ (float). It is also the reciprocal of the scale parameter $\theta$.
b [array_like] The shape parameter of the gamma distribution, sometimes denoted $\alpha$ (float).
x [array_like] The quantile (upper limit of integration; float).

Returns
F [ndarray] The CDF of the gamma distribution with parameters $a$ and $b$ evaluated at $x$.

See also:
gdtrc
1 - CDF of the gamma distribution.

Notes
The evaluation is carried out using the relation to the incomplete gamma integral (regularized gamma function).

References
[1]
scipy.special.gdtrc

The function calculates the gamma distribution survival function.

\[ F = \int_x^{\infty} \frac{a^b}{\Gamma(b)} t^{b-1} e^{-at} dt, \]

where \( \Gamma \) is the gamma function.

**Parameters**

- *a* : array_like
  - The rate parameter of the gamma distribution, sometimes denoted \( \beta \) (float). It is also the reciprocal of the scale parameter \( \theta \).
- *b* : array_like
  - The shape parameter of the gamma distribution, sometimes denoted \( \alpha \) (float).
- *x* : array_like
  - The quantile (lower limit of integration; float).

**Returns**

- *F* : ndarray
  - The survival function of the gamma distribution with parameters \( a \) and \( b \) evaluated at \( x \).

**See also:**

- gdtr, gdtrix

**Notes**

The evaluation is carried out using the relation to the incomplete gamma integral (regularized gamma function).


**References**

[1]

scipy.special.gdtria

The function calculates the inverse of \( p = \text{gdtr}(a, b, x) \), the cumulative distribution function of the gamma distribution.

**Parameters**

- *p* : array_like
  - Probability values.
- *b* : array_like
  - Parameter values of \( \text{gdtr}(a, b, x) \). \( b \) is the “shape” parameter of the gamma distribution.
- *x* : array_like
  - Nonnegative real values, from the domain of the gamma distribution.
- *out* : ndarray, optional
  - If a fourth argument is given, it must be a numpy.ndarray whose size matches the broadcast result of \( a, b \) and \( x \). \( out \) is then the array returned by the function.

**Returns**

- *a* : ndarray
  - Values of the \( a \) parameter such that \( p = \text{gdtr}(a, b, x) \). \( 1/a \) is the “scale” parameter of the gamma distribution.

**See also:**

- gdtr
  - CDF of the gamma distribution.
gdtrib
Inverse with respect to $b$ of $\text{gdtr}(a, b, x)$.

gdtrix
Inverse with respect to $x$ of $\text{gdtr}(a, b, x)$.

Notes
The cumulative distribution function $p$ is computed using a routine by DiDinato and Morris [2]. Computation of $a$ involves a search for a value that produces the desired value of $p$. The search relies on the monotonicity of $p$ with $a$.

References
[1], [2]

Examples
First evaluate $\text{gdtr}$.

```python
>>> from scipy.special import gdtr, gdtria
>>> p = gdtr(1.2, 3.4, 5.6)
>>> print(p)
0.94378087442
```
Verify the inverse.

```python
>>> gdtria(p, 3.4, 5.6)
1.2
```

scipy.special.gdtrib
scipy.special.gdtrib($a$, $p$, $x$, out=None) = <ufunc 'gdtrib'>
Inverse of $\text{gdtr}$ vs $b$.

Returns the inverse with respect to the parameter $b$ of $p = \text{gdtr}(a, b, x)$, the cumulative distribution function of the gamma distribution.

Parameters

- **a** : array_like
  Parameter values of $\text{gdtr}(a, b, x)$. $1/a$ is the “scale” parameter of the gamma distribution.
- **p** : array_like
  Probability values.
- **x** : array_like
  Nonnegative real values, from the domain of the gamma distribution.
- **out** : ndarray, optional
  If a fourth argument is given, it must be a numpy.ndarray whose size matches the broadcast result of $a$, $b$ and $x$. $out$ is then the array returned by the function.

Returns

- **b** : ndarray
  Values of the $b$ parameter such that $p = \text{gdtr}(a, b, x)$. $b$ is the “shape” parameter of the gamma distribution.

See also:

- **gdtr**
  CDF of the gamma distribution.
- **gdtria**
  Inverse with respect to $a$ of $\text{gdtr}(a, b, x)$. 
gdtrix

Inverse with respect to $x$ of $gdtr(a, b, x)$.

**Notes**
The cumulative distribution function $p$ is computed using a routine by DiDinato and Morris [2]. Computation of $b$ involves a search for a value that produces the desired value of $p$. The search relies on the monotonicity of $p$ with $b$.

**References**
[1], [2]

**Examples**
First evaluate $gdtr$.

```python
>>> from scipy.special import gdtr, gdtrib
>>> p = gdtr(1.2, 3.4, 5.6)
>>> print(p)
0.94378087442
```

Verify the inverse.

```python
>>> gdtrib(1.2, p, 5.6)
3.3999999999723882
```

scipy.special.gdtrix

Returns the inverse with respect to the parameter $x$ of $p = gdtr(a, b, x)$, the cumulative distribution function of the gamma distribution. This is also known as the $p$’th quantile of the distribution.

**Parameters**
- `a` [array_like] $a$ parameter values of $gdtr(a, b, x)$. $1/a$ is the “scale” parameter of the gamma distribution.
- `b` [array_like] $b$ parameter values of $gdtr(a, b, x)$. $b$ is the “shape” parameter of the gamma distribution.
- `p` [array_like] Probability values.
- `out` [ndarray, optional] If a fourth argument is given, it must be a numpy.ndarray whose size matches the broadcast result of $a$, $b$ and $x$. $out$ is then the array returned by the function.

**Returns**
- `x` [ndarray] Values of the $x$ parameter such that $p = gdtr(a, b, x)$.

See also:
- `gdtr` CDF of the gamma distribution.
- `gdtria` Inverse with respect to $a$ of $gdtr(a, b, x)$.
- `gdtrib` Inverse with respect to $b$ of $gdtr(a, b, x)$.
Notes

The cumulative distribution function $p$ is computed using a routine by DiDinato and Morris [2]. Computation of $x$ involves a search for a value that produces the desired value of $p$. The search relies on the monotonicity of $p$ with $x$.

References
[1], [2]

Examples
First evaluate $gdtr$.

```python
>>> from scipy.special import gdtr, gdtrix
>>> p = gdtr(1.2, 3.4, 5.6)
>>> print(p)
0.94378087442

Verify the inverse.

```python
>>> gdtrix(1.2, 3.4, p)
5.5999999999999996
```

scipy.special.nbdtr
scipy.special.nbdtr($k$, $n$, $p$) = <ufunc 'nbdtr'>
Negative binomial cumulative distribution function.

Returns the sum of the terms 0 through $k$ of the negative binomial distribution probability mass function,

$$F = \sum_{j=0}^{k} \binom{n+j-1}{j} p^n (1-p)^j.$$

In a sequence of Bernoulli trials with individual success probabilities $p$, this is the probability that $k$ or fewer failures precede the $n$th success.

Parameters

- $k$ [array_like] The maximum number of allowed failures (nonnegative int).
- $n$ [array_like] The target number of successes (positive int).

Returns

- $F$ [ndarray] The probability of $k$ or fewer failures before $n$ successes in a sequence of events with individual success probability $p$.

See also:

nbdtrc

Notes
If floating point values are passed for $k$ or $n$, they will be truncated to integers.

The terms are not summed directly; instead the regularized incomplete beta function is employed, according to the formula,

$$\text{nbdtr}(k, n, p) = I_p(n, k + 1).$$

References
[1]
sympy.special.nbdtrc

Returns the sum of the terms $k + 1$ to infinity of the negative binomial distribution probability mass function,

$$ F = \sum_{j=k+1}^{\infty} \binom{n+j-1}{j} p^n (1-p)^j. $$

In a sequence of Bernoulli trials with individual success probabilities $p$, this is the probability that more than $k$ failures precede the $n$th success.

Parameters
- $k$ [array_like] The maximum number of allowed failures (nonnegative int).
- $n$ [array_like] The target number of successes (positive int).

Returns
- $F$ [ndarray] The probability of $k + 1$ or more failures before $n$ successes in a sequence of events with individual success probability $p$.

Notes
If floating point values are passed for $k$ or $n$, they will be truncated to integers.

The terms are not summed directly; instead the regularized incomplete beta function is employed, according to the formula,

$$ \text{nbdtrc}(k,n,p) = I_{1-p}(k+1,n). $$


References
[1]
sympy.special.nbdtri

Returns the inverse with respect to the parameter $p$ of $y = \text{nbdtr}(k, n, p)$, the negative binomial cumulative distribution function.

Parameters
- $k$ [array_like] The maximum number of allowed failures (nonnegative int).
- $n$ [array_like] The target number of successes (positive int).
- $y$ [array_like] The probability of $k$ or fewer failures before $n$ successes (float).

Returns
- $p$ [ndarray] Probability of success in a single event (float) such that $\text{nbdtr}(k, n, p) = y$.

See also:
nbdtr

Cumulative distribution function of the negative binomial.
nbdtrik
Inverse with respect to \( k \) of \( \text{nbdtr}(k, n, p) \).
nbdtrin
Inverse with respect to \( n \) of \( \text{nbdtr}(k, n, p) \).

Notes
Wrapper for the Cephes [1] routine \text{nbdtri}.

References
[1]

scipy.special.nbdtrik
scipy.special.nbdtrik\( (y, n, p) = \text{<ufunc 'nbdtrik'>} \)

Inverse of \( \text{nbdtr} \) vs \( k \).

Returns the inverse with respect to the parameter \( k \) of \( y = \text{nbdtr}(k, n, p) \), the negative binomial cumulative distribution function.

Parameters
- \( y \) [array_like] The probability of \( k \) or fewer failures before \( n \) successes (float).
- \( n \) [array_like] The target number of successes (positive int).
- \( p \) [array_like] Probability of success in a single event (float).

Returns
- \( k \) [ndarray] The maximum number of allowed failures such that \( \text{nbdtr}(k, n, p) = y \).

See also:

nbdtr
Cumulative distribution function of the negative binomial.
nbdtri
Inverse with respect to \( p \) of \( \text{nbdtr}(k, n, p) \).
nbdtrin
Inverse with respect to \( n \) of \( \text{nbdtr}(k, n, p) \).

Notes
Wrapper for the CDFLIB [1] Fortran routine \text{cdfnbn}.

Formula 26.5.26 of [2],
\[
\sum_{j=k+1}^{\infty} \binom{n+j-1}{j} p^n (1-p)^j = I_{1-p}(k+1, n),
\]
is used to reduce calculation of the cumulative distribution function to that of a regularized incomplete beta \( I \).

Computation of \( k \) involves a search for a value that produces the desired value of \( y \). The search relies on the monotonicity of \( y \) with \( k \).

References
[1], [2]
**scipy.special.nbdtrin**

-scipy.special.nbdtrin(k, y, p) = <ufunc 'nbdtrin'>-

Inverse of \( nbdtr \) vs \( n \).

Returns the inverse with respect to the parameter \( n \) of \( y = nbdtr(k, n, p) \), the negative binomial cumulative distribution function.

**Parameters**

- **k** [array_like] The maximum number of allowed failures (nonnegative int).
- **y** [array_like] The probability of \( k \) or fewer failures before \( n \) successes (float).
- **p** [array_like] Probability of success in a single event (float).

**Returns**

- **n** [ndarray] The number of successes \( n \) such that \( nbdtr(k, n, p) = y \).

See also:

- \( nbdtr \)
  - Cumulative distribution function of the negative binomial.
- \( nbdtri \)
  - Inverse with respect to \( p \) of \( nbdtr(k, n, p) \).
- \( nbdtrik \)
  - Inverse with respect to \( k \) of \( nbdtr(k, n, p) \).

**Notes**

Wrapper for the CDFLIB [1] Fortran routine \( cdfnbn \).

Formula 26.5.26 of [2],

\[
\sum_{j=k+1}^{\infty} \binom{n+j-1}{j} p^n (1-p)^j = I_{1-p}(k+1,n),
\]

is used to reduce calculation of the cumulative distribution function to that of a regularized incomplete beta \( I \).

Computation of \( n \) involves a search for a value that produces the desired value of \( y \). The search relies on the monotonicity of \( y \) with \( n \).

**References**

[1], [2]

**scipy.special.ncf**

-scipy.special.ncf(dfn, dfd, nc, f) = <ufunc 'ncf'>-

Cumulative distribution function of the non-central F distribution.

The non-central F describes the distribution of,

\[
Z = \frac{X/d_n}{Y/d_d}
\]

where \( X \) and \( Y \) are independently distributed, with \( X \) distributed non-central \( \chi^2 \) with noncentrality parameter \( nc \) and \( d_n \) degrees of freedom, and \( Y \) distributed \( \chi^2 \) with \( d_d \) degrees of freedom.

**Parameters**

- **dfn** [array_like] Degrees of freedom of the numerator sum of squares. Range \((0, \infty)\).
- **dfd** [array_like] Degrees of freedom of the denominator sum of squares. Range \((0, \infty)\).
nc  [array_like] Noncentrality parameter. Should be in range (0, 1e4).
f  [array_like] Quantiles, i.e. the upper limit of integration.

Returns

cdf  [float or ndarray] The calculated CDF. If all inputs are scalar, the return will be a float. Otherwise it will be an array.

See also:

ncfdtri
Quantile function; inverse of ncfdtr with respect to f.

ncdtridfd
Inverse of ncfdtr with respect to dfd.

ncdtridfn
Inverse of ncfdtr with respect to dfn.

ncdtrinc
Inverse of ncfdtr with respect to nc.

Notes
The cumulative distribution function is computed using Formula 26.6.20 of [2]:

\[ F(d_n, d_d, n_c, f) = \sum_{j=0}^{\infty} e^{-n_c/2} \left(\frac{n_c/2}{j!}\right) I_x\left(\frac{d_n}{2} + j, \frac{d_d}{2}\right), \]

where \( I \) is the regularized incomplete beta function, and \( x = fd_n/(fd_n + d_d) \).
The computation time required for this routine is proportional to the noncentrality parameter nc. Very large values of this parameter can consume immense computer resources. This is why the search range is bounded by 10,000.

References
[1], [2]

Examples

```python
>>> from scipy import special
cd
```
```python
>>> ax.plot(x, ncf_special, 'r-')
>>> plt.show()
```

```python
scipy.special.ncfdtridfd
scipy.special.ncfdtridfd(dfn, p, nc, f) = <ufunc 'ncfdtridfd'>

Calculate degrees of freedom (denominator) for the noncentral F-distribution.

This is the inverse with respect to dfd of ncfddtr. See ncfddtr for more details.

**Parameters**

- `dfn` [array_like]: Degrees of freedom of the numerator sum of squares. Range (0, inf).
- `p` [array_like]: Value of the cumulative distribution function. Must be in the range [0, 1].
- `nc` [array_like]: Noncentrality parameter. Should be in range (0, 1e4).
- `f` [array_like]: Quantiles, i.e. the upper limit of integration.

**Returns**

- `dfd` [float]: Degrees of freedom of the denominator sum of squares.

See also:

- ncfddtr
  - CDF of the non-central F distribution.
- ncfddtri
  - Quantile function; inverse of ncfddtr with respect to f.
- ncfddtridfn
  - Inverse of ncfddtr with respect to dfn.
- ncfddtrinc
  - Inverse of ncfddtr with respect to nc.
```
Notes
The value of the cumulative noncentral F distribution is not necessarily monotone in either degrees
of freedom. There thus may be two values that provide a given CDF value. This routine assumes
monotonicity and will find an arbitrary one of the two values.

Examples
>>> from scipy.special import ncfdtr, ncfdtridf

Compute the CDF for several values of dfd:

```python
>>> dfd = [1, 2, 3]
>>> p = ncfdtr(2, dfd, 0.25, 15)
>>> p
array([0.8097138 , 0.93020416, 0.96787852])
```

Compute the inverse. We recover the values of dfd, as expected:

```python
>>> ncfdtridf(2, p, 0.25, 15)
array([1. , 2. , 3.])
```

scipy.special.ncfdtridfn

scipy.special.ncfdtridfn(p, dfd, nc, f) = <ufunc 'ncfdtridfn'>

calculate degrees of freedom (numerator) for the noncentral F-distribution.

This is the inverse with respect to dfn of ncfdtr. See ncfdtr for more details.

Parameters

- **p** array_like Value of the cumulative distribution function. Must be in the range [0, 1].
- **dfd** array_like Degrees of freedom of the denominator sum of squares. Range (0, inf).
- **nc** array_like Noncentrality parameter. Should be in range (0, 1e4).
- **f** float Quantiles, i.e. the upper limit of integration.

Returns

- **dfn** float Degrees of freedom of the numerator sum of squares.

See also:

ncfdtr

CDF of the non-central F distribution.

ncfdtri

Quantile function; inverse of ncfdtr with respect to f.

ncfdtridf

Inverse of ncfdtr with respect to dfd.

ncfdtrinc

Inverse of ncfdtr with respect to nc.

Notes

The value of the cumulative noncentral F distribution is not necessarily monotone in either degrees
of freedom. There thus may be two values that provide a given CDF value. This routine assumes
monotonicity and will find an arbitrary one of the two values.
Examples

```python
>>> from scipy.special import ncfdtr, ncfdtridfn
```

Compute the CDF for several values of \( \text{dfn} \):

```python
>>> dfn = [1, 2, 3]
>>> p = ncfdtr(dfn, 2, 0.25, 15)
>>> p
array([0.92562363, 0.93020416, 0.93188394])
```

Compute the inverse. We recover the values of \( \text{dfn} \), as expected:

```python
>>> ncfdtridfn(p, 2, 0.25, 15)
array([1., 2., 3.])
```

**scipy.special.ncfdtri**

scipy.special.ncfdtri(dfn, dfd, nc, p) = <ufunc 'ncfdtri'>

Inverse with respect to \( f \) of the CDF of the non-central F distribution.

See ncfdtr for more details.

**Parameters**

- **dfn**: \([\text{array_like}]\) Degrees of freedom of the numerator sum of squares. Range \((0, \infty)\).
- **dfd**: \([\text{array_like}]\) Degrees of freedom of the denominator sum of squares. Range \((0, \infty)\).
- **nc**: \([\text{array_like}]\) Noncentrality parameter. Should be in range \((0, 1e4)\).
- **p**: \([\text{array_like}]\) Value of the cumulative distribution function. Must be in the range \([0, 1]\).

**Returns**

- **f**: \([\text{float}]\) Quantiles, i.e. the upper limit of integration.

See also:

- ncfdtr 
  CDF of the non-central F distribution.
- ncfdtridfd 
  Inverse of ncfdtr with respect to dfd.
- ncfdtridfn 
  Inverse of ncfdtr with respect to dfn.
- ncfdtrinc 
  Inverse of ncfdtr with respect to nc.

**Examples**

```python
>>> from scipy.special import ncfdtr, ncfdtri
```

Compute the CDF for several values of \( f \):

```python
>>> f = [0.5, 1, 1.5]
>>> p = ncfdtr(2, 3, 1.5, f)
>>> p
array([0.20782291, 0.36107392, 0.47345752])
```
Compute the inverse. We recover the values of $f$, as expected:

```python
>>> ncfdtri(2, 3, 1.5, p)
array([ 0.5, 1. , 1.5])
```

**scipy.special.ncfdtrinc**

Calculates non-centrality parameter for non-central F distribution. This is the inverse with respect to $nc$ of `ncfdtr`. See `ncfdtr` for more details.

**Parameters**

- **dfn** [array_like] Degrees of freedom of the numerator sum of squares. Range (0, inf).
- **dfd** [array_like] Degrees of freedom of the denominator sum of squares. Range (0, inf).
- **p** [array_like] Value of the cumulative distribution function. Must be in the range [0, 1].
- **f** [array_like] Quantiles, i.e. the upper limit of integration.

**Returns**

- **nc** [float] Noncentrality parameter.

**See also:**

- `ncfdtr` CDF of the non-central F distribution.
- `ncfdtri` Quantile function; inverse of `ncfdtr` with respect to $f$.
- `ncfdtridfd` Inverse of `ncfdtr` with respect to $dfd$.
- `ncfdtridfn` Inverse of `ncfdtr` with respect to $dfn$.

**Examples**

```python
>>> from scipy.special import ncfdtr, ncfdtrinc
```

Compute the CDF for several values of $nc$:

```python
>>> nc = [0.5, 1.5, 2.0]
>>> p = ncfdtr(2, 3, nc, 15)
>>> p
array([0.96309246, 0.94327955, 0.93304098])
```

Compute the inverse. We recover the values of $nc$, as expected:

```python
>>> ncfdtrinc(2, 3, p, 15)
array([0.5, 1.5, 2.0])
```

**scipy.special.nctdtr**

Cumulative distribution function of the non-central $t$ distribution.

**Parameters**
df [array_like] Degrees of freedom of the distribution. Should be in range (0, inf).
nc [array_like] Noncentrality parameter. Should be in range (-1e6, 1e6).
t [array_like] Quantiles, i.e. the upper limit of integration.

Returns
cdf [float or ndarray] The calculated CDF. If all inputs are scalar, the return will be a float. Otherwise it will be an array.

See also:
nctdtrit
Inverse CDF (iCDF) of the non-central t distribution.
nctdtridf
Calculate degrees of freedom, given CDF and iCDF values.
nctdtrinc
Calculate non-centrality parameter, given CDF iCDF values.

Examples
>>> from scipy import special
>>> from scipy import stats
>>> import matplotlib.pyplot as plt

Plot the CDF of the non-central t distribution, for nc=0. Compare with the t-distribution from scipy.stats:

```python
>>> x = np.linspace(-5, 5, num=500)
>>> df = 3
>>> nct_stats = stats.t.cdf(x, df)
>>> nct_special = special.nctdtr(df, 0, x)
```

```python
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(x, nct_stats, 'b-', lw=3)
>>> ax.plot(x, nct_special, 'r-')
>>> plt.show()
```

scipy.special.nctdtridf
scipy.special.nctdtridf(p, nc, t) = <ufunc 'nctdtridf'>
Calculate degrees of freedom for non-central t distribution.

See nctdtr for more details.

Parameters

- p [array_like] CDF values, in range (0, 1].
- nc [array_like] Noncentrality parameter. Should be in range (-1e6, 1e6).
- t [array_like] Quantiles, i.e. the upper limit of integration.

scipy.special.nctdtrit
scipy.special.nctdtrit(df, nc, p) = <ufunc 'nctdtrit'>
Inverse cumulative distribution function of the non-central t distribution.

See nctdtr for more details.

Parameters
df  [array_like] Degrees of freedom of the distribution. Should be in range (0, inf).
nc  [array_like] Noncentrality parameter. Should be in range (-1e6, 1e6).
p  [array_like] CDF values, in range (0, 1).

scipy.special.nctdtrinc
s scipy.special.nctdtrinc(df, p, t) = <ufunc 'nctdtrinc'>
Calculate non-centrality parameter for non-central t distribution.

See nctdtr for more details.

Parameters

  df  [array_like] Degrees of freedom of the distribution. Should be in range (0, inf).
  p  [array_like] CDF values, in range (0, 1].
  t  [array_like] Quantiles, i.e. the upper limit of integration.

scipy.special.nrdtrimn
scipy.special.nrdtrimn(p, x, std) = <ufunc 'nrdtrimn'>
Calculate mean of normal distribution given other params.

Parameters

  p  [array_like] CDF values, in range (0, 1].
  x  [array_like] Quantiles, i.e. the upper limit of integration.
  std  [array_like] Standard deviation.

Returns

  mn  [float or ndarray] The mean of the normal distribution.

See also:

  nrdtrimn, ndtr

scipy.special.nrdtrisd
scipy.special.nrdtrisd(p, x, mn) = <ufunc 'nrdtrisd'>
Calculate standard deviation of normal distribution given other params.

Parameters

  p  [array_like] CDF values, in range (0, 1].
  x  [array_like] Quantiles, i.e. the upper limit of integration.
SciPy Reference Guide, Release 1.2.0

nn [float or ndarray] The mean of the normal distribution.

Returns

std [array_like] Standard deviation.

See also:

nrdtristd, ndtr

scipy.special.pdtr

scipy.special.pdtr(k, m) = <ufunc 'pdtr'>

Poisson cumulative distribution function

Returns the sum of the first $k$ terms of the Poisson distribution: $\sum \exp(-m) \times m^j / j!$, $j=0..k) = \text{gammainc}(k+1, m)$. Arguments must both be positive and $k$ an integer.

scipy.special.pdtrc

scipy.special.pdtrc(k, m) = <ufunc 'pdtrc'>

Poisson survival function

Returns the sum of the terms from $k+1$ to infinity of the Poisson distribution: $\sum \exp(-m) \times m^j / j!$, $j=k+1..\infty) = \text{gammainc}(k+1, m)$. Arguments must both be positive and $k$ an integer.

scipy.special.pdtri

scipy.special.pdtri(k, y) = <ufunc 'pdtri'>

Inverse to pdtr vs m

Returns the Poisson variable $m$ such that the sum from 0 to $k$ of the Poisson density is equal to the given probability $y$: calculated by \text{gammaincinv}(k+1, y)$. $k$ must be a nonnegative integer and $y$ between 0 and 1.

scipy.special.pdtrik

scipy.special.pdtrik(p, m) = <ufunc 'pdtrik'>

Inverse to pdtr vs k

Returns the quantile $k$ such that $\text{pdtr}(k, m) = p$

scipy.special.stdtr

scipy.special.stdtr(df, t) = <ufunc 'stdtr'>

Student t distribution cumulative density function

Returns the integral from minus infinity to $t$ of the Student t distribution with $df > 0$ degrees of freedom:

\[
gamma((df+1)/2) / (\sqrt{df \pi}) \times \gamma(df/2)) \times \int_{-\infty}^{t} (1+\pi^2/df)**(-df/2-1/2), x=-\infty..t
\]

scipy.special.stdtridf

scipy.special.stdtridf(p, t) = <ufunc 'stdtridf'>

Inverse of stdtr vs df

Returns the argument $df$ such that stdtr(df, t) is equal to $p$.

scipy.special.stdtrit

scipy.special.stdtrit(df, p) = <ufunc 'stdtrit'>

Inverse of stdtr vs $t$

Returns the argument $t$ such that stdtr(df, t) is equal to $p$.

scipy.special.chdtr

scipy.special.chdtr(v, x) = <ufunc 'chdtr'>

Chi square cumulative distribution function

6.26. Special functions (scipy.special)
Returns the area under the left hand tail (from 0 to \(x\)) of the Chi square probability density function with \(v\) degrees of freedom:

\[
\frac{1}{2^v \Gamma(v/2)} \int_0^x t^{v/2 - 1} e^{-t/2} dt
\]

**scipy.special.chdtrc**

**scipy.special.chdtrc**(\(v, x\)) = \(<ufunc \ 'chdtrc'>\)

Chi square survival function

Returns the area under the right hand tail (from \(x\) to infinity) of the Chi square probability density function with \(v\) degrees of freedom:

\[
\frac{1}{2^v \Gamma(v/2)} \int_x^\infty t^{v/2 - 1} e^{-t/2} dt
\]

**scipy.special.chdtri**

**scipy.special.chdtri**(\(v, p\)) = \(<ufunc \ 'chdtri'>\)

Inverse to \(chdtrc\)

Returns the argument \(x\) such that \(chdtrc(v, x) == p\).

**scipy.special.chdtriv**

**scipy.special.chdtriv**(\(p, x\)) = \(<ufunc \ 'chdtriv'>\)

Inverse to \(chdtr\) vs \(v\)

Returns the argument \(v\) such that \(chdtr(v, x) == p\).

**scipy.special.ndtr**

**scipy.special.ndtr**(\(x\)) = \(<ufunc \ 'ndtr'>\)

Gaussian cumulative distribution function.

Returns the area under the standard Gaussian probability density function, integrated from minus infinity to \(x\)

\[
\frac{1}{\sqrt{2\pi}} \int_{-\infty}^x \exp(-t^2/2) dt
\]

**Parameters**

- \(x\) [array_like, real or complex] Argument

**Returns**

- ndarray The value of the normal CDF evaluated at \(x\)

See also:

\(erf, erfc, scipy.stats.norm, log_ndtr\)

**scipy.special.log_ndtr**

**scipy.special.log_ndtr**(\(x\)) = \(<ufunc \ 'log_ndtr'>\)

Logarithm of Gaussian cumulative distribution function.

Returns the log of the area under the standard Gaussian probability density function, integrated from minus infinity to \(x\):

\[
\log(\frac{1}{\sqrt{2\pi}} \int_{-\infty}^x \exp(-t^2/2) dt)
\]

**Parameters**

- \(x\) [array_like, real or complex] Argument

**Returns**
The value of the log of the normal CDF evaluated at $x$

See also:

- `erf`, `erfc`, `scipy.stats.norm`, `ndtr`

`scipy.special.ndtri`  
`scipy.special.ndtri(y) = <ufunc 'ndtri'>`
Inverse of `ndtr` vs $x$

Returns the argument $x$ for which the area under the Gaussian probability density function (integrated from minus infinity to $x$) is equal to $y$.

`scipy.special.chndtr`  
`scipy.special.chndtr(x, df, nc) = <ufunc 'chndtr'>`
Non-central chi square cumulative distribution function

`scipy.special.chndtridf`  
`scipy.special.chndtridf(x, p, nc) = <ufunc 'chndtridf'>`
Inverse to `chndtr` vs $df$

`scipy.special.chndtrinc`  
`scipy.special.chndtrinc(x, df, p) = <ufunc 'chndtrinc'>`
Inverse to `chndtr` vs $nc$

`scipy.special.chndtrix`  
`scipy.special.chndtrix(p, df, nc) = <ufunc 'chndtrix'>`
Inverse to `chndtr` vs $x$

`scipy.special.smirnov`  
`scipy.special.smirnov(n, d) = <ufunc 'smirnov'>`
Kolmogorov-Smirnov complementary cumulative distribution function

Returns the exact Kolmogorov-Smirnov complementary cumulative distribution function (aka the Survival Function) of $D_n+$ (or $D_n-$) for a one-sided test of equality between an empirical and a theoretical distribution. It is equal to the probability that the maximum difference between a theoretical distribution and an empirical one based on $n$ samples is greater than $d$.

**Parameters**

- `n` [int] Number of samples
- `d` [float, array_like] Deviation between the Empirical CDF (ECDF) and the target CDF.

**Returns**

- `float` The value(s) of smirnov($n$, $d$), Prob($D_n+ >= d$) (Also Prob($D_n- >= d$))

See also:

- `smirnovi`
  The Inverse Survival Function for the distribution

- `scipy.stats.ksone`
  Provides the functionality as a continuous distribution

**Notes**

`smirnov` is used by `stats.kstest` in the application of the Kolmogorov-Smirnov Goodness of Fit test. For historical reasons this function is exposed in `scipy.special`, but the recommended way to achieve the most accurate CDF/SF/PDF/PPF/ISF computations is to use the `stats.ksone` distribution.
Examples

```python
>>> from scipy.special import smirnov

Show the probability of a gap at least as big as 0, 0.5 and 1.0 for a sample of size 5

```python
>>> smirnov(5, [0, 0.5, 1.0])
```
```
array([ 1. , 0.056, 0. ])
```

Compare a sample of size 5 drawn from a source N(0.5, 1) distribution against a target N(0, 1) CDF.

```python
>>> from scipy.stats import norm
>>> n = 5
>>> gendist = norm(0.5, 1)  # Normal distribution, mean 0.5, stddev 1
>>> np.random.seed(seed=233423)  # Set the seed for reproducibility
>>> x = np.sort(gendist.rvs(size=n))
```
```
array([-0.20946287, 0.71688765, 0.95164151, 1.44590852, 3.08880533])
```

```python
>>> target = norm(0)
>>> cdfs = target.cdf(x)
```
```
array([ 0.41704346, 0.76327829, 0.82936059, 0.92589857, 0.99899518])
```

# Construct the Empirical CDF and the K-S statistics (Dn+, Dn-, Dn)
```python
>>> ecdfs = np.arange(n+1, dtype=float)/n
>>> cols = np.column_stack([x, ecdfs[1:], cdfs, cdfs - ecdfs[:n], ecdfs[1:] - cdfs])
>>> np.set_printoptions(precision=3)
```
```
array([[ -2.095e-01, 2.000e-01, 4.170e-01, 4.170e-01, -2.170e-01],
     [ 7.169e-01, 4.000e-01, 7.633e-01, 5.633e-01, -3.633e-01],
     [ 9.516e-01, 6.000e-01, 8.294e-01, 4.294e-01, -2.294e-01],
     [ 1.446e+00, 8.000e-01, 9.259e-01, 3.259e-01, -1.259e-01],
     [ 3.089e+00, 1.000e+00, 9.990e-01, 1.990e-01, 1.005e-03]])
```

```python
gaps = cols[:, -2:]
>>> Dnpm = np.max(gaps, axis=0)
>>> print('Dn-=%s, Dn+=%s' % (Dnpm[0], Dnpm[1]))
Dn- =0.563278, Dn+ =0.001005
```
```
```python
>>> probs = smirnov(n, Dnpm)
>>> print(chr(10).join(['For a sample of size %d drawn from a N(0, 1) distribution:
\[\rightarrow \% n,
\[\[ \% Smirnov n=%s: Prob(Dn- >= %f) = %.4f\] % (n, Dnpm[0], probs[0]),
\[\[ \% Smirnov n=%s: Prob(Dn+ >= %f) = %.4f\]] % (n, Dnpm[1], probs[1]))

For a sample of size 5 drawn from a N(0, 1) distribution:
Smirnov n=5: Prob(Dn- >= 0.563278) = 0.0250
Smirnov n=5: Prob(Dn+ >= 0.001005) = 0.9990
```

Plot the Empirical CDF against the target N(0, 1) CDF.

```python
>>> import matplotlib.pyplot as plt
>>> plt.step(np.concatenate([[-3], x]), ecdfs, where='post', label='Empirical CDF')
>>> x3 = np.linspace(-3, 3, 100)
>>> plt.plot(x3, target.cdf(x3), label='CDF for N(0, 1)')
>>> plt.ylim([0, 1]); plt.grid(True); plt.legend();
```
scipy.special.smirnovi

scipy.special.smirnovi(n, p) = <ufunc 'smirnovi'>

Inverse to \texttt{smirnov}

Returns $d$ such that \texttt{smirnov}(n, d) == p, the critical value corresponding to $p$.

**Parameters**

- \texttt{n} [int] Number of samples
- \texttt{p} [float array_like] Probability

**Returns**

- float The value(s) of \texttt{smirnovi}(n, p), the critical values.

**See also:**

\texttt{smirnov}

The Survival Function (SF) for the distribution

\texttt{scipy.stats.ksone}

Provides the functionality as a continuous distribution

\texttt{kolmogorov, kolmogi, scipy.stats.kstwobign}

**Notes**

\texttt{smirnov} is used by \texttt{stats.kstest} in the application of the Kolmogorov-Smirnov Goodness of Fit test. For historical reasons this function is exposed in \texttt{scipy.special}, but the recommended way to achieve the most accurate CDF/SF/PDF/PPF/ISF computations is to use the \texttt{stats.ksone} distribution.
scipy.special.kolmogorov

scipy.special.kolmogorov(y) = <ufunc 'kolmogorov'>

Complementary cumulative distribution (Survival Function) function of Kolmogorov distribution.

Returns the complementary cumulative distribution function of Kolmogorov’s limiting distribution (D_n*\sqrt(n) as n goes to infinity) of a two-sided test for equality between an empirical and a theoretical distribution. It is equal to the (limit as n->infinity of the) probability that sqrt(n) * max absolute deviation > y.

Parameters

- y [float array_like] Absolute deviation between the Empirical CDF (ECDF) and the target CDF, multiplied by sqrt(n).

Returns

- float The value(s) of kolmogorov(y)

See also:

kolmogi

The Inverse Survival Function for the distribution

scipy.stats.kstwobign

Provides the functionality as a continuous distribution

smirnov, smirnovi

Notes

kolmogorov is used by stats.kstest in the application of the Kolmogorov-Smirnov Goodness of Fit test. For historical reasons this function is exposed in scipy.special, but the recommended way to achieve the most accurate CDF/SF/PDF/PPF/ISF computations is to use the stats.kstwobign distribution.

Examples

Show the probability of a gap at least as big as 0, 0.5 and 1.0.

```python
>>> from scipy.special import kolmogorov
>>> from scipy.stats import kstwobign
>>> kolmogorov([0, 0.5, 1.0])
a[1. , 0.96394524, 0.26999967]
```

Compare a sample of size 1000 drawn from a Laplace(0, 1) distribution against the target distribution, a Normal(0, 1) distribution.

```python
>>> from scipy.stats import norm, laplace
>>> n = 1000
>>> np.random.seed(seed=233423)
>>> lap01 = laplace(0, 1)
>>> x = np.sort(lap01.rvs(n))
>>> np.mean(x), np.std(x)
(-0.083073685397609842, 1.3676426568399822)
```

Construct the Empirical CDF and the K-S statistic D_n.

```python
>>> target = norm(0,1) # Normal mean 0, std dev 1
>>> cdfs = target.cdf(x)
>>> ecdfs = np.arange(n+1, dtype=float)/n
```
gaps = np.column_stack([cdfs - ecdfs[:n], ecdfs[1:] - cdfs])

Dn = np.max(gaps)

Kn = np.sqrt(n) * Dn

print('Dn=%f, sqrt(n)*Dn=%f' % (Dn, Kn))
Dn=0.058286, sqrt(n)*Dn=1.843153

Kn = np.sqrt(n) * Dn

print(chr(10).join(['For a sample of size n drawn from a N(0, 1) distribution:
... ' the approximate Kolmogorov probability that sqrt(n)*Dn>=%f is %f' % (Kn, scipy.special.kolmogi(Kn)),
... ' the approximate Kolmogorov probability that sqrt(n)*Dn<==%f is %f' % (Kn, scipy.special.kstwobign.cdf(Kn))]))

For a sample of size n drawn from a N(0, 1) distribution:
the approximate Kolmogorov probability that sqrt(n)*Dn>=1.843153 is 0.002240
the approximate Kolmogorov probability that sqrt(n)*Dn<=1.843153 is 0.997760

Plot the Empirical CDF against the target N(0, 1) CDF.

import matplotlib.pyplot as plt

plt.step(np.concatenate([[-3], x]], ecdfs, where='post', label='Empirical CDF')

x3 = np.linspace(-3, 3, 100)

plt.plot(x3, target.cdf(x3), label='CDF for N(0, 1)')

plt.ylim([0, 1]); plt.grid(True); plt.legend();

# Add vertical lines marking Dn+ and Dn-

iminus, iplus = np.argmax(gaps, axis=0)

plt.vlines([x[iminus]], ecdfs[iminus], cdfs[iminus], color='r', linestyle='dashed', lw=4)

plt.vlines([x[iplus]], cdfs[iplus], ecdfs[iplus+1], color='r', linestyle='dashed', lw=4)

plt.show()
Parameters

\( p \) [float array_like] Probability

Returns

float The value(s) of kolmogi(p)

See also:

kolmogorov
The Survival Function for the distribution

scipy.stats.kstwobign
Provides the functionality as a continuous distribution

smirnov, smirnovi

Notes

kolmogorov is used by stats.kstest in the application of the Kolmogorov-Smirnov Goodness of Fit test. For historical reasons this function is exposed in scipy.special, but the recommended way to achieve the most accurate CDF/SF/PDF/PPF/ISF computations is to use the stats.kstwobign distribution.

Examples

```python
>>> from scipy.special import kolmogi
>>> kolmogi([0, 0.1, 0.25, 0.5, 0.75, 0.9, 1.0])
array([ inf, 1.22384787, 1.01918472, 0.82757356, 0.67644769,
       0.57117327, 0. ])
```

scipy.special.tklmbda

scipy.special.tklmbda(x, lmbda) = <ufunc 'tklmbda'>
Tukey-Lambda cumulative distribution function

scipy.special.logit

scipy.special.logit(x) = <ufunc 'logit'>
Logit ufunc for ndarrays.

The logit function is defined as \( \logit(p) = \log(p/(1-p)) \). Note that \( \logit(0) = -\infty \), \( \logit(1) = \infty \), and \( \logit(p) \) for \( p<0 \) or \( p>1 \) yields \( \text{nan} \).

Parameters

\( x \) [ndarray] The ndarray to apply logit to element-wise.

Returns

out [ndarray] An ndarray of the same shape as x. Its entries are logit of the corresponding entry of x.

See also:

expit

Notes

As a ufunc logit takes a number of optional keyword arguments. For more information see ufuncs.

New in version 0.10.0.
**Examples**

```python
>>> from scipy.special import logit, expit

```n
```python
>>> logit([0, 0.25, 0.5, 0.75, 1])
array([-inf, -1.09861229, 0., 1.09861229, inf])
```

`expit` is the inverse of `logit`:

```python
>>> expit(logit([0.1, 0.75, 0.999]))
array([0.1, 0.75, 0.999])
```

Plot \( \logit(x) \) for \( x \) in \([0, 1]\):

```python
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(0, 1, 501)
>>> y = logit(x)
>>> plt.plot(x, y)
>>> plt.grid()
>>> plt.ylim(-6, 6)
>>> plt.xlabel('x')
>>> plt.title('logit(x)')
>>> plt.show()
```

---

**scipy.special.expit**

`scipy.special.expit(x) = <ufunc 'expit'>`

Expit (a.k.a. logistic sigmoid) ufunc for ndarrays.

The expit function, also known as the logistic sigmoid function, is defined as \( \expit(x) = 1/(1+\exp(-x)) \). It is the inverse of the logit function.

**Parameters**

- \( x \) [ndarray] The ndarray to apply expit to element-wise.

**Returns**
**expit**

An ndarray of the same shape as x. Its entries are $\expit$ of the corresponding entry of x.

**See also:**

logit

**Notes**

As a ufunc expit takes a number of optional keyword arguments. For more information see ufuncs

New in version 0.10.0.

**Examples**

```python
>>> from scipy.special import expit, logit

>>> expit([-np.inf, -1.5, 0, 1.5, np.inf])
array([ 0.        , 0.18242552, 0.5        , 0.81757448, 1.        ])

logit is the inverse of expit:

>>> logit(expit([-2.5, 0, 3.1, 5.0]))
array([-2.5, 0. , 3.1, 5. ])

Plot expit(x) for x in [-6, 6]:

```python
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(-6, 6, 121)
>>> y = expit(x)
>>> plt.plot(x, y)
>>> plt.grid()
>>> plt.xlim(-6, 6)
>>> plt.xlabel('x')
>>> plt.title('expit(x)')
>>> plt.show()
```

---

**scipy.special.boxcox**

`scipy.special.boxcox(x, lmbda) = <ufunc 'boxcox'>`

Compute the Box-Cox transformation.
The Box-Cox transformation is:

\[
y = \begin{cases} 
    \frac{x^{\lambda} - 1}{\lambda} & \text{if } \lambda \neq 0 \\
    \log(x) & \text{if } \lambda = 0
\end{cases}
\]

Returns \textit{nan} if \(x < 0\). Returns \textit{-inf} if \(x = 0\) and \(\lambda < 0\).

**Parameters**
- \(x\) [array_like] Data to be transformed.
- \(\lambda\) [array_like] Power parameter of the Box-Cox transform.

**Returns**
- \(y\) [array] Transformed data.

**Notes**
New in version 0.14.0.

**Examples**

```python
>>> from scipy.special import boxcox
>>> boxcox([1, 4, 10], 2.5)
array([ 0. , 12.4 , 126.09110641])
>>> boxcox(2, [0, 1, 2])
array([ 0.69314718, 1. , 1.5 ])
```

**scipy.special.boxcox1p**

\(\text{scipy.special.boxcox1p}(x, \lambda) = \text{ufunc \ 'boxcox1p'}\)

Compute the Box-Cox transformation of \(1 + x\).

The Box-Cox transformation computed by \textit{boxcox1p} is:

\[
y = \begin{cases} 
    \frac{(1+x)^{\lambda} - 1}{\lambda} & \text{if } \lambda \neq 0 \\
    \log(1+x) & \text{if } \lambda = 0
\end{cases}
\]

Returns \textit{nan} if \(x < -1\). Returns \textit{-inf} if \(x = -1\) and \(\lambda < 0\).

**Parameters**
- \(x\) [array_like] Data to be transformed.
- \(\lambda\) [array_like] Power parameter of the Box-Cox transform.

**Returns**
- \(y\) [array] Transformed data.

**Notes**
New in version 0.14.0.

**Examples**

```python
>>> from scipy.special import boxcox1p
>>> boxcox1p(1e-4, [0, 0.5, 1])
array([ 9.99950003e-05, 9.99975001e-05, 1.00000000e-04])
>>> boxcox1p([0.01, 0.1], 0.25)
array([ 0.00996272, 0.09645476])
```

**scipy.special.inv_boxcox**

\(\text{scipy.special.inv_boxcox}(y, \lambda) = \text{ufunc \ 'inv_boxcox'}\)

Compute the inverse of the Box-Cox transformation.

Find \(x\) such that:


\[
y = \begin{cases} 
(x**\text{lmbda} - 1) / \text{lmbda} & \text{if } \text{lmbda} \neq 0, \\
\log(x) & \text{if } \text{lmbda} = 0
\end{cases}
\]

**Parameters**

- \(y\) [array_like] Data to be transformed.
- \(\text{lmbda}\) [array_like] Power parameter of the Box-Cox transform.

**Returns**

- \(x\) [array] Transformed data.

**Notes**

New in version 0.16.0.

**Examples**

```python
>>> from scipy.special import boxcox, inv_boxcox
>>> y = boxcox([1, 4, 10], 2.5)
>>> inv_boxcox(y, 2.5)
array([1., 4., 10.])
```

\texttt{scipy.special.inv\_boxcox1p}

\texttt{scipy.special.inv\_boxcox1p}(\(y, \text{lmbda}\)) = <ufunc 'inv\_boxcox1p'>

Compute the inverse of the Box-Cox transformation.

Find \(x\) such that:

\[
y = \begin{cases} 
((1+x)**\text{lmbda} - 1) / \text{lmbda} & \text{if } \text{lmbda} \neq 0, \\
\log(1+x) & \text{if } \text{lmbda} = 0
\end{cases}
\]

**Parameters**

- \(y\) [array_like] Data to be transformed.
- \(\text{lmbda}\) [array_like] Power parameter of the Box-Cox transform.

**Returns**

- \(x\) [array] Transformed data.

**Notes**

New in version 0.16.0.

**Examples**

```python
>>> from scipy.special import boxcox1p, inv_boxcox1p
>>> y = boxcox1p([1, 4, 10], 2.5)
>>> inv_boxcox1p(y, 2.5)
array([1., 4., 10.])
```

\texttt{scipy.special.owens\_t}

\texttt{scipy.special.owens\_t}(\(h, a\)) = <ufunc 'owens\_t'>

Owen's T Function.

The function \(T(h, a)\) gives the probability of the event \((X > h \text{ and } 0 < Y < a \times X)\) where \(X\) and \(Y\) are independent standard normal random variables.

**Parameters**

- \(h\): array_like
  - Input value.
a: array_like
Input value.

Returns
- t: scalar or ndarray
  Probability of the event \(X > h\) and \(0 < Y < a \times X\), where \(X\) and \(Y\) are independent standard normal random variables.

References
[1]

Examples
>>> from scipy import special
>>> a = 3.5
>>> h = 0.78
>>> special.owens_t(h, a)
0.10877216734852274

Information Theory Functions

`entr(x)` Elementwise function for computing entropy.

`rel_entr(x, y)` Elementwise function for computing relative entropy.

`kl_div(x, y)` Elementwise function for computing Kullback-Leibler divergence.

`huber(delta, r)` Huber loss function.

`pseudo_huber(delta, r)` Pseudo-Huber loss function.

scipy.special.entr

scipy.special.entr(x) = <ufunc 'entr'>
Elementwise function for computing entropy.

\[
\text{entr}(x) = \begin{cases}
-x \log(x) & x > 0 \\
0 & x = 0 \\
-\infty & \text{otherwise}
\end{cases}
\]

Parameters
- x [ndarray] Input array.

Returns
- res [ndarray] The value of the elementwise entropy function at the given points \(x\).

See also:
- `kl_div`, `rel_entr`

Notes
This function is concave.
New in version 0.15.0.
The `scipy.special.rel_entr` function is an elementwise function for computing relative entropy. It is defined as follows:

\[
\text{rel}_\text{entr}(x, y) = \begin{cases} 
\log(x/y) & x > 0, y > 0 \\
0 & x = 0, y \geq 0 \\
\infty & \text{otherwise}
\end{cases}
\]

**Parameters**
- **x** [ndarray] First input array.
- **y** [ndarray] Second input array.

**Returns**
- **res** [ndarray] Output array.

**See also:**
- `entr`, `kl_div`

**Notes**
This function is jointly convex in x and y.

New in version 0.15.0.

The `scipy.special.kl_div` function is an elementwise function for computing Kullback-Leibler divergence. It is defined as follows:

\[
\text{kl}_\text{div}(x, y) = \begin{cases} 
\log(x/y) - x + y & x > 0, y > 0 \\
y & x = 0, y \geq 0 \\
\infty & \text{otherwise}
\end{cases}
\]

**Parameters**
- **x** [ndarray] First input array.
- **y** [ndarray] Second input array.

**Returns**
- **res** [ndarray] Output array.

**See also:**
- `entr`, `rel_entr`

**Notes**
This function is non-negative and is jointly convex in x and y.

New in version 0.15.0.

The `scipy.special.huber` function is a Huber loss function. It is defined as follows:

\[
\text{huber}(\delta, r) = \begin{cases} 
\infty & \delta < 0 \\
\frac{1}{2}r^2 & 0 \leq \delta, |r| \leq \delta \\
\delta(|r| - \frac{1}{2}\delta) & \text{otherwise}
\end{cases}
\]

**Parameters**
- **delta** [ndarray] Input array, indicating the quadratic vs. linear loss changepoint.
\( r \) [ndarray] Input array, possibly representing residuals.

**Returns**

\( \text{res} \) [ndarray] The computed Huber loss function values.

**Notes**

This function is convex in \( r \).

New in version 0.15.0.

```python
scipy.special.pseudo_huber
```

\( \text{scipy.special.pseudo_huber}(\text{delta}, r) = \text{ufunc 'pseudo_huber'} \)

Pseudo-Huber loss function.

\[
\text{pseudo}_\text{huber}(\delta, r) = \delta^2 \left( \sqrt{1 + \left( \frac{r}{\delta} \right)^2} - 1 \right)
\]

**Parameters**

\( \text{delta} \) [ndarray] Input array, indicating the soft quadratic vs. linear loss changepoint.

\( r \) [ndarray] Input array, possibly representing residuals.

**Returns**

\( \text{res} \) [ndarray] The computed Pseudo-Huber loss function values.

**Notes**

This function is convex in \( r \).

New in version 0.15.0.

---

### Gamma and Related Functions

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<td>poch(z, m)</td>
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The gamma function is often referred to as the generalized factorial since \( z \cdot \text{gamma}(z) = \text{gamma}(z+1) \) and \( \text{gamma}(n+1) = n! \) for natural number \( n \).

**Parameters**

- **z**
  - [float or complex array_like]

**Returns**

- float or complex
  - The value(s) of \( \text{gamma}(z) \)

**Examples**

```python
>>> from scipy.special import gamma, factorial

>>> gamma([0., 0.5, 1., 5.])
array([ inf, 1.77245385, 1. , 24. ])

>>> z = 2.5 + 1j
>>> gamma(z)
(0.77476210455108352+0.70763120437959293j)
>>> gamma(z+1), z*gamma(z)  # Recurrence property
((1.2292740569981158+2.5438401155000658j),
 (1.2292740569981158+2.5438401155000658j))

>>> gamma(0.5)**2  # gamma(0.5) = sqrt(pi)
3.1415926535897927
```

Plot \( \text{gamma}(x) \) for real \( x \)

```python
>>> x = np.linspace(-3.5, 5.5, 2251)
>>> y = gamma(x)

>>> import matplotlib.pyplot as plt
>>> plt.plot(x, y, 'b', alpha=0.6, label='gamma(x)')
>>> k = np.arange(1, 7)
>>> plt.plot(k, factorial(k-1), 'k*', alpha=0.6, ... label='(x-1)!, x = 1, 2, ...')
>>> plt.xlim(-3.5, 5.5)
>>> plt.ylim(-10, 25)
>>> plt.grid()
>>> plt.xlabel('x')
>>> plt.legend(loc='lower right')
>>> plt.show()
```

**scipy.special.gammaln**

```python
scipy.special.gammaln(x, /, out=None, *, where=True, casting='same_kind', order='K',
                        dtype=None, subok=True[, signature, extobj]) = <ufunc 'gammaln'>
```

Logarithm of the absolute value of the Gamma function.
\gamma(x) = (x-1)!, \ x = 1, 2, ...

**Parameters**

- **x** [array-like] Values on the real line at which to compute \( \gamma(x) \)

**Returns**

- **gamma** [ndarray] Values of \( \gamma(x) \) at x.

See also:

- \( \gamma(x) \) sign of the gamma function
- \( \loggamma \) principal branch of the logarithm of the gamma function

**Notes**

When used in conjunction with \( \gamma(x) \), this function is useful for working in logspace on the real axis without having to deal with complex numbers, via the relation \( \exp(\gamma(x)) = \gamma(x) \).

For complex-valued log-gamma, use \( \loggamma \) instead of \( \gamma(x) \).

**scipy.special.loggamma**

**scipy.special.loggamma**(z, out=None) = <ufunc 'loggamma'>

Principal branch of the logarithm of the Gamma function.

Defined to be \( \log(G(x)) \) for \( x > 0 \) and extended to the complex plane by analytic continuation. The function has a single branch cut on the negative real axis.

New in version 0.18.0.

**Parameters**

- **z** [array-like] Values in the complex plain at which to compute \( \loggamma \)
- **out** [ndarray, optional] Output array for computed values of \( \loggamma \)

**Returns**
loggamma

[ndarray] Values of loggamma at z.

See also:

gammaln
logarithm of the absolute value of the Gamma function

gammasgn
sign of the gamma function

Notes
It is not generally true that \( \log(\Gamma(z)) = \log(\Gamma(z)) \), though the real parts of the functions do agree. The benefit of not defining loggamma as \( \log(\Gamma(z)) \) is that the latter function has a complicated branch cut structure whereas loggamma is analytic except for on the negative real axis.

The identities

\[
\exp(\log(\Gamma(z))) = \Gamma(z) \\
\log(z + 1) = \log(z) + \log(\Gamma(z))
\]

make loggamma useful for working in complex logspace.

On the real line loggamma is related to gammaln via \( \exp(\text{loggamma}(x + 0j)) = \text{gammasgn}(x) \cdot \exp(\text{gammaln}(x)) \), up to rounding error.

The implementation here is based on [hare1997].

References

[hare1997]

scipy.special.gammasgn

scipy.special.gammasgn(x) = <ufunc 'gammasgn'>
Sign of the gamma function.

See also:

gammaln, loggamma

scipy.special.gammainc

scipy.special.gammainc(a, x) = <ufunc 'gammainc'>
Regularized lower incomplete gamma function.

Defined as

\[
\frac{1}{\Gamma(a)} \int_0^x t^{a-1} e^{-t} dt
\]

for \( a > 0 \) and \( x \geq 0 \). The function satisfies the relation \( \text{gammainc}(a, x) + \text{gammaincc}(a, x) = 1 \) where \( \text{gammaincc} \) is the regularized upper incomplete gamma function.

See also:

gammaincc
regularized upper incomplete gamma function

gammaincinv
inverse to gammainc versus x

gammainccinv
inverse to gammaincc versus x

1936 Chapter 6. API Reference
Notes
The implementation largely follows that of [1].

References
[1]

scipy.special.gammaincinv
scipy.special.gammaincinv(a, y) = <ufunc 'gammaincinv'>
Inverse to gammainc

Returns \( x \) such that \( \text{gammainc}(a, x) = y \).

scipy.special.gammaincc
scipy.special.gammaincc(a, x) = <ufunc 'gammaincc'>
Regularized upper incomplete gamma function.

Defined as
\[
\frac{1}{\Gamma(a)} \int_x^\infty t^{a-1}e^{-t}dt
\]
for \( a > 0 \) and \( x \geq 0 \). The function satisfies the relation \( \text{gammainc}(a, x) + \text{gammaincc}(a, x) = 1 \) where \( \text{gammainc} \) is the regularized lower incomplete gamma function.

See also:
gammainc
regularized lower incomplete gamma function
gammaincinv
inverse to \( \text{gammainc} \) versus \( x \)
gammainccinv
inverse to \( \text{gammaincc} \) versus \( x \)

Notes
The implementation largely follows that of [1].

References
[1]

scipy.special.gammainccinv
scipy.special.gammainccinv(a, y) = <ufunc 'gammainccinv'>
Inverse to gammaincc

Returns \( x \) such that \( \text{gammaincc}(a, x) = y \).

scipy.special.beta
scipy.special.beta(a, b) = <ufunc 'beta'>
Beta function.
\[
\beta(a, b) = \frac{\gamma(a) \cdot \gamma(b)}{\gamma(a+b)}
\]

scipy.special.betaln
scipy.special.betaln(a, b) = <ufunc 'betaln'>
Natural logarithm of absolute value of beta function.

Computes \( \ln(\text{abs}(
\beta(a, b))) \).
scipy.special.betainc
scipy.special.betainc(a, b, x) = <ufunc 'betainc'>
Incomplete beta integral.

Compute the incomplete beta integral of the arguments, evaluated from zero to x:

\[
\frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} \int_0^x t^{a-1}(1-t)^{b-1}\,dt.
\]

Notes
The incomplete beta is also sometimes defined without the terms in gamma, in which case the above
definition is the so-called regularized incomplete beta. Under this definition, you can get the incomplete
beta by multiplying the result of the scipy function by beta(a, b).

scipy.special.betaincinv
scipy.special.betaincinv(a, b, y) = <ufunc 'betaincinv'>
Inverse function to beta integral.

Compute x such that betainc(a, b, x) = y.

scipy.special.psi
scipy.special.psi(z, out=None) = <ufunc 'psi'>
The digamma function.

The logarithmic derivative of the gamma function evaluated at z.

Parameters
z [array_like] Real or complex argument.
out [ndarray, optional] Array for the computed values of psi.

Returns
digamma [ndarray] Computed values of psi.

Notes
For large values not close to the negative real axis psi is computed using the asymptotic series (5.11.2)
from [1]. For small arguments not close to the negative real axis the recurrence relation (5.5.2) from [1]
is used until the argument is large enough to use the asymptotic series. For values close to the negative
real axis the reflection formula (5.5.4) from [1] is used first. Note that psi has a family of zeros on
the negative real axis which occur between the poles at nonpositive integers. Around the zeros the
reflection formula suffers from cancellation and the implementation loses precision. The sole positive
zero and the first negative zero, however, are handled separately by precomputing series expansions
using [2], so the function should maintain full accuracy around the origin.

References
[1], [2]

scipy.special.rgamma
scipy.special.rgamma(z) = <ufunc 'rgamma'>
Gamma function inverted

Returns 1/gamma(x)

scipy.special.polygamma
scipy.special.polygamma(n, x)
Polygamma function n.

This is the nth derivative of the digamma (psi) function.

Parameters
n [array_like of int] The order of the derivative of psi.
x [array_like] Where to evaluate the polygamma function.
**Returns**  

polygamma  

[ndarray] The result.

**Examples**

```python
def main():  
    from scipy import special  
    x = [2, 3, 25.5]  
    print(special.polygamma(1, x))  
    print(special.polygamma(0, x) == special.psi(x))

if __name__ == '__main__': main()
```

```python
array([ 0.64493407, 0.39493407, 0.03999467])  
array([ True, True, True], dtype=bool)
```

**scipy.special.multigammaln**

**scipy.special.multigammaln(a, d)**

Returns the log of multivariate gamma, also sometimes called the generalized gamma.

**Parameters**

- `a` [ndarray] The multivariate gamma is computed for each item of `a`.
- `d` [int] The dimension of the space of integration.

**Returns**

- `res` [ndarray] The values of the log multivariate gamma at the given points `a`.

**Notes**

The formal definition of the multivariate gamma of dimension `d` for a real `a` is

$$
\Gamma_d(a) = \int_{A>0} e^{-tr(A)|A|^{a-(d+1)/2}}dA
$$

with the condition $a > (d - 1)/2$, and $A > 0$ being the set of all the positive definite matrices of dimension `d`. Note that `a` is a scalar: the integrand only is multivariate, the argument is not (the function is defined over a subset of the real set).

This can be proven to be equal to the much friendlier equation

$$
\Gamma_d(a) = \pi^{d(d-1)/4} \prod_{i=1}^{d} \Gamma(a - (i - 1)/2).
$$

**References**


**scipy.special.digamma**

**scipy.special.digamma(z, out=None) = <ufunc 'psi'>**

The digamma function.

The logarithmic derivative of the gamma function evaluated at `z`.

**Parameters**

- `z` [array_like] Real or complex argument.
- `out` [ndarray, optional] Array for the computed values of psi.

**Returns**

- `digamma` [ndarray] Computed values of psi.
Notes
For large values not close to the negative real axis \( \psi \) is computed using the asymptotic series (5.11.2) from [1]. For small arguments not close to the negative real axis the recurrence relation (5.5.2) from [1] is used until the argument is large enough to use the asymptotic series. For values close to the negative real axis the reflection formula (5.5.4) from [1] is used first. Note that \( \psi \) has a family of zeros on the negative real axis which occur between the poles at nonpositive integers. Around the zeros the reflection formula suffers from cancellation and the implementation loses precision. The sole positive zero and the first negative zero, however, are handled separately by precomputing series expansions using [2], so the function should maintain full accuracy around the origin.

References
[1], [2]

```
scipy.special.poch
scipy.special.poch(z, m) = <ufunc 'poch'>
```

Rising factorial \( (z)_m \)

The Pochhammer symbol (rising factorial), is defined as

\[
(z)_m = \frac{\Gamma(z + m)}{\Gamma(z)}
\]

For positive integer \( m \) it reads

\[
(z)_m = z(z + 1)...(z + m - 1)
\]

**Parameters**
- \( z \) [array_like] (int or float)
- \( m \) [array_like] (int or float)

**Returns**
- \( \text{poch} \) [ndarray] The value of the function.

Error Function and Fresnel Integrals

```
scipy.special.erf
scipy.special.erf(z) = <ufunc 'erf'>
```

Returns the error function of complex argument.

\[
\text{erf}(z) = \frac{2}{\sqrt{\pi}} \int_0^z \exp(-t^2) \, dt
\]
Parameters

x  [ndarray] Input array.

Returns

res  [ndarray] The values of the error function at the given points x.

See also:

`erfc`, `erfinv`, `erfcinv`, `wofz`, `erfcx`, `erfi`

Notes

The cumulative of the unit normal distribution is given by $\Phi(z) = \frac{1}{2}[1 + \text{erf}(z/\sqrt{2})]$.

References

[1], [2], [3]

Examples

```python
>>> from scipy import special
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(-3, 3)
>>> plt.plot(x, special.erf(x))
>>> plt.xlabel('x')
>>> plt.ylabel('erf(x)')
>>> plt.show()
```

`scipy.special.erfc`

`scipy.special.erfc(x) = <ufunc 'erfc'>`

Complementary error function, $1 - \text{erf}(x)$.

See also:

`erf`, `erfi`, `erfcx`, `dawsn`, `wofz`

References

[1]

Examples
scipy.special.erfcx

scipy.special.erfcx(x) = <ufunc 'erfcx'>

Scaled complementary error function, \( \exp(x^2) \times \text{erfc}(x) \).

See also:

\( \text{erf, erfc, erfi, dawsn, wofz} \)

Notes

New in version 0.12.0.

References

[1]

Examples

```python
>>> from scipy import special
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(-3, 3)
>>> plt.plot(x, special.erfcx(x))
>>> plt.xlabel('x$
>>> plt.ylabel('\text{erfcx}(x)$
>>> plt.show()
```

scipy.special.erfi

scipy.special.erfi(z) = <ufunc 'erfi'>

Imaginary error function, \( -i \text{erf}(i z) \).

See also:

\( \text{erf, erfc, erfcx, dawsn, wofz} \)
Notes
New in version 0.12.0.

References
[1]

Examples
```python
>>> from scipy import special
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(-3, 3)
>>> plt.plot(x, special.erfi(x))
>>> plt.xlabel('$x$')
>>> plt.ylabel('$erfi(x)$')
>>> plt.show()
```
scipy.special.erfinv

scipy.special.erfinv(y)

Inverse of the error function erf.

Computes the inverse of the error function.

In complex domain, there is no unique complex number w satisfying erf(w)=z. This indicates a true inverse function would have multi-value. When the domain restricts to the real, -1 < x < 1, there is a unique real number satisfying erf(erfinv(x)) = x.

Parameters

y [ndarray] Argument at which to evaluate. Domain: [-1, 1]

Returns

erfinv [ndarray] The inverse of erf of y, element-wise

Examples

1. evaluating a float number

```python
>>> from scipy import special
>>> special.erfinv(0.5)
0.4769362762044698
```

2. evaluating a ndarry

```python
>>> from scipy import special
>>> y = np.linspace(-1.0, 1.0, num=10)
>>> special.erfinv(y)
array([-inf, -0.86312307, -0.5407314 , -0.30457019, -0.0987901 ,
       0.0987901 , 0.30457019, 0.5407314 , 0.86312307, inf])
```

scipy.special.erfcinv

scipy.special.erfcinv(y)

Inverse of the complementary error function erfc.

Computes the inverse of the complementary error function function erfc.

In complex domain, there is no unique complex number w satisfying erfc(w)=z. This indicates a true inverse function would have multi-value. When the domain restricts to the real, 0 < x < 2, there is a unique real number satisfying erfc(erfcinv(x)) = erfcinv(erfc(x)).

It is related to inverse of the error function by erfcinv(1-x) = erfinv(x)

Parameters

y [ndarray] Argument at which to evaluate. Domain: [0, 2]

Returns

erfcinv [ndarray] The inverse of erfc of y, element-wise

Examples

1. evaluating a float number

```python
>>> from scipy import special
>>> special.erfcinv(0.5)
0.4769362762044698
```
2. evaluating a ndarray

```python
>>> from scipy import special
>>> y = np.linspace(0.0, 2.0, num=11)
>>> special.erfcinv(y)
array([ inf,  0.9061938 ,  0.59511608,  0.37080716,  0.17914345,
        -0.        , -0.17914345, -0.37080716, -0.59511608, -0.9061938 ,
        -inf])
```

`scipy.special.wofz`

`scipy.special.wofz(z) = <ufunc 'wofz'>`

Faddeeva function

Returns the value of the Faddeeva function for complex argument:

\[
\exp(-z^2) \times \text{erfc}(-i\times z)
\]

See also:

`dawsn`, `erf`, `erfc`, `erfcx`, `erfi`

References

[1]

Examples

```python
>>> from scipy import special
>>> import matplotlib.pyplot as plt

>>> x = np.linspace(-3, 3)
>>> z = special.wofz(x)

>>> plt.plot(x, z.real, label='wofz(x).real')
>>> plt.plot(x, z.imag, label='wofz(x).imag')
>>> plt.xlabel('$x$')
>>> plt.legend(framealpha=1, shadow=True)
>>> plt.grid(alpha=0.25)
>>> plt.show()
```

`scipy.special.dawsn`

`scipy.special.dawsn(x) = <ufunc 'dawsn'>`

Dawson’s integral.

Computes:

\[
\exp(-x^2) \times \int \exp(t^2), t=0..x)
\]

See also:

`wofz`, `erf`, `erfc`, `erfcx`, `erfi`

References

[1]

Examples

```python
>>> from scipy import special
>>> import matplotlib.pyplot as plt

>>> x = np.linspace(-15, 15, num=1000)

(continues on next page)
```
wofz(x).real
wofz(x).imag

```python
>>> plt.plot(x, special.dawsn(x))
>>> plt.xlabel('$x$')
>>> plt.ylabel('$dawsn(x)$')
>>> plt.show()
```

scipy.special.fresnel

scipy.special.fresnel(z) = <ufunc 'fresnel'>

Fresnel sin and cos integrals

Defined as:

```python
ssa = integral(sin(pi/2 * t**2), t=0..z)
csa = integral(cos(pi/2 * t**2), t=0..z)
```
**Parameters**

- `z` [float or complex array_like] Argument

**Returns**

- `ssa, csa` Fresnel sin and cos integral values

**scipy.special.fresnel_zeros**

`scipy.special.fresnel_zeros(nt)`

Compute nt complex zeros of sine and cosine Fresnel integrals $S(z)$ and $C(z)$.

**References**

[1]

**scipy.special.modfresnelp**

`scipy.special.modfresnelp(x) = <ufunc 'modfresnelp'>`

Modified Fresnel positive integrals

**Returns**

- `fp` Integral $F_+(x)$: \( \int_{x}^{\infty} e^{1j*t*t} dt \)
- `kp` Integral $K_+(x)$: \( 1/\sqrt{\pi} e^{-1j*(x*x+\pi/4)} * fp \)

**scipy.special.modfresnelm**

`scipy.special.modfresnelm(x) = <ufunc 'modfresnelm'>`

Modified Fresnel negative integrals

**Returns**

- `fm` Integral $F_-(x)$: \( \int_{x}^{\infty} e^{-1j*t*t} dt \)
- `km` Integral $K_-(x)$: \( 1/\sqrt{\pi} e^{1j*(x*x+\pi/4)} * fp \)

These are not universal functions:

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<td><code>erf_zeros(nt)</code></td>
<td>Compute the first nt zero in the first quadrant, ordered by absolute value.</td>
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<td><code>fresnelc_zeros(nt)</code></td>
<td>Compute nt complex zeros of cosine Fresnel integral $C(z)$.</td>
</tr>
<tr>
<td><code>fresnels_zeros(nt)</code></td>
<td>Compute nt complex zeros of sine Fresnel integral $S(z)$.</td>
</tr>
</tbody>
</table>

**scipy.special.erf_zeros**

`scipy.special.erf_zeros(nt)`

Compute the first nt zero in the first quadrant, ordered by absolute value.

Zeros in the other quadrants can be obtained by using the symmetries \( \text{erf}(-z) = \text{erf}(z) \) and \( \text{erf}(\text{conj}(z)) = \text{conj}(\text{erf}(z)) \).

**Parameters**

- `nt` [int] The number of zeros to compute

**Returns**

- `The locations of the zeros of erf` [ndarray (complex)] Complex values at which zeros of erf($z$)

**References**

[1]
Examples

```python
>>> from scipy import special
>>> special.erf_zeros(1)
array([1.45061616+1.880943j])
```

Check that erf is (close to) zero for the value returned by erf_zeros

```python
>>> special.erf(special.erf_zeros(1))
array([4.95159469e-14-1.16407394e-16j])
```

```python
scipy.special.fresnelc_zeros
scipy.special.fresnelc_zeros(nt)
Compute nt complex zeros of cosine Fresnel integral C(z).

References
[1]
```
```python
scipy.special.fresnels_zeros
scipy.special.fresnels_zeros(nt)
Compute nt complex zeros of sine Fresnel integral S(z).

References
[1]
```

Legendre Functions

```python
lpmv(m, v, x) Associated Legendre function of integer order and real degree.
sph_harm(m, n, theta, phi) Compute spherical harmonics.
```

```python
scipy.special.lpmv
scipy.special.lpmv(m, v, x) = <ufunc 'lpmv'>
Associated Legendre function of integer order and real degree.
```

Defined as

\[ P^m_v = (-1)^m (1 - x^2)^{m/2} \frac{d^m}{dx^m} P_v(x) \]

where

\[ P_v = \sum_{k=0}^{\infty} \frac{(-v)_k (v + 1)_k}{(k!)^2} \left( \frac{1 - x}{2} \right)^k \]

is the Legendre function of the first kind. Here \((\cdot)_k\) is the Pochhammer symbol; see `poch`.

Parameters

- m : array_like Order (int or float). If passed a float not equal to an integer the function returns NaN.
- v : array_like Degree (float).
- x : array_like Argument (float). Must have |x| <= 1.

Returns

- pmv : ndarray Value of the associated Legendre function.

See also:
\texttt{lpmn}

Compute the associated Legendre function for all orders $0, \ldots, m$ and degrees $0, \ldots, n$.

\texttt{clpmn}

Compute the associated Legendre function at complex arguments.

\textbf{Notes}

Note that this implementation includes the Condon-Shortley phase.

\textbf{References}

[1] scipy.special.sph_harm

\texttt{scipy.special.sph_harm(m, n, theta, phi) = <ufunc 'sph_harm'>}

Compute spherical harmonics.

The spherical harmonics are defined as

\[ Y_n^m(\theta, \phi) = \sqrt{\frac{2n + 1}{4\pi} \frac{(n - m)!}{(n + m)!}} e^{im\theta} P_n^m(\cos(\phi)) \]

where $P_n^m$ are the associated Legendre functions; see \texttt{lpmv}.

\textbf{Parameters}

- \texttt{m} [array_like] Order of the harmonic (int); must have $|m| \leq n$.
- \texttt{n} [array_like] Degree of the harmonic (int); must have $n \geq 0$. This is often denoted by $l$ (lower case L) in descriptions of spherical harmonics.
- \texttt{theta} [array_like] Azimuthal (longitudinal) coordinate; must be in $[0, 2\pi]$.
- \texttt{phi} [array_like] Polar (colatitudinal) coordinate; must be in $[0, \pi]$.

\textbf{Returns}

- \texttt{y_mn} [complex float] The harmonic $Y_n^m$ sampled at \texttt{theta} and \texttt{phi}.

\textbf{Notes}

There are different conventions for the meanings of the input arguments \texttt{theta} and \texttt{phi}. In SciPy \texttt{theta} is the azimuthal angle and \texttt{phi} is the polar angle. It is common to see the opposite convention, that is, \texttt{theta} as the polar angle and \texttt{phi} as the azimuthal angle.

Note that SciPy’s spherical harmonics include the Condon-Shortley phase [2] because it is part of \texttt{lpmv}.

With SciPy’s conventions, the first several spherical harmonics are

\[
Y_0^0(\theta, \phi) = \frac{1}{2} \sqrt{\frac{1}{\pi}}
\]

\[
Y_1^{-1}(\theta, \phi) = \frac{1}{2} \sqrt{\frac{3}{2\pi}} e^{-i\theta} \sin(\phi)
\]

\[
Y_1^0(\theta, \phi) = \frac{1}{2} \sqrt{\frac{3}{\pi}} \cos(\phi)
\]

\[
Y_1^1(\theta, \phi) = -\frac{1}{2} \sqrt{\frac{3}{2\pi}} e^{i\phi} \sin(\phi).
\]

\textbf{References}

[1], [2]

These are not universal functions:
### clpmn(m, n, z[, type])

Associated Legendre function of the first kind for complex arguments.

### lpn(n, z)

Legendre function of the first kind.

### lqn(n, z)

Legendre function of the second kind.

### lpmn(m, n, z)

Sequence of associated Legendre functions of the first kind.

### lqmn(m, n, z)

Sequence of associated Legendre functions of the second kind.

### scipy.special.clpmn

Associated Legendre function of the first kind for complex arguments.

Computes the associated Legendre function of the first kind of order \( m \) and degree \( n \), \( P_{m n}(z) = P^m_n(z) \), and its derivative, \( P_{m n}'(z) \). Returns two arrays of size \((m+1, n+1)\) containing \( P_{m n}(z) \) and \( P_{m n}'(z) \) for all orders from 0..\( m \) and degrees from 0..\( n \).

#### Parameters

- **m** ([int]) \(|m| \leq n\): the order of the Legendre function.
- **n** ([int]) \( n \geq 0 \): the degree of the Legendre function. Often called \( L \) in descriptions of the associated Legendre function.
- **z** ([float or complex]): Input value.
- **type** ([int, optional]): takes values 2 or 3:
  - 2: cut on the real axis \(|x| > 1\).
  - 3: cut on the real axis \(-1 < x < 1\) (default).

#### Returns

- **Pmn_z** ([m+1, n+1] array): Values for all orders 0..\( m \) and degrees 0..\( n \)
- **Pmn_d_z** ([m+1, n+1] array): Derivatives for all orders 0..\( m \) and degrees 0..\( n \)

See also:

- **lpn**
  - associated Legendre functions of the first kind for real \( z \)

#### Notes

By default, i.e. for \( type=3 \), phase conventions are chosen according to [1] such that the function is analytic. The cut lies on the interval (-1, 1). Approaching the cut from above or below in general yields a phase factor with respect to Ferrer’s function of the first kind (cf. lpmn).

For \( type=2 \) a cut at \( |x| > 1 \) is chosen. Approaching the real values on the interval (-1, 1) in the complex plane yields Ferrer’s function of the first kind.

#### References

[1], [2]

### scipy.special.lpn

Legendre function of the first kind.

Compute sequence of Legendre functions of the first kind (polynomials), \( P_n(z) \) and derivatives for all degrees from 0 to \( n \) (inclusive).

See also special.legendre for polynomial class.

#### References

[1]
scipy.special.lqn
scipy.special.lqn(n, z)

Legendre function of the second kind.

Compute sequence of Legendre functions of the second kind, \(Q_n(z)\) and derivatives for all degrees from 0 to \(n\) (inclusive).

References
[1]

scipy.special.lpmn
scipy.special.lpmn(m, n, z)

Sequence of associated Legendre functions of the first kind.

Computes the associated Legendre function of the first kind of order \(m\) and degree \(n\), \(P_{mn}(z) = P^m_n(z)\), and its derivative, \(P_{mn}'(z)\). Returns two arrays of size \((m+1, n+1)\) containing \(P_{mn}(z)\) and \(P_{mn}'(z)\) for all orders from 0..\(m\) and degrees from 0..\(n\).

This function takes a real argument \(z\). For complex arguments \(z\) use clpmn instead.

Parameters
\(m\) [int] \(|m| \leq n\); the order of the Legendre function.
\(n\) [int] where \(n \geq 0\); the degree of the Legendre function. Often called \(l\) (lower case \(L\)) in descriptions of the associated Legendre function
\(z\) [float] Input value.

Returns
\(P_{mn}_z\) \([(m+1, n+1)\ array]\) Values for all orders 0..\(m\) and degrees 0..\(n\)
\(P_{mn}_d_z\) \([(m+1, n+1)\ array]\) Derivatives for all orders 0..\(m\) and degrees 0..\(n\)

See also:
clpmn

associated Legendre functions of the first kind for complex \(z\)

Notes
In the interval (-\(1\), 1), Ferrer’s function of the first kind is returned. The phase convention used for the intervals (1, \(\infty\)) and (-\(\infty\), -1) is such that the result is always real.

References
[1], [2]

scipy.special.lqmn
scipy.special.lqmn(m, n, z)

Sequence of associated Legendre functions of the second kind.

Computes the associated Legendre function of the second kind of order \(m\) and degree \(n\), \(Q_{mn}(z) = Q^m_n(z)\), and its derivative, \(Q_{mn}'(z)\). Returns two arrays of size \((m+1, n+1)\) containing \(Q_{mn}(z)\) and \(Q_{mn}'(z)\) for all orders from 0..\(m\) and degrees from 0..\(n\).

Parameters
\(m\) [int] \(|m| \leq n\); the order of the Legendre function.
\(n\) [int] where \(n \geq 0\); the degree of the Legendre function. Often called \(l\) (lower case \(L\)) in descriptions of the associated Legendre function
\(z\) [complex] Input value.

Returns
\(Q_{mn}_z\) \([(m+1, n+1)\ array]\) Values for all orders 0..\(m\) and degrees 0..\(n\)
Qmn_d_z
[(m+1, n+1) array] Derivatives for all orders 0..m and degrees 0..n

References
[1]

Ellipsoidal Harmonics

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<td>Ellipsoidal harmonic normalization constants gamma^p_n</td>
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</table>

**scipy.special.ellip_harm**

These are also known as Lame functions of the first kind, and are solutions to the Lame equation:

$$(s^2 - h^2)(s^2 - k^2)E''(s) + s(2s^2 - h^2 - k^2)E'(s) + (a - qs^2)E(s) = 0$$

where $q = (n + 1)n$ and $a$ is the eigenvalue (not returned) corresponding to the solutions.

**Parameters**

- `h2` [float] $h^2$
- `k2` [float] $k^2$; should be larger than $h^2$
- `n` [int] Degree
- `s` [float] Coordinate
- `p` [int] Order, can range between [1,2n+1]
- `signm` [{1, -1}, optional] Sign of prefactor of functions. Can be +/-1. See Notes.
- `signn` [{1, -1}, optional] Sign of prefactor of functions. Can be +/-1. See Notes.

**Returns**

- `E` [float] the harmonic $E^p_n(s)$

**See also:**

`ellip_harm_2`, `ellip_normal`

**Notes**

The geometric interpretation of the ellipsoidal functions is explained in [2], [3], [4]. The `signm` and `signn` arguments control the sign of prefactors for functions according to their type:

- **K**: +1
- **L**: `signm`
- **M**: `signn`
- **N**: `signm`*`signn`

New in version 0.15.0.

**References**

[1], [2], [3], [4]

**Examples**

```python
>>> from scipy.special import ellip_harm
>>> w = ellip_harm(5,8,1,1,2.5)
```
Check that the functions indeed are solutions to the Lame equation:

```python
>>> from scipy.interpolate import UnivariateSpline
>>> def eigenvalue(f, df, ddf):
...     r = ((s**2 - h**2)*(s**2 - k**2)*ddf + s*(2*s**2 - h**2 - k**2)*df - a*
...         n*(n+1)*s**2*f)/f
...     return -r.mean(), r.std()

>>> s = np.linspace(0.1, 10, 200)
>>> k, h, n, p = 8.0, 2.2, 3, 2
>>> E = ellip_harm(h**2, k**2, n, p, s)
>>> E_spl = UnivariateSpline(s, E)
>>> a, a_err = eigenvalue(E_spl(s), E_spl(s, 1), E_spl(s, 2))
>>> a, a_err
(583.44366156701483, 6.4580890640310646e-11)
```

**scipy.special.ellip_harm_2**

Ellipsoidal harmonic functions $F^p_n(l)$

These are also known as Lame functions of the second kind, and are solutions to the Lame equation:

$$(s^2 - h^2)(s^2 - k^2)F''(s) + s(2s^2 - h^2 - k^2)F'(s) + (a - qs^2)F(s) = 0$$

where $q = (n + 1)n$ and $a$ is the eigenvalue (not returned) corresponding to the solutions.

**Parameters**

- **h2** [float] $h^2$
- **k2** [float] $k^2$; should be larger than $h^2$
- **n** [int] Degree.
- **p** [int] Order, can range between $[1,2n+1]$.
- **s** [float] Coordinate

**Returns**

- **F** [float] The harmonic $F^p_n(s)$

See also:

- el

**Notes**

Lame functions of the second kind are related to the functions of the first kind:

$$F^p_n(s) = (2n + 1)E^p_n(s) \int_0^{1/s} du \frac{(E^p_n(1/u))^2}{(1 - u^2k^2)(1 - u^2h^2)}$$

New in version 0.15.0.

**Examples**

```python
>>> from scipy.special import ellip_harm_2
>>> w = ellip_harm_2(5,8,2,1,10)
>>> w
0.00108056853382
```
scipy.special.ellip_normal
scipy.special.ellip_normal(h2, k2, n, p)

Ellipsoidal harmonic normalization constants gamma^p_n

The normalization constant is defined as
\[ \gamma_n^p = 8 \int_0^h dx \int_h^k dy \frac{(y^2 - x^2)(E_p^n(y)E_p^n(x))^2}{\sqrt{(k^2 - y^2)(y^2 - h^2)(h^2 - x^2)(k^2 - x^2)}} \]

Parameters

- h2 : [float] h**2
- k2 : [float] k**2; should be larger than h**2
- n : [int] Degree.
- p : [int] Order, can range between [1,2n+1].

Returns

gamma : [float] The normalization constant \( \gamma_n^p \)

See also:
ellip_harm, ellip_harm_2

Notes
New in version 0.15.0.

Examples

```python
>>> from scipy.special import ellip_normal
>>> w = ellip_normal(5, 8, 3, 7)
>>> w
1723.38796997
```

Orthogonal polynomials

The following functions evaluate values of orthogonal polynomials:

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<td>Compute the generalized (associated) Laguerre polynomial of degree n and order k.</td>
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<tr>
<td>eval_legendre(n, x[, out])</td>
<td>Evaluate Legendre polynomial at a point.</td>
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<tr>
<td>eval_chebyt(n, x[, out])</td>
<td>Evaluate Chebyshev polynomial of the first kind at a point.</td>
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<tr>
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<td>eval_chebyc(n, x[, out])</td>
<td>Evaluate Chebyshev polynomial of the first kind on [-2, 2] at a point.</td>
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<td><code>eval_sh_chebyt(n, x[, out])</code></td>
<td>Evaluate shifted Chebyshev polynomial of the first kind at a point.</td>
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<td><code>eval_sh_chebyu(n, x[, out])</code></td>
<td>Evaluate shifted Chebyshev polynomial of the second kind at a point.</td>
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<tr>
<td><code>eval_sh_jacobi(n, p, q, x[, out])</code></td>
<td>Evaluate shifted Jacobi polynomial at a point.</td>
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**scipy.special.assoc_laguerre**

`scipy.special.assoc_laguerre(x, n, k=0.0)`

Compute the generalized (associated) Laguerre polynomial of degree `n` and order `k`.

The polynomial \( L_n^{(k)}(x) \) is orthogonal over \([0, \infty)\), with weighting function \( \exp(-x) \cdot x^k \) with \( k > -1 \).

**Notes**

`assoc_laguerre` is a simple wrapper around `eval_genlaguerre`, with reversed argument order (\( x, n, k=0.0 \)) \( \rightarrow \) \( (n, k, x) \).

**scipy.special.eval_legendre**

`scipy.special.eval_legendre(n, x, out=None) = <ufunc 'eval_legendre'>`

Evaluate Legendre polynomial at a point.

The Legendre polynomials can be defined via the Gauss hypergeometric function \( _2F_1 \) as

\[
P_n(x) = _2F_1(-n, n+1; 1; (1-x)/2).
\]

When \( n \) is an integer the result is a polynomial of degree \( n \).

**Parameters**

- `n` [array_like] Degree of the polynomial. If not an integer, the result is determined via the relation to the Gauss hypergeometric function.
- `x` [array_like] Points at which to evaluate the Legendre polynomial

**Returns**

- `P` [ndarray] Values of the Legendre polynomial

**See also:**

- `roots_legendre`
  roots and quadrature weights of Legendre polynomials

- `legendre`
  Legendre polynomial object

- `hyp2f1`
  Gauss hypergeometric function

- `numpy.polynomial.legendre.Legendre`
  Legendre series

**scipy.special.eval_chebyt**

`scipy.special.eval_chebyt(n, x, out=None) = <ufunc 'eval_chebyt'>`

Evaluate Chebyshev polynomial of the first kind at a point.

The Chebyshev polynomials of the first kind can be defined via the Gauss hypergeometric function \( _2F_1 \) as

\[
T_n(x) = _2F_1(n, -n; 1/2; (1-x)/2).
\]
When \( n \) is an integer the result is a polynomial of degree \( n \).

**Parameters**

- \( n \) [array_like] Degree of the polynomial. If not an integer, the result is determined via the relation to the Gauss hypergeometric function.
- \( x \) [array_like] Points at which to evaluate the Chebyshev polynomial

**Returns**

- \( T \) [ndarray] Values of the Chebyshev polynomial

**See also:**

- `roots_chebyt`
  roots and quadrature weights of Chebyshev polynomials of the first kind
- `cheby`
  Chebychev polynomial object
- `eval_chebyu`
  evaluate Chebyshev polynomials of the second kind
- `hyp2f1`
  Gauss hypergeometric function
- `numpy.polynomial.chebyshev.Chebyshev`
  Chebyshev series

**Notes**

This routine is numerically stable for \( x \) in \([-1, 1]\) at least up to order 10000.

scipy.special.eval_chebyu

scipy.special.eval_chebyu(n, x, out=None) = <ufunc 'eval_chebyu'>

Evaluate Chebyshev polynomial of the second kind at a point.

The Chebyshev polynomials of the second kind can be defined via the Gauss hypergeometric function \( _2F_1 \) as

\[
U_n(x) = (n + 1)_2F_1(-n, n + 2; 3/2; (1 - x)/2).
\]

When \( n \) is an integer the result is a polynomial of degree \( n \).

**Parameters**

- \( n \) [array_like] Degree of the polynomial. If not an integer, the result is determined via the relation to the Gauss hypergeometric function.
- \( x \) [array_like] Points at which to evaluate the Chebyshev polynomial

**Returns**

- \( U \) [ndarray] Values of the Chebyshev polynomial

**See also:**

- `roots_chebyu`
  roots and quadrature weights of Chebyshev polynomials of the second kind
- `cheby`
  Chebyshev polynomial object
eval_chebyt

evaluate Chebyshev polynomials of the first kind

hyp2f1

Gauss hypergeometric function

**scipy.special.eval_chebyc**

*scipy.special.eval_chebyc(n, x, out=None) = <ufunc 'eval_chebyc'>*

Evaluate Chebyshev polynomial of the first kind on [-2, 2] at a point.

These polynomials are defined as

\[ S_n(x) = T_n(x/2) \]

where \( T_n \) is a Chebyshev polynomial of the first kind.

**Parameters**

- **n** [array_like] Degree of the polynomial. If not an integer, the result is determined via the relation to eval_chebyt.
- **x** [array_like] Points at which to evaluate the Chebyshev polynomial

**Returns**

- **C** [ndarray] Values of the Chebyshev polynomial

**See also:**

roots_chebyc

roots and quadrature weights of Chebyshev polynomials of the first kind on [-2, 2]

**chebyc**

Chebyshev polynomial object

**numpy.polynomial.chebyshev.Chebyshev**

Chebyshev series

eval_chebyt

evaluate Chebyshev polynomials of the first kind

**scipy.special.eval_chebys**

*scipy.special.eval_chebys(n, x, out=None) = <ufunc 'eval_chebys'>*

Evaluate Chebyshev polynomial of the second kind on [-2, 2] at a point.

These polynomials are defined as

\[ S_n(x) = U_n(x/2) \]

where \( U_n \) is a Chebyshev polynomial of the second kind.

**Parameters**

- **n** [array_like] Degree of the polynomial. If not an integer, the result is determined via the relation to eval_chebyu.
- **x** [array_like] Points at which to evaluate the Chebyshev polynomial

**Returns**

- **S** [ndarray] Values of the Chebyshev polynomial
See also:

roots_chebys
roots and quadrature weights of Chebyshev polynomials of the second kind on [-2, 2]

chebys
Chebyshev polynomial object
eval_chebyu
evaluate Chebyshev polynomials of the second kind

scipy.special.eval_jacobi
scipy.special.eval_jacobi(n, alpha, beta, x, out=None) = <ufunc 'eval_jacobi'>
Evaluate Jacobi polynomial at a point.

The Jacobi polynomials can be defined via the Gauss hypergeometric function \( {}_2F_1 \) as

\[
P_n^{(\alpha,\beta)}(x) = \frac{(\alpha + 1)_n}{\Gamma(n+1)} {}_2F_1(-n, 1 + \alpha + \beta + n; \alpha + 1; (1 - z)/2)
\]

where \((\cdot)_n\) is the Pochhammer symbol; see \(\text{poch}\). When \(n\) is an integer the result is a polynomial of degree \(n\).

Parameters

- \(n\) [array_like] Degree of the polynomial. If not an integer the result is determined via the relation to the Gauss hypergeometric function.
- \(alpha\) [array_like] Parameter
- \(beta\) [array_like] Parameter
- \(x\) [array_like] Points at which to evaluate the polynomial

Returns

- \(P\) [ndarray] Values of the Jacobi polynomial

See also:

roots_jacobi
roots and quadrature weights of Jacobi polynomials

cjacobi
Jacobi polynomial object

hyp2f1
Gauss hypergeometric function

scipy.special.eval_laguerre
scipy.special.eval_laguerre(n, x, out=None) = <ufunc 'eval_laguerre'>
Evaluate Laguerre polynomial at a point.

The Laguerre polynomials can be defined via the confluent hypergeometric function \( {}_1F_1 \) as

\[
L_n(x) = {}_1F_1(-n, 1, x).
\]

When \(n\) is an integer the result is a polynomial of degree \(n\).
n [array_like] Degree of the polynomial. If not an integer the result is determined via the relation to the confluent hypergeometric function.

x [array_like] Points at which to evaluate the Laguerre polynomial

Returns

L [ndarray] Values of the Laguerre polynomial

See also:

roots_laguerre
roots and quadrature weights of Laguerre polynomials

laguerre
Laguerre polynomial object

numpy.polynomial.laguerre.Laguerre
Laguerre series
eval_genlaguerre
evaluate generalized Laguerre polynomials

scipy.special.eval_genlaguerre
scipy.special.eval_genlaguerre(n, alpha, x, out=None) = <ufunc 'eval_genlaguerre'>
Evaluate generalized Laguerre polynomial at a point.

The generalized Laguerre polynomials can be defined via the confluent hypergeometric function $1F_1$ as

$$L^{(\alpha)}_n(x) = \binom{n+\alpha}{n} _1F_1(-n, \alpha + 1, x).$$

When $n$ is an integer the result is a polynomial of degree $n$. The Laguerre polynomials are the special case where $\alpha = 0$.

Parameters

n [array_like] Degree of the polynomial. If not an integer the result is determined via the relation to the confluent hypergeometric function.

alpha [array_like] Parameter; must have alpha > -1

x [array_like] Points at which to evaluate the generalized Laguerre polynomial

Returns

L [ndarray] Values of the generalized Laguerre polynomial

See also:

roots_genlaguerre
roots and quadrature weights of generalized Laguerre polynomials
genlaguerre
generalized Laguerre polynomial object

hyp1f1
confluent hypergeometric function
eval_laguerre
evaluate Laguerre polynomials
scipy.special.eval_hermite

scipy.special.eval_hermite(n, x, out=None) = <ufunc 'eval_hermite'>

Evaluate physicist’s Hermite polynomial at a point.

Defined by

\[ H_n(x) = (-1)^n e^{x^2} \frac{d^n}{dx^n} e^{-x^2}; \]

\(H_n\) is a polynomial of degree \(n\).

Parameters

- n [array_like] Degree of the polynomial
- x [array_like] Points at which to evaluate the Hermite polynomial

Returns

- H [ndarray] Values of the Hermite polynomial

See also:

- roots_hermite: roots and quadrature weights of physicist’s Hermite polynomials
- hermite: physicist’s Hermite polynomial object
- numpy.polynomial.hermite.Hermite: Physicist’s Hermite series
- eval_hermitenorm: evaluate Probabilist’s Hermite polynomials

scipy.special.eval_hermitenorm

scipy.special.eval_hermitenorm(n, x, out=None) = <ufunc 'eval_hermitenorm'>

Evaluate probabilist’s (normalized) Hermite polynomial at a point.

Defined by

\[ H_\epsilon_n(x) = (-1)^n e^{x^2/2} \frac{d^n}{dx^n} e^{-x^2/2}; \]

\(H_\epsilon_n\) is a polynomial of degree \(n\).

Parameters

- n [array_like] Degree of the polynomial
- x [array_like] Points at which to evaluate the Hermite polynomial

Returns

- He [ndarray] Values of the Hermite polynomial

See also:

- roots_hermitenorm: roots and quadrature weights of probabilist’s Hermite polynomials
- hermitenorm: probabilist’s Hermite polynomial object
**numpy.polynomial.hermite_e.HermiteE**

Probabilist’s Hermite series

**eval_hermite**

evaluate physicist’s Hermite polynomials

**scipy.special.eval_gegenbauer**

`scipy.special.eval_gegenbauer(n, alpha, x, out=None) = <ufunc 'eval_gegenbauer'>`

Evaluate Gegenbauer polynomial at a point.

The Gegenbauer polynomials can be defined via the Gauss hypergeometric function $\,_{2}F_{1}$ as

\[
C_n^{(\alpha)} = \frac{(2\alpha)_n}{\Gamma(n+1)} \,_{2}F_{1}(-n, 2\alpha+n; \alpha+1/2; (1-z)/2).
\]

When $n$ is an integer the result is a polynomial of degree $n$.

**Parameters**

- $n$ [array_like] Degree of the polynomial. If not an integer, the result is determined via the relation to the Gauss hypergeometric function.
- $alpha$ [array_like] Parameter
- $x$ [array_like] Points at which to evaluate the Gegenbauer polynomial

**Returns**

- $C$ [ndarray] Values of the Gegenbauer polynomial

See also:

- `roots_gegenbauer`
- `roots and quadrature weights of Gegenbauer polynomials`
- `gegenbauer`
- Gegenbauer polynomial object
- `hyp2f1`
- Gauss hypergeometric function

**scipy.special.eval_sh_legendre**

`scipy.special.eval_sh_legendre(n, x, out=None) = <ufunc 'eval_sh_legendre'>`

Evaluate shifted Legendre polynomial at a point.

These polynomials are defined as

\[
P^*_n(x) = P_n(2x - 1)
\]

where $P_n$ is a Legendre polynomial.

**Parameters**

- $n$ [array_like] Degree of the polynomial. If not an integer, the value is determined via the relation to `eval_legendre`.
- $x$ [array_like] Points at which to evaluate the shifted Legendre polynomial

**Returns**

- $P$ [ndarray] Values of the shifted Legendre polynomial

See also:
roots_sh_legendre
roots and quadrature weights of shifted Legendre polynomials

sh_legendre
shifted Legendre polynomial object

eval_legendre
evaluate Legendre polynomials

numpy.polynomial.legendre.Legendre
Legendre series

scipy.special.eval_sh_chebyt
scipy.special.eval_sh_chebyt(n, x, out=None) = <ufunc 'eval_sh_chebyt'>
Evaluate shifted Chebyshev polynomial of the first kind at a point.

These polynomials are defined as
\[ T_n^*(x) = T_n(2x - 1) \]

where \( T_n \) is a Chebyshev polynomial of the first kind.

Parameters
- n [array_like] Degree of the polynomial. If not an integer, the result is determined via the relation to \texttt{eval_chebyt}.
- x [array_like] Points at which to evaluate the shifted Chebyshev polynomial

Returns
- T [ndarray] Values of the shifted Chebyshev polynomial

See also:

roots_sh_chebyt
roots and quadrature weights of shifted Chebyshev polynomials of the first kind

sh_chebyt
shifted Chebyshev polynomial object

eval_chebyt
evaluate Chebyshev polynomials of the first kind

numpy.polynomial.chebyshev.Chebyshev
Chebyshev series

scipy.special.eval_sh_chebyu
scipy.special.eval_sh_chebyu(n, x, out=None) = <ufunc 'eval_sh_chebyu'>
Evaluate shifted Chebyshev polynomial of the second kind at a point.

These polynomials are defined as
\[ U_n^*(x) = U_n(2x - 1) \]

where \( U_n \) is a Chebyshev polynomial of the first kind.

Parameters
n [array_like] Degree of the polynomial. If not an integer, the result is determined via the relation to eval_chebyu.

x [array_like] Points at which to evaluate the shifted Chebyshev polynomial

Returns

U [ndarray] Values of the shifted Chebyshev polynomial

See also:

roots_sh_chebyu
roots and quadrature weights of shifted Chebychev polynomials of the second kind

sh_chebyu
shifted Chebyshev polynomial object

eval_chebyu
evaluate Chebyshev polynomials of the second kind

scipy.special.eval_sh_jacobi
scipy.special.eval_sh_jacobi(n, p, q, x, out=None) = <ufunc 'eval_sh_jacobi'>
Evaluate shifted Jacobi polynomial at a point.

Defined by

\[ G_n^{(p,q)}(x) = \binom{2n+p-1}{n}^{-1} P_n^{(p-q,q-1)}(2x-1), \]

where \( P_n^{(\cdot)} \) is the n-th Jacobi polynomial.

Parameters

n [int] Degree of the polynomial. If not an integer, the result is determined via the relation to binom and eval_jacobi.
p [float] Parameter
q [float] Parameter

Returns

G [ndarray] Values of the shifted Jacobi polynomial.

See also:

roots_sh_jacobi
roots and quadrature weights of shifted Jacobi polynomials

sh_jacobi
shifted Jacobi polynomial object

eval_jacobi
evaluate Jacobi polynomials

The following functions compute roots and quadrature weights for orthogonal polynomials:

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<td>roots_chebyt(n, mu)</td>
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<td>Gauss-Chebyshev (second kind) quadrature.</td>
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<tr>
<td><code>roots_chebys(n[, mu])</code></td>
<td>Gauss-Chebyshev (second kind) quadrature.</td>
</tr>
<tr>
<td><code>roots_jacobi(n, alpha, beta[, mu])</code></td>
<td>Gauss-Jacobi quadrature.</td>
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<tr>
<td><code>roots_laguerre(n[, mu])</code></td>
<td>Gauss-Laguerre quadrature.</td>
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<td><code>roots_gegenbauer(n, alpha[, mu])</code></td>
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<td><code>roots_sh_chebyu(n[, mu])</code></td>
<td>Gauss-Chebyshev (second kind, shifted) quadrature.</td>
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</table>

`scipy.special.roots_legendre`

`scipy.special.roots_legendre(n, mu=False)`

Gauss-Legendre quadrature.

Computes the sample points and weights for Gauss-Legendre quadrature. The sample points are the roots of the n-th degree Legendre polynomial $P_n(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[-1, 1]$ with weight function $f(x) = 1.0$.

**Parameters**

- `n` [int] quadrature order
- `mu` [bool, optional] If True, return the sum of the weights, optional.

**Returns**

- `x` [ndarray] Sample points
- `w` [ndarray] Weights
- `mu` [float] Sum of the weights

See also:

- `scipy.integrate.quadrature`, `scipy.integrate.fixed_quad`, `numpy.polynomial.legendre.leggauss`

`scipy.special.roots_chebyt`

`scipy.special.roots_chebyt(n, mu=False)`

Gauss-Chebyshev (first kind) quadrature.

Computes the sample points and weights for Gauss-Chebyshev quadrature. The sample points are the roots of the n-th degree Chebyshev polynomial of the first kind, $T_n(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[-1, 1]$ with weight function $f(x) = 1/\sqrt{1-x^2}$.

**Parameters**

- `n` [int] quadrature order
- `mu` [bool, optional] If True, return the sum of the weights, optional.

**Returns**

- `x` [ndarray] Sample points
- `w` [ndarray] Weights
- `mu` [float] Sum of the weights
scipy.special.roots_chebyu

`scipy.special.roots_chebyu(n, mu=False)`

Gauss-Chebyshev (second kind) quadrature.

Computes the sample points and weights for Gauss-Chebyshev quadrature. The sample points are the roots of the n-th degree Chebyshev polynomial of the second kind, \( U_n(x) \). These sample points and weights correctly integrate polynomials of degree \( 2n - 1 \) or less over the interval \([-1, 1]\) with weight function \( f(x) = \sqrt{1 - x^2} \).

**Parameters**

- \( n \) [int] quadrature order
- \( \mu \) [bool, optional] If True, return the sum of the weights, optional.

**Returns**

- \( x \) [ndarray] Sample points
- \( w \) [ndarray] Weights
- \( \mu \) [float] Sum of the weights

See also:

- `scipy.integrate.quadrature`, `scipy.integrate.fixed_quad`
- `numpy.polynomial.chebyshev.chebgauss`

scipy.special.roots_chebyc

`scipy.special.roots_chebyc(n, mu=False)`

Gauss-Chebyshev (first kind) quadrature.

Computes the sample points and weights for Gauss-Chebyshev quadrature. The sample points are the roots of the n-th degree Chebyshev polynomial of the first kind, \( C_n(x) \). These sample points and weights correctly integrate polynomials of degree \( 2n - 1 \) or less over the interval \([-2, 2]\) with weight function \( f(x) = \frac{1}{\sqrt{1 - (x/2)^2}} \).

**Parameters**

- \( n \) [int] quadrature order
- \( \mu \) [bool, optional] If True, return the sum of the weights, optional.

**Returns**

- \( x \) [ndarray] Sample points
- \( w \) [ndarray] Weights
- \( \mu \) [float] Sum of the weights

See also:

- `scipy.integrate.quadrature`, `scipy.integrate.fixed_quad`

scipy.special.roots_chebys

`scipy.special.roots_chebys(n, mu=False)`

Gauss-Chebyshev (second kind) quadrature.

Computes the sample points and weights for Gauss-Chebyshev quadrature. The sample points are the roots of the n-th degree Chebyshev polynomial of the second kind, \( S_n(x) \). These sample points and weights correctly integrate polynomials of degree \( 2n - 1 \) or less over the interval \([-2, 2]\) with weight function \( f(x) = \sqrt{1 - (x/2)^2} \).

**Parameters**

- \( n \) [int] quadrature order
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mu [bool, optional] If True, return the sum of the weights, optional.

Returns

x [ndarray] Sample points
w [ndarray] Weights
mu [float] Sum of the weights

See also:

scipy.integrate.quadrature, scipy.integrate.fixed_quad

scipy.special.roots_jacobi

scipy.special.roots_jacobi(n, alpha, beta, mu=False)

Gauss-Jacobi quadrature.

Computes the sample points and weights for Gauss-Jacobi quadrature. The sample points are the roots
of the n-th degree Jacobi polynomial, $P_n^{\alpha,\beta}(x)$. These sample points and weights correctly integrate
polynomials of degree $2n-1$ or less over the interval $[-1, 1]$ with weight function $f(x) = (1-x)^\alpha(1+x)^\beta$.

Parameters

n [int] quadrature order
alpha [float] alpha must be > -1
beta [float] beta must be > -1
mu [bool, optional] If True, return the sum of the weights, optional.

Returns

x [ndarray] Sample points
w [ndarray] Weights
mu [float] Sum of the weights

See also:

scipy.integrate.quadrature, scipy.integrate.fixed_quad

scipy.special.roots_laguerre

scipy.special.roots_laguerre(n, mu=False)

Gauss-Laguerre quadrature.

Computes the sample points and weights for Gauss-Laguerre quadrature. The sample points are the
roots of the n-th degree Laguerre polynomial, $L_n(x)$. These sample points and weights correctly integrate
polynomials of degree $2n-1$ or less over the interval $[0, \infty]$ with weight function $f(x) = e^{-x}$.

Parameters

n [int] quadrature order
mu [bool, optional] If True, return the sum of the weights, optional.

Returns

x [ndarray] Sample points
w [ndarray] Weights
mu [float] Sum of the weights

See also:

scipy.integrate.quadrature, scipy.integrate.fixed_quad, numpy.polynomial.laguerre.laggauss
scipy.special.roots_genlaguerre

**scipy.special.roots_genlaguerre(n, alpha, mu=False)**

Gauss-generalized Laguerre quadrature.

Computes the sample points and weights for Gauss-generalized Laguerre quadrature. The sample points are the roots of the n-th degree generalized Laguerre polynomial, \( L_n^\alpha(x) \). These sample points and weights correctly integrate polynomials of degree \( 2n - 1 \) or less over the interval \([0, \infty]\) with weight function \( f(x) = x^\alpha e^{-x} \).

**Parameters**

- **n** : [int] quadrature order
- **alpha** : [float] alpha must be > -1
- **mu** : [bool, optional] If True, return the sum of the weights, optional.

**Returns**

- **x** : [ndarray] Sample points
- **w** : [ndarray] Weights
- **mu** : [float] Sum of the weights

**See also:**

- scipy.integrate.quadrature, scipy.integrate.fixed_quad

scipy.special.roots_hermite

**scipy.special.roots_hermite(n, mu=False)**

Gauss-Hermite (physicst’s) quadrature.

Computes the sample points and weights for Gauss-Hermite quadrature. The sample points are the roots of the n-th degree Hermite polynomial, \( H_n(x) \). These sample points and weights correctly integrate polynomials of degree \( 2n - 1 \) or less over the interval \([-\infty, \infty]\) with weight function \( f(x) = e^{-x^2} \).

**Parameters**

- **n** : [int] quadrature order
- **mu** : [bool, optional] If True, return the sum of the weights, optional.

**Returns**

- **x** : [ndarray] Sample points
- **w** : [ndarray] Weights
- **mu** : [float] Sum of the weights

**See also:**

- scipy.integrate.quadrature, scipy.integrate.fixed_quad, numpy.polynomial.hermite.hermgauss, roots_hermitenorm

**Notes**

For small \( n \) up to 150 a modified version of the Golub-Welsch algorithm is used. Nodes are computed from the eigenvalue problem and improved by one step of a Newton iteration. The weights are computed from the well-known analytical formula.

For \( n \) larger than 150 an optimal asymptotic algorithm is applied which computes nodes and weights in a numerically stable manner. The algorithm has linear runtime making computation for very large \( n \) (several thousand or more) feasible.

**References**

- [townsend.trogdon.olver-2014], [townsend.trogdon.olver-2015]
**scipy.special.roots_hermitenorm**  

**scipy.special.roots_hermitenorm(n, mu=False)**  

Gauss-Hermite (statistician’s) quadrature.

Computes the sample points and weights for Gauss-Hermite quadrature. The sample points are the roots of the n-th degree Hermite polynomial, $H_n(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[-\infty, \infty]$ with weight function $f(x) = e^{-x^2/2}$.

**Parameters**

- **n** [int] quadrature order
- **mu** [bool, optional] If True, return the sum of the weights, optional.

**Returns**

- **x** [ndarray] Sample points
- **w** [ndarray] Weights
- **mu** [float] Sum of the weights

See also:

- `scipy.integrate.quadrature`, `scipy.integrate.fixed_quad`, `numpy.polynomial.hermite_e.hermegauss`

**Notes**

For small $n$ up to 150 a modified version of the Golub-Welsch algorithm is used. Nodes are computed from the eigenvalue problem and improved by one step of a Newton iteration. The weights are computed from the well-known analytical formula.

For $n$ larger than 150 an optimal asymptotic algorithm is used which computes nodes and weights in a numerical stable manner. The algorithm has linear runtime making computation for very large $n$ (several thousand or more) feasible.

**scipy.special.roots_gegenbauer**  

**scipy.special.roots_gegenbauer(n, alpha, mu=False)**  

Gauss-Gegenbauer quadrature.

Computes the sample points and weights for Gauss-Gegenbauer quadrature. The sample points are the roots of the n-th degree Gegenbauer polynomial, $C_n^\alpha(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[-1, 1]$ with weight function $f(x) = (1 - x^2)^{\alpha-1/2}$.

**Parameters**

- **n** [int] quadrature order
- **alpha** [float] $\alpha$ must be $> -0.5$
- **mu** [bool, optional] If True, return the sum of the weights, optional.

**Returns**

- **x** [ndarray] Sample points
- **w** [ndarray] Weights
- **mu** [float] Sum of the weights

See also:

- `scipy.integrate.quadrature`, `scipy.integrate.fixed_quad`
**scipy.special.roots_sh_legendre**

`scipy.special.roots_sh_legendre(n, mu=False)`  
Gauss-Legendre (shifted) quadrature.

Computes the sample points and weights for Gauss-Legendre quadrature. The sample points are the roots of the n-th degree shifted Legendre polynomial $P_n^*(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[0, 1]$ with weight function $f(x) = 1.0$.

**Parameters**

- `n` [int] quadrature order
- `mu` [bool, optional] If True, return the sum of the weights, optional.

**Returns**

- `x` [ndarray] Sample points
- `w` [ndarray] Weights
- `mu` [float] Sum of the weights

**See also:**

`scipy.integrate.quadrature`, `scipy.integrate.fixed_quad`

**scipy.special.roots_sh_chebyt**

`scipy.special.roots_sh_chebyt(n, mu=False)`  
Gauss-Chebyshev (first kind, shifted) quadrature.

Computes the sample points and weights for Gauss-Chebyshev quadrature. The sample points are the roots of the n-th degree shifted Chebyshev polynomial of the first kind, $T_n(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[0, 1]$ with weight function $f(x) = 1/\sqrt{1-x^2}$.

**Parameters**

- `n` [int] quadrature order
- `mu` [bool, optional] If True, return the sum of the weights, optional.

**Returns**

- `x` [ndarray] Sample points
- `w` [ndarray] Weights
- `mu` [float] Sum of the weights

**See also:**

`scipy.integrate.quadrature`, `scipy.integrate.fixed_quad`

**scipy.special.roots_sh_chebyu**

`scipy.special.roots_sh_chebyu(n, mu=False)`  
Gauss-Chebyshev (second kind, shifted) quadrature.

Computes the sample points and weights for Gauss-Chebyshev quadrature. The sample points are the roots of the n-th degree shifted Chebyshev polynomial of the second kind, $U_n(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[0, 1]$ with weight function $f(x) = \sqrt{x - x^2}$.

**Parameters**

- `n` [int] quadrature order
- `mu` [bool, optional] If True, return the sum of the weights, optional.

**Returns**

- `x` [ndarray] Sample points
- `w` [ndarray] Weights
mu [float] Sum of the weights

See also:

*scipy.integrate.quadrature, scipy.integrate.fixed_quad*

**scipy.special.roots_sh_jacobi**

`scipy.special.roots_sh_jacobi(n, p1, q1, mu=False)`

Gauss-Jacobi (shifted) quadrature.

Computes the sample points and weights for Gauss-Jacobi (shifted) quadrature. The sample points are the roots of the n-th degree shifted Jacobi polynomial, $G^n_{p,q}(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval [0, 1] with weight function $f(x) = (1 - x)^{p - q} x^{q-1}$

**Parameters**

- **n** [int] quadrature order
- **p1** [float] $(p1 - q1)$ must be $> -1$
- **q1** [float] $q1$ must be $> 0$
- **mu** [bool, optional] If True, return the sum of the weights, optional.

**Returns**

- **x** [ndarray] Sample points
- **w** [ndarray] Weights
- **mu** [float] Sum of the weights

See also:

*scipy.integrate.quadrature, scipy.integrate.fixed_quad*

The functions below, in turn, return the polynomial coefficients in `orthopoly1d` objects, which function similarly as `numpy.poly1d`. The `orthopoly1d` class also has an attribute `weights` which returns the roots, weights, and total weights for the appropriate form of Gaussian quadrature. These are returned in an n x 3 array with roots in the first column, weights in the second column, and total weights in the final column. Note that `orthopoly1d` objects are converted to `poly1d` when doing arithmetic, and lose information of the original orthogonal polynomial.

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**scipy.special.legendre**

`scipy.special.legendre(n, monic=False)`

Legendre polynomial.
Defined to be the solution of

\[
\frac{d}{dx} \left[ (1 - x^2) \frac{d}{dx} P_n(x) \right] + n(n+1)P_n(x) = 0;
\]

\(P_n(x)\) is a polynomial of degree \(n\).

**Parameters**
- \(n\) [int] Degree of the polynomial.
- \(monic\) [bool, optional] If True, scale the leading coefficient to be 1. Default is False.

**Returns**
- \(P\) [orthopoly1d] Legendre polynomial.

**Notes**
The polynomials \(P_n\) are orthogonal over \([-1, 1]\) with weight function 1.

**Examples**
Generate the 3rd-order Legendre polynomial \(1/2*(5x^3 + 0x^2 - 3x + 0)\):

```python
>>> from scipy.special import legendre
>>> legendre(3)
poly1d([ 2.5, 0. , -1.5, 0. ])
```

```
scipy.special.chebyt
```

scipy.special.chebyt\(n, monic=False\)
Chebyshev polynomial of the first kind.

Defined to be the solution of

\[
(1 - x^2) \frac{d^2}{dx^2} T_n - x \frac{d}{dx} T_n + n^2 T_n = 0;
\]

\(T_n\) is a polynomial of degree \(n\).

**Parameters**
- \(n\) [int] Degree of the polynomial.
- \(monic\) [bool, optional] If True, scale the leading coefficient to be 1. Default is False.

**Returns**
- \(T\) [orthopoly1d] Chebyshev polynomial of the first kind.

**See also:**

```
cheby
```

Chebyshev polynomial of the second kind.

**Notes**
The polynomials \(T_n\) are orthogonal over \([-1, 1]\) with weight function \((1 - x^2)^{-1/2}\).

```
scipy.special.chebyu
```

scipy.special.chebyu\(n, monic=False\)
Chebyshev polynomial of the second kind.

Defined to be the solution of

\[
(1 - x^2) \frac{d^2}{dx^2} U_n - 3x \frac{d}{dx} U_n + n(n + 2) U_n = 0;
\]

\(U_n\) is a polynomial of degree \(n\).
Parameters

- n [int] Degree of the polynomial.
- monic [bool, optional] If True, scale the leading coefficient to be 1. Default is False.

Returns

- U [orthopoly1d] Chebyshev polynomial of the second kind.

See also:

- chebyt
  Chebyshev polynomial of the first kind.

Notes

The polynomials $U_n$ are orthogonal over $[-1, 1]$ with weight function $(1 - x^2)^{1/2}$.

scipy.special.chebyc

scipy.special.chebyc(n, monic=False)

Chebyshev polynomial of the first kind on $[-2, 2]$.

Defined as $C_n(x) = 2T_n(x/2)$, where $T_n$ is the $n$th Chebychev polynomial of the first kind.

Parameters

- n [int] Degree of the polynomial.
- monic [bool, optional] If True, scale the leading coefficient to be 1. Default is False.

Returns

- C [orthopoly1d] Chebyshev polynomial of the first kind on $[-2, 2]$.

See also:

- chebyt
  Chebyshev polynomial of the first kind.

Notes

The polynomials $C_n(x)$ are orthogonal over $[-2, 2]$ with weight function $1/\sqrt{1-(x/2)^2}$.

References

/[1/]

scipy.special.chebys

scipy.special.chebys(n, monic=False)

Chebyshev polynomial of the second kind on $[-2, 2]$.

Defined as $S_n(x) = U_n(x/2)$ where $U_n$ is the $n$th Chebychev polynomial of the second kind.

Parameters

- n [int] Degree of the polynomial.
- monic [bool, optional] If True, scale the leading coefficient to be 1. Default is False.

Returns

- S [orthopoly1d] Chebyshev polynomial of the second kind on $[-2, 2]$.

See also:

- chebyu
  Chebyshev polynomial of the second kind
Notes
The polynomials $S_n(x)$ are orthogonal over $[-2, 2]$ with weight function $\sqrt{1 - (x/2)^2}$.

References
[1]

scipy.special.jacobi

scipy.special.jacobi($n$, $alpha$, $beta$, monic=False)

Jacobi polynomial.

Defined to be the solution of

$$(1 - x^2) \frac{d^2}{dx^2} P_n^{(\alpha, \beta)} + (\beta - \alpha - (\alpha + \beta + 2)x) \frac{d}{dx} P_n^{(\alpha, \beta)} + n(n + \alpha + \beta + 1) P_n^{(\alpha, \beta)} = 0$$

for $\alpha, \beta > -1$; $P_n^{(\alpha, \beta)}$ is a polynomial of degree $n$.

Parameters

- $n$ [int] Degree of the polynomial.
- $alpha$ [float] Parameter, must be greater than -1.
- $beta$ [float] Parameter, must be greater than -1.
- $monic$ [bool, optional] If True, scale the leading coefficient to be 1. Default is False.

Returns

- $P$ [orthopoly1d] Jacobi polynomial.

Notes

For fixed $\alpha, \beta$, the polynomials $P_n^{(\alpha, \beta)}$ are orthogonal over $[-1, 1]$ with weight function $(1 - x)^{\alpha + 1}(1 + x)^{\beta}$.

scipy.special.laguerre

scipy.special.laguerre($n$, monic=False)

Laguerre polynomial.

Defined to be the solution of

$$x \frac{d^2}{dx^2} L_n + (1 - x) \frac{d}{dx} L_n + nL_n = 0;$$

$L_n$ is a polynomial of degree $n$.

Parameters

- $n$ [int] Degree of the polynomial.
- $monic$ [bool, optional] If True, scale the leading coefficient to be 1. Default is False.

Returns

- $L$ [orthopoly1d] Laguerre Polynomial.

Notes

The polynomials $L_n$ are orthogonal over $[0, \infty)$ with weight function $e^{-x}$.

scipy.special.genlaguerre

scipy.special.genlaguerre($n$, $alpha$, monic=False)

Generalized (associated) Laguerre polynomial.

Defined to be the solution of

$$x \frac{d^2}{dx^2} L_n^{(\alpha)} + (\alpha + 1 - x) \frac{d}{dx} L_n^{(\alpha)} + nL_n^{(\alpha)} = 0,$$

where $\alpha > -1$; $L_n^{(\alpha)}$ is a polynomial of degree $n$.

Parameters


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n  [int] Degree of the polynomial.
alpha [float] Parameter, must be greater than -1.
monic [bool, optional] If True, scale the leading coefficient to be 1. Default is False.

**Returns**

See also:
laguerre
Laguerre polynomial.

**Notes**
For fixed $\alpha$, the polynomials $L_n^{(\alpha)}$ are orthogonal over $[0, \infty)$ with weight function $e^{-x}x^\alpha$.
The Laguerre polynomials are the special case where $\alpha = 0$.

**scipy.special.hermite**
scipy.special.hermite(n, monic=False)
Physicist’s Hermite polynomial.
Defined by

$$H_n(x) = (-1)^n e^{x^2} \frac{d^n}{dx^n} e^{-x^2};$$

$H_n$ is a polynomial of degree $n$.

**Parameters**
n  [int] Degree of the polynomial.
monic [bool, optional] If True, scale the leading coefficient to be 1. Default is False.

**Returns**
H  [orthopoly1d] Hermite polynomial.

**Notes**
The polynomials $H_n$ are orthogonal over $(-\infty, \infty)$ with weight function $e^{-x^2}$.

**scipy.special.hermitenorm**
scipy.special.hermitenorm(n, monic=False)
Normalized (probabilist’s) Hermite polynomial.
Defined by

$$He_n(x) = (-1)^n e^{x^2/2} \frac{d^n}{dx^n} e^{-x^2/2};$$

$He_n$ is a polynomial of degree $n$.

**Parameters**
n  [int] Degree of the polynomial.
monic [bool, optional] If True, scale the leading coefficient to be 1. Default is False.

**Returns**
He  [orthopoly1d] Hermite polynomial.

**Notes**
The polynomials $He_n$ are orthogonal over $(-\infty, \infty)$ with weight function $e^{-x^2/2}$.
scipy.special.gegenbauer

scipy.special.gegenbauer(n, alpha, monic=False)

Gegenbauer (ultraspherical) polynomial.

Defined to be the solution of

\[(1 - x^2) \frac{d^2}{dx^2} C_n^{(\alpha)} - (2 \alpha + 1)x \frac{d}{dx} C_n^{(\alpha)} + n(n + 2\alpha)C_n^{(\alpha)} = 0\]

for \(\alpha > -1/2\); \(C_n^{(\alpha)}\) is a polynomial of degree \(n\).

**Parameters**

- **n** [int] Degree of the polynomial.
- **monic** [bool, optional] If True, scale the leading coefficient to be 1. Default is False.

**Returns**

- **C** [orthopoly1d] Gegenbauer polynomial.

**Notes**

The polynomials \(C_n^{(\alpha)}\) are orthogonal over \([-1, 1]\) with weight function \((1 - x^2)^{(\alpha-1/2)}\).

scipy.special.sh_legendre

scipy.special.sh_legendre(n, monic=False)

Shifted Legendre polynomial.

Defined as \(P_n^*(x) = P_n(2x - 1)\) for \(P_n\) the nth Legendre polynomial.

**Parameters**

- **n** [int] Degree of the polynomial.
- **monic** [bool, optional] If True, scale the leading coefficient to be 1. Default is False.

**Returns**

- **P** [orthopoly1d] Shifted Legendre polynomial.

**Notes**

The polynomials \(P_n^*\) are orthogonal over \([0, 1]\) with weight function 1.

scipy.special.sh_chebyt

scipy.special.sh_chebyt(n, monic=False)

Shifted Chebyshev polynomial of the first kind.

Defined as \(T_n^*(x) = T_n(2x - 1)\) for \(T_n\) the nth Chebyshev polynomial of the first kind.

**Parameters**

- **n** [int] Degree of the polynomial.
- **monic** [bool, optional] If True, scale the leading coefficient to be 1. Default is False.

**Returns**

- **T** [orthopoly1d] Shifted Chebyshev polynomial of the first kind.

**Notes**

The polynomials \(T_n^*\) are orthogonal over \([0, 1]\) with weight function \((x - x^2)^{-1/2}\).

scipy.special.sh_chebyu

scipy.special.sh_chebyu(n, monic=False)

Shifted Chebyshev polynomial of the second kind.

Defined as \(U_n^*(x) = U_n(2x - 1)\) for \(U_n\) the nth Chebyshev polynomial of the second kind.

**Parameters**

**
.. _orthopoly1d-reference:

orthopoly1d

.. autofunction:: scipy.special.orthopoly1d

.. _shifted_chebyshev-polynomials-reference:

Shifting Chebyshev Polynomials

.. autofunction:: scipy.special.shifted_chebyu

.. automodule:: scipy.special
   :members:

.. _shifted_jacobi-polynomials-reference:

Shifting Jacobi Polynomials

.. autofunction:: scipy.special.shifted_jacobi

.. automodule:: scipy.special
   :members:

Hypergeometric Functions

.. autofunction:: scipy.special.hyp2f1
   :return: Gauss hypergeometric function \(2F1(a, b; c; z)\)

.. autoclass:: scipy.special.hyp2f1
   :members:

   .. automodule:: scipy.special
      :members:

.. _warning-shifting-polynomials:

**Warning:** Computing values of high-order polynomials (around order \(> 20\)) using polynomial coefficients is numerically unstable. To evaluate polynomial values, the :func:`eval_*` functions should be used instead.
Parameters

- \(a, b, c\) [array_like] Arguments, should be real-valued.
- \(z\) [array_like] Argument, real or complex.

Returns

- \(\text{hyp2f1}\) [scalar or ndarray] The values of the gaussian hypergeometric function.

See also:

- \(\text{hyp0f1}\) confluent hypergeometric limit function.
- \(\text{hyp1f1}\) Kummer’s (confluent hypergeometric) function.

Notes

This function is defined for \(|z| < 1\) as

\[
\text{hyp2f1}(a, b, c, z) = \sum_{n=0}^{\infty} \frac{(a)_n (b)_n}{(c)_n} \frac{z^n}{n!},
\]

and defined on the rest of the complex \(z\)-plane by analytic continuation. Here \((\cdot)_n\) is the Pochhammer symbol; see \texttt{poch}. When \(n\) is an integer the result is a polynomial of degree \(n\).

The implementation for complex values of \(z\) is described in [1].

References

[1], [2], [3]

\texttt{scipy.special.hyp1f1}

\texttt{scipy.special.hyp1f1(a, b, x) = <ufunc 'hyp1f1'>}

Confluent hypergeometric function 1F1(a, b; x)

\texttt{scipy.special.hyperu}

\texttt{scipy.special.hyperu(a, b, x) = <ufunc 'hyperu'>}

Confluent hypergeometric function U(a, b; x) of the second kind

\texttt{scipy.special.hyp0f1}

\texttt{scipy.special.hyp0f1(v, x) = <ufunc 'hyp0f1'>}

Confluent hypergeometric limit function 0F1.

Parameters

- \(v, z\) [array_like] Input values.

Returns

- \(\text{hyp0f1}\) [ndarray] The confluent hypergeometric limit function.

Notes

This function is defined as:

\[
0F1(v, z) = \sum_{k=0}^{\infty} \frac{z^k}{(v)_k k!}.
\]

It’s also the limit as \(q \to \infty\) of \(1F1(q; v; z/q)\), and satisfies the differential equation \(f''(z) + vf'(z) = f(z)\).
scipy.special.hyp2f0

scipy.special.hyp2f0(*args, **kwds)

g2f0 is deprecated! hyp2f0 is deprecated in SciPy 1.2

hyp2f0(x1, x2, x3, x4[, out1, out2], / [, out=(None, None)], *, where=True, casting='same_kind', order='K', dtype=Although, subok=True, signature, extobj])

hyp2f0(a, b, c, x)

Hypergeometric function 2F0 in y and an error estimate

The parameter type determines a convergence factor and can be either 1 or 2.

Returns

y Value of the function
err Error estimate

scipy.special.hyp1f2

scipy.special.hyp1f2(*args, **kwds)

g1f2 is deprecated! hyp1f2 is deprecated in SciPy 1.2

hyp1f2(x1, x2, x3, x4[, out1, out2], / [, out=(None, None)], *, where=True, casting='same_kind', order='K', dtype=Although, subok=True, signature, extobj])

hyp1f2(a, b, c, x)

Hypergeometric function 1F2 and error estimate

Returns

y Value of the function
err Error estimate

scipy.special.hyp3f0

scipy.special.hyp3f0(*args, **kwds)

g3f0 is deprecated! hyp3f0 is deprecated in SciPy 1.2

hyp3f0(x1, x2, x3, x4[, out1, out2], / [, out=(None, None)], *, where=True, casting='same_kind', order='K', dtype=Although, subok=True, signature, extobj])

hyp3f0(a, b, c, x)

Hypergeometric function 3F0 in y and an error estimate

Returns

y Value of the function
err Error estimate

Parabolic Cylinder Functions

<table>
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<th>Description</th>
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<td>pbdv(v, x)</td>
<td>Parabolic cylinder function D</td>
</tr>
<tr>
<td>pbvv(v, x)</td>
<td>Parabolic cylinder function V</td>
</tr>
<tr>
<td>pbwa(a, x)</td>
<td>Parabolic cylinder function W.</td>
</tr>
</tbody>
</table>

scipy.special.pbdv

scipy.special.pbdv(v, x) = <ufunc 'pbdv'>

Parabolic cylinder function D

Returns (d, dp) the parabolic cylinder function Dv(x) in d and the derivative, Dv'(x) in dp.

Returns


```
d  Value of the function
dp  Value of the derivative vs x

\texttt{scipy.special.pbvv}
\texttt{scipy.special.pbvv(v, x) = ufunc 'pbvv'>}
Parabolic cylinder function $V$

Returns the parabolic cylinder function $Vv(x)$ in $v$ and the derivative, $Vv'(x)$ in $vp$.

**Returns**

$v$  Value of the function
$v_p$  Value of the derivative vs $x$

\texttt{scipy.special.pbwa}
\texttt{scipy.special.pbwa(a, x) = ufunc 'pbwa'>}
Parabolic cylinder function $W$.

The function is a particular solution to the differential equation

\[
y'' + \left( \frac{1}{4}x^2 - a \right) y = 0,
\]

for a full definition see section 12.14 in [1].

**Parameters**

- $a$  [array_like] Real parameter
- $x$  [array_like] Real argument

**Returns**

- $w$  [scalar or ndarray] Value of the function
- $w_p$  [scalar or ndarray] Value of the derivative in $x$

**Notes**

The function is a wrapper for a Fortran routine by Zhang and Jin [2]. The implementation is accurate only for $|a|, |x| < 5$ and returns NaN outside that range.

**References**

[1], [2]

These are not universal functions:

- `pbdv_seq(v, x)`  Parabolic cylinder functions $Dv(x)$ and derivatives.
- `pbvv_seq(v, x)`  Parabolic cylinder functions $Vv(x)$ and derivatives.
- `pbdn_seq(n, z)`  Parabolic cylinder functions $Dn(z)$ and derivatives.

\texttt{scipy.special.pbdv_seq}
\texttt{scipy.special.pbdv_seq(v, x)}
Parabolic cylinder functions $Dv(x)$ and derivatives.

**Parameters**

- $v$  [float] Order of the parabolic cylinder function
- $x$  [float] Value at which to evaluate the function and derivatives

**Returns**

- $dv$  [ndarray] Values of $D_{vi}(x)$, for $vi=v-int(v)$, $vi=1+v-int(v)$, ..., $vi=v$.
- $dp$  [ndarray] Derivatives $D_{vi}'(x)$, for $vi=v-int(v)$, $vi=1+v-int(v)$, ..., $vi=v$.
```
scipy.special.pbvv_seq
scipy.special.pbvv_seq(v, x)
Parabolic cylinder functions \( V_v(x) \) and derivatives.

Parameters

- \( v \) [float] Order of the parabolic cylinder function
- \( x \) [float] Value at which to evaluate the function and derivatives

Returns

- \( dv \) [ndarray] Values of \( V_{vi}(x) \), for \( vi=v-int(v) \), \( vi=1+v-int(v) \), \ldots, \( vi=v \).
- \( dp \) [ndarray] Derivatives \( V_{vi}'(x) \), for \( vi=v-int(v) \), \( vi=1+v-int(v) \), \ldots, \( vi=v \).

References

[1]

scipy.special.pbdn_seq
scipy.special.pbdn_seq(n, z)
Parabolic cylinder functions \( D_n(z) \) and derivatives.

Parameters

- \( n \) [int] Order of the parabolic cylinder function
- \( z \) [complex] Value at which to evaluate the function and derivatives

Returns

- \( dv \) [ndarray] Values of \( D_i(z) \), for \( i=0, \ldots, i=n \).
- \( dp \) [ndarray] Derivatives \( D_i'(z) \), for \( i=0, \ldots, i=n \).

References

[1]

Mathieu and Related Functions

<table>
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<tr>
<th>Function</th>
<th>Description</th>
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<tbody>
<tr>
<td>\texttt{mathieu_a}(m, q)</td>
<td>Characteristic value of even Mathieu functions</td>
</tr>
<tr>
<td>\texttt{mathieu_b}(m, q)</td>
<td>Characteristic value of odd Mathieu functions</td>
</tr>
</tbody>
</table>

scipy.special.mathieu\_a
scipy.special.mathieu\_a(m, q) = \texttt{ufunc 'mathieu\_a'}

Characteristic value of even Mathieu functions

Returns the characteristic value for the even solution, \( ce\_m(z, \ q) \), of Mathieu’s equation.

scipy.special.mathieu\_b
scipy.special.mathieu\_b(m, q) = \texttt{ufunc 'mathieu\_b'}

Characteristic value of odd Mathieu functions

Returns the characteristic value for the odd solution, \( se\_m(z, \ q) \), of Mathieu’s equation.

These are not universal functions:

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>\texttt{mathieu_even_coef}(m, q)</td>
<td>Fourier coefficients for even Mathieu and modified Mathieu functions.</td>
</tr>
<tr>
<td>\texttt{mathieu_odd_coef}(m, q)</td>
<td>Fourier coefficients for even Mathieu and modified Mathieu functions.</td>
</tr>
</tbody>
</table>
scipy.special.mathieu_even_coef
scipy.special.mathieu_even_coef(m, q)

Fourier coefficients for even Mathieu and modified Mathieu functions.

The Fourier series of the even solutions of the Mathieu differential equation are of the form

\[ ce_{2n}(z, q) = \sum_{k=0}^{\infty} A_{(2n)}^{(2k)} \cos 2kz \]
\[ ce_{2n+1}(z, q) = \sum_{k=0}^{\infty} A_{(2n+1)}^{(2k+1)} \cos(2k + 1)z \]

This function returns the coefficients \( A_{(2n)}^{(2k)} \) for even input \( m=2n \), and the coefficients \( A_{(2n+1)}^{(2k+1)} \) for odd input \( m=2n+1 \).

**Parameters**

- **m** [int] Order of Mathieu functions. Must be non-negative.
- **q** [float (>=0)] Parameter of Mathieu functions. Must be non-negative.

**Returns**

- **Ak** [ndarray] Even or odd Fourier coefficients, corresponding to even or odd \( m \).

**References**

[1], [2]

scipy.special.mathieu_odd_coef
scipy.special.mathieu_odd_coef(m, q)

Fourier coefficients for even Mathieu and modified Mathieu functions.

The Fourier series of the odd solutions of the Mathieu differential equation are of the form

\[ se_{2n+1}(z, q) = \sum_{k=0}^{\infty} B_{(2n+1)}^{(2k+1)} \sin(2k + 1)z \]
\[ se_{2n+2}(z, q) = \sum_{k=0}^{\infty} B_{(2n+2)}^{(2k+2)} \sin(2k + 2)z \]

This function returns the coefficients \( B_{(2n+2)}^{(2k+2)} \) for even input \( m=2n+2 \), and the coefficients \( B_{(2n+1)}^{(2k+1)} \) for odd input \( m=2n+1 \).

**Parameters**

- **m** [int] Order of Mathieu functions. Must be non-negative.
- **q** [float (>=0)] Parameter of Mathieu functions. Must be non-negative.

**Returns**

- **Bk** [ndarray] Even or odd Fourier coefficients, corresponding to even or odd \( m \).

**References**

[1]

The following return both function and first derivative:

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
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<tbody>
<tr>
<td>mathieu_cem(m, q, x)</td>
<td>Even Mathieu function and its derivative</td>
</tr>
<tr>
<td>mathieu_sem(m, q, x)</td>
<td>Odd Mathieu function and its derivative</td>
</tr>
<tr>
<td>mathieu_modcem1(m, q, x)</td>
<td>Even modified Mathieu function of the first kind and its derivative</td>
</tr>
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<tbody>
<tr>
<td><code>mathieu_modcem2</code></td>
<td>Even modified Mathieu function of the second kind and its derivative</td>
</tr>
<tr>
<td><code>mathieu_modsem1</code></td>
<td>Odd modified Mathieu function of the first kind and its derivative</td>
</tr>
<tr>
<td><code>mathieu_modsem2</code></td>
<td>Odd modified Mathieu function of the second kind and its derivative</td>
</tr>
</tbody>
</table>

**scipy.special.mathieu_cem**

```python
scipy.special.mathieu_cem(m, q, x) = <ufunc 'mathieu_cem'>
```

Even Mathieu function and its derivative

Returns the even Mathieu function, \( ce_m(x, q) \), of order \( m \) and parameter \( q \) evaluated at \( x \) (given in degrees). Also returns the derivative with respect to \( x \) of \( ce_m(x, q) \)

**Parameters**

- \( m \) Order of the function
- \( q \) Parameter of the function
- \( x \) Argument of the function, *given in degrees, not radians*

**Returns**

- \( y \) Value of the function
- \( yp \) Value of the derivative vs \( x \)

**scipy.special.mathieu_sem**

```python
scipy.special.mathieu_sem(m, q, x) = <ufunc 'mathieu_sem'>
```

Odd Mathieu function and its derivative

Returns the odd Mathieu function, \( se_m(x, q) \), of order \( m \) and parameter \( q \) evaluated at \( x \) (given in degrees). Also returns the derivative with respect to \( x \) of \( se_m(x, q) \).

**Parameters**

- \( m \) Order of the function
- \( q \) Parameter of the function
- \( x \) Argument of the function, *given in degrees, not radians.*

**Returns**

- \( y \) Value of the function
- \( yp \) Value of the derivative vs \( x \)

**scipy.special.mathieu_modcem1**

```python
scipy.special.mathieu_modcem1(m, q, x) = <ufunc 'mathieu_modcem1'>
```

Even modified Mathieu function of the first kind and its derivative

Evaluates the even modified Mathieu function of the first kind, \( Mc1m(x, q) \), and its derivative at \( x \) for order \( m \) and parameter \( q \).

**Returns**

- \( y \) Value of the function
- \( yp \) Value of the derivative vs \( x \)

**scipy.special.mathieu_modcem2**

```python
scipy.special.mathieu_modcem2(m, q, x) = <ufunc 'mathieu_modcem2'>
```

Even modified Mathieu function of the second kind and its derivative

Evaluates the even modified Mathieu function of the second kind, \( Mc2m(x, q) \), and its derivative at \( x \) (given in degrees) for order \( m \) and parameter \( q \).
Returns

- \( y \): Value of the function
- \( y_p \): Value of the derivative vs \( x \)

`scipy.special.mathieu_modsem1`

`scipy.special.mathieu_modsem1(m, q, x) = <ufunc 'mathieu_modsem1'>`

Odd modified Mathieu function of the first kind and its derivative

Evaluates the odd modified Mathieu function of the first kind, \( Ms_1m(x, q) \), and its derivative at \( x \) (given in degrees) for order \( m \) and parameter \( q \).

Returns

- \( y \): Value of the function
- \( y_p \): Value of the derivative vs \( x \)

`scipy.special.mathieu_modsem2`

`scipy.special.mathieu_modsem2(m, q, x) = <ufunc 'mathieu_modsem2'>`

Odd modified Mathieu function of the second kind and its derivative

Evaluates the odd modified Mathieu function of the second kind, \( Ms_2m(x, q) \), and its derivative at \( x \) (given in degrees) for order \( m \) and parameter \( q \).

Returns

- \( y \): Value of the function
- \( y_p \): Value of the derivative vs \( x \)

Spheroidal Wave Functions

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<th>Description</th>
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<td>Prolate spheroidal angular function of the first kind and its derivative</td>
</tr>
<tr>
<td><code>pro_rad1(m, n, c, x)</code></td>
<td>Prolate spheroidal radial function of the first kind and its derivative</td>
</tr>
<tr>
<td><code>pro_rad2(m, n, c, x)</code></td>
<td>Prolate spheroidal radial function of the second kind and its derivative</td>
</tr>
<tr>
<td><code>obl_ang1(m, n, c, x)</code></td>
<td>Oblate spheroidal angular function of the first kind and its derivative</td>
</tr>
<tr>
<td><code>obl_rad1(m, n, c, x)</code></td>
<td>Oblate spheroidal radial function of the first kind and its derivative</td>
</tr>
<tr>
<td><code>obl_rad2(m, n, c, x)</code></td>
<td>Oblate spheroidal radial function of the second kind and its derivative</td>
</tr>
<tr>
<td><code>pro_cv(m, n, c)</code></td>
<td>Characteristic value of prolate spheroidal function</td>
</tr>
<tr>
<td><code>obl_cv(m, n, c)</code></td>
<td>Characteristic value of oblate spheroidal function</td>
</tr>
<tr>
<td><code>pro_cv_seq(m, n, c)</code></td>
<td>Characteristic values for prolate spheroidal wave functions.</td>
</tr>
<tr>
<td><code>obl_cv_seq(m, n, c)</code></td>
<td>Characteristic values for oblate spheroidal wave functions.</td>
</tr>
</tbody>
</table>

`scipy.special.pro_ang1`

`scipy.special.pro_ang1(m, n, c, x) = <ufunc 'pro_ang1'>`

Prolate spheroidal angular function of the first kind and its derivative

Computes the prolate spheroidal angular function of the first kind and its derivative (with respect to \( x \)) for mode parameters \( m \geq 0 \) and \( n \geq m \), spheroidal parameter \( c \) and \( |x| < 1.0 \).

Returns
scipy.special.pro_rad1

scipy.special.pro_rad1(m, n, c, x) = <ufunc 'pro_rad1'>

Prolate spheroidal radial function of the first kind and its derivative

Computes the prolate spheroidal radial function of the first kind and its derivative (with respect to \( x \)) for mode parameters \( m\geq0 \) and \( n\geq m \), spheroidal parameter \( c \) and \(|x| < 1.0\).

Returns

- **s**: Value of the function
- **sp**: Value of the derivative vs \( x \)

scipy.special.pro_rad2

scipy.special.pro_rad2(m, n, c, x) = <ufunc 'pro_rad2'>

Prolate spheroidal radial function of the second kind and its derivative

Computes the prolate spheroidal radial function of the second kind and its derivative (with respect to \( x \)) for mode parameters \( m\geq0 \) and \( n\geq m \), spheroidal parameter \( c \) and \(|x| < 1.0\).

Returns

- **s**: Value of the function
- **sp**: Value of the derivative vs \( x \)

scipy.special.obl_ang1

scipy.special.obl_ang1(m, n, c, x) = <ufunc 'obl_ang1'>

Oblate spheroidal angular function of the first kind and its derivative

Computes the oblate spheroidal angular function of the first kind and its derivative (with respect to \( x \)) for mode parameters \( m\geq0 \) and \( n\geq m \), spheroidal parameter \( c \) and \(|x| < 1.0\).

Returns

- **s**: Value of the function
- **sp**: Value of the derivative vs \( x \)

scipy.special.obl_rad1

scipy.special.obl_rad1(m, n, c, x) = <ufunc 'obl_rad1'>

Oblate spheroidal radial function of the first kind and its derivative

Computes the oblate spheroidal radial function of the first kind and its derivative (with respect to \( x \)) for mode parameters \( m\geq0 \) and \( n\geq m \), spheroidal parameter \( c \) and \(|x| < 1.0\).

Returns

- **s**: Value of the function
- **sp**: Value of the derivative vs \( x \)

scipy.special.obl_rad2

scipy.special.obl_rad2(m, n, c, x) = <ufunc 'obl_rad2'>

Oblate spheroidal radial function of the second kind and its derivative

Computes the oblate spheroidal radial function of the second kind and its derivative (with respect to \( x \)) for mode parameters \( m\geq0 \) and \( n\geq m \), spheroidal parameter \( c \) and \(|x| < 1.0\).

Returns

- **s**: Value of the function
- **sp**: Value of the derivative vs \( x \)
directives

The following functions require pre-computed characteristic value:

<table>
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<td>pro_ang1_cv</td>
<td>Prolate spheroidal angular function pro_ang1 for precomputed characteristic value</td>
</tr>
<tr>
<td>pro_rad1_cv</td>
<td>Prolate spheroidal radial function pro_rad1 for precomputed characteristic value</td>
</tr>
<tr>
<td>pro_rad2_cv</td>
<td>Prolate spheroidal radial function pro_rad2 for precomputed characteristic value</td>
</tr>
<tr>
<td>obl_ang1_cv</td>
<td>Oblate spheroidal angular function obl_ang1 for precomputed characteristic value</td>
</tr>
<tr>
<td>obl_rad1_cv</td>
<td>Oblate spheroidal radial function obl_rad1 for precomputed characteristic value</td>
</tr>
<tr>
<td>obl_rad2_cv</td>
<td>Oblate spheroidal radial function obl_rad2 for precomputed characteristic value</td>
</tr>
</tbody>
</table>

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sp  Value of the derivative vs x

scipy.special.pro_rad1_cv
scipy.special.pro_rad1_cv(m, n, c, cv, x) = <ufunc 'pro_rad1_cv'>
  Prolate spheroidal radial function pro_rad1 for precomputed characteristic value

  Computes the prolate spheroidal radial function of the first kind and its derivative (with respect to x) for
  mode parameters m>=0 and n>=m, spheroidal parameter c and |x| < 1.0. Requires pre-computed
  characteristic value.

  Returns
  s  Value of the function
  sp Value of the derivative vs x

scipy.special.pro_rad2_cv
scipy.special.pro_rad2_cv(m, n, c, cv, x) = <ufunc 'pro_rad2_cv'>
  Prolate spheroidal radial function pro_rad2 for precomputed characteristic value

  Computes the prolate spheroidal radial function of the second kind and its derivative (with respect to x) for
  mode parameters m>=0 and n>=m, spheroidal parameter c and |x| < 1.0. Requires pre-
  computed characteristic value.

  Returns
  s  Value of the function
  sp Value of the derivative vs x

scipy.special.obl_ang1_cv
scipy.special.obl_ang1_cv(m, n, c, cv, x) = <ufunc 'obl_ang1_cv'>
  Oblate spheroidal angular function obl_ang1 for precomputed characteristic value

  Computes the oblate spheroidal angular function of the first kind and its derivative (with respect to x) for
  mode parameters m>=0 and n>=m, spheroidal parameter c and |x| < 1.0. Requires pre-
  computed characteristic value.

  Returns
  s  Value of the function
  sp Value of the derivative vs x

scipy.special.obl_rad1_cv
scipy.special.obl_rad1_cv(m, n, c, cv, x) = <ufunc 'obl_rad1_cv'>
  Oblate spheroidal radial function obl_rad1 for precomputed characteristic value

  Computes the oblate spheroidal radial function of the first kind and its derivative (with respect to x) for
  mode parameters m>=0 and n>=m, spheroidal parameter c and |x| < 1.0. Requires pre-computed
  characteristic value.

  Returns
  s  Value of the function
  sp Value of the derivative vs x

scipy.special.obl_rad2_cv
scipy.special.obl_rad2_cv(m, n, c, cv, x) = <ufunc 'obl_rad2_cv'>
  Oblate spheroidal radial function obl_rad2 for precomputed characteristic value

  Computes the oblate spheroidal radial function of the second kind and its derivative (with respect to x) for
  mode parameters m>=0 and n>=m, spheroidal parameter c and |x| < 1.0. Requires pre-
  computed characteristic value.

  Returns
  s  Value of the function
Kelvin Functions

<table>
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<th>Function</th>
<th>Description</th>
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<td><code>kelvin(x)</code></td>
<td>Kelvin functions as complex numbers</td>
</tr>
<tr>
<td><code>kelvin_zeros(nt)</code></td>
<td>Compute nt zeros of all Kelvin functions.</td>
</tr>
<tr>
<td><code>ber(x)</code></td>
<td>Kelvin function ber.</td>
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<tr>
<td><code>bei(x)</code></td>
<td>Kelvin function bei</td>
</tr>
<tr>
<td><code>berp(x)</code></td>
<td>Derivative of the Kelvin function ber</td>
</tr>
<tr>
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</tr>
<tr>
<td><code>ker(x)</code></td>
<td>Kelvin function ker</td>
</tr>
<tr>
<td><code>kei(x)</code></td>
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<tr>
<td><code>kerp(x)</code></td>
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<td><code>keip(x)</code></td>
<td>Derivative of the Kelvin function kei</td>
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**scipy.special.kelvin**

```python
def kelvin(x)
```

Kelvin functions as complex numbers

**Returns**

Be, Ke, Bep, Kep

The tuple (Be, Ke, Bep, Kep) contains complex numbers representing the real and imaginary Kelvin functions and their derivatives evaluated at x. For example, \( \text{kelvin}(x)[0].\text{real} = \text{ber}(x) \) and \( \text{kelvin}(x)[0].\text{imag} = \text{bei}(x) \) with similar relationships for ker and kei.

**scipy.special.kelvin_zeros**

```python
def kelvin_zeros(nt)
```

Compute nt zeros of all Kelvin functions.

Returned in a length-8 tuple of arrays of length nt. The tuple contains the arrays of zeros of (ber, bei, ker, kei, ber', bei', ker', kei').

**References**

[1]

**scipy.special.ber**

```python
def ber(x)
```

Kelvin function ber.

**scipy.special.bei**

```python
def bei(x)
```

Kelvin function bei

**scipy.special.berp**

```python
def berp(x)
```

Derivative of the Kelvin function ber

**scipy.special.beip**

```python
def beip(x)
```

Derivative of the Kelvin function bei

**scipy.special.ker**

```python
def ker(x)
```

Kelvin function ker

**scipy.special.kei**

```python
def kei(x)
```

Kelvin function kei
scipy.special.kerp
scipy.special.kerp(x) = ufunc 'kerp'
    Derivative of the Kelvin function ker

scipy.special.keip
scipy.special.keip(x) = ufunc 'keip'
    Derivative of the Kelvin function kei

These are not universal functions:

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<td>Compute nt zeros of the Kelvin function ber(x).</td>
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<td>berp_zeros(nt)</td>
<td>Compute nt zeros of the Kelvin function ber'(x).</td>
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References

[1]
References
[1]

scipy.special.keip_zeros
scipy.special.keip_zeros(nt)
Compute nt zeros of the Kelvin function kei'(x).

References
[1]

Combinatorics

\[
\begin{align*}
\text{comb}(N, k[, \text{exact}, \text{repetition}]) & \quad \text{The number of combinations of N things taken k at a time.} \\
\text{perm}(N, k[, \text{exact}]) & \quad \text{Permutations of N things taken k at a time, i.e., k-permutations of N.}
\end{align*}
\]

scipy.special.comb
scipy.special.comb(N, k, exact=False, repetition=False)
The number of combinations of N things taken k at a time.

This is often expressed as “N choose k”.

Parameters

- N [int, ndarray] Number of things.
- k [int, ndarray] Number of elements taken.
- exact [bool, optional] If exact is False, then floating point precision is used, otherwise exact long integer is computed.
- repetition [bool, optional] If repetition is True, then the number of combinations with repetition is computed.

Returns

- val [int, float, ndarray] The total number of combinations.

See also:

- binom
  Binomial coefficient ufunc

Notes
- Array arguments accepted only for exact=False case.
- If k > N, N < 0, or k < 0, then a 0 is returned.

Examples

```python
>>> from scipy.special import comb
>>> k = np.array([3, 4])
>>> n = np.array([10, 10])
>>> comb(n, k, exact=False)
array([ 120.,  210.])
>>> comb(10, 3, exact=True)
120L
>>> comb(10, 3, exact=True, repetition=True)
220L
```
scipy.special.perm

scipy.special.perm(N, k, exact=False)

Permutations of N things taken k at a time, i.e., k-permutations of N.

It’s also known as “partial permutations”.

**Parameters**

- `N` [int, ndarray]: Number of things.
- `k` [int, ndarray]: Number of elements taken.
- `exact` [bool, optional]: If `exact` is False, then floating point precision is used, otherwise exact long integer is computed.

**Returns**

- `val` [int, ndarray]: The number of k-permutations of N.

**Notes**

- Array arguments accepted only for exact=False case.
- If k > N, N < 0, or k < 0, then a 0 is returned.

**Examples**

```python
>>> from scipy.special import perm
>>> k = np.array([3, 4])
>>> n = np.array([10, 10])
>>> perm(n, k)
array([ 720., 5040.])
>>> perm(10, 3, exact=True)
720
```

---

Lambert W and Related Functions

- `lambertw(z[, k, tol])`: Lambert W function.
- `wrightomega(z[, out])`: Wright Omega function.

Other Special Functions

- `agm(a, b)`: Compute the arithmetic-geometric mean of a and b.
- `bermoulli(n)`: Bernoulli numbers B0..Bn (inclusive).
- `binom(n, k)`: Binomial coefficient
- `diric(x, n)`: Periodic sinc function, also called the Dirichlet function.
- `euler(n)`: Euler numbers E(0), E(1), ..., E(n).
- `expn(n, x)`: Exponential integral E_n
- `exp1(z)`: Exponential integral E_1 of complex argument z
- `expi(x)`: Exponential integral Ei
- `factorial(n[, exact])`: The factorial of a number or array of numbers.
- `factorial2(n[, exact])`: Double factorial.
- `factorialk(n, k[, exact])`: Multifactorial of n of order k, n!!...!
- `shichi(x[, out])`: Hyperbolic sine and cosine integrals.
- `sici(x[, out])`: Sine and cosine integrals.
- `softmax(x[, axis])`: Softmax function

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<td><code>spence(z[, out])</code></td>
<td>Spence’s function, also known as the dilogarithm.</td>
</tr>
<tr>
<td><code>zeta(x[, q, out])</code></td>
<td>Riemann or Hurwitz zeta function.</td>
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<tr>
<td><code>zetac(x)</code></td>
<td>Riemann zeta function minus 1.</td>
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**scipy.special.agm**

scipy.special.agm(a, b) = <ufunc 'agm'>

Compute the arithmetic-geometric mean of \(a\) and \(b\).

Start with \(a_0 = a\) and \(b_0 = b\) and iteratively compute:

\[
\begin{align*}
    a_{n+1} &= (a_n + b_n)/2 \\
    b_{n+1} &= \sqrt{a_n \times b_n}
\end{align*}
\]

\(a_n\) and \(b_n\) converge to the same limit as \(n\) increases; their common limit is \(agm(a, b)\).

**Parameters**

- **a**, **b** [array_like] Real values only. If the values are both negative, the result is negative. If one value is negative and the other is positive, \(nan\) is returned.

**Returns**

- **float** The arithmetic-geometric mean of \(a\) and \(b\).

**Examples**

```python
>>> from scipy.special import agm
>>> a, b = 24.0, 6.0
>>> agm(a, b)
13.458171481725614
```

Compare that result to the iteration:

```python
>>> while a != b:
...     a, b = (a + b)/2, np.sqrt(a*b)
...     print("a = {0:.16f} b={1:.16f}" % (a, b))
...
  a = 15.00000000000000  b=12.00000000000000  
  a = 13.50000000000000  b=13.4164078649987388  
  a = 13.45820393249937  b=13.4581714817256159  
  a = 13.4581714817256159  b=13.4581714817256159
```

When array-like arguments are given, broadcasting applies:

```python
>>> a = np.array([[1.5], [3], [6]])  # a has shape (3, 1).
>>> b = np.array([6, 12, 24, 48])  # b has shape (4,).
>>> agm(a, b)
array([[  3.36454287,   5.42363427,   9.05798751,  15.63650756],
       [  4.37037309,  10.84726853,  18.11597502,  21.69453707],
       [  6.74074619,  13.45817148,  21.69453707]])
```

**scipy.special.bernoulli**

scipy.special.bernoulli(n)

Bernoulli numbers B0..Bn (inclusive).

**References**

[1]
scipy.special.binom

scipy.special.binom(n, k) = <ufunc 'binom'>

Binomial coefficient

See also:

comb

The number of combinations of N things taken k at a time.

scipy.special.dirc

scipy.special.dirc(x, n)

Periodic sinc function, also called the Dirichlet function.

The Dirichlet function is defined as:

\[ \text{dirc}(x, n) = \frac{\sin(x \cdot n / 2)}{(n \cdot \sin(x / 2))}, \]

where \( n \) is a positive integer.

Parameters

x : [array_like] Input data

n : [int] Integer defining the periodicity.

Returns

dirc : [ndarray]

Examples

```python
>>> from scipy import special
>>> import matplotlib.pyplot as plt

>>> x = np.linspace(-8*np.pi, 8*np.pi, num=201)
>>> plt.figure(figsize=(8, 8));
>>> for idx, n in enumerate([2, 3, 4, 9]):
...     plt.subplot(2, 2, idx+1)
...     plt.plot(x, special.dirc(x, n))
...     plt.title('dirc, n={}'.format(n))
>>> plt.show()
```

The following example demonstrates that \textit{dirc} gives the magnitudes (modulo the sign and scaling) of the Fourier coefficients of a rectangular pulse.

Suppress output of values that are effectively 0:

```python
>>> np.set_printoptions(suppress=True)
```

Create a signal \( x \) of length \( m \) with \( k \) ones:

```python
>>> m = 8
>>> k = 3
>>> x = np.zeros(m)
>>> x[:k] = 1
```

Use the FFT to compute the Fourier transform of \( x \), and inspect the magnitudes of the coefficients:
6.26. Special functions (scipy.special)
Now find the same values (up to sign) using `diric`. We multiply by $k$ to account for the different scaling conventions of `numpy.fft.fft` and `diric`:

```
>>> theta = np.linspace(0, 2*np.pi, m, endpoint=False)
>>> k * special.diric(theta, k)
array([ 3.00000000, 2.41421356, 1.00000000, -0.41421356, -1.00000000,
       -0.41421356, 1.00000000, 2.41421356])
```

### scipy.special.euler

The Euler numbers $[1]$ are also known as the secant numbers.

Because `euler(n)` returns floating point values, it does not give exact values for large $n$. The first inexact value is $E(22)$.

**Parameters**

- $n$ [int] The highest index of the Euler number to be returned.

**Returns**

- ndarray The Euler numbers $[E(0), E(1), ..., E(n)]$. The odd Euler numbers, which are all zero, are included.

**Examples**

```
>>> from scipy.special import euler
>>> euler(6)
array([ 1., 0., -1., 0., 5., 0., -61.])
```

```
>>> euler(13).astype(np.int64)
array([ 1, 0, -1, 0, 5, 0, -61, 0, 1385, 0, -50521, 0, 2702765, 0])
```

```
>>> euler(22)[-1]  # Exact value of E(22) is -69348874393137901.
-69348874393137976.0
```

### scipy.special.expn

Returns the exponential integral for integer $n$ and non-negative $x$ and $n$:

```
integral(exp(-x*t) / t**n, t=1..inf).
```

### scipy.special.expl1

Exponential integral $E_1$ of complex argument $z$
**integral**

`integral(exp(-z*t)/t, t=1..inf)`.

**scipy.special.expi**

```python
scipy.special.expi(x) = <ufunc 'expi'>
```

Exponential integral Ei

Defined as:

```
integral(exp(t)/t, t=-inf..x)
```

See `expn` for a different exponential integral.

**scipy.special.factorial**

```python
scipy.special.factorial(n, exact=False)
```

The factorial of a number or array of numbers.

The factorial of non-negative integer n is the product of all positive integers less than or equal to n:

\[ n! = n \times (n - 1) \times (n - 2) \times \ldots \times 1 \]

**Parameters**

- `n` [int or array_like of ints] Input values. If `n < 0`, the return value is 0.
- `exact` [bool, optional] If True, calculate the answer exactly using long integer arithmetic. If False, result is approximated in floating point rapidly using the `gamma` function. Default is False.

**Returns**

- `nf` [float or int or ndarray] Factorial of `n`, as integer or float depending on `exact`.

**Notes**

For arrays with `exact=True`, the factorial is computed only once, for the largest input, with each other result computed in the process. The output dtype is increased to `int64` or `object` if necessary.

With `exact=False` the factorial is approximated using the gamma function:

\[ n! = \Gamma(n + 1) \]

**Examples**

```python
>>> from scipy.special import factorial
>>> arr = np.array([3, 4, 5])
>>> factorial(arr, exact=False)
array([  6.,  24., 120.])
>>> factorial(arr, exact=True)
array([  6,  24, 120])
>>> factorial(5, exact=True)
120L
```

**scipy.special.factorial2**

```python
scipy.special.factorial2(n, exact=False)
```

Double factorial.

This is the factorial with every second value skipped. E.g., \( 7!! = 7 \times 5 \times 3 \times 1 \). It can be approximated numerically as:
n!! = special.gamma(n/2+1)*2**((m+1)/2)/sqrt(pi)  n odd
= 2**(n/2) * (n/2)!                          n even

Parameters
n        [int or array_like] Calculate n!! . Arrays are only supported with exact set to False. If n < 0, the return value is 0.
exact    [bool, optional] The result can be approximated rapidly using the gamma-formula above (default). If exact is set to True, calculate the answer exactly using integer arithmetic.

Returns
nff      [float or int] Double factorial of n, as an int or a float depending on exact.

Examples
>>> from scipy.special import factorial2
>>> factorial2(7, exact=False)
a(105.00000000000001)
>>> factorial2(7, exact=True)
105L

scipy.special.factorialk

scipy.special.factorialk(n, k, exact=True)
Multifactorial of n of order k, n(k!!...!).
This is the multifactorial of n skipping k values. For example,
factorialk(17, 4) = 17!!!! = 17 * 13 * 9 * 5 * 1
In particular, for any integer n, we have
factorialk(n, 1) = factorial(n)
factorialk(n, 2) = factorial2(n)

Parameters
n        [int] Calculate multifactorial. If n < 0, the return value is 0.
k        [int] Order of multifactorial.
exact    [bool, optional] If exact is set to True, calculate the answer exactly using integer arithmetic.

Returns

Raises
NotImplementedError
Raises when exact is False

Examples
>>> from scipy.special import factorialk
>>> factorialk(5, 1, exact=True)
120L
>>> factorialk(5, 3, exact=True)
10L
scipy.special.shichi

scipy.special.shichi(x, out=None) = <ufunc 'shichi'>

Hyperbolic sine and cosine integrals.

The hyperbolic sine integral is

\[ \int_0^x \frac{\sinh t}{t} dt \]

and the hyperbolic cosine integral is

\[ \gamma + \log(x) + \int_0^x \frac{\cosh t - 1}{t} dt \]

where \( \gamma \) is Euler’s constant and \( \log \) is the principle branch of the logarithm.

Parameters

- x [array_like] Real or complex points at which to compute the hyperbolic sine and cosine integrals.

Returns

- si [ndarray] Hyperbolic sine integral at x
- ci [ndarray] Hyperbolic cosine integral at x

Notes

For real arguments with \( x < 0 \), \( \chi \) is the real part of the hyperbolic cosine integral. For such points \( \chi(x) \) and \( \chi(x + 0j) \) differ by a factor of \( 1j*\pi \).

For real arguments the function is computed by calling Cephes’ [1] shichi routine. For complex arguments the algorithm is based on Mpmath’s [2] shi and \( \chi \) routines.

References

[1], [2]

scipy.special.sici

scipy.special.sici(x, out=None) = <ufunc 'sici'>

Sine and cosine integrals.

The sine integral is

\[ \int_0^x \frac{\sin t}{t} dt \]

and the cosine integral is

\[ \gamma + \log(x) + \int_0^x \frac{\cos t - 1}{t} dt \]

where \( \gamma \) is Euler’s constant and \( \log \) is the principle branch of the logarithm.

Parameters

- x [array_like] Real or complex points at which to compute the sine and cosine integrals.

Returns

- si [ndarray] Sine integral at x
- ci [ndarray] Cosine integral at x
Notes
For real arguments with $x < 0$, $ci$ is the real part of the cosine integral. For such points $ci(x)$ and $ci(x + 0j)$ differ by a factor of $1j \cdot \pi$.

For real arguments the function is computed by calling Cephes’ [1] $sici$ routine. For complex arguments the algorithm is based on Mpmath’s [2] $si$ and $ci$ routines.

References
[1], [2]

`scipy.special.softmax`

The softmax function transforms each element of a collection by computing the exponential of each element divided by the sum of the exponentials of all the elements. That is, if $x$ is a one-dimensional numpy array:

$$softmax(x) = \frac{\exp(x)}{\sum \exp(x)}$$

Parameters
- $x$: [array_like] Input array.
- $axis$: [int or tuple of ints, optional] Axis to compute values along. Default is None and softmax will be computed over the entire array $x$.

Returns
- $s$: [ndarray] An array the same shape as $x$. The result will sum to 1 along the specified axis.

Notes
The formula for the softmax function $\sigma(x)$ for a vector $x = \{x_0, x_1, ..., x_{n-1}\}$ is

$$\sigma(x)_j = \frac{e^{x_j}}{\sum_k e^{x_k}}$$

The softmax function is the gradient of $\logsumexp$.

New in version 1.2.0.

Examples

```python
>>> from scipy.special import softmax
>>> np.set_printoptions(precision=5)

>>> x = np.array([[1, 0.5, 0.2, 3],
...                [1, -1, 7, 3],
...                [2, 12, 13, 3]])

Compute the softmax transformation over the entire array.

>>> m = softmax(x)
>>> m
array([[ 4.48309e-06,  2.71913e-06,  2.01438e-06,  3.31258e-05],
        [ 4.48309e-06,  6.06720e-07,  1.80861e-03,  3.31258e-05],
        [ 1.21863e-05,  2.68421e-01,  7.29644e-01,  3.31258e-05]])
```
>>> m.sum()
1.0000000000000002

Compute the softmax transformation along the first axis (i.e. the columns).

```python
>>> m = softmax(x, axis=0)
```

```python
array([[ 2.11942e-01, 1.01300e-05, 2.75394e-06, 3.33333e-01],
       [ 2.11942e-01, 2.26030e-06, 2.47262e-03, 3.33333e-01],
       [ 5.76117e-01, 9.99988e-01, 9.97525e-01, 3.33333e-01]])
```

```python
>>> m.sum(axis=0)
array([ 1., 1., 1., 1.])
```

Compute the softmax transformation along the second axis (i.e. the rows).

```python
>>> m = softmax(x, axis=1)
```

```python
array([[ 1.05877e-01, 6.42177e-02, 4.75736e-02, 7.82332e-01],
       [ 2.42746e-03, 3.28521e-04, 9.79307e-01, 1.79366e-02],
       [ 1.22094e-05, 2.68929e-01, 7.31025e-01, 3.31885e-05]])
```

```python
>>> m.sum(axis=1)
array([ 1., 1., 1.])
```

**scipy.special.spence**

```python
scipy.special.spence(z, out=None) = <ufunc 'spence'>
```

Spence’s function, also known as the dilogarithm.

It is defined to be

\[ \int_0^z \log(t) \frac{dt}{1 - t} \]

for complex \( z \), where the contour of integration is taken to avoid the branch cut of the logarithm. Spence’s function is analytic everywhere except the negative real axis where it has a branch cut.

**Parameters**

- **z**: [array_like] Points at which to evaluate Spence’s function

**Returns**

- **s**: [ndarray] Computed values of Spence’s function

**Notes**

There is a different convention which defines Spence’s function by the integral

\[ -\int_0^z \log(1 - t) \frac{dt}{t} \]  

this is our \( \text{spence}(1 - z) \).

**scipy.special.zeta**

```python
scipy.special.zeta(x, q=None, out=None)
```

Riemann or Hurwitz zeta function.

**Parameters**

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x [array_like of float] Input data, must be real.
q [array_like of float, optional] Input data, must be real. Defaults to Riemann zeta.
out [ndarray, optional] Output array for the computed values.

Returns
out [array_like] Values of zeta(x).

See also:
zetac

Notes
The two-argument version is the Hurwitz zeta function:
\[ \zeta(x, q) = \sum_{k=0}^{\infty} \frac{1}{(k + q)^x}, \]

Riemann zeta function corresponds to q = 1.

Examples

```python
>>> from scipy.special import zeta, polygamma, factorial

Some specific values:

>>> zeta(2), np.pi**2/6
(1.6449340668482266, 1.6449340668482264)

>>> zeta(4), np.pi**4/90
(1.082323237111381, 1.08232323711138)

Relation to the polygamma function:

```python
>>> m = 3
>>> x = 1.25
>>> polygamma(m, x)
array(2.782144009188397)

>>> (-1)**(m+1) * factorial(m) * zeta(m+1, x)
2.7821440091883969
```

scipy.special.zetac
scipy.special.zetac(x) = <ufunc 'zetac'>

Riemann zeta function minus 1.

This function is defined as
\[ \zeta(x) = \sum_{k=2}^{\infty} \frac{1}{k^x}, \]

where x > 1. For x < 1, the analytic continuation is computed.

Because of limitations of the numerical algorithm, zetac(x) returns nan for x less than -30.8148.

Parameters
x [array_like of float] Values at which to compute zeta(x) - 1 (must be real).

Returns
out [array_like] Values of zeta(x) - 1.
See also:

zeta

Examples

```python
>>> from scipy.special import zetac, zeta
```

Some special values:

```python
>>> zetac(2), np.pi**2/6 - 1
(0.64493406684822641, 0.6449340668482264)

>>> zetac(-1), -1.0/12 - 1
(-1.0833333333333333, -1.0833333333333333)
```

Compare zetac(x) to zeta(x) - 1 for large x:

```python
>>> zetac(60), zeta(60) - 1
(8.673617380119933e-19, 0.0)
```

Convenience Functions

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<td>Element-wise cube root of x.</td>
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<tr>
<td>exp10(x)</td>
<td>Compute $10^{x}$ element-wise.</td>
</tr>
<tr>
<td>exp2(x)</td>
<td>Compute $2^{x}$ element-wise.</td>
</tr>
<tr>
<td>radian(d, m, s)</td>
<td>Convert from degrees to radians.</td>
</tr>
<tr>
<td>cosdg(x)</td>
<td>Cosine of the angle $x$ given in degrees.</td>
</tr>
<tr>
<td>sindg(x)</td>
<td>Sine of angle given in degrees.</td>
</tr>
<tr>
<td>tandg(x)</td>
<td>Tangent of angle $x$ given in degrees.</td>
</tr>
<tr>
<td>cotdg(x)</td>
<td>Cotangent of the angle $x$ given in degrees.</td>
</tr>
<tr>
<td>log1p(x)</td>
<td>Calculates log(1+x) for use when $x$ is near zero</td>
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<tr>
<td>expm1(x)</td>
<td>Compute $e^{x} - 1$.</td>
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<td>round(x)</td>
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<td>xlogy(x, y)</td>
<td>Compute $x \log(y)$ so that the result is 0 if $x = 0$.</td>
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<td>xlog1py(x, y)</td>
<td>Compute $x \log1p(y)$ so that the result is 0 if $x = 0$.</td>
</tr>
<tr>
<td>logsumexp(a[, axis, b, keepdims, return_sign])</td>
<td>Compute the log of the sum of exponentials of input elements.</td>
</tr>
<tr>
<td>exprel(x)</td>
<td>Relative error exponential, $(e^x - 1)/x$.</td>
</tr>
<tr>
<td>sinc(x)</td>
<td>Return the sinc function.</td>
</tr>
</tbody>
</table>

scipy.special.cbrt

scipy.special.cbrt(x) = <ufunc 'cbrt'>

Element-wise cube root of x.

Parameters

- x [array_like] x must contain real numbers.

Returns

- float The cube root of each value in x.
Examples

```python
>>> from scipy.special import cbrt

>>> cbrt(8)
2.0
>>> cbrt([-8, -3, 0.125, 1.331])
array([-2. , -1.44224957, 0.5 , 1.1 ])
```

**scipy.special.exp10**

scipy.special.exp10(x) = <ufunc 'exp10'>

Compute \(10^x\) element-wise.

**Parameters**

- x [array_like] x must contain real numbers.

**Returns**

- float \(10^x\), computed element-wise.

**Examples**

```python
>>> from scipy.special import exp10

>>> exp10(3)
1000.0
>>> x = np.array([[-1, -0.5, 0], [0.5, 1, 1.5]])
>>> exp10(x)
array([[ 0.1 , 0.31622777, 1. ],
       [ 3.16227766, 10. , 31.6227766 ]])
```

**scipy.special.exp2**

scipy.special.exp2(x) = <ufunc 'exp2'>

Compute \(2^x\) element-wise.

**Parameters**

- x [array_like] x must contain real numbers.

**Returns**

- float \(2^x\), computed element-wise.

**Examples**

```python
>>> from scipy.special import exp2

>>> exp2(3)
8.0
>>> x = np.array([[-1, -0.5, 0], [0.5, 1, 1.5]])
>>> exp2(x)
array([[ 0.5 , 0.70710678, 1. ],
       [ 1.41421356, 2. , 2.82842712]])
```

**scipy.special.radian**

scipy.special.radian(d, m, s) = <ufunc 'radian'>

Convert from degrees to radians

Returns the angle given in \((d)egrees, (m)inutes, and (s)econds in radians.
scipy.special.cosdg
scipy.special.cosdg(x) = <ufunc 'cosdg'>
Cosine of the angle \(x\) given in degrees.

scipy.special.sindg
scipy.special.sindg(x) = <ufunc 'sindg'>
Sine of angle given in degrees

scipy.special.tandg
scipy.special.tandg(x) = <ufunc 'tandg'>
Tangent of angle \(x\) given in degrees.

scipy.special.cotdg
scipy.special.cotdg(x) = <ufunc 'cotdg'>
Cotangent of the angle \(x\) given in degrees.

scipy.special.log1p
scipy.special.log1p(x) = <ufunc 'log1p'>
Calculates \(\log(1+x)\) for use when \(x\) is near zero

scipy.special.expm1
scipy.special.expm1(x) = <ufunc 'expm1'>
Compute \(\exp(x) - 1\).

When \(x\) is near zero, \(\exp(x)\) is near 1, so the numerical calculation of \(\exp(x) - 1\) can suffer from catastrophic loss of precision. \(\text{expm1}(x)\) is implemented to avoid the loss of precision that occurs when \(x\) is near zero.

Parameters
x [array_like] \(x\) must contain real numbers.

Returns
float \(\exp(x) - 1\) computed element-wise.

Examples
>>> from scipy.special import expm1

>>> expm1(1.0)
1.7182818284590451

>>> expm1([-0.2, -0.1, 0, 0.1, 0.2])
array([-0.18126925, -0.09516258, 0. , 0.10517092, 0.22140276])

The exact value of \(\exp(7.5e-13) - 1\) is:

7.5000000000000007031250000001318...*10**-13.

Here is what \(\text{expm1}(7.5e-13)\) gives:

>>> expm1(7.5e-13)
7.5006667543675576e-13

Compare that to \(\exp(7.5e-13) - 1\), where the subtraction results in a “catastrophic” loss of precision:

>>> np.exp(7.5e-13) - 1
7.5006667557666662e-13

scipy.special.cosm1
scipy.special.cosm1(x) = <ufunc 'cosm1'>
\(\cos(x) - 1\) for use when \(x\) is near zero.
scipy.special.round

scipy.special.round(x) = <ufunc 'round'>

Round to nearest integer

Returns the nearest integer to \( x \) as a double precision floating point result. If \( x \) ends in 0.5 exactly, the nearest even integer is chosen.

scipy.special.xlogy

scipy.special.xlogy(x, y) = <ufunc 'xlogy'>

Compute \( x \times \log(y) \) so that the result is 0 if \( x = 0 \).

Parameters

- \( x \) [array_like] Multiplier
- \( y \) [array_like] Argument

Returns

- \( z \) [array_like] Computed \( x \times \log(y) \)

Notes

New in version 0.13.0.

scipy.special.xlog1py

scipy.special.xlog1py(x, y) = <ufunc 'xlog1py'>

Compute \( x \times \log_1p(y) \) so that the result is 0 if \( x = 0 \).

Parameters

- \( x \) [array_like] Multiplier
- \( y \) [array_like] Argument

Returns

- \( z \) [array_like] Computed \( x \times \log_1p(y) \)

Notes

New in version 0.13.0.

scipy.special.logsumexp

scipy.special.logsumexp(a, axis=None, b=None, keepdims=False, return_sign=False)

Compute the log of the sum of exponentials of input elements.

Parameters

- \( a \) [array_like] Input array.
- \( axis \) [None or int or tuple of ints, optional] Axis or axes over which the sum is taken. By default \( axis \) is None, and all elements are summed. New in version 0.11.0.
- \( keepdims \) [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original array. New in version 0.15.0.
- \( b \) [array-like, optional] Scaling factor for \( \exp(a) \) must be of the same shape as \( a \) or broadcastable to \( a \). These values may be negative in order to implement subtraction. New in version 0.12.0.
- \( return\_sign \) [bool, optional] If this is set to True, the result will be a pair containing sign information; if False, results that are negative will be returned as NaN. Default is False (no sign information). New in version 0.16.0.
Returns
res [ndarray] The result, \( \text{np.log(np.sum(np.exp(a)))} \) calculated in a numerically more stable way. If \( b \) is given then \( \text{np.log(np.sum(b*np.exp(a)))} \) is returned.
sgn [ndarray] If return_sign is True, this will be an array of floating-point numbers matching \( \text{res} \) and +1, 0, or -1 depending on the sign of the result. If False, only one result is returned.

See also:
numpy.logaddexp, numpy.logaddexp2

Notes
Numpy has a logaddexp function which is very similar to logsumexp, but only handles two arguments. logaddexp.reduce is similar to this function, but may be less stable.

Examples

```python
>>> from scipy.special import logsumexp
>>> a = np.arange(10)
>>> np.log(np.sum(np.exp(a)))
9.4586297444267107
>>> logsumexp(a)
9.4586297444267107
```

With weights

```python
>>> a = np.arange(10)
>>> b = np.arange(10, 0, -1)
>>> logsumexp(a, b=b)
9.9170178533034665
>>> np.log(np.sum(b*np.exp(a)))
9.9170178533034647
```

Returning a sign flag

```python
>>> logsumexp([1,2],b=[1,-1],return_sign=True)
(1.5413248546129181, -1.0)
```

Notice that logsumexp does not directly support masked arrays. To use it on a masked array, convert the mask into zero weights:

```python
>>> a = np.ma.array([np.log(2), 2, np.log(3)],
... mask=[False, True, False])
>>> b = (~a.mask).astype(int)
>>> logsumexp(a.data, b=b, np.log(5)
1.6094379124341005, 1.6094379124341005
```

scipy.special.exprel

scipy.special.exprel(x) = <ufunc 'exprel'>

Relative error exponential, \( \frac{\exp(x) - 1}{x} \).

When \( x \) is near zero, \( \exp(x) \) is near 1, so the numerical calculation of \( \exp(x) - 1 \) can suffer from catastrophic loss of precision. exprel(x) is implemented to avoid the loss of precision that occurs when \( x \) is near zero.

Parameters

- x [ndarray] Input array. \( x \) must contain real numbers.
**Returns**

float   \((\exp(x) - 1)/x\), computed element-wise.

See also:

expm1

Notes
New in version 0.17.0.

Examples

```python
>>> from scipy.special import exprel

>>> exprel(0.01)
1.0050167084168056
>>> exprel([-0.25, -0.1, 0, 0.1, 0.25])
array([ 0.88479687, 0.95162582, 1. , 1.05170918, 1.13610167])
```

Compare `exprel(5e-9)` to the naive calculation. The exact value is `1.00000000250000000416...`

```python
>>> exprel(5e-9)
1.0000000025
>>> (np.exp(5e-9) - 1)/5e-9
0.99999999392252903
```

**scipy.special.sinc**

scipy.special.sinc(x)

Return the sinc function.

The sinc function is \(\sin(x)/(\pi x)\).

**Parameters**

- **x**  
  [ndarray] Array (possibly multi-dimensional) of values for which to calculate \(\text{sinc}(x)\).

**Returns**

- **out**  
  [ndarray] \(\text{sinc}(x)\), which has the same shape as the input.

**Notes**

\(\text{sinc}(0)\) is the limit value 1.

The name sinc is short for “sine cardinal” or “sinus cardinalis”.

The sinc function is used in various signal processing applications, including in anti-aliasing, in the construction of a Lanczos resampling filter, and in interpolation.

For bandlimited interpolation of discrete-time signals, the ideal interpolation kernel is proportional to the sinc function.

**References**

[1], [2]

**Examples**

```python
>>> x = np.linspace(-4, 4, 41)
>>> np.sinc(x)
array([-3.89804309e-17, -4.92362781e-02, -8.40918587e-02,
    -8.90384387e-02, -5.84680802e-02, 3.89804309e-17,
```

(continues on next page)
6.68206631e-02, 1.16434881e-01, 1.26137788e-01,
8.50444803e-02, -3.89804309e-17, -1.03943254e-01,
-1.89206682e-01, -2.16236208e-01, -1.55914881e-01,
3.89804309e-17, 2.33872321e-01, 5.04551152e-01,
7.56826729e-01, 9.35489284e-01, 1.00000000e+00,
9.35489284e-01, 7.56826729e-01, 5.04551152e-01,
2.33872321e-01, 3.89804309e-01, -1.55914881e-01,
-2.16236208e-01, -1.89206682e-01, -1.03943254e-01,
-3.89804309e-17, 8.50444803e-02, 1.26137788e-01,
1.16434881e-01, 6.68206631e-02, 3.89804309e-17,
-5.84680802e-02, -8.90384387e-02, -8.40918587e-02,
-4.92362781e-02, -3.89804309e-17
>>>
plt.plot(x, np.sinc(x))
[<matplotlib.lines.Line2D object at 0x...>]
>>>
plt.title("Sinc Function")
<matplotlib.text.Text object at 0x...>
>>>
plt.ylabel("Amplitude")
<matplotlib.text.Text object at 0x...>
>>>
plt.xlabel("X")
<matplotlib.text.Text object at 0x...>
>>>
plt.show()

It works in 2-D as well:

>>> x = np.linspace(-4, 4, 401)
>>> xx = np.outer(x, x)
>>> plt.imshow(np.sinc(xx))
<matplotlib.image.AxesImage object at 0x...>

6.27 Statistical functions (scipy.stats)

This module contains a large number of probability distributions as well as a growing library of statistical functions.

Each univariate distribution is an instance of a subclass of `rv_continuous` (`rv_discrete` for discrete distributions):

```python
rv_continuous([momtype, a, b, xtol, ...])  # A generic continuous random variable class meant for subclassing.
rv_discrete([a, b, name, badvalue, ...])  # A generic discrete random variable class meant for subclassing.
rv_histogram(histogram, *args, **kwargs)  # Generates a distribution given by a histogram.
```

### 6.27.1 scipy.stats.rv_continuous

```python
class scipy.stats.rv_continuous(momtype=1, a=None, b=None, xtol=1e-14, badvalue=None,
name=None, longname=None, shapes=None, extradoc=None,
seed=None)
```

A generic continuous random variable class meant for subclassing.
rv_continuous is a base class to construct specific distribution classes and instances for continuous random variables. It cannot be used directly as a distribution.

**Parameters**

- **momtype**
  [int, optional] The type of generic moment calculation to use: 0 for pdf, 1 (default) for ppf.

- **a**
  [float, optional] Lower bound of the support of the distribution, default is minus infinity.

- **b**
  [float, optional] Upper bound of the support of the distribution, default is plus infinity.

- **xtol**
  [float, optional] The tolerance for fixed point calculation for generic ppf.

- **badvalue**
  [float, optional] The value in a result arrays that indicates a value that for which some argument restriction is violated, default is np.nan.

- **name**
  [str, optional] The name of the instance. This string is used to construct the default example for distributions.

- **longname**
  [str, optional] This string is used as part of the first line of the docstring returned when a subclass has no docstring of its own. Note: longname exists for backwards compatibility, do not use for new subclasses.

- **shapes**
  [str, optional] The shape of the distribution. For example "m, n" for a distribution that takes two integers as the two shape arguments for all its methods. If not provided, shape parameters will be inferred from the signature of the private methods, _pdf and _cdf of the instance.

- **extradoc**
  [str, optional, deprecated] This string is used as the last part of the docstring returned when a subclass has no docstring of its own. Note: extradoc exists for backwards compatibility, do not use for new subclasses.

- **seed**
  [None or int or numpy.random.RandomState instance, optional] This parameter defines the RandomState object to use for drawing random variates. If None (or np.random), the global np.random state is used. If integer, it is used to seed the local RandomState instance. Default is None.

**Notes**

Public methods of an instance of a distribution class (e.g., pdf, cdf) check their arguments and pass valid arguments to private, computational methods (_pdf, _cdf). For pdf(x), x is valid if it is within the support of a distribution, self.a <= x <= self.b. Whether a shape parameter is valid is decided by an _argcheck method (which defaults to checking that its arguments are strictly positive.)

**Subclassing**

New random variables can be defined by subclassing the rv_continuous class and re-defining at least the _pdf or the _cdf method (normalized to location 0 and scale 1).

If positive argument checking is not correct for your RV then you will also need to re-define the _argcheck method.

Correct, but potentially slow defaults exist for the remaining methods but for speed and/or accuracy you can over-ride:

\[
_{\text{logpdf, _cdf, _logcdf, _ppf, _rvs, _isf, _sf, _logsf}}
\]

The default method _rvs relies on the inverse of the cdf, _ppf, applied to a uniform random variate. In order to generate random variates efficiently, either the default _ppf needs to be overwritten (e.g. if the inverse cdf can expressed in an explicit form) or a sampling method needs to be implemented in a custom _rvs method.
If possible, you should override __isf__, __sf__ or __logsf__. The main reason would be to improve numerical accuracy: for example, the survival function __sf__ is computed as $1 - __cdf__$ which can result in loss of precision if $\_cdf(x)$ is close to one.

**Methods that can be overwritten by subclasses**

__rvs__, __pdf__, __cdf__, __sf__, __ppf__, __isf__, __stats__, __munp__, __entropy__, __argcheck__

There are additional (internal and private) generic methods that can be useful for cross-checking and for debugging, but might work in all cases when directly called.

A note on **shapes**: subclasses need not specify them explicitly. In this case, **shapes** will be automatically deduced from the signatures of the overridden methods (pdf, cdf etc). If, for some reason, you prefer to avoid relying on introspection, you can specify **shapes** explicitly as an argument to the instance constructor.

**Frozen Distributions**

Normally, you must provide shape parameters (and, optionally, location and scale parameters to each call of a method of a distribution.

Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a “frozen” continuous RV object:

$$rv = \text{generic}(\langle shape(s)\rangle, \text{loc}=0, \text{scale}=1)$$

__rv_frozen__ object with the same methods but holding the given shape, location, and scale fixed

**Statistics**

Statistics are computed using numerical integration by default. For speed you can redefine this using __stats__:

- take shape parameters and return mu, mu2, g1, g2
- If you can’t compute one of these, return it as None
- Can also be defined with a keyword argument **moments**, which is a string composed of “m”, “v”, “s”, and/or “k”. Only the components appearing in string should be computed and returned in the order “m”, “v”, “s”, or “k” with missing values returned as None.

Alternatively, you can override __munp__, which takes n and shape parameters and returns the n-th non-central moment of the distribution.

**Examples**

To create a new Gaussian distribution, we would do the following:

```python
>>> from scipy.stats import rv_continuous
>>> class gaussian_gen(rv_continuous):
...     "Gaussian distribution"
...     def pdf(self, x):
```
```python
...     return np.exp(-x**2 / 2.) / np.sqrt(2.0 * np.pi)
>>> gaussian = gaussian_gen(name='gaussian')
```

The `scipy.stats` distributions are instances, so here we subclass `rv_continuous` and create an instance. With this, we now have a fully functional distribution with all relevant methods automatically generated by the framework.

Note that above we defined a standard normal distribution, with zero mean and unit variance. Shifting and scaling of the distribution can be done by using `loc` and `scale` parameters: `gaussian.pdf(x, loc, scale)` essentially computes $y = (x - \text{loc}) / \text{scale}$ and `gaussian._pdf(y) / \text{scale}`.

**Attributes**

- `random_state`
  
  Get or set the RandomState object for generating random variates.

**Methods**

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<th>Method</th>
<th>Description</th>
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<td><code>rvs(*args, **kwds)</code></td>
<td>Random variates of given type.</td>
</tr>
<tr>
<td><code>pdf(x, *args, **kwds)</code></td>
<td>Probability density function at $x$ of the given RV.</td>
</tr>
<tr>
<td><code>logpdf(x, *args, **kwds)</code></td>
<td>Log of the probability density function at $x$ of the given RV.</td>
</tr>
<tr>
<td><code>cdf(x, *args, **kwds)</code></td>
<td>Cumulative distribution function of the given RV.</td>
</tr>
<tr>
<td><code>logcdf(x, *args, **kwds)</code></td>
<td>Log of the cumulative distribution function at $x$ of the given RV.</td>
</tr>
<tr>
<td><code>sf(x, *args, **kwds)</code></td>
<td>Survival function $(1 - \text{cdf})$ at $x$ of the given RV.</td>
</tr>
<tr>
<td><code>logsf(x, *args, **kwds)</code></td>
<td>Log of the survival function of the given RV.</td>
</tr>
<tr>
<td><code>ppf(q, *args, **kwds)</code></td>
<td>Percent point function (inverse of <code>cdf</code>) at $q$ of the given RV.</td>
</tr>
<tr>
<td><code>isf(q, *args, **kwds)</code></td>
<td>Inverse survival function (inverse of <code>sf</code>) at $q$ of the given RV.</td>
</tr>
<tr>
<td><code>moment(n, *args, **kwds)</code></td>
<td>$n$-th order non-central moment of distribution.</td>
</tr>
<tr>
<td><code>stats(*args, **kwds)</code></td>
<td>Some statistics of the given RV.</td>
</tr>
<tr>
<td><code>entropy(*args, **kwds)</code></td>
<td>Differential entropy of the RV.</td>
</tr>
<tr>
<td><code>expect([func, args, loc, scale, lb, ub, ...])</code></td>
<td>Calculate expected value of a function with respect to the distribution by numerical integration.</td>
</tr>
<tr>
<td><code>median(*args, **kwds)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(*args, **kwds)</code></td>
<td>Mean of the distribution.</td>
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<tr>
<td><code>std(*args, **kwds)</code></td>
<td>Standard deviation of the distribution.</td>
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<tr>
<td><code>var(*args, **kwds)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, *args, **kwds)</code></td>
<td>Confidence interval with equal areas around the median.</td>
</tr>
<tr>
<td><code>__call__(*args, **kwds)</code></td>
<td>Freeze the distribution for the given arguments.</td>
</tr>
<tr>
<td><code>fit(data, *args, **kwds)</code></td>
<td>Return MLEs for shape (if applicable), location, and scale parameters from data.</td>
</tr>
<tr>
<td><code>fit_loc_scale(data, *args)</code></td>
<td>Estimate loc and scale parameters from data using 1st and 2nd moments.</td>
</tr>
<tr>
<td><code>nnlf(theta, x)</code></td>
<td>Return negative loglikelihood function.</td>
</tr>
</tbody>
</table>
**scipy.stats.rv_continuous.rvs**

`rv_continuous.rvs(*args, **kwds)`

Random variates of given type.

**Parameters**

- `arg1, arg2, arg3, ...`
  - [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
- `loc`  
  - [array_like, optional] Location parameter (default=0).
- `scale`  
  - [array_like, optional] Scale parameter (default=1).
- `size`  
  - [int or tuple of ints, optional] Defining number of random variates (default is 1).
- `random_state`  
  - [None or int or np.random.RandomState instance, optional] If int or RandomState, use it for drawing the random variates. If None, rely on self.

**Returns**

- `rvs`  
  - [ndarray or scalar] Random variates of given size.

**scipy.stats.rv_continuous.pdf**

`rv_continuous.pdf(x, *args, **kwds)`

Probability density function at x of the given RV.

**Parameters**

- `x`
  - [array_like] quantiles
- `arg1, arg2, arg3, ...`
  - [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
- `loc`  
  - [array_like, optional] location parameter (default=0)
- `scale`  
  - [array_like, optional] scale parameter (default=1)

**Returns**

- `pdf`  
  - [ndarray] Probability density function evaluated at x

**scipy.stats.rv_continuous.logpdf**

`rv_continuous.logpdf(x, *args, **kwds)`

Log of the probability density function at x of the given RV.

This uses a more numerically accurate calculation if available.

**Parameters**

- `x`
  - [array_like] quantiles
- `arg1, arg2, arg3, ...`
  - [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
- `loc`  
  - [array_like, optional] location parameter (default=0)
- `scale`  
  - [array_like, optional] scale parameter (default=1)

**Returns**

- `logpdf`  
  - [array_like] Log of the probability density function evaluated at x
scipy.stats.rv_continuous.cdf

rv_continuous.cdf(x, *args, **kwds)
Cumulative distribution function of the given RV.

Parameters

x
[array_like] quantiles
arg1, arg2, arg3,...
[array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc
[array_like, optional] location parameter (default=0)
scale
[array_like, optional] scale parameter (default=1)

Returns
cdf
[ndarray] Cumulative distribution function evaluated at x

scipy.stats.rv_continuous.logcdf

rv_continuous.logcdf(x, *args, **kwds)
Log of the cumulative distribution function at x of the given RV.

Parameters

x
[array_like] quantiles
arg1, arg2, arg3,...
[array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc
[array_like, optional] location parameter (default=0)
scale
[array_like, optional] scale parameter (default=1)

Returns
logcdf
[array_like] Log of the cumulative distribution function evaluated at x

scipy.stats.rv_continuous.sf

rv_continuous.sf(x, *args, **kwds)
Survival function (1 - cdf) at x of the given RV.

Parameters

x
[array_like] quantiles
arg1, arg2, arg3,...
[array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc
[array_like, optional] location parameter (default=0)
scale
[array_like, optional] scale parameter (default=1)

Returns
sf
[array_like] Survival function evaluated at x

scipy.stats.rv_continuous.logsf

rv_continuous.logsf(x, *args, **kwds)
Log of the survival function of the given RV.

Returns the log of the “survival function,” defined as (1 - cdf), evaluated at x.

Parameters
x = [array_like] quantiles
arg1, arg2, arg3,... [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc = [array_like, optional] location parameter (default=0)
scale = [array_like, optional] scale parameter (default=1)

Returns
logsf = [ndarray] Log of the survival function evaluated at x.

scipy.stats.rv_continuous.ppf

rv_continuous.ppf(q, *args, **kwds)
Percent point function (inverse of cdf) at q of the given RV.

Parameters
q = [array_like] lower tail probability
arg1, arg2, arg3,... [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc = [array_like, optional] location parameter (default=0)
scale = [array_like, optional] scale parameter (default=1)

Returns
x = [array_like] quantile corresponding to the lower tail probability q.

scipy.stats.rv_continuous.isf

rv_continuous.isf(q, *args, **kwds)
Inverse survival function (inverse of sf) at q of the given RV.

Parameters
q = [array_like] upper tail probability
arg1, arg2, arg3,... [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc = [array_like, optional] location parameter (default=0)
scale = [array_like, optional] scale parameter (default=1)

Returns
x = [ndarray or scalar] Quantile corresponding to the upper tail probability q.

scipy.stats.rv_continuous.moment

rv_continuous.moment(n, *args, **kwds)
n-th order non-central moment of distribution.

Parameters
n = [int, n >= 1] Order of moment.
arg1, arg2, arg3,... [float] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
loc = [array_like, optional] location parameter (default=0)
scale = [array_like, optional] scale parameter (default=1)
scipy.stats.rv_continuous.stats

rv_continuous.stats(*args, **kwds)
Some statistics of the given RV.

Parameters
arg1, arg2, arg3,...
[array_like] The shape parameter(s) for the distribution (see docstring of the
instance object for more information)
loc
[array_like, optional] location parameter (default=0)
scale
[array_like, optional (continuous RVs only)] scale parameter (default=1)
moments
[str, optional] composed of letters ['mvsk'] defining which moments to compute:
'm' = mean, 'v' = variance, 's' = (Fisher's) skew, 'k' = (Fisher's) kurtosis.
(default is 'mv')

Returns
stats
[sequence] of requested moments.

scipy.stats.rv_continuous.entropy

rv_continuous.entropy(*args, **kwds)
Differential entropy of the RV.

Parameters
arg1, arg2, arg3,...
[array_like] The shape parameter(s) for the distribution (see docstring of the
instance object for more information).
loc
[array_like, optional] Location parameter (default=0).
scale
[array_like, optional (continuous distributions only).] Scale parameter (de-
fault=1).

Notes
Entropy is defined base e:

```python
>>> drv = rv_discrete(values=((0, 1), (0.5, 0.5)))
>>> np.allclose(drv.entropy(), np.log(2.0))
True
```

scipy.stats.rv_continuous.expect

rv_continuous.expect(func=None, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)
Calculate expected value of a function with respect to the distribution by numerical integration.
The expected value of a function \( f(x) \) with respect to a distribution \( \text{dist} \) is defined as:

\[
\mathbb{E}[f(x)] = \text{Integral}(f(x) \times \text{dist}.pdf(x)),
\]

where \( \text{ub} \) and \( \text{lb} \) are arguments and \( x \) has the \( \text{dist}.pdf(x) \) distribution. If the bounds \( \text{lb} \) and \( \text{ub} \) correspond to the support of the distribution, e.g. \([-\infty, \infty]\) in the default case, then the integral is the unrestricted expectation of \( f(x) \). Also, the function \( f(x) \) may be defined such that \( f(x) \) is 0 outside a finite interval in which case the expectation is calculated within the finite range \([\text{lb}, \text{ub}]\).
Parameters

- `func` [callable, optional] Function for which integral is calculated. Takes only one argument. The default is the identity mapping \( f(x) = x \).
- `args` [tuple, optional] Shape parameters of the distribution.
- `loc` [float, optional] Location parameter (default=0).
- `scale` [float, optional] Scale parameter (default=1).
- `lb, ub` [scalar, optional] Lower and upper bound for integration. Default is set to the support of the distribution.
- `conditional` [bool, optional] If True, the integral is corrected by the conditional probability of the integration interval. The return value is the expectation of the function, conditional on being in the given interval. Default is False.

Additional keyword arguments are passed to the integration routine.

Returns

- `expect` [float] The calculated expected value.

Notes

The integration behavior of this function is inherited from `scipy.integrate.quad`. Neither this function nor `scipy.integrate.quad` can verify whether the integral exists or is finite. For example `cauchy(0).mean()` returns `np.nan` and `cauchy(0).expect()` returns 0.0.

Examples

To understand the effect of the bounds of integration consider >>> from scipy.stats import expon

```python
>>> expon(1).expect(lambda x: 1, lb=0.0, ub=2.0)
0.6321205588285578
```

This is close to

```python
>>> expon(1).cdf(2.0) - expon(1).cdf(0.0)
0.6321205588285577
```

If `conditional=True`

```python
>>> expon(1).expect(lambda x: 1, lb=0.0, ub=2.0, conditional=True)
1.0000000000000002
```

The slight deviation from 1 is due to numerical integration.

`scipy.stats.rv_continuous.median`

```python
rv_continuous.median(*args, **kwds)
```

Median of the distribution.

Parameters

- `arg1, arg2, arg3,...` [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
- `loc` [float, optional] Location parameter, Default is 0.
- `scale` [float, optional] Scale parameter, Default is 1.

Returns

- `median` [float] The median of the distribution.

See also:
inverse of the CDF

**scipy.stats.rv_continuous.mean**

```
rv_continuous.mean(*args, **kwds)
```

Mean of the distribution.

**Parameters**

- `arg1, arg2, arg3,...`
  - `[array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
- `loc`  
  - `[array_like, optional] location parameter (default=0)
- `scale`  
  - `[array_like, optional] scale parameter (default=1)

**Returns**

- `mean`  
  - `[float] the mean of the distribution

**scipy.stats.rv_continuous.std**

```
rv_continuous.std(*args, **kwds)
```

Standard deviation of the distribution.

**Parameters**

- `arg1, arg2, arg3,...`
  - `[array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
- `loc`  
  - `[array_like, optional] location parameter (default=0)
- `scale`  
  - `[array_like, optional] scale parameter (default=1)

**Returns**

- `std`  
  - `[float] standard deviation of the distribution

**scipy.stats.rv_continuous.var**

```
rv_continuous.var(*args, **kwds)
```

Variance of the distribution.

**Parameters**

- `arg1, arg2, arg3,...`
  - `[array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
- `loc`  
  - `[array_like, optional] location parameter (default=0)
- `scale`  
  - `[array_like, optional] scale parameter (default=1)

**Returns**

- `var`  
  - `[float] the variance of the distribution

---

**stats.distributions.rv_discrete.ppf**

Inverse of the CDF
scipy.stats.rv_continuous.interval

rv_continuous.interval(alpha, *args, **kwds)
Confidence interval with equal areas around the median.

Parameters

- **alpha**: [array_like of float] Probability that an rv will be drawn from the returned range. Each value should be in the range [0, 1].
- arg1, arg2, ...:
  [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
- loc:
  [array_like, optional] location parameter, Default is 0.
- scale:
  [array_like, optional] scale parameter, Default is 1.

Returns

- a, b:
  [ndarray of float] end-points of range that contain 100 * alpha % of the rv’s possible values.

scipy.stats.rv_continuous.__call__

rv_continuous.__call__(*args, **kwds)
Freeze the distribution for the given arguments.

Parameters

- arg1, arg2, arg3,....:
  [array_like] The shape parameter(s) for the distribution. Should include all the non-optional arguments, may include loc and scale.

Returns

- rv_frozen:
  [rv_frozen instance] The frozen distribution.

scipy.stats.rv_continuous.fit

rv_continuous.fit(data, *args, **kwds)
Return MLEs for shape (if applicable), location, and scale parameters from data.

MLE stands for Maximum Likelihood Estimate. Starting estimates for the fit are given by input arguments; for any arguments not provided with starting estimates, self._fitstart(data) is called to generate such.

One can hold some parameters fixed to specific values by passing in keyword arguments f0, f1, ..., fn (for shape parameters) and floc and fscale (for location and scale parameters, respectively).

Parameters

- **data**: [array_like] Data to use in calculating the MLEs.
- **args**: [floats, optional] Starting value(s) for any shape-characterizing arguments (those not provided will be determined by a call to _fitstart(data)). No default value.
- **kwds**: [floats, optional] Starting values for the location and scale parameters; no default. Special keyword arguments are recognized as holding certain parameters fixed:
  - f0...fn : hold respective shape parameters fixed. Alternatively, shape parameters to fix can be specified by name. For example, if self.shapes == "a, b", fa`and `fix_a are equivalent to f0, and fb and fix_b are equivalent to f1.
- **floc**: hold location parameter fixed to specified value.
- **fscale**: hold scale parameter fixed to specified value.
- **optimizer**: The optimizer to use. The optimizer must take `func`, and starting position as the first two arguments, plus `args` (for extra arguments to pass to the function to be optimized) and `disp=0` to suppress output as keyword arguments.

**Returns**

`mle_tuple`

[tuple of floats] MLEs for any shape parameters (if applicable), followed by those for location and scale. For most random variables, shape statistics will be returned, but there are exceptions (e.g. `norm`).

**Notes**

This fit is computed by maximizing a log-likelihood function, with penalty applied for samples outside of range of the distribution. The returned answer is not guaranteed to be the globally optimal MLE, it may only be locally optimal, or the optimization may fail altogether.

**Examples**

Generate some data to fit: draw random variates from the `beta` distribution

```python
>>> from scipy.stats import beta
>>> a, b = 1., 2.
>>> x = beta.rvs(a, b, size=1000)
```

Now we can fit all four parameters (`a`, `b`, `loc` and `scale`):

```python
>>> a1, b1, loc1, scale1 = beta.fit(x)
```

We can also use some prior knowledge about the dataset: let’s keep `loc` and `scale` fixed:

```python
>>> a1, b1, loc1, scale1 = beta.fit(x, floc=0, fscale=1)
>>> loc1, scale1
(0, 1)
```

We can also keep shape parameters fixed by using `f`-keywords. To keep the zero-th shape parameter a equal 1, use `f0=1` or, equivalently, `fa=1`:

```python
>>> a1, b1, loc1, scale1 = beta.fit(x, fa=1, floc=0, fscale=1)
>>> a1
1
```

Not all distributions return estimates for the shape parameters. `norm` for example just returns estimates for location and scale:

```python
>>> from scipy.stats import norm
>>> x = norm.rvs(a, b, size=1000, random_state=123)
>>> loc1, scale1 = norm.fit(x)
>>> loc1, scale1
(0.9208717275841631, 2.0015750750324668)
```

**scipy.stats.rv_continuous.fit_loc_scale**

`rv_continuous.fit_loc_scale(data, *args)`

Estimate loc and scale parameters from data using 1st and 2nd moments.

**Parameters**
data   [array_like] Data to fit.
arg1, arg2, arg3,...
       [array_like] The shape parameter(s) for the distribution (see docstring of the
       instance object for more information).

Returns
Lhat   [float] Estimated location parameter for the data.
Shat   [float] Estimated scale parameter for the data.

scipy.stats.rv_continuous.nnlf

rv_continuous.nnlf(\theta, x)

Return negative loglikelihood function.

Notes
This is \(-\sum(\log \text{pdf}(x, \theta), \text{axis}=0)\) where \(\theta\) are the parameters (including loc and
scale).

6.27.2 scipy.stats.rv_discrete

class scipy.stats.rv_discrete(a=0, b=\infty, name=None, badvalue=None, moment_tol=1e-08,
values=None, inc=1, longname=None, shapes=None, extradoc=None, seed=None)

A generic discrete random variable class meant for subclassing.

rv_discrete is a base class to construct specific distribution classes and instances for discrete random
variables. It can also be used to construct an arbitrary distribution defined by a list of support points
and corresponding probabilities.

Parameters
a      [float, optional] Lower bound of the support of the distribution, default: 0
b      [float, optional] Upper bound of the support of the distribution, default: plus
inf
moment_tol  [float, optional] The tolerance for the generic calculation of moments.
values   [tuple of two array_like, optional] (xk, pk) where xk are integers with non-zero
probabilities pk with \(\sum(pk) = 1\).
inc      [integer, optional] Increment for the support of the distribution. Default is 1.
(other values have not been tested)
badvalue  [float, optional] The value in a result arrays that indicates a value that for which
some argument restriction is violated, default is np.nan.
name     [str, optional] The name of the instance. This string is used to construct the default
example for distributions.
longname  [str, optional] This string is used as part of the first line of the docstring returned
when a subclass has no docstring of its own. Note: longname exists for backwards
compatibility, do not use for new subclasses.
shapes   [str, optional] The shape of the distribution. For example “m, n” for a distribution
that takes two integers as the two shape arguments for all its methods If not
provided, shape parameters will be inferred from the signatures of the private
methods, _pmf and _cdf of the instance.
extradoc  [str, optional] This string is used as the last part of the docstring returned when a
subclass has no docstring of its own. Note: extradoc exists for backwards compat-
ibility, do not use for new subclasses.
seed  [None or int or numpy.random.RandomState instance, optional] This parameter defines the RandomState object to use for drawing random variates. If None, the global np.random state is used. If integer, it is used to seed the local RandomState instance. Default is None.

Notes
This class is similar to _rv_continuous. Whether a shape parameter is valid is decided by an _argcheck method (which defaults to checking that its arguments are strictly positive.) The main differences are:

- the support of the distribution is a set of integers
- instead of the probability density function, pdf (and the corresponding private _pdf), this class defines the probability mass function, pmf (and the corresponding private _pmf.)
- scale parameter is not defined.

To create a new discrete distribution, we would do the following:

```python
>>> from scipy.stats import rv_discrete
>>> class poisson_gen(rv_discrete):
...     "Poisson distribution"
...     def _pmf(self, k, mu):
...         return exp(-mu) * mu**k / factorial(k)
```

and create an instance:

```python
>>> poisson = poisson_gen(name="poisson")
```

Note that above we defined the Poisson distribution in the standard form. Shifting the distribution can be done by providing the loc parameter to the methods of the instance. For example, poisson.pmf(x, mu, loc) delegates the work to poisson._pmf(x-loc, mu).

Discrete distributions from a list of probabilities
Alternatively, you can construct an arbitrary discrete rv defined on a finite set of values xk with Prob{X=xk} = pk by using the values keyword argument to the _rv_discrete constructor.

Examples
Custom made discrete distribution:

```python
>>> from scipy import stats
>>> xk = np.arange(7)
>>> pk = (0.1, 0.2, 0.3, 0.1, 0.1, 0.1, 0.2)
>>> custm = stats.rv_discrete(name='custm', values=(xk, pk))
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
>>> ax.plot(xk, custm.pmf(xk), 'ro', ms=12, mec='r')
>>> ax.vlines(xk, 0, custm.pmf(xk), colors='r', lw=4)
>>> plt.show()
```

Random number generation:

```python
>>> R = custm.rvs(size=100)
```

Attributes
random_state
Get or set the RandomState object for generating random variates.
Methods

- `rvs(*args, **kwargs)` Random variates of given type.
- `pmf(k, *args, **kwds)` Probability mass function at k of the given RV.
- `logpmf(k, *args, **kwds)` Log of the probability mass function at k of the given RV.
- `cdf(k, *args, **kwds)` Cumulative distribution function of the given RV.
- `logcdf(k, *args, **kwds)` Log of the cumulative distribution function at k of the given RV.
- `sf(k, *args, **kwds)` Survival function (1 - cdf) at k of the given RV.
- `logsf(k, *args, **kwds)` Log of the survival function of the given RV.
- `ppf(q, *args, **kwds)` Percent point function (inverse of cdf) at q of the given RV.
- `isf(q, *args, **kwds)` Inverse survival function (inverse of sf) at q of the given RV.
- `moment(n, *args, **kwds)` n-th order non-central moment of distribution.
- `stats(*args, **kwds)` Some statistics of the given RV.
- `entropy(*args, **kwds)` Differential entropy of the RV.
- `interval(alpha, *args, **kwds)` Confidence interval with equal areas around the median.
- `__call__(*args, **kwds)` Freeze the distribution for the given arguments.

`scipy.stats.rv_discrete.rvs` [scipy.stats]

`rv_discrete.rvs(*args, **kwargs)`
Random variates of given type.

Parameters

- `arg1, arg2, arg3` [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
- `loc` [int or tuple of ints, optional] Location parameter (default=0).
- `size` [int or tuple of ints, optional] Defining number of random variates (Default is 1).
Parameters

- **k**: array_like Quantiles.
- **arg1, arg2, arg3,...**: array_like The shape parameter(s) for the distribution (see docstring of the instance object for more information).
- **loc**: array_like, optional Location parameter (default=0).

Returns

- **pmf**: array_like Probability mass function evaluated at k.

**scipy.stats.rv_discrete.logpmf**

```
rv_discrete.logpmf(k, *args, **kwds)
```

Log of the probability mass function at k of the given RV.

Parameters

- **k**: array_like Quantiles.
- **arg1, arg2, arg3,...**: array_like The shape parameter(s) for the distribution (see docstring of the instance object for more information).
- **loc**: array_like, optional Location parameter. Default is 0.

Returns

- **logpmf**: array_like Log of the probability mass function evaluated at k.

**scipy.stats.rv_discrete.cdf**

```
rv_discrete.cdf(k, *args, **kwds)
```

Cumulative distribution function of the given RV.

Parameters

- **k**: array_like, int Quantiles.
- **arg1, arg2, arg3,...**: array_like The shape parameter(s) for the distribution (see docstring of the instance object for more information).
- **loc**: array_like, optional Location parameter (default=0).

Returns

- **cdf**: ndarray Cumulative distribution function evaluated at k.

**scipy.stats.rv_discrete.logcdf**

```
rv_discrete.logcdf(k, *args, **kwds)
```

Log of the cumulative distribution function at k of the given RV.

Parameters

- **k**: array_like, int Quantiles.
- **arg1, arg2, arg3,...**: array_like The shape parameter(s) for the distribution (see docstring of the instance object for more information).
- **loc**: array_like, optional Location parameter (default=0).

Returns

- **logcdf**: array_like Log of the cumulative distribution function evaluated at k.
scipy.stats.rv_discrete.sf

rv_discrete.sf(k, *args, **kwds)
Survival function (1 - cdf) at k of the given RV.

Parameters
k [array_like] Quantiles.
arg1, arg2, arg3,... [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
loc [array_like, optional] Location parameter (default=0).

Returns
sf [array_like] Survival function evaluated at k.

scipy.stats.rv_discrete.logsf

rv_discrete.logsf(k, *args, **kwds)
Log of the survival function of the given RV.
Returns the log of the “survival function,” defined as 1 - cdf, evaluated at k.

Parameters
k [array_like] Quantiles.
arg1, arg2, arg3,... [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
loc [array_like, optional] Location parameter (default=0).

Returns
logsf [ndarray] Log of the survival function evaluated at k.

scipy.stats.rv_discrete.ppf

rv_discrete.ppf(q, *args, **kwds)
Percent point function (inverse of cdf) at q of the given RV.

Parameters
q [array_like] Lower tail probability.
arg1, arg2, arg3,... [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
loc [array_like, optional] Location parameter (default=0).

Returns
k [array_like] Quantile corresponding to the lower tail probability, q.

scipy.stats.rv_discrete.isf

rv_discrete.isf(q, *args, **kwds)
Inverse survival function (inverse of sf) at q of the given RV.

Parameters
q [array_like] Upper tail probability.
arg1, arg2, arg3,...
    [array_like] The shape parameter(s) for the distribution (see docstring of the
    instance object for more information).
loc
    [array_like, optional] Location parameter (default=0).

Returns
k
    [ndarray or scalar] Quantile corresponding to the upper tail probability, q.

scipy.stats.rv_discrete.moment
rv_discrete.moment(n, *args, **kwds)
n-th order non-central moment of distribution.

Parameters
n
    [int, n >= 1] Order of moment.
arg1, arg2, arg3,...
    [float] The shape parameter(s) for the distribution (see docstring of the in-
loc
    [array_like, optional] location parameter (default=0)
scale
    [array_like, optional] scale parameter (default=1)

scipy.stats.rv_discrete.stats
rv_discrete.stats(*args, **kwds)
Some statistics of the given RV.

Parameters
arg1, arg2, arg3,...
    [array_like] The shape parameter(s) for the distribution (see docstring of the
loc
    [array_like, optional] location parameter (default=0)
scale
    [array_like, optional (continuous RVs only)] scale parameter (default=1)
moments
    [str, optional] composed of letters ['mvsk'] defining which moments to compute:
    'm' = mean, 'v' = variance, 's' = (Fisher’s) skew, 'k' = (Fisher’s) kurtosis. (default is 'mv')

Returns
stats
    [sequence] of requested moments.

scipy.stats.rv_discrete.entropy
rv_discrete.entropy(*args, **kwds)
Differential entropy of the RV.

Parameters
arg1, arg2, arg3,...
    [array_like] The shape parameter(s) for the distribution (see docstring of the
loc
    [array_like, optional] Location parameter (default=0).
scale
    [array_like, optional (continuous distributions only).] Scale parameter (de-

Notes
Entropy is defined base $e$:

```python
>>> drv = rv_discrete(values=((0, 1), (0.5, 0.5)))
>>> np.allclose(drv.entropy(), np.log(2.0))
True
```

`scipy.stats.rv_discrete.expect`

`rv_discrete.expect(func=None, args=(), loc=0, lb=None, ub=None, conditional=False, maxcount=1000, tolerance=1e-10, chunksize=32)`

Calculate expected value of a function with respect to the distribution for discrete distribution by numerical summation.

**Parameters**

- `func` [callable, optional] Function for which the expectation value is calculated. Takes only one argument. The default is the identity mapping $f(k) = k$.
- `args` [tuple, optional] Shape parameters of the distribution.
- `loc` [float, optional] Location parameter. Default is 0.
- `lb`, `ub` [int, optional] Lower and upper bound for the summation, default is set to the support of the distribution, inclusive (ul <= k <= ub).
- `conditional` [bool, optional] If true then the expectation is corrected by the conditional probability of the summation interval. The return value is the expectation of the function, `func`, conditional on being in the given interval (k such that ul <= k <= ub). Default is False.
- `maxcount` [int, optional] Maximal number of terms to evaluate (to avoid an endless loop for an infinite sum). Default is 1000.
- `tolerance` [float, optional] Absolute tolerance for the summation. Default is 1e-10.
- `chunksize` [int, optional] Iterate over the support of a distributions in chunks of this size. Default is 32.

**Returns**

- `expect` [float] Expected value.

**Notes**

For heavy-tailed distributions, the expected value may or may not exist, depending on the function, `func`. If it does exist, but the sum converges slowly, the accuracy of the result may be rather low. For instance, for `zipf(4)`, accuracy for mean, variance in example is only 1e-5. increasing `maxcount` and/or `chunksize` may improve the result, but may also make `zipf` very slow.

The function is not vectorized.

`scipy.stats.rv_discrete.median`

`rv_discrete.median(*args, **kwds)`

Median of the distribution.

**Parameters**

- `arg1, arg2, arg3,...` [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
- `loc` [array_like, optional] Location parameter, Default is 0.
scale [array_like, optional] Scale parameter, Default is 1.

Returns
median [float] The median of the distribution.

See also:

stats.distributions.rv_discrete.ppf
Inverse of the CDF

scipy.stats.rv_discrete.mean
rv_discrete.mean(*args, **kwds)
Mean of the distribution.

Parameters
arg1, arg2, arg3,...
[array_like] The shape parameter(s) for the distribution (see docstring of the
instance object for more information)
loc [array_like, optional] location parameter (default=0)
scale [array_like, optional] scale parameter (default=1)

Returns
mean [float] the mean of the distribution

scipy.stats.rv_discrete.std
rv_discrete.std(*args, **kwds)
Standard deviation of the distribution.

Parameters
arg1, arg2, arg3,...
[array_like] The shape parameter(s) for the distribution (see docstring of the
instance object for more information)
loc [array_like, optional] location parameter (default=0)
scale [array_like, optional] scale parameter (default=1)

Returns
std [float] standard deviation of the distribution

scipy.stats.rv_discrete.var
rv_discrete.var(*args, **kwds)
Variance of the distribution.

Parameters
arg1, arg2, arg3,...
[array_like] The shape parameter(s) for the distribution (see docstring of the
instance object for more information)
loc [array_like, optional] location parameter (default=0)
scale [array_like, optional] scale parameter (default=1)

Returns
var [float] the variance of the distribution
scipy.stats.rv_discrete.interval

`rv_discrete.interval(alpha, *args, **kwds)`
Confidence interval with equal areas around the median.

**Parameters**

- `alpha`  
  [array_like of float] Probability that an rv will be drawn from the returned range. Each value should be in the range \([0, 1]\).

- `arg1, arg2, ...`  
  [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).

- `loc`  
  [array_like, optional] location parameter, Default is 0.

- `scale`  
  [array_like, optional] scale parameter, Default is 1.

**Returns**

- `a, b`  
  [ndarray of float] end-points of range that contain 100 * `alpha` % of the rv’s possible values.

scipy.stats.rv_discrete.__call__

`rv_discrete.__call__(*args, **kwds)`
Freeze the distribution for the given arguments.

**Parameters**

- `arg1, arg2, arg3,...`  
  [array_like] The shape parameter(s) for the distribution. Should include all the non-optional arguments, may include `loc` and `scale`.

**Returns**

- `rv_frozen`  
  [rv_frozen instance] The frozen distribution.

### 6.27.3 scipy.stats.rv_histogram

**class**  `scipy.stats.rv_histogram(histogram, *args, **kwargs)`
Generates a distribution given by a histogram. This is useful to generate a template distribution from a binned datasample.

As a subclass of the `rv_continuous` class, `rv_histogram` inherits from it a collection of generic methods (see `rv_continuous` for the full list), and implements them based on the properties of the provided binned datasample.

**Parameters**

- `histogram`  
  [tuple of array_like] Tuple containing two array_like objects The first containing the content of \(n\) bins The second containing the \((n+1)\) bin boundaries In particular the return value np.histogram is accepted

**Notes**

There are no additional shape parameters except for the `loc` and `scale`. The pdf is defined as a stepwise function from the provided histogram The cdf is a linear interpolation of the pdf.

New in version 0.19.0.
Examples
Create a scipy.stats distribution from a numpy histogram

```python
>>> import scipy.stats
>>> import numpy as np
>>> data = scipy.stats.norm.rvs(size=100000, loc=0, scale=1.5, random_state=123)
>>> hist = np.histogram(data, bins=100)
>>> hist_dist = scipy.stats.rv_histogram(hist)
```

Behaves like an ordinary scipy rv_continuous distribution

```python
>>> hist_dist.pdf(1.0)
0.20538577847618705
>>> hist_dist.cdf(2.0)
0.90818568543056499
```

PDF is zero above (below) the highest (lowest) bin of the histogram, defined by the max (min) of the original dataset

```python
>>> hist_dist.pdf(np.max(data))
0.0
>>> hist_dist.cdf(np.max(data))
1.0
>>> hist_dist.pdf(np.min(data))
7.7591907244498314e-05
>>> hist_dist.cdf(np.min(data))
0.0
```

PDF and CDF follow the histogram

```python
>>> import matplotlib.pyplot as plt
>>> X = np.linspace(-5.0, 5.0, 100)
>>> plt.title("PDF from Template")
>>> plt.hist(data, density=True, bins=100)
>>> plt.plot(X, hist_dist.pdf(X), label='PDF')
>>> plt.plot(X, hist_dist.cdf(X), label='CDF')
>>> plt.show()
```

Attributes
random_state
Get or set the RandomState object for generating random variates.

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**scipy.stats.rv_histogram.__call__**

`rv_histogram.__call__(*args, **kwds*)`

Freeze the distribution for the given arguments.

**Parameters**

- arg1, arg2, arg3, ...
  - [array_like] The shape parameter(s) for the distribution. Should include all the non-optional arguments, may include `loc` and `scale`.

**Returns**

- rv_frozen
  - [rv_frozen instance] The frozen distribution.

**scipy.stats.rv_histogram.cdf**

`rv_histogram.cdf(x, *args, **kwds)`

Cumulative distribution function of the given RV.

**Parameters**

- x
  - [array_like] quantiles
- arg1, arg2, arg3, ...
  - [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
- loc
  - [array_like, optional] location parameter (default=0)
- scale
  - [array_like, optional] scale parameter (default=1)

**Returns**
```python
cdf [ndarray] Cumulative distribution function evaluated at x

scipy.stats.rv_histogram.entropy
rv_histogram.entropy(*args, **kwds)
Differential entropy of the RV.

Parameters
arg1, arg2, arg3,... [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
loc [array_like, optional] Location parameter (default=0).
scale [array_like, optional (continuous distributions only)] Scale parameter (default=1).

Notes
Entropy is defined base e:

```python
>>> drv = rv_discrete(values=((0, 1), (0.5, 0.5)))
>>> np.allclose(drv.entropy(), np.log(2.0))
True

scipy.stats.rv_histogram.expect
rv_histogram.expect(func=None, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)
Calculate expected value of a function with respect to the distribution by numerical integration.

The expected value of a function f(x) with respect to a distribution dist is defined as:

```python
ub
E[f(x)] = \int_{lb}^{ub} f(x) \cdot dist.pdf(x) dx
```

where \( ub \) and \( lb \) are arguments and \( x \) has the \( dist.pdf(x) \) distribution. If the bounds \( lb \) and \( ub \) correspond to the support of the distribution, e.g. \([-\infty, \infty]\) in the default case, then the
integral is the unrestricted expectation of \( f(x) \). Also, the function \( f(x) \) may be defined such that \( f(x) = 0 \) outside a finite interval in which case the expectation is calculated within the finite range \([lb, ub]\).

**Parameters**

- **func** [callable, optional] Function for which integral is calculated. Takes only one argument. The default is the identity mapping \( f(x) = x \).
- **args** [tuple, optional] Shape parameters of the distribution.
- **loc** [float, optional] Location parameter (default=0).
- **scale** [float, optional] Scale parameter (default=1).
- **lb, ub** [scalar, optional] Lower and upper bound for integration. Default is set to the support of the distribution.
- **conditional** [bool, optional] If True, the integral is corrected by the conditional probability of the integration interval. The return value is the expectation of the function, conditional on being in the given interval. Default is False.

**Returns**

- **expect** [float] The calculated expected value.

**Notes**

The integration behavior of this function is inherited from `scipy.integrate.quad`. Neither this function nor `scipy.integrate.quad` can verify whether the integral exists or is finite. For example `cauchy(0).mean()` returns `np.nan` and `cauchy(0).expect()` returns `0.0`.

**Examples**

To understand the effect of the bounds of integration consider >>> from scipy.stats import expon >>> expon(1).expect(lambda x: 1, lb=0.0, ub=2.0) 0.6321205588285578

This is close to

```python
>>> expon(1).cdf(2.0) - expon(1).cdf(0.0)
0.6321205588285577
```

If `conditional=True`

```python
>>> expon(1).expect(lambda x: 1, lb=0.0, ub=2.0, conditional=True)
1.0000000000000002
```

The slight deviation from 1 is due to numerical integration.

**scipy.stats.rv_histogram.fit**

`rv_histogram.fit(data, *args, **kwds)`

Return MLEs for shape (if applicable), location, and scale parameters from data.

MLE stands for Maximum Likelihood Estimate. Starting estimates for the fit are given by input arguments; for any arguments not provided with starting estimates, `self._fitstart(data)` is called to generate such.

One can hold some parameters fixed to specific values by passing in keyword arguments `f0, f1, ...`, `fn` (for shape parameters) and `floc` and `fscale` (for location and scale parameters, respectively).

**Parameters**

- **data** [array_like] Data to use in calculating the MLEs.
args [floats, optional] Starting value(s) for any shape-characterizing arguments (those not provided will be determined by a call to \_fitstart(data)). No default value.

kwds [floats, optional] Starting values for the location and scale parameters; no default. Special keyword arguments are recognized as holding certain parameters fixed:

- f0..fn: hold respective shape parameters fixed. Alternatively, shape parameters to fix can be specified by name. For example, if self.shapes == "a, b", fa and \_fix_a are equivalent to f0, and fb and \_fix_b are equivalent to f1.
- floc: hold location parameter fixed to specified value.
- fscale: hold scale parameter fixed to specified value.
- optimizer: The optimizer to use. The optimizer must take func, and starting position as the first two arguments, plus args (for extra arguments to pass to the function to be optimized) and disp=0 to suppress output as keyword arguments.

Returns

mle_tuple [tuple of floats] MLEs for any shape parameters (if applicable), followed by those for location and scale. For most random variables, shape statistics will be returned, but there are exceptions (e.g. norm).

Notes

This fit is computed by maximizing a log-likelihood function, with penalty applied for samples outside of range of the distribution. The returned answer is not guaranteed to be the globally optimal MLE, it may only be locally optimal, or the optimization may fail altogether.

Examples

Generate some data to fit: draw random variates from the beta distribution

```python
>>> from scipy.stats import beta
>>> a, b = 1., 2.
>>> x = beta.rvs(a, b, size=1000)
```

Now we can fit all four parameters (a, b, loc and scale):

```python
>>> a1, b1, loc1, scale1 = beta.fit(x)
```

We can also use some prior knowledge about the dataset: let’s keep loc and scale fixed:

```python
>>> a1, b1, loc1, scale1 = beta.fit(x, floc=0, fscale=1)
>>> loc1, scale1
(0, 1)
```

We can also keep shape parameters fixed by using f-keys. To keep the zero-th shape parameter a equal 1, use f0=1 or, equivalently, fa=1:

```python
>>> a1, b1, loc1, scale1 = beta.fit(x, fa=1, floc=0, fscale=1)
>>> a1
1
```

Not all distributions return estimates for the shape parameters. norm for example just returns estimates for location and scale:
```
>>> from scipy.stats import norm
>>> x = norm.rvs(a, b, size=1000, random_state=123)
>>> loc1, scale1 = norm.fit(x)
>>> loc1, scale1
(0.92087172783841631, 2.0015750750324668)
```

**scipy.stats.rv_histogram.fit_loc_scale**

`rv_histogram.fit_loc_scale(data, *args)`

Estimate loc and scale parameters from data using 1st and 2nd moments.

**Parameters**

- `data` [array_like] Data to fit.
- `arg1, arg2, arg3,...` [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).

**Returns**

- `Lhat` [float] Estimated location parameter for the data.
- `Shat` [float] Estimated scale parameter for the data.

**scipy.stats.rv_histogram.freeze**

`rv_histogram.freeze(*args, **kwds)`

Freeze the distribution for the given arguments.

**Parameters**

- `arg1, arg2, arg3,...` [array_like] The shape parameter(s) for the distribution. Should include all the non-optional arguments, may include `loc` and `scale`.

**Returns**

- `rv_frozen` [rv_frozen instance] The frozen distribution.

**scipy.stats.rv_histogram.interval**

`rv_histogram.interval(alpha, *args, **kwds)`

Confidence interval with equal areas around the median.

**Parameters**

- `alpha` [array_like of float] Probability that an rv will be drawn from the returned range. Each value should be in the range [0, 1].
- `arg1, arg2, ...` [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
- `loc` [array_like, optional] location parameter, Default is 0.
- `scale` [array_like, optional] scale parameter, Default is 1.

**Returns**

- `a, b` [ndarray of float] end-points of range that contain 100 * `alpha` % of the rv’s possible values.
scipy.stats.rv_histogram.isf

rv_histogram.isf(q, *args, **kwds)
Inverse survival function (inverse of sf) at q of the given RV.

Parameters
q [array_like] upper tail probability
arg1, arg2, arg3,... [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc [array_like, optional] location parameter (default=0)
scale [array_like, optional] scale parameter (default=1)

Returns
x [ndarray or scalar] Quantile corresponding to the upper tail probability q.

scipy.stats.rv_histogram.logcdf

rv_histogram.logcdf(x, *args, **kwds)
Log of the cumulative distribution function at x of the given RV.

Parameters
x [array_like] quantiles
arg1, arg2, arg3,... [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc [array_like, optional] location parameter (default=0)
scale [array_like, optional] scale parameter (default=1)

Returns
logcdf [array_like] Log of the cumulative distribution function evaluated at x

scipy.stats.rv_histogram.logpdf

rv_histogram.logpdf(x, *args, **kwds)
Log of the probability density function at x of the given RV.
This uses a more numerically accurate calculation if available.

Parameters
x [array_like] quantiles
arg1, arg2, arg3,... [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc [array_like, optional] location parameter (default=0)
scale [array_like, optional] scale parameter (default=1)

Returns
logpdf [array_like] Log of the probability density function evaluated at x
scipy.stats.rv_histogram.logsf

`rv_histogram.logsf(x, *args, **kwds)`

Log of the survival function of the given RV.

Returns the log of the “survival function,” defined as (1 - \text{cdf}), evaluated at \(x\).

**Parameters**

- \(x\) [array_like] quantiles
- \(\text{arg1}, \text{arg2}, \text{arg3},...\) [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
- loc [array_like, optional] location parameter (default=0)
- scale [array_like, optional] scale parameter (default=1)

**Returns**

- \(\text{logsf}\) [ndarray] Log of the survival function evaluated at \(x\).

scipy.stats.rv_histogram.mean

`rv_histogram.mean(*args, **kwds)`

Mean of the distribution.

**Parameters**

- \(\text{arg1}, \text{arg2}, \text{arg3},...\) [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
- loc [array_like, optional] location parameter, Default is 0.
- scale [array_like, optional] scale parameter, Default is 1.

**Returns**

- \(\text{mean}\) [float] the mean of the distribution

scipy.stats.rv_histogram.median

`rv_histogram.median(*args, **kwds)`

Median of the distribution.

**Parameters**

- \(\text{arg1}, \text{arg2}, \text{arg3},...\) [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
- loc [array_like, optional] Location parameter, Default is 0.
- scale [array_like, optional] Scale parameter, Default is 1.

**Returns**

- \(\text{median}\) [float] The median of the distribution.

See also:

stats.distributions.rv_discrete.ppf

Inverse of the CDF
scipy.stats.rv_histogram.moment

rv_histogram.moment(n, *args, **kwds)

n-th order non-central moment of distribution.

Parameters

- **n**: [int, n >= 1] Order of moment.
- **arg1, arg2, arg3,...**: [float] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
- **loc**: [array_like, optional] location parameter (default=0)
- **scale**: [array_like, optional] scale parameter (default=1)

scipy.stats.rv_histogram.nnlf

rv_histogram.nnlf(theta, x)

Return negative loglikelihood function.

Notes

This is -sum(log pdf(x, theta), axis=0) where theta are the parameters (including loc and scale).

scipy.stats.rv_histogram.pdf

rv_histogram.pdf(x, *args, **kwds)

Probability density function at x of the given RV.

Parameters

- **x**: [array_like] quantiles
- **arg1, arg2, arg3,...**: [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
- **loc**: [array_like, optional] location parameter (default=0)
- **scale**: [array_like, optional] scale parameter (default=1)

Returns

- **pdf**: [ndarray] Probability density function evaluated at x

scipy.stats.rv_histogram.ppf

rv_histogram.ppf(q, *args, **kwds)

Percent point function (inverse of cdf) at q of the given RV.

Parameters

- **q**: [array_like] lower tail probability
- **arg1, arg2, arg3,...**: [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
- **loc**: [array_like, optional] location parameter (default=0)
- **scale**: [array_like, optional] scale parameter (default=1)

Returns

- **x**: [array_like] quantile corresponding to the lower tail probability q.
scipy.stats.rv_histogram.rvs

rv_histogram.rvs(*args, **kwds)

Random variates of given type.

Parameters

arg1, arg2, arg3,...

[array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc

[array_like, optional] Location parameter (default=0).

scale

[array_like, optional] Scale parameter (default=1).

size

[int or tuple of ints, optional] Defining number of random variates (default is 1).

random_state

[None or int or np.random.RandomState instance, optional] If int or RandomState, use it for drawing the random variates. If None, rely on self.random_state. Default is None.

Returns

rvs

[ndarray or scalar] Random variates of given size.

scipy.stats.rv_histogram.sf

rv_histogram.sf(x, *args, **kwds)

Survival function (1 - cdf) at x of the given RV.

Parameters

x

[array_like] quantiles

arg1, arg2, arg3,...

[array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc

[array_like, optional] location parameter (default=0)

scale

[array_like, optional] scale parameter (default=1)

Returns

sf

[array_like] Survival function evaluated at x

scipy.stats.rv_histogram.stats

rv_histogram.stats(*args, **kwds)

Some statistics of the given RV.

Parameters

arg1, arg2, arg3,...

[array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc

[array_like, optional] location parameter (default=0)

scale

[array_like, optional (continuous RVs only)] scale parameter (default=1)

moments

[str, optional] composed of letters ['mvsk'] defining which moments to compute: 'm' = mean, 'v' = variance, 's' = (Fisher's) skew, 'k' = (Fisher's) kurtosis. (default is 'mv')

Returns

stats

[sequence] of requested moments.
scipy.stats.rv_histogram.std

rv_histogram.std(*args, **kwds)
Standard deviation of the distribution.

Parameters
arg1, arg2, arg3,

[array_like] The shape parameter(s) for the distribution (see docstring of the
instance object for more information)
loc
[array_like, optional] location parameter (default=0)
scale
[array_like, optional] scale parameter (default=1)

Returns
std
[float] standard deviation of the distribution

scipy.stats.rv_histogram.var

rv_histogram.var(*args, **kwds)
Variance of the distribution.

Parameters
arg1, arg2, arg3,

[array_like] The shape parameter(s) for the distribution (see docstring of the
instance object for more information)
loc
[array_like, optional] location parameter (default=0)
scale
[array_like, optional] scale parameter (default=1)

Returns
var
[float] the variance of the distribution

6.27.4 Continuous distributions

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<th>Description</th>
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</thead>
<tbody>
<tr>
<td>alpha</td>
<td>An alpha continuous random variable.</td>
</tr>
<tr>
<td>anglit</td>
<td>An anglit continuous random variable.</td>
</tr>
<tr>
<td>arcsine</td>
<td>An arcsine continuous random variable.</td>
</tr>
<tr>
<td>argus</td>
<td>Argus distribution</td>
</tr>
<tr>
<td>beta</td>
<td>A beta continuous random variable.</td>
</tr>
<tr>
<td>betaprime</td>
<td>A beta prime continuous random variable.</td>
</tr>
<tr>
<td>bradford</td>
<td>A Bradford continuous random variable.</td>
</tr>
<tr>
<td>burr</td>
<td>A Burr (Type III) continuous random variable.</td>
</tr>
<tr>
<td>burr12</td>
<td>A Burr (Type XII) continuous random variable.</td>
</tr>
<tr>
<td>cauchy</td>
<td>A Cauchy continuous random variable.</td>
</tr>
<tr>
<td>chi</td>
<td>A chi continuous random variable.</td>
</tr>
<tr>
<td>chi2</td>
<td>A chi-squared continuous random variable.</td>
</tr>
<tr>
<td>cosine</td>
<td>A cosine continuous random variable.</td>
</tr>
<tr>
<td>crystalball</td>
<td>Crystalball distribution</td>
</tr>
<tr>
<td>dgamma</td>
<td>A double gamma continuous random variable.</td>
</tr>
<tr>
<td>dweibull</td>
<td>A double Weibull continuous random variable.</td>
</tr>
<tr>
<td>erlang</td>
<td>An Erlang continuous random variable.</td>
</tr>
<tr>
<td>exp</td>
<td>An exponential continuous random variable.</td>
</tr>
<tr>
<td>expnorm</td>
<td>An exponentially modified Normal continuous random variable.</td>
</tr>
</tbody>
</table>

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<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>exponweib</td>
<td>An exponentiated Weibull continuous random variable.</td>
</tr>
<tr>
<td>exponpow</td>
<td>An exponential power continuous random variable.</td>
</tr>
<tr>
<td>f</td>
<td>An F continuous random variable.</td>
</tr>
<tr>
<td>fatiguelife</td>
<td>A fatigue-life (Birnbaum-Saunders) continuous random variable.</td>
</tr>
<tr>
<td>fisk</td>
<td>A Fisk continuous random variable.</td>
</tr>
<tr>
<td>foldcauchy</td>
<td>A folded Cauchy continuous random variable.</td>
</tr>
<tr>
<td>foldnorm</td>
<td>A folded normal continuous random variable.</td>
</tr>
<tr>
<td>frechet_r</td>
<td>A frechet_r continuous random variable.</td>
</tr>
<tr>
<td>frechet_l</td>
<td>A frechet_l continuous random variable.</td>
</tr>
<tr>
<td>genlogistic</td>
<td>A generalized logistic continuous random variable.</td>
</tr>
<tr>
<td>gennorm</td>
<td>A generalized normal continuous random variable.</td>
</tr>
<tr>
<td>genpareto</td>
<td>A generalized Pareto continuous random variable.</td>
</tr>
<tr>
<td>genexpon</td>
<td>A generalized exponential continuous random variable.</td>
</tr>
<tr>
<td>genextreme</td>
<td>A generalized extreme value continuous random variable.</td>
</tr>
<tr>
<td>gausshyper</td>
<td>A Gauss hypergeometric continuous random variable.</td>
</tr>
<tr>
<td>gamma</td>
<td>A gamma continuous random variable.</td>
</tr>
<tr>
<td>gengamma</td>
<td>A generalized gamma continuous random variable.</td>
</tr>
<tr>
<td>genhalflogistic</td>
<td>A generalized half-logistic continuous random variable.</td>
</tr>
<tr>
<td>gilbrat</td>
<td>A Gilbrat continuous random variable.</td>
</tr>
<tr>
<td>gompertz</td>
<td>A Gompertz (or truncated Gumbel) continuous random variable.</td>
</tr>
<tr>
<td>gumbel_r</td>
<td>A right-skewed Gumbel continuous random variable.</td>
</tr>
<tr>
<td>gumbel_l</td>
<td>A left-skewed Gumbel continuous random variable.</td>
</tr>
<tr>
<td>halfcauchy</td>
<td>A Half-Cauchy continuous random variable.</td>
</tr>
<tr>
<td>halflogistic</td>
<td>A half-logistic continuous random variable.</td>
</tr>
<tr>
<td>halfnorm</td>
<td>A half-normal continuous random variable.</td>
</tr>
<tr>
<td>halfgennorm</td>
<td>The upper half of a generalized normal continuous random variable.</td>
</tr>
<tr>
<td>hypsecant</td>
<td>A hyperbolic secant continuous random variable.</td>
</tr>
<tr>
<td>invgamma</td>
<td>An inverted gamma continuous random variable.</td>
</tr>
<tr>
<td>invgauss</td>
<td>An inverse Gaussian continuous random variable.</td>
</tr>
<tr>
<td>invweibull</td>
<td>An inverted Weibull continuous random variable.</td>
</tr>
<tr>
<td>johnsonsib</td>
<td>A Johnson SB continuous random variable.</td>
</tr>
<tr>
<td>johnsonsu</td>
<td>A Johnson SU continuous random variable.</td>
</tr>
<tr>
<td>kappa4</td>
<td>Kappa 4 parameter distribution.</td>
</tr>
<tr>
<td>kappa3</td>
<td>Kappa 3 parameter distribution.</td>
</tr>
<tr>
<td>ksone</td>
<td>General Kolmogorov-Smirnov one-sided test.</td>
</tr>
<tr>
<td>kstwobign</td>
<td>Kolmogorov-Smirnov two-sided test for large N.</td>
</tr>
<tr>
<td>laplace</td>
<td>A Laplace continuous random variable.</td>
</tr>
<tr>
<td>levy</td>
<td>A Levy continuous random variable.</td>
</tr>
<tr>
<td>levy_l</td>
<td>A left-skewed Levy continuous random variable.</td>
</tr>
<tr>
<td>levy_stable</td>
<td>A Levy-stable continuous random variable.</td>
</tr>
<tr>
<td>logistic</td>
<td>A logistic (or Sech-squared) continuous random variable.</td>
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<table>
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<td>loggamma</td>
<td>A log gamma continuous random variable.</td>
</tr>
<tr>
<td>loglaplace</td>
<td>A log-Laplace continuous random variable.</td>
</tr>
<tr>
<td>lognorm</td>
<td>A lognormal continuous random variable.</td>
</tr>
<tr>
<td>lomax</td>
<td>A Lomax (Pareto of the second kind) continuous random variable.</td>
</tr>
<tr>
<td>maxwell</td>
<td>A Maxwell continuous random variable.</td>
</tr>
<tr>
<td>mielke</td>
<td>A Mielke’s Beta-Kappa continuous random variable.</td>
</tr>
<tr>
<td>moyal</td>
<td>A Moyal continuous random variable.</td>
</tr>
<tr>
<td>nakagami</td>
<td>A Nakagami continuous random variable.</td>
</tr>
<tr>
<td>ncx2</td>
<td>A non-central chi-squared continuous random variable.</td>
</tr>
<tr>
<td>ncf</td>
<td>A non-central F distribution continuous random variable.</td>
</tr>
<tr>
<td>nct</td>
<td>A non-central Student’s t continuous random variable.</td>
</tr>
<tr>
<td>norm</td>
<td>A normal continuous random variable.</td>
</tr>
<tr>
<td>normingauss</td>
<td>A Normal Inverse Gaussian continuous random variable.</td>
</tr>
<tr>
<td>pareto</td>
<td>A Pareto continuous random variable.</td>
</tr>
<tr>
<td>pearson3</td>
<td>A Pearson type III continuous random variable.</td>
</tr>
<tr>
<td>powerlaw</td>
<td>A power-function continuous random variable.</td>
</tr>
<tr>
<td>powerlognorm</td>
<td>A power log-normal continuous random variable.</td>
</tr>
<tr>
<td>powernorm</td>
<td>A power normal continuous random variable.</td>
</tr>
<tr>
<td>rdist</td>
<td>An R-distributed continuous random variable.</td>
</tr>
<tr>
<td>reciproc2</td>
<td>A reciprocal continuous random variable.</td>
</tr>
<tr>
<td>rayleigh</td>
<td>A Rayleigh continuous random variable.</td>
</tr>
<tr>
<td>rice</td>
<td>A Rice continuous random variable.</td>
</tr>
<tr>
<td>recipinvgauss</td>
<td>A reciprocal inverse Gaussian continuous random variable.</td>
</tr>
<tr>
<td>semicircular</td>
<td>A semicircular continuous random variable.</td>
</tr>
<tr>
<td>skewnorm</td>
<td>A skew-normal random variable.</td>
</tr>
<tr>
<td>t</td>
<td>A Student’s t continuous random variable.</td>
</tr>
<tr>
<td>trapz</td>
<td>A trapezoidal continuous random variable.</td>
</tr>
<tr>
<td>triang</td>
<td>A triangular continuous random variable.</td>
</tr>
<tr>
<td>truncexpon</td>
<td>A truncated exponential continuous random variable.</td>
</tr>
<tr>
<td>truncnorm</td>
<td>A truncated normal continuous random variable.</td>
</tr>
<tr>
<td>tukeylambda</td>
<td>A Tukey-Lamdba continuous random variable.</td>
</tr>
<tr>
<td>uniform</td>
<td>A uniform continuous random variable.</td>
</tr>
<tr>
<td>vonmises</td>
<td>A Von Mises continuous random variable.</td>
</tr>
<tr>
<td>vonmises_line</td>
<td>A Von Mises continuous random variable.</td>
</tr>
<tr>
<td>wald</td>
<td>A Wald continuous random variable.</td>
</tr>
<tr>
<td>weibull_min</td>
<td>Weibull minimum continuous random variable.</td>
</tr>
<tr>
<td>weibull_max</td>
<td>Weibull maximum continuous random variable.</td>
</tr>
<tr>
<td>wrapcauchy</td>
<td>A wrapped Cauchy continuous random variable.</td>
</tr>
</tbody>
</table>

**scipy.stats.alpha**

*scipy.stats.alpha* = <scipy.stats._continuous_distns.alpha_gen object>

An alpha continuous random variable.

As an instance of the *rv_continuous* class, *alpha* object inherits from it a collection of generic methods...
Notes
The probability density function for alpha is:

\[ f(x; a) = \frac{1}{x^2 \Phi(a) \sqrt{2\pi}} \exp\left(-\frac{1}{2}(a - 1/x)^2\right) \]

where \( \Phi \) is the normal CDF, \( x > 0 \), and \( a > 0 \).

alpha takes \( a \) as a shape parameter.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, alpha.pdf(x, a, loc, scale) is identically equivalent to alpha.pdf(y, a) / scale with \( y = (x - loc) / scale \).

Examples

```python
>>> from scipy.stats import alpha
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> a = 3.57
>>> mean, var, skew, kurt = alpha.stats(a, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(alpha.ppf(0.01, a),
... alpha.ppf(0.99, a), 100)
>>> ax.plot(x, alpha.pdf(x, a),
... 'r-', lw=5, alpha=0.6, label='alpha pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = alpha(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = alpha.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], alpha.cdf(vals, a))
True
```

Generate random numbers:

```python
>>> r = alpha.rvs(a, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

<table>
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<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rvs(a, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, a, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, a, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, a, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, a, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, a, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, a, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, a, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, a, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, a, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(a, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(a, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, a, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(a,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(a, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(a, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(a, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(a, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, a, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

### scipy.stats.anglit

**scipy.stats.anglit**

scipy.stats.anglit = <scipy.stats._continuous_distns.anglit_gen object>

An anglit continuous random variable.
As an instance of the `rv_continuous` class, `anglit` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `anglit` is:

\[ f(x) = \sin(2x + \pi/2) = \cos(2x) \]

for \(-\pi/4 \leq x \leq \pi/4\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `anglit.pdf(x, loc, scale)` is identically equivalent to `anglit.pdf(y) / scale` with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
>>> from scipy.stats import anglit
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> mean, var, skew, kurt = anglit.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(anglit.ppf(0.01), ...
...     anglit.ppf(0.99), 100)
>>> ax.plot(x, anglit.pdf(x), ...
...     'r-', lw=5, alpha=0.6, label='anglit pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = anglit()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = anglit.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], anglit.cdf(vals))
True
```

Generate random numbers:

```python
>>> r = anglit.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

<table>
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<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rvs(loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, loc=0, scale=1)</td>
<td>Survival function (also defined as (1 - \text{cdf}), but (sf) is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, loc=0, scale=1)</td>
<td>Percent point function (inverse of (\text{cdf}) — percentiles).</td>
</tr>
<tr>
<td>isf(q, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of (\text{sf})).</td>
</tr>
<tr>
<td>moment(n, loc=0, scale=1)</td>
<td>Non-central moment of order (n).</td>
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<tr>
<td>stats(loc=0, scale=1, moments='mv')</td>
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<tr>
<td>entropy(loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
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<tr>
<td>fit(data, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(loc=0, scale=1)</td>
<td>Median of the distribution.</td>
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<td>mean(loc=0, scale=1)</td>
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<td>Variance of the distribution.</td>
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<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
</tr>
</tbody>
</table>

scipy.stats.arcsine

scipy.stats.arcsine = <scipy.stats._continuous_distns.arcsine_gen object>
An arcsine continuous random variable.
As an instance of the `rv_continuous` class, `arcsine` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `arcsine` is:

\[
f(x) = \frac{1}{\pi \sqrt{x(1-x)}}
\]

for \(0 < x < 1\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `arcsine.pdf(x, loc, scale)` is identically equivalent to `arcsine.pdf(y) / scale` with \(y = (x - loc) / scale\).

**Examples**

```python
>>> from scipy.stats import arcsine
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:
```
```python
>>> mean, var, skew, kurt = arcsine.stats(moments='mvsk')
```

Display the probability density function (pdf):
```
```python
>>> x = np.linspace(arcsine.ppf(0.01), ...
                  arcsine.ppf(0.99), 100)
>>> ax.plot(x, arcsine.pdf(x), ...
          'r-', lw=5, alpha=0.6, label='arcsine pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:
```
```python
>>> rv = arcsine()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:
```
```python
>>> vals = arcsine.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], arcsine.cdf(vals))
```

Generate random numbers:
```
```python
>>> r = arcsine.rvs(size=1000)
```

And compare the histogram:
```
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
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<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
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<td>sf(x, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
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<tr>
<td>ppf(q, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(loc=0, scale=1)</td>
<td>Median of the distribution.</td>
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<td>Mean of the distribution.</td>
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<td>std(loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

scipy.stats.argus

scipy.stats.argus = <scipy.stats._continuous_distns.argus_gen object>

Argus distribution
As an instance of the `rv_continuous` class, `argus` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `argus` is:

\[
f(x, \chi) = \frac{\chi^3}{\sqrt{2\pi} \Psi(\chi)} x^2 \sqrt{1 - x^2} \exp(-\chi^2 (1 - x^2)/2)
\]

for \(0 < x < 1\), where

\[
\Psi(\chi) = \Phi(\chi) - \chi \phi(\chi) - 1/2
\]

with \(\Phi\) and \(\phi\) being the CDF and PDF of a standard normal distribution, respectively.

`argus` takes \(\chi\) as shape a parameter.

**References**
The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, \(\text{argus.pdf}(x, \chi, \text{loc}, \text{scale})\) is identically equivalent to \(\text{argus.pdf}(y, \chi) / \text{scale}\) with \(y = (x - \text{loc}) / \text{scale}\).

New in version 0.19.0.

/1/

**Examples**

```python
>>> from scipy.stats import argus
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> chi = 1
>>> mean, var, skew, kurt = argus.stats(chi, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(argus.ppf(0.01, chi), ...
...                   argus.ppf(0.99, chi), 100)
>>> ax.plot(x, argus.pdf(x, chi), ...
...         'r-', lw=5, alpha=0.6, label='argus pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = argus(chi)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = argus.pdf([0.001, 0.5, 0.999], chi)
>>> np.allclose([0.001, 0.5, 0.999], argus.cdf(vals, chi))
True
```

Generate random numbers:
>>> r = argus.rvs(chi, size=1000)

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
## Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rvs(chi, loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, chi, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, chi, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, chi, loc=0, scale=1)</code></td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td><code>logcdf(x, chi, loc=0, scale=1)</code></td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td><code>sf(x, chi, loc=0, scale=1)</code></td>
<td>Survival function (also defined as (1 - \text{cdf}), but <code>sf</code> is sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, chi, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, chi, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of <code>cdf</code> — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, chi, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of <code>sf</code>).</td>
</tr>
<tr>
<td><code>moment(n, chi, loc=0, scale=1)</code></td>
<td>Non-central moment of order <code>n</code>.</td>
</tr>
<tr>
<td><code>stats(chi, loc=0, scale=1, moments='mv')</code></td>
<td>Mean(‘m’), variance(‘v’), skew(‘s’), and/or kurtosis(‘k’).</td>
</tr>
<tr>
<td><code>entropy(chi, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, chi, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, args=(chi,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td><code>median(chi, loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(chi, loc=0, scale=1)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(chi, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(chi, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, chi, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

### scipy.stats.beta

`scipy.stats.beta = <scipy.stats._continuous_distns.beta_gen object>`

A beta continuous random variable.

As an instance of the `rv_continuous` class, `beta` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

#### Notes

The probability density function for `beta` is:

\[
f(x, a, b) = \frac{\Gamma(a + b)x^{a-1}(1-x)^{b-1}}{\Gamma(a)\Gamma(b)}
\]

for \(0 < x < 1, a > 0, b > 0\), where \(\Gamma\) is the gamma function (`scipy.special.gamma`).

`beta` takes `a` and `b` as shape parameters.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `beta.pdf(x, a, b, loc, scale)` is identically equivalent to `beta.pdf(y, a, b) / scale` with `y = (x - loc) / scale`.

#### Examples

```python
>>> from scipy.stats import beta
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```
Calculate a few first moments:

```python
>>> a, b = 2.31, 0.627
>>> mean, var, skew, kurt = beta.stats(a, b, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(beta.ppf(0.01, a, b),
...                 beta.ppf(0.99, a, b), 100)
>>> ax.plot(x, beta.pdf(x, a, b),
...         'r-', lw=5, alpha=0.6, label='beta pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = beta(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = beta.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], beta.cdf(vals, a, b))
True
```

Generate random numbers:

```python
>>> r = beta.rvs(a, b, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

<table>
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<tbody>
<tr>
<td><code>rvs(a, b, loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, a, b, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, a, b, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, a, b, loc=0, scale=1)</code></td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td><code>logcdf(x, a, b, loc=0, scale=1)</code></td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td><code>sf(x, a, b, loc=0, scale=1)</code></td>
<td>Survival function (also defined as (1 - cdf), but <code>sf</code> is sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, a, b, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, a, b, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of <code>cdf</code> — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, a, b, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of <code>sf</code>).</td>
</tr>
<tr>
<td><code>moment(n, a, b, loc=0, scale=1)</code></td>
<td>Non-central moment of order <code>n</code></td>
</tr>
<tr>
<td><code>stats(a, b, loc=0, scale=1, moments='mv')</code></td>
<td>Mean(‘m’), variance(‘v’), skew(‘s’), and/or kurtosis(‘k’).</td>
</tr>
<tr>
<td><code>entropy(a, b, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, a, b, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, args=(a, b), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td><code>median(a, b, loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
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<td><code>mean(a, b, loc=0, scale=1)</code></td>
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</tr>
<tr>
<td><code>std(a, b, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, a, b, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains <code>alpha</code> percent of the distribution.</td>
</tr>
</tbody>
</table>

### scipy.stats.betaprime

**scipy.stats.betaprime = <scipy.stats._continuous_distns.betaprime_gen object>**

A beta prime continuous random variable.

As an instance of the `rv_continuous` class, `betaprime` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `betaprime` is:

\[
f(x, a, b) = \frac{x^{a-1}(1 + x)^{-a-b}}{\beta(a, b)}
\]

for \(x > 0, a > 0, b > 0\), where \(\beta(a, b)\) is the beta function (see `scipy.special.beta`).

`betaprime` takes `a` and `b` as shape parameters.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `betaprime.pdf(x, a, b, loc, scale)` is identically equivalent to `betaprime.pdf(y, a, b) / scale` with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
code
>>> from scipy.stats import betaprime
code
>>> import matplotlib.pyplot as plt
code
>>> fig, ax = plt.subplots(1, 1)
```
Calculate a few first moments:

```python
>>> a, b = 5, 6
>>> mean, var, skew, kurt = betaprime.stats(a, b, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(betaprime.ppf(0.01, a, b),
...                betaprime.ppf(0.99, a, b), 100)
>>> ax.plot(x, betaprime.pdf(x, a, b),
...          'r-', lw=5, alpha=0.6, label='betaprime pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = betaprime(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = betaprime.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], betaprime.cdf(vals, a, b))
```

Generate random numbers:

```python
>>> r = betaprime.rvs(a, b, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
## Methods

<table>
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<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, a, b, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, a, b, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, a, b, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, a, b, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, a, b, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, a, b, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, a, b, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, a, b, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, a, b, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(a, b, loc=0, scale=1, moments='mv')</td>
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</tr>
<tr>
<td>entropy(a, b, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, a, b, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(a, b), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(a, b, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(a, b, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(a, b, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(a, b, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, a, b, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

### scipy.stats.bradford

`scipy.stats.bradford = <scipy.stats._continuous_distns.bradford_gen object>`

A Bradford continuous random variable.

As an instance of the `rv_continuous` class, `bradford` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

#### Notes

The probability density function for `bradford` is:

\[
f(x, c) = \frac{c}{\log(1 + c)(1 + cx)}
\]

for \(0 < x < 1\) and \(c > 0\).

`bradford` takes \(c\) as a shape parameter for \(c\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `bradford.pdf(x, c, loc, scale)` is identically equivalent to `bradford.pdf(y, c) / scale` with \(y = (x - loc) / scale\).

#### Examples

```python
>>> from scipy.stats import bradford
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```
Calculate a few first moments:

```python
>>> c = 0.299
>>> mean, var, skew, kurt = bradford.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(bradford.ppf(0.01, c),
...                   bradford.ppf(0.99, c), 100)
>>> ax.plot(x, bradford.pdf(x, c),
...          'r-', lw=5, alpha=0.6, label='bradford pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = bradford(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = bradford.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], bradford.cdf(vals, c))
True
```

Generate random numbers:

```python
>>> r = bradford.rvs(c, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
## Methods

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rvs(c, loc=0, scale=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, c, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, c, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, c, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, c, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, c, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, c, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, c, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, c, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, c, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(c, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(c, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, c, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(c, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
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<td>mean(c, loc=0, scale=1)</td>
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<tr>
<td>var(c, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(c, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, c, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

### scipy.stats.burr

scipy.stats.burr = <scipy.stats._continuous_distns.burr_gen object>

A Burr (Type III) continuous random variable.

As an instance of the rv_continuous class, burr object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

- **fisk**
  - a special case of either burr or burr12 with d=1

- **burr12**
  - Burr Type XII distribution

### Notes

The probability density function for burr is:

\[
f(x, c, d) = cdx^{-c-1}(1 + x^{-c})^{-d-1}
\]

for \( x > 0 \) and \( c, d > 0 \).

burr takes \( c \) and \( d \) as shape parameters.
This is the PDF corresponding to the third CDF given in Burr’s list; specifically, it is equation (11) in Burr’s paper [1].

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, burr.pdf(x, c, d, loc, scale) is identically equivalent to burr.pdf(y, c, d) / scale with y = (x - loc) / scale.

References
[1]

Examples

```python
>>> from scipy.stats import burr
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> c, d = 10.5, 4.3
>>> mean, var, skew, kurt = burr.stats(c, d, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(burr.ppf(0.01, c, d),
... burr.ppf(0.99, c, d), 100)
>>> ax.plot(x, burr.pdf(x, c, d),
... 'r-', lw=5, alpha=0.6, label='burr pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = burr(c, d)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = burr.ppf([0.001, 0.5, 0.999], c, d)
>>> np.allclose([0.001, 0.5, 0.999], burr.cdf(vals, c, d))
True
```

Generate random numbers:

```python
>>> r = burr.rvs(c, d, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
## Methods

<table>
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<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, c, d, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, c, d, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, c, d, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
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<td>logcdf(x, c, d, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, c, d, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, c, d, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, c, d, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, c, d, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, c, d, loc=0, scale=1)</td>
<td>Non-central moment of order n.</td>
</tr>
<tr>
<td>stats(c, d, loc=0, scale=1, moments='mv')</td>
<td>Mean(‘m’), variance(‘v’), skew(‘s’), and/or kurtosis(‘k’).</td>
</tr>
<tr>
<td>entropy(c, d, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, c, d, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(c, d), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
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<td>median(c, d, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
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<td>Variance of the distribution.</td>
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<tr>
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<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, c, d, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
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</table>

### scipy.stats.burr12

**scipy.stats.burr12**

*scipy.stats.burr12* = *<scipy.stats._continuous_distns.burr12_gen object>*

A Burr (Type XII) continuous random variable.
As an instance of the `rv_continuous` class, `burr12` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**See also:**

- `fisk`  
  a special case of either `burr` or `burr12` with \( d=1 \)
- `burr`  
  Burr Type III distribution

**Notes**

The probability density function for `burr` is:

\[
f(x; c, d) = cd x^{c-1} (1 + x^c)^{-d-1}\]

for \( x > 0 \) and \( c, d > 0 \).

`burr12` takes \( c \) and \( d \) as shape parameters for \( c \) and \( d \).

This is the PDF corresponding to the twelfth CDF given in Burr’s list; specifically, it is equation (20) in Burr’s paper [1].

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `burr12.pdf(x, c, d, loc, scale)` is identically equivalent to `burr12.pdf(y, c, d) / scale` with \( y = (x - \text{loc}) / \text{scale} \).

The Burr type 12 distribution is also sometimes referred to as the Singh-Maddala distribution from NIST [2].

**References**

[1], [2]

**Examples**

```python
>>> from scipy.stats import burr12
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> c, d = 10, 4
>>> mean, var, skew, kurt = burr12.stats(c, d, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(burr12.ppf(0.01, c, d),
...                 burr12.ppf(0.99, c, d), 100)
>>> ax.plot(x, burr12.pdf(x, c, d),
...         'r-', lw=5, alpha=0.6, label='burr12 pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = burr12(c, d)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```
Check accuracy of cdf and ppf:

```python
>>> vals = burr12.ppf([0.001, 0.5, 0.999], c, d)
>>> np.allclose([0.001, 0.5, 0.999], burr12.cdf(vals, c, d))
True
```

Generate random numbers:

```python
>>> r = burr12.rvs(c, d, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

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<td>Random variates.</td>
</tr>
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<td>Probability density function.</td>
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<td>logpdf(x, c, d, loc=0, scale=1)</td>
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<td>cdf(x, c, d, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, c, d, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, c, d, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf; but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, c, d, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, c, d, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
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<tr>
<td>isf(q, c, d, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
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<td>moment(n, c, d, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
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<tr>
<td>stats(c, d, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
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<td>entropy(c, d, loc=0, scale=1)</td>
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<td>fit(data, c, d, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(c, d), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
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<td>median(c, d, loc=0, scale=1)</td>
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<tr>
<td>interval(alpha, c, d, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
</tr>
</tbody>
</table>

**scipy.stats.cauchy**

A Cauchy continuous random variable.

As an instance of the `rv_continuous` class, `cauchy` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `cauchy` is

$$f(x) = \frac{1}{\pi(1 + x^2)}$$

for a real number $x$.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `cauchy.pdf(x, loc, scale)` is identically equivalent to `cauchy.pdf(y) / scale` with $y = (x - loc) / scale$.

**Examples**

```python
>>> from scipy.stats import cauchy
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:
Display the probability density function (pdf):

```python
>>> x = np.linspace(cauchy.ppf(0.01),
...                   cauchy.ppf(0.99), 100)
>>> ax.plot(x, cauchy.pdf(x),
...          'r-', lw=5, alpha=0.6, label='cauchy pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = cauchy()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = cauchy.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], cauchy.cdf(vals))
```

Generate random numbers:

```python
>>> r = cauchy.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

<table>
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<tr>
<td>rvs(loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
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<td>cdf(x, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
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<td>logcdf(x, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
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<td>sf(x, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
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<td>ppf(q, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
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<td>isf(q, loc=0, scale=1)</td>
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<td>moment(n, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
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<td>stats(loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
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<tr>
<td>entropy(loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(loc=0, scale=1)</td>
<td>Median of the distribution.</td>
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<td>interval(alpha, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

**scipy.stats.chi**

`scipy.stats.chi = <scipy.stats._continuous_distns.chi_gen object>`

A chi continuous random variable.

As an instance of the `rv_continuous` class, `chi` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `chi` is:

\[
 f(x, k) = \frac{1}{2^{k/2-1} \Gamma(k/2)} x^{k-1} \exp\left(-x^2/2\right)
\]

for \(x > 0\) and \(k > 0\) (degrees of freedom, denoted `df` in the implementation). \(\Gamma\) is the gamma function (`scipy.special.gamma`).

Special cases of `chi` are:

- `chi(1, loc, scale)` is equivalent to `halfnorm`
- `chi(2, 0, scale)` is equivalent to `rayleigh`
- `chi(3, 0, scale)` is equivalent to `maxwell`

`chi` takes `df` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `chi.pdf(x, df, loc, scale)` is identically
equivalent to `chi.pdf(y, df) / scale` with `y = (x - loc) / scale`.

**Examples**

```python
>>> from scipy.stats import chi
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> df = 78
>>> mean, var, skew, kurt = chi.stats(df, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(chi.ppf(0.01, df), ...
...                 chi.ppf(0.99, df), 100)
>>> ax.plot(x, chi.pdf(x, df), ...
...          'r-', lw=5, alpha=0.6, label='chi pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = chi(df)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

```python
>>> vals = chi.ppf([0.001, 0.5, 0.999], df)
>>> np.allclose([0.001, 0.5, 0.999], chi.cdf(vals, df))
```

Generate random numbers:

```python
>>> r = chi.rvs(df, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', alpha=0.2)
>>> plt.show()
```
Methods

<table>
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<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, df, loc=0, scale=1)</td>
<td>Probability density function.</td>
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</tr>
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<td>sf(x, df, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
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<td>ppf(q, df, loc=0, scale=1)</td>
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<td>entropy(df, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
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<tr>
<td>fit(data, df, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(df,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(df, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
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<td>std(df, loc=0, scale=1)</td>
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<tr>
<td>interval(alpha, df, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
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</table>

scipy.stats.chi2

scipy.stats.chi2 = <scipy.stats._continuous_distns.chi2_gen object>

A chi-squared continuous random variable.
As an instance of the `rv_continuous` class, `chi2` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `chi2` is:

\[ f(x, k) = \frac{1}{2^{k/2} \Gamma(k/2)} x^{k/2 - 1} \exp(-x/2) \]

for \( x > 0 \) and \( k > 0 \) (degrees of freedom, denoted \( df \) in the implementation).

`chi2` takes \( df \) as a shape parameter.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the \( \text{loc} \) and \( \text{scale} \) parameters. Specifically, \( \text{chi2.pdf}(x, df, \text{loc}, \text{scale}) \) is identically equivalent to \( \text{chi2.pdf}(y, df) / \text{scale} \) with \( y = (x - \text{loc}) / \text{scale} \).

**Examples**
```python
>>> from scipy.stats import chi2
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:
```n
>>> df = 55
>>> mean, var, skew, kurt = chi2.stats(df, moments='mvsk')

Display the probability density function (pdf):
```n
>>> x = np.linspace(chi2.ppf(0.01, df), chi2.ppf(0.99, df), 100)
>>> ax.plot(x, chi2.pdf(x, df), 'r-', lw=5, alpha=0.6, label='chi2 pdf')

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:
```n
>>> rv = chi2(df)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')

Check accuracy of cdf and ppf:
```n
>>> vals = chi2.ppf([0.001, 0.5, 0.999], df)
>>> np.allclose([0.001, 0.5, 0.999], chi2.cdf(vals, df))
```

Generate random numbers:
```n
>>> r = chi2.rvs(df, size=1000)

And compare the histogram:
```n
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
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<tr>
<td>pdf(x, df, loc=0, scale=1)</td>
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<td>logsf(x, df, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, df, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, df, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, df, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(df, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(df, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, df, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(df,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(df, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(df, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(df, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(df, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, df, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

`scipy.stats.cosine`

`scipy.stats.cosine = <scipy.stats._continuous_distns.cosine_gen object>`

A cosine continuous random variable.
As an instance of the \texttt{rv\_continuous} class, \texttt{cosine} object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The cosine distribution is an approximation to the normal distribution. The probability density function for \texttt{cosine} is:

\[
f(x) = \frac{1}{2\pi}(1 + \cos(x))
\]

for \(-\pi \leq x \leq \pi\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the \texttt{loc} and \texttt{scale} parameters. Specifically, \texttt{cosine.pdf(x, loc, scale)} is identically equivalent to \texttt{cosine.pdf(y) / scale} with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
>>> from scipy.stats import cosine
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> mean, var, skew, kurt = cosine.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(cosine.ppf(0.01),
...                 cosine.ppf(0.99), 100)
>>> ax.plot(x, cosine.pdf(x),
...         'r-', lw=5, alpha=0.6, label='cosine pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = cosine()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = cosine.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], cosine.cdf(vals))
True
```

Generate random numbers:

```python
>>> r = cosine.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### scipy.stats.crystalball

```python
scipy.stats.crystalball = <scipy.stats._continuous_distns.crystalball_gen object>
```

Crystalball distribution
As an instance of the `rv_continuous` class, `crystalball` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `crystalball` is:

\[
f(x, \beta, m) = \begin{cases} 
N \exp(-x^2/2), & \text{for } x > -\beta \\
NA(B - x)^{-m} & \text{for } x \leq -\beta 
\end{cases}
\]

where \( A = (m/|\beta|)^n \exp(-\beta^2/2) \), \( B = m/|\beta| - |\beta| \) and \( N \) is a normalisation constant.

`crystalball` takes \( \beta > 0 \) and \( m > 1 \) as shape parameters. \( \beta \) defines the point where the pdf changes from a power-law to a Gaussian distribution. \( m \) is the power of the power-law tail.

**References**
The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `crystalball.pdf(x, beta, m, loc, scale)` is identically equivalent to `crystalball.pdf(y, beta, m) / scale` with \( y = (x - \text{loc}) / \text{scale} \).

New in version 0.19.0.

[1]

**Examples**
```python
>>> from scipy.stats import crystalball
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> beta, m = 2, 3
>>> mean, var, skew, kurt = crystalball.stats(beta, m, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(crystalball.ppf(0.01, beta, m),...
...                  crystalball.ppf(0.99, beta, m), 100)
>>> ax.plot(x, crystalball.pdf(x, beta, m),...
...          'r-', lw=5, alpha=0.6, label='crystalball pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = crystalball(beta, m)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = crystalball.ppf([0.001, 0.5, 0.999], beta, m)
>>> np.allclose([0.001, 0.5, 0.999], crystalball.cdf(vals, beta, m))
True
```

Generate random numbers:
```python
>>> r = crystalball.rvs(beta, m, size=1000)

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rvs(beta, m, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, beta, m, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, beta, m, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, beta, m, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, beta, m, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, beta, m, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, beta, m, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, beta, m, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, beta, m, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, beta, m, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(beta, m, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
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<tr>
<td>entropy(beta, m, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, beta, m, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(beta, m), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
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<tr>
<td>median(beta, m, loc=0, scale=1)</td>
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<td>mean(beta, m, loc=0, scale=1)</td>
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<td>var(beta, m, loc=0, scale=1)</td>
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<tr>
<td>std(beta, m, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, beta, m, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

**scipy.stats.dgamma**

A double gamma continuous random variable.

As an instance of the `rv_continuous` class, `dgamma` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `dgamma` is:

\[
f(x,a) = \frac{1}{2\Gamma(a)} |x|^{a-1} \exp(-|x|)
\]

for a real number \(x\) and \(a > 0\). \(\Gamma\) is the gamma function (`scipy.special.gamma`).

`dgamma` takes \(a\) as a shape parameter for \(a\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `dgamma.pdf(x, a, loc, scale)` is identically equivalent to `dgamma.pdf(y, a) / scale` with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
>>> from scipy.stats import dgamma
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```
Calculate a few first moments:

```python
>>> a = 1.1
>>> mean, var, skew, kurt = dgamma.stats(a, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(dgamma.ppf(0.01, a), dgamma.ppf(0.99, a), 100)
>>> ax.plot(x, dgamma.pdf(x, a), 'r-', lw=5, alpha=0.6, label='dgamma pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = dgamma(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = dgamma.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], dgamma.cdf(vals, a))
True
```

Generate random numbers:

```python
>>> r = dgamma.rvs(a, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

<table>
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<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, a, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, a, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, a, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, a, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, a, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, a, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, a, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, a, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, a, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(a, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(a, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, a, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(a,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(a, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
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<td>mean(a, loc=0, scale=1)</td>
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<td>var(a, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(a, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, a, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

scipy.stats.dweibull

scipy.stats.dweibull = <scipy.stats._continuous_distns.dweibull_gen object>

A double Weibull continuous random variable.

As an instance of the rv_continuous class, dweibull object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes
The probability density function for dweibull is given by

\[ f(x, c) = \frac{c}{2}x^{c-1}\exp(-|x|^c) \]

for a real number \( x \) and \( c > 0 \).

dweibull takes \( c \) as a shape parameter for \( c \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, dweibull.pdf(\( x, c, loc, scale \)) is identically equivalent to dweibull.pdf(\( y, c \)) / scale with \( y = (x - loc) / scale \).

Examples

```python
>>> from scipy.stats import dweibull
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```
Calculate a few first moments:

```python
>>> c = 2.07
>>> mean, var, skew, kurt = dweibull.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(dweibull.ppf(0.01, c), ...
... dweibull.ppf(0.99, c), 100)
>>> ax.plot(x, dweibull.pdf(x, c), ...
... 'r-', lw=5, alpha=0.6, label='dweibull pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = dweibull(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = dweibull.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], dweibull.cdf(vals, c))
True
```

Generate random numbers:

```python
>>> r = dweibull.rvs(c, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

<table>
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<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rvs(c, loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, c, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, c, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
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<tr>
<td><code>cdf(x, c, loc=0, scale=1)</code></td>
<td>Cumulative distribution function.</td>
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<tr>
<td><code>logcdf(x, c, loc=0, scale=1)</code></td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td><code>sf(x, c, loc=0, scale=1)</code></td>
<td>Survival function (also defined as $1 - cdf$, but $sf$ is sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, c, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, c, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of $cdf$ — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, c, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of $sf$).</td>
</tr>
<tr>
<td><code>moment(n, c, loc=0, scale=1)</code></td>
<td>Non-central moment of order $n$.</td>
</tr>
<tr>
<td><code>stats(c, loc=0, scale=1, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy(c, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, c, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td><code>median(c, loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(c, loc=0, scale=1)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(c, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(c, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, c, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
</tr>
</tbody>
</table>

### scipy.stats.erlang

**scipy.stats.erlang**

`scipy.stats.erlang = <scipy.stats._continuous_distns.erlang_gen object>`

An Erlang continuous random variable.

As an instance of the `rv_continuous` class, `erlang` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**See also:**

`gamma`

**Notes**

The Erlang distribution is a special case of the Gamma distribution, with the shape parameter $a$ an integer. Note that this restriction is not enforced by `erlang`. It will, however, generate a warning the first time a non-integer value is used for the shape parameter.

Refer to `gamma` for examples.
Methods

<table>
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</thead>
<tbody>
<tr>
<td><code>rvs(a, loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, a, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, a, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, a, loc=0, scale=1)</code></td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td><code>logcdf(x, a, loc=0, scale=1)</code></td>
<td>Log of the cumulative distribution function.</td>
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<td><code>sf(x, a, loc=0, scale=1)</code></td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
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<td><code>logsf(x, a, loc=0, scale=1)</code></td>
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<tr>
<td><code>ppf(q, a, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, a, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>moment(n, a, loc=0, scale=1)</code></td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td><code>stats(a, loc=0, scale=1, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
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<td><code>entropy(a, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
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<td><code>fit(data, a, loc=0, scale=1)</code></td>
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<td><code>var(a, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
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<tr>
<td><code>std(a, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, a, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

scipy.stats.expon

`scipy.stats.expon = <scipy.stats._continuous_distns.expon_gen object>`

An exponential continuous random variable.

As an instance of the `rv_continuous` class, `expon` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `expon` is:

\[ f(x) = \exp(-x) \]

for \( x \geq 0 \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `expon.pdf(x, loc, scale)` is identically equivalent to `expon.pdf(y) / scale` with \( y = (x - loc) / scale \).

A common parameterization for `expon` is in terms of the rate parameter `lambda`, such that `pdf = lambda * exp(-lambda * x)`. This parameterization corresponds to using `scale = 1 / lambda`.

Examples

```python
>>> from scipy.stats import expon
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```
Calculate a few first moments:

```python
>>> mean, var, skew, kurt = expon.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(expon.ppf(0.01),
...                   expon.ppf(0.99), 100)
>>> ax.plot(x, expon.pdf(x),
...          'r-', lw=5, alpha=0.6, label='expon pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = expon()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = expon.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], expon.cdf(vals))
```

Generate random numbers:

```python
>>> r = expon.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

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</tr>
<tr>
<td>pdf(x, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
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<tr>
<td>var(loc=0, scale=1)</td>
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</tr>
<tr>
<td>std(loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

scipy.stats.exponnorm

scipy.stats.exponnorm = <scipy.stats._continuous_distns.exponnorm_gen object>

An exponentially modified Normal continuous random variable.

As an instance of the rv_continuous class, exponnorm object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for exponnorm is:

\[
f(x, K) = \frac{1}{2K} \exp \left( -\frac{1}{2K^2} - \frac{x}{K} \right) \text{erfc} \left( -\frac{x - 1/K}{\sqrt{2}} \right)
\]

where \( x \) is a real number and \( K > 0 \).

It can be thought of as the sum of a standard normal random variable and an independent exponentially distributed random variable with rate \( 1/K \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, \( \text{exponnorm.pdf}(x, K, \text{loc}, \text{scale}) \) is identically equivalent to \( \text{exponnorm.pdf}(y, K) / \text{scale} \) with \( y = (x - \text{loc}) / \text{scale} \).

An alternative parameterization of this distribution (for example, in Wikipedia) involves three parameters, \( \mu \), \( \lambda \) and \( \sigma \). In the present parameterization this corresponds to having \( \text{loc} \) and \( \text{scale} \) equal to \( \mu \) and \( \sigma \), respectively, and shape parameter \( K = \frac{1}{\sigma \lambda} \).
New in version 0.16.0.

Examples

```python
>>> from scipy.stats import exponnorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> K = 1.5
>>> mean, var, skew, kurt = exponnorm.stats(K, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(exponnorm.ppf(0.01, K), ...
...                 exponnorm.ppf(0.99, K), 100)
>>> ax.plot(x, exponnorm.pdf(x, K), ...
...          'r-', lw=5, alpha=0.6, label='exponnorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = exponnorm(K)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = exponnorm.ppf([0.001, 0.5, 0.999], K)
>>> np.allclose([0.001, 0.5, 0.999], exponnorm.cdf(vals, K))
True
```

Generate random numbers:

```python
>>> r = exponnorm.rvs(K, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', alpha=0.2)
>>> plt.show()
```
## Methods

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<tbody>
<tr>
<td>rvs(K, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, K, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, K, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, K, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, K, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, K, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, K, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, K, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, K, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, K, loc=0, scale=1)</td>
<td>Non-central moment of order n.</td>
</tr>
<tr>
<td>stats(K, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(K, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, K, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(K,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(K, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(K, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(K, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(K, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, K, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

```python
scipy.stats.exponweib
```

An exponentiated Weibull continuous random variable.
As an instance of the \texttt{rv_continuous} class, \texttt{exponweib} object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

\textbf{Notes}

The probability density function for \texttt{exponweib} is:

\[
f(x,a,c) = ac(1 - \exp(-x^c))^{a-1}\exp(-x^c)x^{c-1}
\]

for \(x > 0, \ a > 0, \ c > 0\).

\texttt{exponweib} takes \(a\) and \(c\) as shape parameters.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the \texttt{loc} and \texttt{scale} parameters. Specifically, \texttt{exponweib.pdf}(x, a, c, loc, scale) is identically equivalent to \texttt{exponweib.pdf}(y, a, c) / scale with \(y = (x - \text{loc}) / \text{scale}\).

\textbf{Examples}

```python
>>> from scipy.stats import exponweib
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> a, c = 2.89, 1.95
>>> mean, var, skew, kurt = exponweib.stats(a, c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(exponweib.ppf(0.01, a, c),
                     ...                   exponweib.ppf(0.99, a, c), 100)
>>> ax.plot(x, exponweib.pdf(x, a, c),
                     ...                   'r-', lw=5, alpha=0.6, label='exponweib pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = exponweib(a, c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = exponweib.ppf([0.001, 0.5, 0.999], a, c)
>>> np.allclose([0.001, 0.5, 0.999], exponweib.cdf(vals, a, c))
True
```

Generate random numbers:

```python
>>> r = exponweib.rvs(a, c, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

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<td>rvs(a, c, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, a, c, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, a, c, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
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<tr>
<td>cdf(x, a, c, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, a, c, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
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<tr>
<td>sf(x, a, c, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
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<td>ppf(q, a, c, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, a, c, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, a, c, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(a, c, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(a, c, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, a, c, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(a, c), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(a, c, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(a, c, loc=0, scale=1)</td>
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<tr>
<td>var(a, c, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
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<tr>
<td>std(a, c, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, a, c, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

**scipy.stats.exponpow**

```python
scipy.stats.exponpow = <scipy.stats._continuous_distns.exponpow_gen object>
```

An exponential power continuous random variable.
As an instance of the `rv_continuous` class, `exponpow` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `exponpow` is:

\[ f(x, b) = bx^{b-1}\exp(1 + x^b - \exp(x^b)) \]

for \( x \geq 0, b > 0 \). Note that this is a different distribution from the exponential power distribution that is also known under the names “generalized normal” or “generalized Gaussian”.

`exponpow` takes \( b \) as a shape parameter for \( b \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `exponpow.pdf(x, b, loc, scale)` is identically equivalent to `exponpow.pdf(y, b) / scale` with \( y = (x - loc) / scale \).

**References**

http://www.math.wm.edu/~leemis/chart/UDR/PDFs/Exponentialpower.pdf

**Examples**

```python
>>> from scipy.stats import exponpow
>>> import matplotlib.pyplot as plt

>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> b = 2.7
>>> mean, var, skew, kurt = exponpow.stats(b, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(exponpow.ppf(0.01, b),
                  exponpow.ppf(0.99, b), 100)
>>> ax.plot(x, exponpow.pdf(x, b),
          'r-', lw=5, alpha=0.6, label='exponpow pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = exponpow(b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = exponpow.ppf([0.001, 0.5, 0.999], b)
>>> np.allclose([0.001, 0.5, 0.999], exponpow.cdf(vals, b))
```

Generate random numbers:

```python
>>> r = exponpow.rvs(b, size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Methods

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<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, b, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, b, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
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<tr>
<td><code>cdf(x, b, loc=0, scale=1)</code></td>
<td>Cumulative distribution function.</td>
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<td><code>logcdf(x, b, loc=0, scale=1)</code></td>
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<tr>
<td><code>sf(x, b, loc=0, scale=1)</code></td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
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<td><code>logsf(x, b, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
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<tr>
<td><code>ppf(q, b, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, b, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>moment(n, b, loc=0, scale=1)</code></td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td><code>stats(b, loc=0, scale=1, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy(b, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, b, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, args=(b,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td><code>median(b, loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(b, loc=0, scale=1)</code></td>
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<td><code>var(b, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(b, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, b, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
</tr>
</tbody>
</table>
scipy.stats.f

scipy.stats.f = <scipy.stats._continuous_distns.f_gen object>

An F continuous random variable.

As an instance of the `rv_continuous` class, `f` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `f` is:

\[
    f(x, df_1, df_2) = \frac{df_2^{df_2/2} df_1^{df_1/2} x^{df_1/2-1}}{(df_2 + df_1 x)^{(df_1 + df_2)/2} B(df_1/2, df_2/2)}
\]

for \( x > 0 \).

`f` takes `dfn` and `dfd` as shape parameters.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `f.pdf(x, dfn, dfd, loc, scale)` is identically equivalent to `f.pdf(y, dfn, dfd) / scale` with `y = (x - loc) / scale`.

**Examples**

```python
>>> from scipy.stats import f
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> dfn, dfd = 29, 18
>>> mean, var, skew, kurt = f.stats(dfn, dfd, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(f.ppf(0.01, dfn, dfd), ...
...                  f.ppf(0.99, dfn, dfd), 100)
>>> ax.plot(x, f.pdf(x, dfn, dfd), '
...              r-', lw=5, alpha=0.6, label='f pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = f(dfn, dfd)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = f.ppf([0.001, 0.5, 0.999], dfn, dfd)
>>> np.allclose([0.001, 0.5, 0.999], f.cdf(vals, dfn, dfd))
True
```

Generate random numbers:

```python
>>> r = f.rvs(dfn, dfd, size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Histogram with probability density function](image)

**Methods**

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</thead>
<tbody>
<tr>
<td><code>rvs(dfn, dfd, loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, dfn, dfd, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, dfn, dfd, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, dfn, dfd, loc=0, scale=1)</code></td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td><code>logcdf(x, dfn, dfd, loc=0, scale=1)</code></td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td><code>sf(x, dfn, dfd, loc=0, scale=1)</code></td>
<td>Survival function (also defined as (1 - \text{cdf}), but (sf) is sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, dfn, dfd, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, dfn, dfd, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of (\text{cdf}) — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, dfn, dfd, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of (sf)).</td>
</tr>
<tr>
<td><code>moment(n, dfn, dfd, loc=0, scale=1)</code></td>
<td>Non-central moment of order (n)</td>
</tr>
<tr>
<td><code>stats(dfn, dfd, loc=0, scale=1, moments='mv')</code></td>
<td>Mean('(m)'), variance('(v)'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy(dfn, dfd, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, dfn, dfd, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, args=(dfn, dfd), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td><code>median(dfn, dfd, loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
</tr>
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<td><code>mean(dfn, dfd, loc=0, scale=1)</code></td>
<td>Mean of the distribution.</td>
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<td><code>var(dfn, dfd, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
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<tr>
<td><code>std(dfn, dfd, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, dfn, dfd, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>
scipy.stats.fatiguelife

scipy.stats.fatiguelife = <scipy.stats._continuous_distns.fatiguelife_gen object>
A fatigue-life (Birnbaum-Saunders) continuous random variable.

As an instance of the rv_continuous class, fatiguelife object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes
The probability density function for fatiguelife is:

\[ f(x, c) = \frac{x + 1}{2c \sqrt{2\pi x^3}} \exp\left(-\frac{(x - 1)^2}{2xc^2}\right) \]

for \( x > 0 \) and \( c > 0 \).

fatiguelife takes \( c \) as a shape parameter for \( c \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, fatiguelife.pdf(x, c, loc, scale) is identically equivalent to fatiguelife.pdf(y, c) / scale with \( y = (x - \text{loc}) / \text{scale} \).

References
[1]

Examples

```python
>>> from scipy.stats import fatiguelife
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> c = 29
>>> mean, var, skew, kurt = fatiguelife.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(fatiguelife.ppf(0.01, c), ...
...                   fatiguelife.ppf(0.99, c), 100)
>>> ax.plot(x, fatiguelife.pdf(x, c), ...
...         'r-', lw=5, alpha=0.6, label='fatiguelife pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = fatiguelife(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = fatiguelife.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], fatiguelife.cdf(vals, c))
```

Generate random numbers:
```python
>>> r = fatiguelife.rvs(c, size=1000)
And compare the histogram:
```
Methods

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
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<tr>
<td>rvs(c, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, c, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, c, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, c, loc=0, scale=1)</td>
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<td>logcdf(x, c, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
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<tr>
<td>sf(x, c, loc=0, scale=1)</td>
<td>Survival function (also defined as (1 - cdf), but (sf) is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, c, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, c, loc=0, scale=1)</td>
<td>Percent point function (inverse of (cdf) — percentiles).</td>
</tr>
<tr>
<td>isf(q, c, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of (sf)).</td>
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<td>moment(n, c, loc=0, scale=1)</td>
<td>Non-central moment of order (n)</td>
</tr>
<tr>
<td>stats(c, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(c, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, c, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
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<tr>
<td>median(c, loc=0, scale=1)</td>
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<td>mean(c, loc=0, scale=1)</td>
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<td>var(c, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(c, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, c, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
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</table>

**scipy.stats.fisk**

*scipy.stats.fisk = <scipy.stats._continuous_distns.fisk_gen object>*

A Fisk continuous random variable.

The Fisk distribution is also known as the log-logistic distribution.

As an instance of the `rv_continuous` class, `fisk` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**See also:**

`burr`

**Notes**

The probability density function for `fisk` is:

\[
f(x, c) = cx^{-c-1}(1 + x^{-c})^{-2}
\]

for \(x > 0\) and \(c > 0\).

`fisk` takes \(c\) as a shape parameter for \(c\).

`fisk` is a special case of `burr` or `burr12` with \(d=1\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `fisk.pdf(x, c, loc, scale)` is identically equivalent to `fisk.pdf(y, c) / scale` with \(y = (x - loc) / scale\).
Examples

```python
>>> from scipy.stats import fisk
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> c = 3.09
>>> mean, var, skew, kurt = fisk.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(fisk.ppf(0.01, c),
...                  fisk.ppf(0.99, c), 100)
>>> ax.plot(x, fisk.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='fisk pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = fisk(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = fisk.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], fisk.cdf(vals, c))
True
```

Generate random numbers:

```python
>>> r = fisk.rvs(c, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

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<td>Random variates.</td>
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<td><code>logcdf(x, c, loc=0, scale=1)</code></td>
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<td><code>sf(x, c, loc=0, scale=1)</code></td>
<td>Survival function (also defined as $1 - \text{cdf}$, but $sf$ is sometimes more accurate).</td>
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<tr>
<td><code>logsf(x, c, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, c, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of <code>cdf</code> — percentiles).</td>
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<td>Inverse survival function (inverse of $sf$).</td>
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<td><code>moment(n, c, loc=0, scale=1)</code></td>
<td>Non-central moment of order $n$</td>
</tr>
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<td><code>stats(c, loc=0, scale=1, moments='mv')</code></td>
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**scipy.stats.foldcauchy**

`scipy.stats.foldcauchy = <scipy.stats._continuous_distns.foldcauchy_gen object>`

A folded Cauchy continuous random variable.
As an instance of the \texttt{rv\_continuous} class, \texttt{foldcauchy} object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

\textbf{Notes}

The probability density function for \texttt{foldcauchy} is:

$$f(x,c) = \frac{1}{\pi(1 + (x - c)^2)} + \frac{1}{\pi(1 + (x + c)^2)}$$

for $x \geq 0$.

\texttt{foldcauchy} takes $c$ as a shape parameter for $c$.

\textbf{Examples}

```python
>>> from scipy.stats import foldcauchy
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> c = 4.72
>>> mean, var, skew, kurt = foldcauchy.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(foldcauchy.ppf(0.01, c), ...
... foldcauchy.ppf(0.99, c), 100)
>>> ax.plot(x, foldcauchy.pdf(x, c), ...
... 'r-', lw=5, alpha=0.6, label='foldcauchy pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = foldcauchy(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = foldcauchy.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], foldcauchy.cdf(vals, c))
```

Generate random numbers:

```python
>>> r = foldcauchy.rvs(c, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

<table>
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<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, c, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
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<td>logcdf(x, c, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
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<tr>
<td>sf(x, c, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
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<td>logsf(x, c, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, c, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, c, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, c, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(c, loc=0, scale=1, moments='mv')</td>
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<tr>
<td>entropy(c, loc=0, scale=1)</td>
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</tr>
<tr>
<td>interval(alpha, c, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

scipy.stats.foldnorm

scipy.stats.foldnorm = <scipy.stats._continuous_distns.foldnorm_gen object>  
A folded normal continuous random variable.

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As an instance of the `rv_continuous` class, `foldnorm` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `foldnorm` is:

\[
    f(x, c) = \sqrt{\frac{2}{\pi \cosh(cx)}} \exp(-\frac{x^2 + c^2}{2})
\]

for \(c \geq 0\).

`foldnorm` takes \(c\) as a shape parameter for \(c\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `foldnorm.pdf(x, c, loc, scale)` is identically equivalent to `foldnorm.pdf(y, c) / scale` with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**
```python
>>> from scipy.stats import foldnorm
>>> import matplotlib.pyplot as plt

>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:
```n
c = 1.95
>>> mean, var, skew, kurt = foldnorm.stats(c, moments='mvsk')

Display the probability density function (pdf):
```n
>>> x = np.linspace(foldnorm.ppf(0.01, c), ...
... foldnorm.ppf(0.99, c), 100)
>>> ax.plot(x, foldnorm.pdf(x, c), 'r-', lw=5, alpha=0.6, label='foldnorm pdf')

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:
```n
```n
Check accuracy of cdf and ppf:
```n
Generate random numbers:
```n
And compare the histogram:
```n
Methods

- `rvs(c, loc=0, scale=1, size=1, random_state=None)`
  - Random variates.
- `pdf(x, c, loc=0, scale=1)`
  - Probability density function.
- `logpdf(x, c, loc=0, scale=1)`
  - Log of the probability density function.
- `cdf(x, c, loc=0, scale=1)`
  - Cumulative distribution function.
- `logcdf(x, c, loc=0, scale=1)`
  - Log of the cumulative distribution function.
- `sf(x, c, loc=0, scale=1)`
  - Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).
- `logsf(x, c, loc=0, scale=1)`
  - Log of the survival function.
- `ppf(q, c, loc=0, scale=1)`
  - Percent point function (inverse of cdf — percentiles).
- `isf(q, c, loc=0, scale=1)`
  - Inverse survival function (inverse of sf).
- `moment(n, c, loc=0, scale=1)`
  - Non-central moment of order n
- `stats(c, loc=0, scale=1, moments='mv')`
  - Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
- `entropy(c, loc=0, scale=1)`
  - (Differential) entropy of the RV.
- `fit(data, c, loc=0, scale=1)`
  - Parameter estimates for generic data.
- `expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`
  - Expected value of a function (of one argument) with respect to the distribution.
- `median(c, loc=0, scale=1)`
  - Median of the distribution.
- `mean(c, loc=0, scale=1)`
  - Mean of the distribution.
- `var(c, loc=0, scale=1)`
  - Variance of the distribution.
- `std(c, loc=0, scale=1)`
  - Standard deviation of the distribution.
- `interval(alpha, c, loc=0, scale=1)`
  - Endpoints of the range that contains alpha percent of the distribution.

`scipy.stats.frechet_r`

`scipy.stats.frechet_r = <scipy.stats._continuous_distns.frechet_r_gen object>`

A frechet_r continuous random variable.
As an instance of the `rv_continuous` class, `frechet_r` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Examples**

```python
>>> from scipy.stats import frechet_r
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> c =
>>> mean, var, skew, kurt = frechet_r.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(frechet_r.ppf(0.01, c),
...                 frechet_r.ppf(0.99, c), 100)
>>> ax.plot(x, frechet_r.pdf(x, c),
...          'r-', lw=5, alpha=0.6, label='frechet_r pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = frechet_r(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = frechet_r.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], frechet_r.cdf(vals, c))
True
```

Generate random numbers:

```python
>>> r = frechet_r.rvs(c, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

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<tr>
<td><code>stats(c, loc=0, scale=1, moments='mvsk')</code></td>
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<td><code>interval(alpha, c, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains <code>alpha</code> percent of the distribution</td>
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</table>

### scipy.stats.frechet_l

`scipy.stats.frechet_l = <scipy.stats._continuous_distns.frechet_l_gen object>`

A frechet_l continuous random variable.

As an instance of the `rv_continuous` class, `frechet_l` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Examples**

```python
>>> from scipy.stats import frechet_l
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> c = ...
>>> mean, var, skew, kurt = frechet_l.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(frechet_l.ppf(0.01, c), ...
                           frechet_l.ppf(0.99, c), 100)
>>> ax.plot(x, frechet_l.pdf(x, c),
```

(continues on next page)
Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = frechet_l(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=5, alpha=0.6, label='frechet_l pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = frechet_l.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], frechet_l.cdf(vals, c))
True
```

Generate random numbers:

```python
>>> r = frechet_l.rvs(c, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

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### scipy.stats.genlogistic

**scipy.stats.genlogistic** = \(<\text{scipy.stats._continuous_distns.genlogistic_gen object}\> 

A generalized logistic continuous random variable.

As an instance of the \text{rv_continuous} class, \text{genlogistic} object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for \text{genlogistic} is:

\[
f(x, c) = c \frac{\exp(-x)}{(1 + \exp(-x))^{c+1}}
\]

for \(x > 0, c > 0\).

\text{genlogistic} takes \(c\) as a shape parameter for \(c\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the \text{loc} and \text{scale} parameters. Specifically, \text{genlogistic.pdf}(x, c, loc, scale) is identically equivalent to \text{genlogistic.pdf}(y, c) / scale with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
>>> from scipy.stats import genlogistic
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```
Calculate a few first moments:

```python
>>> c = 0.412
>>> mean, var, skew, kurt = genlogistic.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(genlogistic.ppf(0.01, c),
...                  genlogistic.ppf(0.99, c), 100)
>>> ax.plot(x, genlogistic.pdf(x, c),
...          'r-', lw=5, alpha=0.6, label='genlogistic pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = genlogistic(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = genlogistic.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], genlogistic.cdf(vals, c))
True
```

Generate random numbers:

```python
>>> r = genlogistic.rvs(c, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

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**scipy.stats.gennorm**

`scipy.stats.gennorm = <scipy.stats._continuous_distns.gennorm_gen object>`  
A generalized normal continuous random variable.

As an instance of the `rv_continuous` class, `gennorm` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**See also:**

- `laplace`
  - Laplace distribution
- `norm`
  - normal distribution

**Notes**

The probability density function for `gennorm` is [1]:

\[ f(x; \beta) = \frac{\beta}{2\Gamma(1/\beta)} \exp(-|x|^\beta) \]

\( \Gamma \) is the gamma function (`scipy.special.gamma`).
`gennorm` takes `beta` as a shape parameter for $\beta$. For $\beta = 1$, it is identical to a Laplace distribution. For $\beta = 2$, it is identical to a normal distribution (with `scale=1/sqrt(2)`).

**References**

[1]

**Examples**

```python
>>> from scipy.stats import gennorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> beta = 1.3
>>> mean, var, skew, kurt = gennorm.stats(beta, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(gennorm.ppf(0.01, beta),
...                  gennorm.ppf(0.99, beta), 100)
>>> ax.plot(x, gennorm.pdf(x, beta),
...         'r-', lw=5, alpha=0.6, label='gennorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = gennorm(beta)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = gennorm.ppf([0.001, 0.5, 0.999], beta)
>>> np.allclose([0.001, 0.5, 0.999], gennorm.cdf(vals, beta))
True
```

Generate random numbers:

```python
>>> r = gennorm.rvs(beta, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
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<td><code>pdf(x, beta, loc=0, scale=1)</code></td>
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#### scipy.stats.genpareto

`scipy.stats.genpareto = <scipy.stats._continuous_distns.genpareto_gen object>`

A generalized Pareto continuous random variable.
As an instance of the \texttt{rv\_continuous} class, \texttt{genpareto} object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

\textbf{Notes}

The probability density function for \texttt{genpareto} is:

\[
f(x, c) = (1 + cx)^{-1 - 1/c}
\]

defined for \( x \geq 0 \) if \( c \geq 0 \), and for \( 0 \leq x \leq -1/c \) if \( c < 0 \).

\texttt{genpareto} takes \( c \) as a shape parameter for \( c \).

For \( c = 0 \), \texttt{genpareto} reduces to the exponential distribution, \texttt{expon}:

\[
f(x, 0) = \exp(-x)
\]

For \( c = -1 \), \texttt{genpareto} is uniform on \([0, 1] \):

\[
f(x, -1) = 1
\]

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the \texttt{loc} and \texttt{scale} parameters. Specifically, \texttt{genpareto.pdf}(\( x, c, \texttt{loc}, \texttt{scale} \)) is identically equivalent to \texttt{genpareto.pdf}(\( y, c \)) / \texttt{scale} with \( y = (x - \texttt{loc}) / \texttt{scale} \).

\textbf{Examples}

```python
>>> from scipy.stats import genpareto
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> c = 0.1
>>> mean, var, skew, kurt = genpareto.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(genpareto.ppf(0.01, c),
...                   genpareto.ppf(0.99, c), 100)
>>> ax.plot(x, genpareto.pdf(x, c),
...          'r-', lw=5, alpha=0.6, label='genpareto pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = genpareto(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of \texttt{cdf} and \texttt{ppf}:

```python
>>> vals = genpareto.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], genpareto.cdf(vals, c))
True
```

Generate random numbers:
```python
>>> r = genpareto.rvs(c, size=1000)

And compare the histogram:
```
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<tr>
<td><code>interval(alpha, c, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

**scipy.stats.genexpon**

`scipy.stats.genexpon = <scipy.stats._continuous_distns.genexpon_gen object>`

A generalized exponential continuous random variable.

As an instance of the `rv_continuous` class, `genexpon` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `genexpon` is:

$$f(x, a, b, c) = \left(a + b(1 - \exp(-cx))\right) \exp(-ax - bx + \frac{b}{c}(1 - \exp(-cx)))$$

for \( x \geq 0, \ a, b, c > 0 \).

`genexpon` takes \( a, b \) and \( c \) as shape parameters.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `genexpon.pdf(x, a, b, c, loc, scale)` is identically equivalent to `genexpon.pdf(y, a, b, c) / scale` with \( y = (x - \text{loc}) / \text{scale} \).

**References**


Examples

```python
>>> from scipy.stats import genexpon
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> a, b, c = 9.13, 16.2, 3.28
>>> mean, var, skew, kurt = genexpon.stats(a, b, c, moments='mvsk')
```

Display the probability density function (pdf):

```
>>> x = np.linspace(genexpon.ppf(0.01, a, b, c), ...
>>>                      genexpon.ppf(0.99, a, b, c), 100)
>>> ax.plot(x, genexpon.pdf(x, a, b, c), ...
>>>                      'r-', lw=5, alpha=0.6, label='genexpon pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```
>>> rv = genexpon(a, b, c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```
>>> vals = genexpon.ppf([0.001, 0.5, 0.999], a, b, c)
>>> np.allclose([0.001, 0.5, 0.999], genexpon.cdf(vals, a, b, c))
True
```

Generate random numbers:

```
>>> r = genexpon.rvs(a, b, c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

<table>
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<tbody>
<tr>
<td>rvs(a, b, c, loc=0, scale=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, a, b, c, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, a, b, c, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, a, b, c, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, a, b, c, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, a, b, c, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, a, b, c, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, a, b, c, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, a, b, c, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, a, b, c, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(a, b, c, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(a, b, c, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, a, b, c, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(a, b, c), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(a, b, c, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(a, b, c, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(a, b, c, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(a, b, c, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, a, b, c, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

```python
scipy.stats.genextreme
```

A generalized extreme value continuous random variable.
As an instance of the `rv_continuous` class, `genextreme` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

`gumbel_r`

Notes

For $c = 0$, `genextreme` is equal to `gumbel_r`. The probability density function for `genextreme` is:

$$f(x, c) = \begin{cases} \exp(-\exp(-x)) \exp(-x) & \text{for } c = 0 \\ \exp(-(1-cx)^{1/c})(1-cx)^{1/c-1} & \text{for } x \leq 1/c, c > 0 \end{cases}$$

Note that several sources and software packages use the opposite convention for the sign of the shape parameter $c$.

`genextreme` takes $c$ as a shape parameter for $c$.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `genextreme.pdf(x, c, loc, scale)` is identically equivalent to `genextreme.pdf(y, c) / scale` with $y = (x - \text{loc}) / \text{scale}$.

Examples

```python
>>> from scipy.stats import genextreme
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
c = -0.1
>>> mean, var, skew, kurt = genextreme.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(genextreme.ppf(0.01, c),
...                  genextreme.ppf(0.99, c), 100)
>>> ax.plot(x, genextreme.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='genextreme pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = genextreme(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

```python
>>> vals = genextreme.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], genextreme.cdf(vals, c))
True
```

Generate random numbers:

```python
>>> r = genextreme.rvs(c, size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Plot of genextreme and frozen PDFs]

**Methods**

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rvs(c, loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, c, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, c, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, c, loc=0, scale=1)</code></td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td><code>logcdf(x, c, loc=0, scale=1)</code></td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td><code>sf(x, c, loc=0, scale=1)</code></td>
<td>Survival function (also defined as (1 - \text{cdf}), but (sf) is sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, c, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, c, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of (cdf) — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, c, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of (sf)).</td>
</tr>
<tr>
<td><code>moment(n, c, loc=0, scale=1)</code></td>
<td>Non-central moment of order (n).</td>
</tr>
<tr>
<td><code>stats(c, loc=0, scale=1, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy(c, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, c, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td><code>median(c, loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(c, loc=0, scale=1)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(c, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(c, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, c, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains (alpha) percent of the distribution.</td>
</tr>
</tbody>
</table>
**scipy.stats.gausshyper**

`scipy.stats.gausshyper = <scipy.stats._continuous_distns.gausshyper_gen object>`

A Gauss hypergeometric continuous random variable.

As an instance of the `rv_continuous` class, `gausshyper` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `gausshyper` is:

\[ f(x; a, b, c, z) = C x^{a-1} (1 - x)^{b-1} (1 + z x)^{-c} \]

for \( 0 \leq x \leq 1, a > 0, b > 0, \) and \( C = \frac{1}{B(a, b) F[2, 1][c, a, a+b, -z]} \). \( F[2, 1] \) is the Gauss hypergeometric function `scipy.special.hyp2f1`.

`gausshyper` takes \( a, b, c \) and \( z \) as shape parameters.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gausshyper.pdf(x, a, b, c, z, loc, scale)` is identically equivalent to `gausshyper.pdf(y, a, b, c, z) / scale` with \( y = (x - loc) / scale \).

**Examples**

```python
>>> from scipy.stats import gausshyper
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> a, b, c, z = 13.8, 3.12, 2.51, 5.18
>>> mean, var, skew, kurt = gausshyper.stats(a, b, c, z, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(gausshyper.ppf(0.01, a, b, c, z),
...                   gausshyper.ppf(0.99, a, b, c, z), 100)
>>> ax.plot(x, gausshyper.pdf(x, a, b, c, z), 'r-', lw=5, alpha=0.6, label='gausshyper pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = gausshyper(a, b, c, z)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=5, alpha=0.6, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = gausshyper.ppf([0.001, 0.5, 0.999], a, b, c, z)
>>> np.allclose([0.001, 0.5, 0.999], gausshyper.cdf(vals, a, b, c, z))
True
```

Generate random numbers:

```python
```
```python
>>> r = gausshyper.rvs(a, b, c, z, size=1000)

And compare the histogram:
```
Methods

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rvs(a, b, c, z, loc=0, scale=1, random_state=None, size=1)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, a, b, c, z, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, a, b, c, z, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, a, b, c, z, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, a, b, c, z, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, a, b, c, z, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, a, b, c, z, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, a, b, c, z, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, a, b, c, z, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, a, b, c, z, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(a, b, c, z, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(a, b, c, z, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, a, b, c, z, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(a, b, c, z), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(a, b, c, z, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(a, b, c, z, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(a, b, c, z, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(a, b, c, z, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, a, b, c, z, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

**scipy.stats.gamma**

```python
scipy.stats.gamma = <scipy.stats._continuous_distns.gamma_gen object>
```

A gamma continuous random variable.

As an instance of the `rv_continuous` class, `gamma` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**See also:**

`erlang`, `expon`

**Notes**

The probability density function for `gamma` is:

$$f(x, a) = \frac{x^{a-1}\exp(-x)}{\Gamma(a)}$$

for $x \geq 0$, $a > 0$. Here $\Gamma(a)$ refers to the gamma function.

`gamma` takes $a$ as a shape parameter for $a$.

When $a$ is an integer, `gamma` reduces to the Erlang distribution, and when $a = 1$ to the exponential distribution.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gamma.pdf(x, a, loc, scale)` is identically equivalent to `gamma.pdf(y, a) / scale` with $y = (x - loc) / scale$. 

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Examples

```python
from scipy.stats import gamma
import matplotlib.pyplot as plt

fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> a = 1.99
>>> mean, var, skew, kurt = gamma.stats(a, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(gamma.ppf(0.01, a), ...
...                 gamma.ppf(0.99, a), 100)
>>> ax.plot(x, gamma.pdf(x, a), ...
...         'r-', lw=5, alpha=0.6, label='gamma pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = gamma(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = gamma.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], gamma.cdf(vals, a))
True
```

Generate random numbers:

```python
>>> r = gamma.rvs(a, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

<table>
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<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rvs(a, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, a, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, a, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, a, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, a, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, a, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
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<tr>
<td>ppf(q, a, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, a, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, a, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
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<td>stats(a, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(a, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, a, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(a,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(a, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(a, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(a, loc=0, scale=1)</td>
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<tr>
<td>std(a, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, a, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
</tr>
</tbody>
</table>

**scipy.stats.gengamma**

`scipy.stats.gengamma = <scipy.stats._continuous_distns.gengamma_gen object>`

A generalized gamma continuous random variable.
As an instance of the `rv_continuous` class, `gengamma` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `gengamma` is:

\[
f(x, a, c) = \frac{|c|x^{ca-1}\exp(-xc)}{\Gamma(a)}
\]

for \( x \geq 0, \; a > 0, \; \text{and} \; c \neq 0 \). \( \Gamma(a) \) is the gamma function (scipy.special.gamma).

`gengamma` takes \( a \) and \( c \) as shape parameters.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the \( \text{loc} \) and \( \text{scale} \) parameters. Specifically, `gengamma.pdf(x, a, c, loc, scale)` is identically equivalent to `gengamma.pdf(y, a, c) / scale` with \( y = (x - \text{loc}) / \text{scale} \).

**Examples**

```python
>>> from scipy.stats import gengamma
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> a, c = 4.42, -3.12
>>> mean, var, skew, kurt = gengamma.stats(a, c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(gengamma.ppf(0.01, a, c),
...                  gengamma.ppf(0.99, a, c), 100)
>>> ax.plot(x, gengamma.pdf(x, a, c),
...         'r-', lw=5, alpha=0.6, label='gengamma pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = gengamma(a, c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = gengamma.ppf([0.001, 0.5, 0.999], a, c)
>>> np.allclose([0.001, 0.5, 0.999], gengamma.cdf(vals, a, c))
True
```

Generate random numbers:

```python
>>> r = gengamma.rvs(a, c, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

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<td>Non-central moment of order n</td>
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<td>interval(alpha, a, c, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
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**scipy.stats.genhalflogistic**

`scipy.stats.genhalflogistic = <scipy.stats._continuous_distns.genhalflogistic_gen object>`

A generalized half-logistic continuous random variable.
As an instance of the `rv_continuous` class, `genhalflogistic` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `genhalflogistic` is:

\[
f(x, c) = \frac{2(1 - cx)^{1/(c-1)}}{[1 + (1 - cx)^{1/c}]^2}
\]

for \(0 \leq x \leq 1/c\), and \(c > 0\).

`genhalflogistic` takes \(c\) as a shape parameter for \(c\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `genhalflogistic.pdf(x, c, loc, scale)` is identically equivalent to `genhalflogistic.pdf(y, c) / scale` with \(y = (x - loc) / scale\).

**Examples**
```python
>>> from scipy.stats import genhalflogistic
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> c = 0.773
>>> mean, var, skew, kurt = genhalflogistic.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(genhalflogistic.ppf(0.01, c), ...
...                   genhalflogistic.ppf(0.99, c), 100)
>>> ax.plot(x, genhalflogistic.pdf(x, c), ...
...          'r-', lw=5, alpha=0.6, label='genhalflogistic pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = genhalflogistic(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = genhalflogistic.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], genhalflogistic.cdf(vals, c))
True
```

Generate random numbers:

```python
>>> r = genhalflogistic.rvs(c, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
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### scipy.stats.gilbrat

`scipy.stats.gilbrat = <scipy.stats._continuous_distns.gilbrat_gen object>`

A Gilbrat continuous random variable.
As an instance of the `rv_continuous` class, `gilbrat` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `gilbrat` is:

\[
f(x) = \frac{1}{x \sqrt{2\pi}} \exp\left(-\frac{1}{2} (\log(x))^2\right)
\]

`gilbrat` is a special case of `lognorm` with \(s=1\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gilbrat.pdf(x, loc, scale)` is identically equivalent to `gilbrat.pdf(y) / scale` with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
>>> from scipy.stats import gilbrat
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> mean, var, skew, kurt = gilbrat.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(gilbrat.ppf(0.01),
...                  gilbrat.ppf(0.99), 100)
>>> ax.plot(x, gilbrat.pdf(x),
...         'r-', lw=5, alpha=0.6, label='gilbrat pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = gilbrat()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = gilbrat.pdf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], gilbrat.cdf(vals))
True
```

Generate random numbers:

```python
>>> r = gilbrat.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
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scipy.stats.gompertz

scipy.stats.gompertz = <scipy.stats._continuous_distns.gompertz_gen object>
A Gompertz (or truncated Gumbel) continuous random variable.
As an instance of the `rv_continuous` class, `gompertz` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `gompertz` is:

\[ f(x, c) = c \exp(x) \exp(-c(e^x - 1)) \]

for \( x \geq 0, c > 0 \).

`gompertz` takes \( c \) as a shape parameter for \( c \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gompertz.pdf(x, c, loc, scale)` is identically equivalent to `gompertz.pdf(y, c) / scale` with \( y = (x - loc) / scale \).

**Examples**
```python
>>> from scipy.stats import gompertz
>>> import matplotlib.pyplot as plt

>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:
```n
c = 0.947

>>> mean, var, skew, kurt = gompertz.stats(c, moments='mvsk')

Display the probability density function (pdf):
```n
>>> x = np.linspace(gompertz.ppf(0.01, c), ...
...                  gompertz.ppf(0.99, c), 100)

>>> ax.plot(x, gompertz.pdf(x, c), ...
...          'r-', lw=5, alpha=0.6, label='gompertz pdf')

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:
```n
>>> rv = gompertz(c)

Check accuracy of cdf and ppf:
```n
>>> vals = gompertz.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], gompertz.cdf(vals, c))
True

Generate random numbers:
```n
>>> r = gompertz.rvs(c, size=1000)
And compare the histogram:
```n
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
### gompertz pdf

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```python
scipy.stats.gumbel_r
```

A right-skewed Gumbel continuous random variable.
As an instance of the `rv_continuous` class, `gumbel_r` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**See also:**
- `gumbel_l`
- `gompertz`
- `genextreme`

**Notes**

The probability density function for `gumbel_r` is:

\[
f(x) = \exp(-(x + e^{-x}))
\]

The Gumbel distribution is sometimes referred to as a type I Fisher-Tippett distribution. It is also related to the extreme value distribution, log-Weibull and Gompertz distributions.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gumbel_r.pdf(x, loc, scale)` is identically equivalent to `gumbel_r.pdf(y) / scale` with \( y = (x - \text{loc}) / \text{scale} \).

**Examples**

```python
>>> from scipy.stats import gumbel_r
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> mean, var, skew, kurt = gumbel_r.stats(moments='mvsk')
>>> mean
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(gumbel_r.ppf(0.01),
...                   gumbel_r.ppf(0.99), 100)
>>> ax.plot(x, gumbel_r.pdf(x),
...          'r-', lw=5, alpha=0.6, label='gumbel_r pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = gumbel_r()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

```python
>>> vals = gumbel_r.pdf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], gumbel_r.cdf(vals))
```

Generate random numbers:

```python
>>> r = gumbel_r.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
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<td><code>interval(alpha, loc=0, scale=1)</code></td>
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</table>

### scipy.stats.gumbel_l

`scipy.stats.gumbel_l = <scipy.stats._continuous_distns.gumbel_l_gen object>`

A left-skewed Gumbel continuous random variable.
As an instance of the `rv_continuous` class, `gumbel_l` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

`gumbel_r`, `gompertz`, `genextreme`

Notes
The probability density function for `gumbel_l` is:

\[ f(x) = \exp(x - e^x) \]

The Gumbel distribution is sometimes referred to as a type I Fisher-Tippett distribution. It is also related to the extreme value distribution, log-Weibull and Gompertz distributions.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gumbel_l.pdf(x, loc, scale)` is identically equivalent to `gumbel_l.pdf(y) / scale` with \( y = (x - \text{loc}) / \text{scale} \).

Examples

```python
>>> from scipy.stats import gumbel_l
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> mean, var, skew, kurt = gumbel_l.stats(moments='mvsk')
``` Display the probability density function (pdf):

```python
>>> x = np.linspace(gumbel_l.ppf(0.001),
...                 gumbel_l.ppf(0.999), 100)
>>> ax.plot(x, gumbel_l.pdf(x),
...          'r-', lw=5, alpha=0.6, label='gumbel_l pdf')
``` Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = gumbel_l()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
``` Check accuracy of cdf and ppf:

```python
>>> vals = gumbel_l.pdf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], gumbel_l.cdf(vals))
True
``` Generate random numbers:

```python
>>> r = gumbel_l.rvs(size=1000)
``` And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

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### scipy.stats.halfcauchy

`scipy.stats.halfcauchy = <scipy.stats._continuous_distns.halfcauchy_gen object>`

A Half-Cauchy continuous random variable.
As an instance of the `rv_continuous` class, `halfcauchy` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `halfcauchy` is:

\[ f(x) = \frac{2}{\pi(1 + x^2)} \]

for \( x \geq 0 \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, \( \text{halfcauchy.pdf}(x, \text{loc}, \text{scale}) \) is identically equivalent to \( \text{halfcauchy.pdf}(y) / \text{scale} \) with \( y = (x - \text{loc}) / \text{scale} \).

**Examples**

```python
>>> from scipy.stats import halfcauchy
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> mean, var, skew, kurt = halfcauchy.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(halfcauchy.ppf(0.01),
...                 halfcauchy.ppf(0.99), 100)
>>> ax.plot(x, halfcauchy.pdf(x),
...          'r-', lw=5, alpha=0.6, label='halfcauchy pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = halfcauchy()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = halfcauchy.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], halfcauchy.cdf(vals))
```

Generate random numbers:

```python
>>> r = halfcauchy.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()```
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**scipy.stats.halflogistic**

`scipy.stats.halflogistic = <scipy.stats._continuous_distns.halflogistic_gen object>`

A half-logistic continuous random variable.
As an instance of the `rv_continuous` class, `halflogistic` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `halflogistic` is:

\[
f(x) = \frac{2e^{-x}}{(1 + e^{-x})^2} = \frac{1}{2} \text{sech}(x/2)^2
\]

for \( x \geq 0 \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `halflogistic.pdf(x, loc, scale)` is identically equivalent to `halflogistic.pdf(y) / scale` with \( y = (x - \text{loc}) / \text{scale} \).

**Examples**

```python
>>> from scipy.stats import halflogistic
>>> import matplotlib.pyplot as plt

>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> mean, var, skew, kurt = halflogistic.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(halflogistic.ppf(0.01),
...                 halflogistic.ppf(0.99), 100)
>>> ax.plot(x, halflogistic.pdf(x),
...         'r-', lw=5, alpha=0.6, label='halflogistic pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = halflogistic()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = halflogistic.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], halflogistic.cdf(vals))
True
```

Generate random numbers:

```python
>>> r = halflogistic.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
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**scipy.stats.halfnorm**

`scipy.stats.halfnorm = <scipy.stats._continuous_distns.halfnorm_gen object>`

A half-normal continuous random variable.
As an instance of the `rv_continuous` class, `halfnorm` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `halfnorm` is:

\[
f(x) = \sqrt{2/\pi} \exp(-x^2/2)
\]

for \(x > 0\).

`halfnorm` is a special case of `chi` with \(df=1\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `halfnorm.pdf(x, loc, scale)` is identically equivalent to `halfnorm.pdf(y) / scale` with \(y = (x - loc) / scale\).

**Examples**

```python
>>> from scipy.stats import halfnorm
>>> import matplotlib.pyplot as plt

>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> mean, var, skew, kurt = halfnorm.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(halfnorm.ppf(0.01), halfnorm.ppf(0.99), 100)
>>> ax.plot(x, halfnorm.pdf(x), 'r-', lw=5, alpha=0.6, label='halfnorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = halfnorm()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = halfnorm.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], halfnorm.cdf(vals))
```

True

Generate random numbers:

```python
>>> r = halfnorm.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
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scipy.stats.halfgennorm

scipy.stats.halfgennorm = <scipy.stats._continuous_distns.halfgennorm_gen object>

The upper half of a generalized normal continuous random variable.
As an instance of the \texttt{rv_continuous} class, \texttt{halfgennorm} object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

\textbf{See also:}

gennorm

generalized normal distribution

expon

exponential distribution

halfnorm

half normal distribution

\textbf{Notes}

The probability density function for \texttt{halfgennorm} is:

\begin{equation}
    f(x, \beta) = \frac{\beta}{\Gamma(1/\beta)} \exp(-|x|^\beta)
\end{equation}

for $x > 0$. $\Gamma$ is the gamma function (\texttt{scipy.special.gamma}).

gennorm takes \texttt{beta} as a shape parameter for $\beta$. For $\beta = 1$, it is identical to an exponential distribution. For $\beta = 2$, it is identical to a half normal distribution (with \texttt{scale}=1/sqrt(2)).

\textbf{References}

[1]

\textbf{Examples}

```python
>>> from scipy.stats import halfgennorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> beta = 0.675
>>> mean, var, skew, kurt = halfgennorm.stats(beta, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(halfgennorm.ppf(0.01, beta),
...                  halfgennorm.ppf(0.99, beta), 100)
>>> ax.plot(x, halfgennorm.pdf(x, beta),
...         'r-', lw=5, alpha=0.6, label='halfgennorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = halfgennorm(beta)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:
>>> vals = halfgennorm.ppf([0.001, 0.5, 0.999], beta)
>>> np.allclose([0.001, 0.5, 0.999], halfgennorm.cdf(vals, beta))
True

Generate random numbers:

>>> r = halfgennorm.rvs(beta, size=1000)

And compare the histogram:

>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
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<td>cdf(x, beta, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, beta, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, beta, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, beta, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, beta, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, beta, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, beta, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(beta, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(beta, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, beta, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(beta,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(beta, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(beta, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(beta, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(beta, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, beta, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

### scipy.stats.hypsecant

`scipy.stats.hypsecant = <scipy.stats._continuous_distns.hypsecant_gen object>`

A hyperbolic secant continuous random variable.

As an instance of the `rv_continuous` class, `hypsecant` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `hypsecant` is:

\[ f(x) = \frac{1}{\pi} \text{sech}(x) \]

for a real number \( x \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `hypsecant.pdf(x, loc, scale)` is identically equivalent to `hypsecant.pdf(y) / scale` with \( y = (x - \text{loc}) / \text{scale} \).

**Examples**

```python
>>> from scipy.stats import hypsecant
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:
```python
mean, var, skew, kurt = hypsecant.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
x = np.linspace(hypsecant.ppf(0.01),
...     hypsecant.ppf(0.99), 100)
ax.plot(x, hypsecant.pdf(x),
...     'r-', lw=5, alpha=0.6, label='hypsecant pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
rv = hypsecant()
ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
vals = hypsecant.ppf([0.001, 0.5, 0.999])
np.allclose([0.001, 0.5, 0.999], hypsecant.cdf(vals))
```

Generate random numbers:

```python
r = hypsecant.rvs(size=1000)
```

And compare the histogram:

```python
ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
ax.legend(loc='best', frameon=False)
plt.show()
```

---

### 6.27. Statistical functions (scipy.stats)

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Methods

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<td>interval(alpha, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
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</table>

**scipy.stats.invgamma**

`scipy.stats.invgamma = <scipy.stats._continuous_distns.invgamma_gen object>`

An inverted gamma continuous random variable.

As an instance of the `rv_continuous` class, `invgamma` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `invgamma` is:

\[
    f(x, a) = x^{-a-1} \frac{\exp(-\frac{1}{x})}{\Gamma(a)}
\]

for \( x > 0, \ a > 0 \). \( \Gamma \) is the gamma function (`scipy.special.gamma`).

`invgamma` takes \( a \) as a shape parameter for \( a \).

`invgamma` is a special case of `gengamma` with \( c=-1 \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `invgamma.pdf(x, a, loc, scale)` is identically equivalent to `invgamma.pdf(y, a) / scale` with \( y = (x - \text{loc}) / \text{scale} \).

**Examples**
```python
>>> from scipy.stats import invgamma
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> a = 4.07
>>> mean, var, skew, kurt = invgamma.stats(a, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(invgamma.ppf(0.01, a), ...
...       invgamma.ppf(0.99, a), 100)
>>> ax.plot(x, invgamma.pdf(x, a), ...
...       'r-', lw=5, alpha=0.6, label='invgamma pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = invgamma(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = invgamma.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], invgamma.cdf(vals, a))
True
```

Generate random numbers:

```python
>>> r = invgamma.rvs(a, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

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<td>Random variates.</td>
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<tr>
<td><code>pdf(x, a, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
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<tr>
<td><code>logpdf(x, a, loc=0, scale=1)</code></td>
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<td><code>ppf(q, a, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
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<td><code>isf(q, a, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of sf).</td>
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<tr>
<td><code>moment(n, a, loc=0, scale=1)</code></td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td><code>stats(a, loc=0, scale=1, moments='mv')</code></td>
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<tr>
<td><code>entropy(a, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, a, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, args=(a,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
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<tr>
<td><code>median(a, loc=0, scale=1)</code></td>
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<td><code>interval(alpha, a, loc=0, scale=1)</code></td>
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</table>

### scipy.stats.invgauss

`scipy.stats.invgauss = <scipy.stats._continuous_distns.invgauss_gen object>`

An inverse Gaussian continuous random variable.
As an instance of the `rv_continuous` class, `invgauss` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `invgauss` is:

\[
 f(x, \mu) = \frac{1}{\sqrt{2\pi x^3}} \exp\left(-\frac{(x - \mu)^2}{2x\mu^2}\right)
\]

for \( x > 0 \) and \( \mu > 0 \).

`invgauss` takes \( \mu \) as a shape parameter for \( \mu \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, \( \text{invgauss.pdf}(x, \mu, \text{loc}, \text{scale}) \) is identically equivalent to \( \text{invgauss.pdf}(y, \mu) / \text{scale} \) with \( y = (x - \text{loc}) / \text{scale} \).

When \( \mu \) is too small, evaluating the cumulative distribution function will be inaccurate due to \( \text{cdf}(\mu \to 0) = \infty \times 0 \). NaNs are returned for \( \mu \leq 0.0028 \).

**Examples**
```python
>>> from scipy.stats import invgauss
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:
```n
```python
>>> mu = 0.145
>>> mean, var, skew, kurt = invgauss.stats(mu, moments='mvsk')
```

Display the probability density function (pdf):
```python
>>> x = np.linspace(invgauss.ppf(0.01, mu),
... invgauss.ppf(0.99, mu), 100)
>>> ax.plot(x, invgauss.pdf(x, mu),
... 'r-', lw=5, alpha=0.6, label='invgauss pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:
```python
>>> rv = invgauss(mu)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:
```python
>>> vals = invgauss.ppf([0.001, 0.5, 0.999], mu)
>>> np.allclose([0.001, 0.5, 0.999], invgauss.cdf(vals, mu))
True
```

Generate random numbers:
```python
>>> r = invgauss.rvs(mu, size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Graph showing invgauss pdf and frozen pdf](image)

### Methods

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</tr>
</thead>
<tbody>
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<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, mu, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, mu, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
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<td><code>cdf(x, mu, loc=0, scale=1)</code></td>
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<td><code>sf(x, mu, loc=0, scale=1)</code></td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
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<td><code>logsf(x, mu, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
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<td><code>ppf(q, mu, loc=0, scale=1)</code></td>
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<td><code>isf(q, mu, loc=0, scale=1)</code></td>
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</tr>
<tr>
<td><code>moment(n, mu, loc=0, scale=1)</code></td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td><code>stats(mu, loc=0, scale=1, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy(mu, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, mu=0, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, args=(mu,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td><code>median(mu, loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
</tr>
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<td><code>mean(mu, loc=0, scale=1)</code></td>
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<td><code>var(mu, loc=0, scale=1)</code></td>
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<td><code>std(mu, loc=0, scale=1)</code></td>
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<tr>
<td><code>interval(alpha, mu, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
</tr>
</tbody>
</table>
scipy.stats.invweibull

scipy.stats.invweibull = <scipy.stats._continuous_distns.invweibull_gen object>
An inverted Weibull continuous random variable.

This distribution is also known as the Fréchet distribution or the type II extreme value distribution.

As an instance of the rv_continuous class, invweibull object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes
The probability density function for invweibull is:

\[ f(x;c) = cx^{-c-1}\exp(-x^{-c}) \]

for \( x > 0, \ c > 0 \).

invweibull takes \( c \) as a shape parameter for \( c \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, invweibull.pdf(x, c, loc, scale) is identically equivalent to invweibull.pdf(y, c) / scale with y = (x - loc) / scale.

References

Examples

```python
>>> from scipy.stats import invweibull
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> c = 10.6
>>> mean, var, skew, kurt = invweibull.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(invweibull.ppf(0.01, c),
...                  invweibull.ppf(0.99, c), 100)
>>> ax.plot(x, invweibull.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='invweibull pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = invweibull(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = invweibull.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], invweibull.cdf(vals, c))
```

Generate random numbers:

```python
```
```python
>>> r = invweibull.rvs(c, size=1000)

And compare the histogram:
```
Methods

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<tr>
<td>pdf(x, c, loc=0, scale=1)</td>
<td>Probability density function.</td>
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<td>entropy(c, loc=0, scale=1)</td>
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<td>fit(data, c, loc=0, scale=1)</td>
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</tr>
<tr>
<td>expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
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scipy.stats.johnsonsb

scipy.stats.johnsonsb = <scipy.stats._continuous_distns.johnsonsb_gen object>

A Johnson SB continuous random variable.

As an instance of the rv_continuous class, johnsonsb object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

johnsonsu

Notes

The probability density function for johnsonsb is:

\[ f(x, a, b) = \frac{b}{x(1 - x)} \phi(a + b \log \frac{x}{1 - x}) \]

for \(0 < x < 1\) and \(a, b > 0\), and \(\phi\) is the normal pdf.

johnsonsb takes \(a\) and \(b\) as shape parameters.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, johnsonsb.pdf(x, a, b, loc, scale) is identically equivalent to johnsonsb.pdf(y, a, b) / scale with y = (x - loc) / scale.
Examples

```python
>>> from scipy.stats import johnsonsb
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> a, b = 4.32, 3.18
>>> mean, var, skew, kurt = johnsonsb.stats(a, b, moments='mvsk')
```  
Display the probability density function (pdf):

```python
>>> x = np.linspace(johnsonsb.ppf(0.01, a, b),
...                  johnsonsb.ppf(0.99, a, b), 100)
>>> ax.plot(x, johnsonsb.pdf(x, a, b),
...          'r-', lw=5, alpha=0.6, label='johnsonsb pdf')
```  
Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = johnsonsb(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```  
Check accuracy of cdf and ppf:

```python
>>> vals = johnsonsb.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], johnsonsb.cdf(vals, a, b))
True
```  
Generate random numbers:

```python
>>> r = johnsonsb.rvs(a, b, size=1000)
```  
And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rvs(a, b, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, a, b, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, a, b, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, a, b, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, a, b, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, a, b, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, a, b, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, a, b, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, a, b, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, a, b, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(a, b, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(a, b, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, a, b, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
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<td>expect(func, args=(a, b), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
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</tr>
<tr>
<td>var(a, b, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(a, b, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, a, b, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

**scipy.stats.johnsonsu**

A Johnson SU continuous random variable.
As an instance of the `rv_continuous` class, `johnsonsu` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**See also:**

`johnsonsb`

**Notes**

The probability density function for `johnsonsu` is:

\[
f(x, a, b) = \frac{b}{\sqrt{x^2 + 1}} \phi(a + b \log(x + \sqrt{x^2 + 1}))
\]

for all \(x, a, b > 0\), and \(\phi\) is the normal pdf.

`johnsonsu` takes \(a\) and \(b\) as shape parameters.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `johnsonsu.pdf(x, a, b, loc, scale)` is identically equivalent to `johnsonsu.pdf(y, a, b) / scale` with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
>>> from scipy.stats import johnsonsu
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> a, b = 2.55, 2.25
>>> mean, var, skew, kurt = johnsonsu.stats(a, b, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(johnsonsu.ppf(0.01, a, b),
...                  johnsonsu.ppf(0.99, a, b), 100)
>>> ax.plot(x, johnsonsu.pdf(x, a, b),
...         'r-', lw=5, alpha=0.6, label='johnsonsu pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = johnsonsu(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = johnsonsu.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], johnsonsu.cdf(vals, a, b))
```

Generate random numbers:

```python
>>> r = johnsonsu.rvs(a, b, size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Graph showing johnsonsu pdf and frozen pdf]

## Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rvs(a, b, loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, a, b, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, a, b, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, a, b, loc=0, scale=1)</code></td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td><code>logcdf(x, a, b, loc=0, scale=1)</code></td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td><code>sf(x, a, b, loc=0, scale=1)</code></td>
<td>Survival function (also defined as $1 - cdf$, but $sf$ is sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, a, b, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, a, b, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
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<td><code>isf(q, a, b, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of sf).</td>
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<td><code>moment(n, a, b, loc=0, scale=1)</code></td>
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<tr>
<td><code>interval(alpha, a, b, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>
scipy.stats.kappa4

scipy.stats.kappa4 = <scipy.stats._continuous_distns.kappa4_gen object>

Kappa 4 parameter distribution.

As an instance of the `rv_continuous` class, `kappa4` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes
The probability density function for kappa4 is:

\[
f(x, h, k) = (1 - kx)^{1/k-1}(1 - h(1 - kx)^{1/k})^{1/h-1}
\]

if \( h \) and \( k \) are not equal to 0.

If \( h \) or \( k \) are zero then the pdf can be simplified:

\( h = 0 \) and \( k \neq 0 \):

\[
kappa4.pdf(x, h, k) = (1.0 - k*x)^{(1.0/k - 1.0)}*\exp(-(1.0 - k*x)^{(1.0/k)})
\]

\( h \neq 0 \) and \( k = 0 \):

\[
kappa4.pdf(x, h, k) = \exp(-x)*(1.0 - h*\exp(-x))^{(1.0/h - 1.0)}
\]

\( h = 0 \) and \( k = 0 \):

\[
kappa4.pdf(x, h, k) = \exp(-x)*\exp(-\exp(-x))
\]

kappa4 takes \( h \) and \( k \) as shape parameters.

The kappa4 distribution returns other distributions when certain \( h \) and \( k \) values are used.

<table>
<thead>
<tr>
<th>( h )</th>
<th>( k=0.0 )</th>
<th>( k=1.0 )</th>
<th>(-\infty \leq k \leq \infty )</th>
</tr>
</thead>
<tbody>
<tr>
<td>-1.0</td>
<td>Logistic</td>
<td></td>
<td>Generalized Logistic(1)</td>
</tr>
<tr>
<td>0.0</td>
<td>Gumbel</td>
<td></td>
<td>Reverse Exponential(2)</td>
</tr>
<tr>
<td>1.0</td>
<td>Exponential</td>
<td>Uniform</td>
<td>Generalized Pareto</td>
</tr>
<tr>
<td></td>
<td>gumbel_r(x)</td>
<td>uniform(x)</td>
<td>genpareto(x, -k)</td>
</tr>
</tbody>
</table>


2. This distribution is currently not in scipy.

References
J.C. Finney, “Optimization of a Skewed Logistic Distribution With Respect to the Kolmogorov-Smirnov Test”, A Dissertation Submitted to the Graduate Faculty of the Louisiana State University and Agricultural and Mechanical College, (August, 2004); https://digitalcommons.lsu.edu/gradschool_dissertations/3672


The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, kappa4.pdf(x, h, k, loc, scale) is identically equivalent to kappa4.pdf(y, h, k) / scale with y = (x - loc) / scale.

Examples

```python
>>> from scipy.stats import kappa4
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> h, k = 0.1, 0
>>> mean, var, skew, kurt = kappa4.stats(h, k, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(kappa4.ppf(0.01, h, k),
                  kappa4.ppf(0.99, h, k), 100)
>>> ax.plot(x, kappa4.pdf(x, h, k),
          'r-', lw=5, alpha=0.6, label='kappa4 pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = kappa4(h, k)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = kappa4.ppf([0.001, 0.5, 0.999], h, k)
>>> np.allclose([0.001, 0.5, 0.999], kappa4.cdf(vals, h, k))
True
```

Generate random numbers:

```python
>>> r = kappa4.rvs(h, k, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

<table>
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<td>rvs(h, k, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, h, k, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, h, k, loc=0, scale=1)</td>
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<td>cdf(x, h, k, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
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<td>logcdf(x, h, k, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, h, k, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, h, k, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, h, k, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, h, k, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, h, k, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(h, k, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(h, k, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, h, k, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(h, k), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(h, k, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
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<td>mean(h, k, loc=0, scale=1)</td>
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<td>var(h, k, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
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<tr>
<td>std(h, k, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, h, k, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
</tr>
</tbody>
</table>

**scipy.stats.kappa3**

scipy.stats.kappa3 = <scipy.stats._continuous_distns.kappa3_gen object>

Kappa 3 parameter distribution.
As an instance of the `rv_continuous` class, `kappa3` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `kappa3` is:

\[ f(x, a) = a(a + x)^{-\frac{a+1}{a}} \]

for \( x > 0 \) and \( a > 0 \).

`kappa3` takes \( a \) as a shape parameter for \( a \).

**References**


The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `kappa3.pdf(x, a, loc, scale)` is identically equivalent to `kappa3.pdf(y, a) / scale` with \( y = (x - loc) / scale \).

**Examples**
```python
>>> from scipy.stats import kappa3
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:
```n
```python
>>> a = 1
>>> mean, var, skew, kurt = kappa3.stats(a, moments='mvsk')
```

Display the probability density function (pdf):
```python
>>> x = np.linspace(kappa3.ppf(0.01, a),
...                  kappa3.ppf(0.99, a), 100)
>>> ax.plot(x, kappa3.pdf(x, a),
...          'r-', lw=5, alpha=0.6, label='kappa3 pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:
```python
>>> rv = kappa3(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:
```python
>>> vals = kappa3.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], kappa3.cdf(vals, a))
True
```

Generate random numbers:
```python
>>> r = kappa3.rvs(a, size=1000)

And compare the histogram:

```
Methods

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rvs(a, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, a, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, a, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, a, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, a, loc=0, scale=1)</td>
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<td>sf(x, a, loc=0, scale=1)</td>
<td>Survival function (also defined as $1 - cdf$, but $sf$ is sometimes more accurate).</td>
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<td>logsf(x, a, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, a, loc=0, scale=1)</td>
<td>Percent point function (inverse of $cdf$ — percentiles).</td>
</tr>
<tr>
<td>isf(q, a, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of $sf$).</td>
</tr>
<tr>
<td>moment(n, a, loc=0, scale=1)</td>
<td>Non-central moment of order $n$</td>
</tr>
<tr>
<td>stats(a, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(a, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, a, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(a,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(a, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(a, loc=0, scale=1)</td>
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<td>var(a, loc=0, scale=1)</td>
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</tr>
<tr>
<td>interval(alpha, a, loc=0, scale=1)</td>
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</table>

**scipy.stats.ksone**

`scipy.stats.ksone = <scipy.stats._continuous_distns.ksone_gen object>`

General Kolmogorov-Smirnov one-sided test.

This is the distribution of the one-sided Kolmogorov-Smirnov (KS) statistics $\sqrt{n}D_n^+$ and $\sqrt{n}D_n^-$ for a finite sample size $n$ (the shape parameter).

As an instance of the `rv_continuous` class, `ksone` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**See also:**

kstwobign, kstest

**Notes**

$\sqrt{n}D_n^+$ and $\sqrt{n}D_n^-$ are given by

$$D_n^+ = \sup_x(F_n(x) - F(x)),$$
$$D_n^- = \sup_x(F(x) - F_n(x)),$$

where $F$ is a CDF and $F_n$ is an empirical CDF. `ksone` describes the distribution under the null hypothesis of the KS test that the empirical CDF corresponds to $n$ i.i.d. random variates with CDF $F$.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `ksone.pdf(x, n, loc, scale)` is identically equivalent to `ksone.pdf(y, n) / scale` with $y = (x - loc) / scale$. 

6.27. Statistical functions (`scipy.stats`)
References

Examples

```python
>>> from scipy.stats import ksone
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> n = 1e+03
>>> mean, var, skew, kurt = ksone.stats(n, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(ksone.ppf(0.01, n), ...
...               ksone.ppf(0.99, n), 100)
>>> ax.plot(x, ksone.pdf(x, n), ...
...         'r-', lw=5, alpha=0.6, label='ksone pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = ksone(n)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = ksone.ppf([0.001, 0.5, 0.999], n)
>>> np.allclose([0.001, 0.5, 0.999], ksone.cdf(vals, n))
True
```

Generate random numbers:

```python
>>> r = ksone.rvs(n, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

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**scipy.stats.kstwobign**

`scipy.stats.kstwobign = <scipy.stats._continuous_distns.kstwobign_gen object>`

Kolmogorov-Smirnov two-sided test for large N.
This is the asymptotic distribution of the two-sided Kolmogorov-Smirnov statistic \( \sqrt{n}D_n \) that measures the maximum absolute distance of the theoretical CDF from the empirical CDF (see \textit{kstest}).

As an instance of the \textit{rv_continuous} class, \textit{kstwobign} object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

\textbf{See also:}

\textit{ksone, kstest}

\textbf{Notes}

\( \sqrt{n}D_n \) is given by

\[
D_n = \sup_x |F_n(x) - F(x)|
\]

where \( F \) is a CDF and \( F_n \) is an empirical CDF. \textit{kstwobign} describes the asymptotic distribution (i.e. the limit of \( \sqrt{n}D_n \)) under the null hypothesis of the KS test that the empirical CDF corresponds to i.i.d. random variates with CDF \( F \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the \textit{loc} and \textit{scale} parameters. Specifically, \textit{kstwobign.pdf(x, loc, scale)} is identically equivalent to \textit{kstwobign.pdf(y)} / \textit{scale} with \( y = (x - \text{loc}) / \text{scale} \).

\textbf{References}

[1]

\textbf{Examples}

```python
>>> from scipy.stats import kstwobign
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> mean, var, skew, kurt = kstwobign.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(kstwobign.ppf(0.01),
...                 kstwobign.ppf(0.99), 100)
>>> ax.plot(x, kstwobign.pdf(x),
...          'r-', lw=5, alpha=0.6, label='kstwobign pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = kstwobign()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of \textit{cdf} and \textit{ppf}:

```python
>>> vals = kstwobign.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], kstwobign.cdf(vals))
True
```

Generate random numbers:
```python
>>> r = kstwobign.rvs(size=1000)

And compare the histogram:
```
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<td>Mean(‘m’), variance(‘v’), skew(‘s’), and/or kurtosis(‘k’).</td>
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### scipy.stats.laplace

A Laplace continuous random variable.

As an instance of the `rv_continuous` class, `laplace` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `laplace` is

\[
f(x) = \frac{1}{2} \exp(-|x|)
\]

for a real number \(x\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `laplace.pdf(x, loc, scale)` is identically equivalent to `laplace.pdf(y) / scale` with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
def from scipy.stats import laplace
def import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:
Display the probability density function (pdf):

```python
>>> x = np.linspace(laplace.ppf(0.01),
...                   laplace.ppf(0.99), 100)
>>> ax.plot(x, laplace.pdf(x),
...          'r-', lw=5, alpha=0.6, label='laplace pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = laplace()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = laplace.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], laplace.cdf(vals))
True
```

Generate random numbers:

```python
>>> r = laplace.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
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Methods

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scipy.stats.levy

scipy.stats.levy = <scipy.stats._continuous_distns.levy_gen object>

A Levy continuous random variable.

As an instance of the rv_continuous class, levy object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

levy_stable, levy_l

Notes

The probability density function for levy is:

\[
f(x) = \frac{1}{\sqrt{2\pi x^3}} \exp\left(-\frac{1}{2x}\right)
\]

for \( x > 0 \).

This is the same as the Levy-stable distribution with \( a = 1/2 \) and \( b = 1 \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, levy.pdf(x, loc, scale) is identically equivalent to levy.pdf(y) / scale with y = (x - loc) / scale.
Examples

```python
>>> from scipy.stats import levy
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> mean, var, skew, kurt = levy.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(levy.ppf(0.01),
...                 levy.ppf(0.99), 100)
>>> ax.plot(x, levy.pdf(x),
...         'r-', lw=5, alpha=0.6, label='levy pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = levy()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = levy.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], levy.cdf(vals))
True
```

Generate random numbers:

```python
>>> r = levy.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
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scipy.stats.levy_l

scipy.stats.levy_l = <scipy.stats._continuous_distns.levy_l_gen object>

A left-skewed Levy continuous random variable.
As an instance of the `rv_continuous` class, `levy_l` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**See also:**

`levy`, `levy_stable`

**Notes**
The probability density function for `levy_l` is:

\[
f(x) = \frac{1}{|x|\sqrt{2\pi |x|}} \exp\left(-\frac{1}{2|x|}\right)
\]

for \(x < 0\).

This is the same as the Levy-stable distribution with \(a = 1/2\) and \(b = -1\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `levy_l.pdf(x, loc, scale)` is identically equivalent to `levy_l.pdf(y) / scale` with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
>>> from scipy.stats import levy_l
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
Calculate a few first moments:

```python
>>> mean, var, skew, kurt = levy_l.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(levy_l.ppf(0.01),
...                 levy_l.ppf(0.99), 100)
>>> ax.plot(x, levy_l.pdf(x),
...          'r-', lw=5, alpha=0.6, label='levy_l pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = levy_l()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = levy_l.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], levy_l.cdf(vals))
True
```

Generate random numbers:

```python
>>> r = levy_l.rvs(size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Graph showing levy_l pdf and frozen pdf]

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<td><code>expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False,**kwds)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
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</tr>
<tr>
<td><code>interval(alpha, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
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</tbody>
</table>
scipy.stats.levy_stable

scipy.stats.levy_stable = <scipy.stats._continuous_distns.levy_stable_gen object>

A Levy-stable continuous random variable.

As an instance of the rv_continuous class, levy_stable object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:
levy, levy_l

Notes

The distribution for levy_stable has characteristic function:

\[ \varphi(t, \alpha, \beta, c, \mu) = e^{it\mu-|ct|^{\alpha}(1-i\beta \text{sign}(t))\Phi(\alpha, t)} \]

where:

\[ \Phi = \begin{cases} \tan \left( \frac{\pi \alpha}{2} \right) & \alpha \neq 1 \\ -\frac{2}{\pi} \log |t| & \alpha = 1 \end{cases} \]

The probability density function for levy_stable is:

\[ f(x) = \frac{1}{2\pi} \int_{-\infty}^{\infty} \varphi(t)e^{-ixt} dt \]

where \(-\infty < t < \infty\). This integral does not have a known closed form.

For evaluation of pdf we use either Zolotarev \( S_0 \) parameterization with integration, direct integration of standard parameterization of characteristic function or FFT of characteristic function. If set to other than None and if number of points is greater than \( \text{levy_stable.pdf_fft_min_points_threshold} \) (defaults to None) we use FFT otherwise we use one of the other methods.

The default method is 'best' which uses Zolotarev’s method if alpha = 1 and integration of characteristic function otherwise. The default method can be changed by setting \( \text{levy_stable.pdf_default_method} \) to either ‘zolotarev’, ‘quadrature’ or ‘best’.

To increase accuracy of FFT calculation one can specify \( \text{levy_stable.pdf_fft_grid_spacing} \) (defaults to 0.001) and \( \text{pdf_fft_n_points_two_power} \) (defaults to a value that covers the input range * 4). Setting \( \text{pdf_fft_n_points_two_power} \) to 16 should be sufficiently accurate in most cases at the expense of CPU time.

For evaluation of cdf we use Zolotarev \( S_0 \) parameterization with integration or integral of the pdf FFT interpolated spline. The settings affecting FFT calculation are the same as for pdf calculation. Setting the threshold to None (default) will disable FFT. For cdf calculations the Zolotarev method is superior in accuracy, so FFT is disabled by default.

Fitting estimate uses quantile estimation method in [MC]. MLE estimation of parameters in fit method uses this quantile estimate initially. Note that MLE doesn’t always converge if using FFT for pdf calculations; so it’s best that \( \text{pdf_fft_min_points_threshold} \) is left unset.

Warning: For pdf calculations implementation of Zolotarev is unstable for values where alpha = 1 and beta != 0. In this case the quadrature method is recommended. FFT calculation is also considered experimental.

For cdf calculations FFT calculation is considered experimental. Use Zolotarev’s method instead (default).
The probability density above is defined in the “standardized” form. To shift and/or scale the
distribution use the \texttt{loc} and \texttt{scale} parameters. Specifically, \texttt{levy\_stable.pdf}(x, alpha, beta, 
loc, scale) is identically equivalent to \texttt{levy\_stable.pdf}(y, alpha, beta) / scale with 
y = (x - loc) / scale.

\textbf{References}
[MC], [MS], [BS]

\textbf{Examples}

\begin{verbatim}
>>> from scipy.stats import levy_stable
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

>>> alpha, beta = 1.8, -0.5

>>> mean, var, skew, kurt = levy_stable.stats(alpha, beta, moments='mvsk')

Display the probability density function (pdf):

>>> x = np.linspace(levy_stable.ppf(0.01, alpha, beta),
...                  levy_stable.ppf(0.99, alpha, beta), 100)

>>> ax.plot(x, levy_stable.pdf(x, alpha, beta),
...          'r-', lw=5, alpha=0.6, label='levy_stable pdf')

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale
parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

>>> rv = levy_stable(alpha, beta)

>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')

Check accuracy of cdf and ppf:

>>> vals = levy_stable.ppf([0.001, 0.5, 0.999], alpha, beta)
>>> np.allclose([0.001, 0.5, 0.999], levy_stable.cdf(vals, alpha, beta))
True

Generate random numbers:

>>> r = levy_stable.rvs(alpha, beta, size=1000)

And compare the histogram:

>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
\end{verbatim}
Methods

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<tr>
<td><code>pdf(x, alpha, beta, loc=0, scale=1)</code></td>
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<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td><code>sf(x, alpha, beta, loc=0, scale=1)</code></td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
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</tr>
<tr>
<td><code>moment(n, alpha, beta, loc=0, scale=1)</code></td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td><code>stats(alpha, beta, loc=0, scale=1, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy(alpha, beta, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, alpha, beta, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expected(func, args=(alpha, beta), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
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<td><code>interval(alpha, beta, loc=0, scale=1)</code></td>
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</table>
scipy.stats.logistic

scipy.stats.logistic = <scipy.stats._continuous_distns.logistic_gen object>
A logistic (or Sech-squared) continuous random variable.

As an instance of the rv_continuous class, logistic object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes
The probability density function for logistic is:

\[ f(x) = \frac{\exp(-x)}{(1 + \exp(-x))^2} \]

logistic is a special case of genlogistic with c=1.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, logistic.pdf(x, loc, scale) is identically equivalent to logistic.pdf(y) / scale with y = (x - loc) / scale.

Examples

```python
def from scipy.stats import logistic
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
>>> mean, var, skew, kurt = logistic.stats(moments='mvsk')
```

Calculate a few first moments:

```python
def mean, var, skew, kurt = logistic.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
def x = np.linspace(logistic.ppf(0.01),
... logistic.ppf(0.99), 100)
>>> ax.plot(x, logistic.pdf(x),
... 'r-', lw=5, alpha=0.6, label='logistic pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
def rv = logistic()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
def vals = logistic.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], logistic.cdf(vals))
```

Generate random numbers:

```python
def r = logistic.rvs(size=1000)
```

And compare the histogram:
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
scipy.stats.loggamma

scipy.stats.loggamma = <scipy.stats._continuous_distns.loggamma_gen object>

A log gamma continuous random variable.

As an instance of the rv_continuous class, loggamma object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes
The probability density function for loggamma is:

\[ f(x; c) = \frac{\exp(cx - \exp(x))}{\Gamma(c)} \]

for all \( x, c > 0 \). Here, \( \Gamma \) is the gamma function (scipy.special.gamma).

loggamma takes \( c \) as a shape parameter for \( c \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, loggamma.pdf(\( x \), \( c \), loc, scale) is identically equivalent to loggamma.pdf(\( y \), \( c \)) / scale with \( y = (x - \text{loc}) / \text{scale} \).

Examples

```
>>> from scipy.stats import loggamma
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> c = 0.414
>>> mean, var, skew, kurt = loggamma.stats(c, moments='mvsk')

Display the probability density function (pdf):

```python
>>> x = np.linspace(loggamma.ppf(0.01, c),
...                  loggamma.ppf(0.99, c), 100)
>>> ax.plot(x, loggamma.pdf(x, c),
...          'r-', lw=5, alpha=0.6, label='loggamma pdf')

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = loggamma(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = loggamma.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], loggamma.cdf(vals, c))
True
```

Generate random numbers:

```python
>>> r = loggamma.rvs(c, size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Graph showing loggamma pdf and frozen pdf]

### Methods

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</tr>
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<td>Random variates.</td>
</tr>
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</table>
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scipy.stats.loglaplace

`scipy.stats.loglaplace = <scipy.stats._continuous_distns.loglaplace_gen object>`

A log-Laplace continuous random variable.

As an instance of the `rv_continuous` class, `loglaplace` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `loglaplace` is:

\[
  f(x, c) = \begin{cases} 
  \frac{cx^{-1}}{2} & \text{for } 0 < x < 1 \\
  \frac{cx^{-1}}{2} & \text{for } x \geq 1 
  \end{cases}
\]

for \( c > 0 \).

`loglaplace` takes \( c \) as a shape parameter for \( c \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `loglaplace.pdf(x, c, loc, scale)` is identically equivalent to `loglaplace.pdf(y, c) / scale` with \( y = (x - loc) / scale \).

References


Examples

```python
>>> from scipy.stats import loglaplace
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> c = 3.25
>>> mean, var, skew, kurt = loglaplace.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(loglaplace.ppf(0.01, c),
...                  loglaplace.ppf(0.99, c), 100)
>>> ax.plot(x, loglaplace.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='loglaplace pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = loglaplace(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = loglaplace.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], loglaplace.cdf(vals, c))
True
```

Generate random numbers:
```python
>>> r = loglaplace.rvs(c, size=1000)

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

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**scipy.stats.lognorm**

scipy.stats.lognorm = <scipy.stats._continuous_distns.lognorm_gen object>

A lognormal continuous random variable.

As an instance of the **rv_continuous** class, **lognorm** object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for **lognorm** is:

\[ f(x, s) = \frac{1}{sx\sqrt{2\pi}} \exp \left( -\frac{\log^2(x)}{2s^2} \right) \]

for \( x > 0, s > 0 \).

**lognorm** takes \( s \) as a shape parameter for \( s \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the **loc** and **scale** parameters. Specifically, **lognorm.pdf(x, s, loc, scale)** is identically equivalent to **lognorm.pdf(y, s) / scale** with \( y = (x - \text{loc}) / \text{scale} \).

A common parametrization for a lognormal random variable \( Y \) is in terms of the mean, \( \mu \), and standard deviation, \( \sigma \), of the unique normally distributed random variable \( X \) such that \( \exp(X) = Y \). This parametrization corresponds to setting \( s = \sigma \) and \( \text{scale} = \exp(\mu) \).
Examples

```python
>>> from scipy.stats import lognorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> s = 0.954
>>> mean, var, skew, kurt = lognorm.stats(s, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(lognorm.ppf(0.01, s),
...                 lognorm.ppf(0.99, s), 100)
>>> ax.plot(x, lognorm.pdf(x, s),
...          'r-', lw=5, alpha=0.6, label='lognorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = lognorm(s)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = lognorm.ppf([0.001, 0.5, 0.999], s)
>>> np.allclose([0.001, 0.5, 0.999], lognorm.cdf(vals, s))
True
```

Generate random numbers:

```python
>>> r = lognorm.rvs(s, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

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<td>pdf(x, s, loc=0, scale=1)</td>
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<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, s, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, s, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, s, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, s, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(s, loc=0, scale=1, moments=’mv”)</td>
<td>Mean(‘m’), variance(‘v’), skew(‘s’), and/or kurtosis(‘k’).</td>
</tr>
<tr>
<td>entropy(s, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, s, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(s), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(s, loc=0, scale=1)</td>
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<td>mean(s, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(s, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(s, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, s, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

**scipy.stats.lomax**

`scipy.stats.lomax = <scipy.stats._continuous_distns.lomax_gen object>`

A Lomax (Pareto of the second kind) continuous random variable.
As an instance of the `rv_continuous` class, `lomax` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `lomax` is:

\[
f(x,c) = \frac{c}{(1 + x)^{c+1}}
\]

for \( x \geq 0, \ c > 0 \).

`lomax` takes \( c \) as a shape parameter for \( c \).

`lomax` is a special case of `pareto` with `loc=-1.0`.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `lomax.pdf(x, c, loc, scale)` is identically equivalent to `lomax.pdf(y, c) / scale` with \( y = (x - loc) / scale \).

**Examples**

```python
>>> from scipy.stats import lomax
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> c = 1.88
>>> mean, var, skew, kurt = lomax.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(lomax.ppf(0.01, c),
...     lomax.ppf(0.99, c), 100)
>>> ax.plot(x, lomax.pdf(x, c),
...     'r-', lw=5, alpha=0.6, label='lomax pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = lomax(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = lomax.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], lomax.cdf(vals, c))
True
```

Generate random numbers:

```python
>>> r = lomax.rvs(c, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

<table>
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</tr>
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<tbody>
<tr>
<td><code>rvs(c, loc=0, scale=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, c, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, c, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, c, loc=0, scale=1)</code></td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td><code>logcdf(x, c, loc=0, scale=1)</code></td>
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<td><code>isf(q, c, loc=0, scale=1)</code></td>
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</tr>
<tr>
<td><code>moment(n, c, loc=0, scale=1)</code></td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td><code>stats(c, loc=0, scale=1, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy(c, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, c, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td><code>median(c, loc=0, scale=1)</code></td>
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`scipy.stats.maxwell`

`scipy.stats.maxwell = <scipy.stats._continuous_distns.maxwell_gen object>`

A Maxwell continuous random variable.
As an instance of the `rv_continuous` class, `maxwell` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

A special case of a `chi` distribution, with \( \text{df}=3 \), \( \text{loc}=0.0 \), and given \( \text{scale} = a \), where \( a \) is the parameter used in the Mathworld description \(^1\).

The probability density function for `maxwell` is:

\[
    f(x) = \sqrt{2/\pi} x^2 \exp(-x^2/2)
\]

for \( x > 0 \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, \( \text{maxwell.pdf}(x, \text{loc}, \text{scale}) \) is identically equivalent to \( \text{maxwell.pdf}(y) / \text{scale} \) with \( y = (x - \text{loc}) / \text{scale} \).

**References**

\(^1\)

**Examples**

```python
>>> from scipy.stats import maxwell
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
def maxwell.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
def maxwell.pdf(x, loc=0.0, scale=1.0, size=None)
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
def maxwell.rvs(size=1000)
```

Check accuracy of cdf and ppf:

```python
def maxwell.cdf(x, loc=0.0, scale=1.0)
```

Generate random numbers:

```python
def maxwell.rvs(size=1000)
```

And compare the histogram:
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()

```

Methods

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```
scipy.stats.mielke

scipy.stats.mielke = <scipy.stats._continuous_distns.mielke_gen object>
A Mielke's Beta-Kappa continuous random variable.

As an instance of the rv_continuous class, mielke object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes
The probability density function for mielke is:

\[ f(x; k, s) = k x^{k-1} \left(1 + x^s\right)^{1+k/s} \]

for \( x > 0 \) and \( k, s > 0 \).

mielke takes \( k \) and \( s \) as shape parameters.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, mielke.pdf\((x, k, s, \text{loc}, \text{scale})\) is identically equivalent to mielke.pdf\((y, k, s) / \text{scale}\) with \( y = (x - \text{loc}) / \text{scale}\).

Examples
>>> from scipy.stats import mielke
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

>>> k, s = 10.4, 3.6
>>> mean, var, skew, kurt = mielke.stats(k, s, moments='mvsk')

Display the probability density function (pdf):

>>> x = np.linspace(mielke.ppf(0.01, k, s),
...                 mielke.ppf(0.99, k, s), 100)
>>> ax.plot(x, mielke.pdf(x, k, s),
...          'r-', lw=5, alpha=0.6, label='mielke pdf')

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

>>> rv = mielke(k, s)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')

Check accuracy of cdf and ppf:

>>> vals = mielke.ppf([0.001, 0.5, 0.999], k, s)
>>> np.allclose([0.001, 0.5, 0.999], mielke.cdf(vals, k, s))
True

Generate random numbers:

>>> r = mielke.rvs(k, s, size=1000)

And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

### Methods

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<td><code>pdf(x, k, s, loc=0, scale=1)</code></td>
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<td><code>ppf(q, k, s, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of (cdf) — percentiles).</td>
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<td><code>moment(n, k, s, loc=0, scale=1)</code></td>
<td>Non-central moment of order (n).</td>
</tr>
<tr>
<td><code>stats(k, s, loc=0, scale=1, moments='mv')</code></td>
<td>Mean (‘m’), variance (‘v’), skew (‘s’), and/or kurtosis (‘k’).</td>
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<td>(Differential) entropy of the RV.</td>
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<tr>
<td><code>fit(data, k, s, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, args=(k, s), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td><code>median(k, s, loc=0, scale=1)</code></td>
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<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, k, s, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
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</table>
scipy.stats.moyal

scipy.stats.moyal = <scipy.stats._continuous_distns.moyal_gen object>

A Moyal continuous random variable.

As an instance of the rv_continuous class, moyal object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for moyal is:

\[ f(x) = \exp(-x + \exp(-x))/\sqrt{2\pi} \]

for a real number \( x \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, moyal.pdf(x, loc, scale) is identically equivalent to moyal.pdf(y) / scale with \( y = (x - \text{loc}) / \text{scale} \).

This distribution has utility in high-energy physics and radiation detection. It describes the energy loss of a charged relativistic particle due to ionization of the medium [1]. It also provides an approximation for the Landau distribution. For an in depth description see [2]. For additional description, see [3].

References

New in version 1.1.0.

[1], [2], [3]

Examples

```python
>>> from scipy.stats import moyal
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> mean, var, skew, kurt = moyal.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(moyal.ppf(0.01), ...
...                   moyal.ppf(0.99), 100)
>>> ax.plot(x, moyal.pdf(x), ...
...         'r-', lw=5, alpha=0.6, label='moyal pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = moyal()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = moyal.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], moyal.cdf(vals))
True
```

Generate random numbers:
>>> r = moyal.rvs(size=1000)

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

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<td>Survival function (also defined as (1 - \text{cdf}), but (sf) is sometimes more accurate).</td>
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<td>ppf(q, loc=0, scale=1)</td>
<td>Percent point function (inverse of (\text{cdf} - \text{percentiles})).</td>
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**scipy.stats.nakagami**

A Nakagami continuous random variable.

As an instance of the `rv_continuous` class, `nakagami` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `nakagami` is:

\[
f(x, \nu) = \frac{2\nu^\nu}{\Gamma(\nu)} x^{2\nu-1} \exp(-\nu x^2)
\]

for \(x > 0, \nu > 0\).

`nakagami` takes \(\nu\) as a shape parameter for \(\nu\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `nakagami.pdf(x, nu, loc, scale)` is identically equivalent to `nakagami.pdf(y, nu) / scale` with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
>>> from scipy.stats import nakagami
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```
Calculate a few first moments:

```python
>>> nu = 4.97
>>> mean, var, skew, kurt = nakagami.stats(nu, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(nakagami.ppf(0.01, nu),
...                   nakagami.ppf(0.99, nu), 100)
>>> ax.plot(x, nakagami.pdf(x, nu),
...          'r-', lw=5, alpha=0.6, label='nakagami pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = nakagami(nu)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = nakagami.ppf([0.001, 0.5, 0.999], nu)
>>> np.allclose([0.001, 0.5, 0.999], nakagami.cdf(vals, nu))
True
```

Generate random numbers:

```python
>>> r = nakagami.rvs(nu, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

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<td>Random variates.</td>
</tr>
<tr>
<td>random_state=None)`</td>
<td></td>
</tr>
<tr>
<td><code>pdf(x, nu, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td>`logpdf(x, nu, loc=0, scale=</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>1)`</td>
<td></td>
</tr>
<tr>
<td><code>cdf(x, nu, loc=0, scale=1)</code></td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>`logcdf(x, nu, loc=0, scale=</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>1)`</td>
<td></td>
</tr>
<tr>
<td><code>sf(x, nu, loc=0, scale=1)</code></td>
<td>Survival function (also defined as $1 - cdf$, but $sf$ is sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, nu, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, nu, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, nu, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>`moment(n, nu, loc=0, scale=</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>1)`</td>
<td></td>
</tr>
<tr>
<td>`stats(nu, loc=0, scale=1,</td>
<td>Mean(‘m’), variance(‘v’), skew(‘s’), and/or kurtosis(‘k’).</td>
</tr>
<tr>
<td>moments=’mv’)</td>
<td></td>
</tr>
<tr>
<td><code>entropy(nu, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>`fit(data, nu, loc=0, scale=</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>1)`</td>
<td></td>
</tr>
<tr>
<td>`expect(func, args=(nu,),</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>loc=0, scale=1, lb=None, ub=</td>
<td></td>
</tr>
<tr>
<td>None, conditional=False,</td>
<td></td>
</tr>
<tr>
<td>**kwds)`</td>
<td></td>
</tr>
<tr>
<td><code>median(nu, loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(nu, loc=0, scale=1)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(nu, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(nu, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>`interval(alpha, nu, loc=0,</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
<tr>
<td>scale=1)`</td>
<td></td>
</tr>
</tbody>
</table>

`scipy.stats.ncx2`

`scipy.stats.ncx2 = <scipy.stats._continuous_distns.ncx2_gen object>`

A non-central chi-squared continuous random variable.

As an instance of the `rv_continuous` class, `ncx2` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `ncx2` is:

\[
f(x, k, \lambda) = \frac{1}{2} \exp(-(\lambda + x)/2) x^{(k-2)/4} I_{(k-2)/2}(\sqrt{\lambda x})
\]

for $x > 0$ and $k, \lambda > 0$. $k$ specifies the degrees of freedom (denoted `df` in the implementation) and $\lambda$ is the non-centrality parameter (denoted `nc` in the implementation). $I_{\nu}$ denotes the modified Bessel function of first order of degree $\nu$ (`scipy.special.iv`).

`ncx2` takes `df` and `nc` as shape parameters.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `ncx2.pdf(x, df, nc, loc, scale)` is identically equivalent to `ncx2.pdf(y, df, nc) / scale` with $y = (x - loc) / scale$.

**Examples**
```python
from scipy.stats import ncx2
import matplotlib.pyplot as plt

fig, ax = plt.subplots(1, 1)

calculate a few first moments:

```python
>>> df, nc = 21, 1.06
>>> mean, var, skew, kurt = ncx2.stats(df, nc, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(ncx2.ppf(0.01, df, nc), ...
...                 ncx2.ppf(0.99, df, nc), 100)
>>> ax.plot(x, ncx2.pdf(x, df, nc), ...
...          'r-', lw=5, alpha=0.6, label='ncx2 pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = ncx2(df, nc)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = ncx2.ppf([0.001, 0.5, 0.999], df, nc)
>>> np.allclose([0.001, 0.5, 0.999], ncx2.cdf(vals, df, nc))
True
```

Generate random numbers:

```python
>>> r = ncx2.rvs(df, nc, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
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<tbody>
<tr>
<td>rvs(df, nc, loc=0, scale=1, random_state=None, size=1)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, df, nc, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, df, nc, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, df, nc, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, df, nc, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, df, nc, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, df, nc, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, df, nc, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, df, nc, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, df, nc, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(df, nc, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(df, nc, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, df, nc, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(df, nc), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(df, nc, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(df, nc, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(df, nc, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(df, nc, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, df, nc, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

### scipy.stats.ncf

scipy.stats.ncf = <scipy.stats._continuous_distns.ncf_gen object>
A non-central F distribution continuous random variable.
As an instance of the `rv_continuous` class, `ncf` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `ncf` is:

\[
    f(x; n_1, n_2) = \exp\left(\frac{\lambda}{2} + \lambda n_1 \frac{x}{2(n_1 x + n_2)}\right)n_1^{n_1/2}n_2^{n_2/2}x^{n_1/2-1}
    (n_2 + n_1 x)^{-(n_1+n_2)/2} \gamma(n_1/2)\gamma(1 + n_2/2)
    L_{n_2/2}^{n_1/2}(-\lambda n_1 \frac{2(n_1 x + n_2)}{(n_1 + n_2)})
    B(v_1/2, v_2/2)\gamma(\frac{n_1 + n_2}{2})
\]

for \( n_1 > 1, n_2 > 0 \). Here \( n_1 \) is the degrees of freedom in the numerator, \( n_2 \) the degrees of freedom in the denominator, \( \lambda \) the non-centrality parameter, \( \gamma \) is the logarithm of the Gamma function, \( L_k^n \) is a generalized Laguerre polynomial and \( B \) is the beta function.

`ncf` takes `df1`, `df2` and `nc` as shape parameters.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `ncf.pdf(x, dfn, dfd, nc, loc, scale)` is identically equivalent to `ncf.pdf(y, dfn, dfd, nc) / scale` with \( y = (x - loc) / scale \).

**Examples**
```python
>>> from scipy.stats import ncf
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
>>> dfn, dfd, nc = 27, 27, 0.416
>>> mean, var, skew, kurt = ncf.stats(dfn, dfd, nc, moments='mvsk')
>>> x = np.linspace(ncf.ppf(0.01, dfn, dfd, nc),
...                  ncf.ppf(0.99, dfn, dfd, nc), 100)
>>> ax.plot(x, ncf.pdf(x, dfn, dfd, nc), 'r--', lw=5,
...          label='ncf pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:
```python
>>> rv = ncf(dfn, dfd, nc)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=5, alpha=0.6, label='frozen pdf')
```

Check accuracy of cdf and ppf:
```python
>>> vals = ncf.ppf([0.001, 0.5, 0.999], dfn, dfd, nc)
>>> np.allclose([0.001, 0.5, 0.999], ncf.cdf(vals, dfn, dfd, nc))
True
```

Generate random numbers:
```python
>>> r = ncf.rvs(dfn, dfd, nc, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

<table>
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<th>Description</th>
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<tr>
<td>rvs(dfn, dfd, nc, loc=0, scale=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, dfn, dfd, nc, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, dfn, dfd, nc, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, dfn, dfd, nc, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, dfn, dfd, nc, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, dfn, dfd, nc, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, dfn, dfd, nc, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, dfn, dfd, nc, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, dfn, dfd, nc, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, dfn, dfd, nc, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(dfn, dfd, nc, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(dfn, dfd, nc, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, dfn, dfd, nc, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(dfn, dfd, nc), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(dfn, dfd, nc, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(dfn, dfd, nc, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(dfn, dfd, nc, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(dfn, dfd, nc, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, dfn, dfd, nc, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

**scipy.stats.nct**

```
scipy.stats.nct = <scipy.stats._continuous_distns.nct_gen object>
```

A non-central Student’s t continuous random variable.

As an instance of the `rv_continuous` class, `nct` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

If $Y$ is a standard normal random variable and $V$ is an independent chi-square random variable ($\chi^2$) with $k$ degrees of freedom, then

$$X = \frac{Y + c}{\sqrt{V/k}}$$

has a non-central Student’s t distribution on the real line. The degrees of freedom parameter $k$ (denoted df in the implementation) satisfies $k > 0$ and the noncentrality parameter $c$ (denoted nct in the implementation) is a real number.

The probability density above is defined in the “standardized form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, `nct.pdf(x, df, nc, loc, scale)` is identically equivalent to `nct.pdf(y, df, nc) / scale` with $y = (x - loc) / scale$. 

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Examples

```python
>>> from scipy.stats import nct
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> df, nc = 14, 0.24
>>> mean, var, skew, kurt = nct.stats(df, nc, moments='mvsk')
```  
Display the probability density function (pdf):

```python
>>> x = np.linspace(nct.ppf(0.01, df, nc),
                 ...           nct.ppf(0.99, df, nc), 100)
>>> ax.plot(x, nct.pdf(x, df, nc),
                 ...             'r-', lw=5, alpha=0.6, label='nct pdf')
```  
Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = nct(df, nc)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```  
Check accuracy of cdf and ppf:

```python
>>> vals = nct.ppf([0.001, 0.5, 0.999], df, nc)
>>> np.allclose([0.001, 0.5, 0.999], nct.cdf(vals, df, nc))
True
```  
Generate random numbers:

```python
>>> r = nct.rvs(df, nc, size=1000)
```  
And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

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<td>Random variates.</td>
</tr>
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<td>pdf(x, df, nc, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, df, nc, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, df, nc, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
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<tr>
<td>logcdf(x, df, nc, loc=0, scale=1)</td>
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<td>sf(x, df, nc, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
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<td>ppf(q, df, nc, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
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<td>moment(n, df, nc, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
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<td>fit(data, df, nc, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(df, nc), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(df, nc, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(df, nc, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(df, nc, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(df, nc, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, df, nc, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

scipy.stats.norm

scipy.stats.norm = <scipy.stats._continuous_distns.norm_gen object>

A normal continuous random variable.
The location (loc) keyword specifies the mean. The scale (scale) keyword specifies the standard deviation.

As an instance of the `rv_continuous` class, `norm` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `norm` is:

\[
f(x) = \frac{\exp(-x^2/2)}{\sqrt{2\pi}}
\]

for a real number \(x\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, `norm.pdf(x, loc, scale)` is identically equivalent to `norm.pdf(y) / scale` with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**
```python
>>> from scipy.stats import norm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:
```n
```python
>>> mean, var, skew, kurt = norm.stats(moments='mvsk')
```

Display the probability density function (pdf):
```python
>>> x = np.linspace(norm.ppf(0.01), norm.ppf(0.99), 100)
>>> ax.plot(x, norm.pdf(x), 'r-', lw=5, alpha=0.6, label='norm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:
```python
>>> rv = norm()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:
```python
>>> vals = norm.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], norm.cdf(vals))
```

Generate random numbers:
```python
>>> r = norm.rvs(size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

<table>
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</tr>
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<td>Probability density function.</td>
</tr>
<tr>
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<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, loc=0, scale=1)</td>
<td>Survival function (also defined as $1 - \text{cdf}$, but $sf$ is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
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<td>ppf(q, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
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<tr>
<td>isf(q, loc=0, scale=1)</td>
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<tr>
<td>moment(n, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
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<tr>
<td>entropy(loc=0, scale=1)</td>
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</tr>
<tr>
<td>fit(data, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
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<tr>
<td>median(loc=0, scale=1)</td>
<td>Median of the distribution.</td>
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<tr>
<td>interval(alpha, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
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**scipy.stats.norminvgauss**

`scipy.stats.norminvgauss` = <scipy.stats._continuous_distns.norminvgauss_gen object>

A Normal Inverse Gaussian continuous random variable.
As an instance of the \texttt{rv\_continuous} class, \texttt{norminvgauss} object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for \texttt{norminvgauss} is:

\[
f(x, a, b) = \frac{a \exp(\sqrt{a^2 - b^2 + bx})}{\pi \sqrt{1 + x^2} K_1(a \sqrt{1 + x^2})}\]

where \( x \) is a real number, the parameter \( a \) is the tail heaviness and \( b \) is the asymmetry parameter satisfying \( a > 0 \) and \( \text{abs}(b) \leq a \). \( K_1 \) is the modified Bessel function of second kind (\texttt{scipy.special.k1}).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the \texttt{loc} and \texttt{scale} parameters. Specifically, \texttt{norminvgauss.pdf(x, a, b, loc, scale)} is identically equivalent to \texttt{norminvgauss.pdf(y, a, b) / scale} with \( y = (x - \text{loc}) / \text{scale} \).

A normal inverse Gaussian random variable \( Y \) with parameters \( a \) and \( b \) can be expressed as a normal mean-variance mixture: \( Y = b * V + \sqrt{V} * X \) where \( X \sim \text{norm}(0,1) \) and \( V \sim \text{invgauss}(\mu=1/\sqrt{a^2 - b^2}) \). This representation is used to generate random variates.

**References**


**Examples**

```python
>>> from scipy.stats import norminvgauss
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> a, b = 1, 0.5
>>> mean, var, skew, kurt = norminvgauss.stats(a, b, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(norminvgauss.ppf(0.01, a, b),
...                 norminvgauss.ppf(0.99, a, b), 100)
>>> ax.plot(x, norminvgauss.pdf(x, a, b),
...          'r-', lw=5, alpha=0.6, label='norminvgauss pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = norminvgauss(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of \texttt{cdf} and \texttt{ppf}:

```python
>>> vals = norminvgauss.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], norminvgauss.cdf(vals, a, b))
```

6.27. Statistical functions (\texttt{scipy.stats})
Generate random numbers:

```python
>>> r = norminvgauss.rvs(a, b, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

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<td>Percent point function (inverse of (cdf) — percentiles).</td>
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<td><code>isf(q, a, b, loc=0, scale=1)</code></td>
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<td>Non-central moment of order (n)</td>
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<td><code>entropy(a, b, loc=0, scale=1)</code></td>
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<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, a, b, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains (alpha) percent of the distribution</td>
</tr>
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</table>

**scipy.stats.pareto**

`scipy.stats.pareto = <scipy.stats._continuous_distns.pareto_gen object>`  
A Pareto continuous random variable.

As an instance of the `rv_continuous` class, `pareto` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `pareto` is:

\[
 f(x, b) = \frac{b}{x^{b+1}}
\]

for \(x \geq 1, b > 0\).

`pareto` takes \(b\) as a shape parameter for \(b\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `pareto.pdf(x, b, loc, scale)` is identically equivalent to `pareto.pdf(y, b) / scale` with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
globals()['__file__'] = __file__
from scipy.stats import pareto
import matplotlib.pyplot as plt
fig, ax = plt.subplots(1, 1)
```
Calculate a few first moments:

```python
>>> b = 2.62
>>> mean, var, skew, kurt = pareto.stats(b, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(pareto.ppf(0.01, b),
...                   pareto.ppf(0.99, b), 100)
>>> ax.plot(x, pareto.pdf(x, b),
...          'r-', lw=5, alpha=0.6, label='pareto pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = pareto(b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = pareto.ppf([0.001, 0.5, 0.999], b)
>>> np.allclose([0.001, 0.5, 0.999], pareto.cdf(vals, b))
```

Generate random numbers:

```python
>>> r = pareto.rvs(b, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

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<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, b, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, b, loc=0, scale=1)</td>
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</tr>
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<td>cdf(x, b, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
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<td>logcdf(x, b, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, b, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, b, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, b, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, b, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, b, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(b, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(b, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, b, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(b,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(b, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(b, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(b, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(b, loc=0, scale=1)</td>
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</tr>
<tr>
<td>interval(alpha, b, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

**scipy.stats.pearson3**

A Pearson type III continuous random variable.

As an instance of the `rv_continuous` class, `pearson3` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `pearson3` is:

\[
f(x, \text{skew}) = \frac{|\beta|}{\Gamma(\alpha)} (\beta (x - \zeta))^{\alpha - 1} \exp(-\beta (x - \zeta))
\]

where:

\[
\beta = \frac{2}{\text{skewstddev}} \alpha = (\text{stddev} \beta)^2 \zeta = \text{loc} - \frac{\alpha}{\beta}
\]

\(\Gamma\) is the gamma function (scipy.special.gamma). `pearson3` takes `skew` as a shape parameter for `skew`.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `pearson3.pdf(x, skew, loc, scale)` is identically equivalent to `pearson3.pdf(y, skew) / scale` with \(y = (x - \text{loc}) / \text{scale}\).
References

Examples
```python
>>> from scipy.stats import pearson3
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:
```n
```python
>>> skew = 0.1
>>> mean, var, skew, kurt = pearson3.stats(skew, moments='mvsk')
```

Display the probability density function (pdf):
```python
>>> x = np.linspace(pearson3.ppf(0.01, skew),
...                  pearson3.ppf(0.99, skew), 100)
>>> ax.plot(x, pearson3.pdf(x, skew),
...          'r-', lw=5, alpha=0.6, label='pearson3 pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:
```python
>>> rv = pearson3(skew)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:
```python
>>> vals = pearson3.ppf([0.001, 0.5, 0.999], skew)
>>> np.allclose([0.001, 0.5, 0.999], pearson3.cdf(vals, skew))
True
```

Generate random numbers:
```python
>>> r = pearson3.rvs(skew, size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

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<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, skew, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, skew, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, skew, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, skew, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, skew, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, skew, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, skew, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, skew, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, skew, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(skew, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(skew, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, skew, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(skew,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(skew, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(skew, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
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<td>var(skew, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(skew, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, skew, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
</tr>
</tbody>
</table>

**scipy.stats.powerlaw**

```python
scipy.stats.powerlaw = <scipy.stats._continuous_distns.powerlaw_gen object>
```

A power-function continuous random variable.
As an instance of the \texttt{rv\_continuous} class, \texttt{powerlaw} object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

\textbf{Notes}

The probability density function for \texttt{powerlaw} is:

\[ f(x, a) = ax^{a-1} \]

for \(0 \leq x \leq 1, \ a > 0\).

\texttt{powerlaw} takes \(a\) as a shape parameter for \(a\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the \texttt{loc} and \texttt{scale} parameters. Specifically, \texttt{powerlaw.pdf(x, a, loc, scale)} is identically equivalent to \texttt{powerlaw.pdf(y, a) / scale} with \(y = (x - \text{loc}) / \text{scale}\).

\texttt{powerlaw} is a special case of \texttt{beta} with \(b=1\).

\textbf{Examples}

```python
>>> from scipy.stats import powerlaw
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> a = 1.66
>>> mean, var, skew, kurt = powerlaw.stats(a, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(powerlaw.ppf(0.01, a), ...
... powerlaw.ppf(0.99, a), 100)
>>> ax.plot(x, powerlaw.pdf(x, a), ...
... 'r-', lw=5, alpha=0.6, label='powerlaw pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = powerlaw(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = powerlaw.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], powerlaw.cdf(vals, a))
True
```

Generate random numbers:

```python
>>> r = powerlaw.rvs(a, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### scipy.stats.powerlognorm

```python
scipy.stats.powerlognorm = <scipy.stats._continuous_distns.powerlognorm_gen object>
```

A power log-normal continuous random variable.

### Methods

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<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
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<td>Log of the survival function.</td>
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<tr>
<td>ppf(q, a, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
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<tr>
<td>isf(q, a, loc=0, scale=1)</td>
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<td>Non-central moment of order n</td>
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<tr>
<td>stats(a, loc=0, scale=1, moments='mv')</td>
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<td>entropy(a, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, a, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(a,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(a, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(a, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(a, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(a, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, a, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>
As an instance of the `rv_continuous` class, `powerlognorm` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `powerlognorm` is:

\[ f(x, c, s) = \frac{c}{xs} \phi(\log(x)/s)(\Phi(-\log(x)/s))^{c-1} \]

where \( \phi \) is the normal pdf, and \( \Phi \) is the normal cdf, and \( x > 0, s, c > 0 \).

`powerlognorm` takes \( c \) and \( s \) as shape parameters.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `powerlognorm.pdf(x, c, s, loc, scale)` is identically equivalent to `powerlognorm.pdf(y, c, s) / scale` with \( y = (x - loc) / scale \).

**Examples**

```python
>>> from scipy.stats import powerlognorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> c, s = 2.14, 0.446
>>> mean, var, skew, kurt = powerlognorm.stats(c, s, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(powerlognorm.ppf(0.01, c, s),
...                  powerlognorm.ppf(0.99, c, s), 100)
>>> ax.plot(x, powerlognorm.pdf(x, c, s),
...         'r-', lw=5, alpha=0.6, label='powerlognorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = powerlognorm(c, s)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = powerlognorm.ppf([0.001, 0.5, 0.999], c, s)
>>> np.allclose([0.001, 0.5, 0.999], powerlognorm.cdf(vals, c, s))
True
```

Generate random numbers:

```python
>>> r = powerlognorm.rvs(c, s, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
scipy.stats.powernorm

scipy.stats.powernorm = <scipy.stats._continuous_distns.powernorm_gen object>

A power normal continuous random variable.

### Statistical functions (scipy.stats)

Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
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<tbody>
<tr>
<td>rvs(c, s, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, c, s, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, c, s, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, c, s, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, c, s, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, c, s, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, c, s, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, c, s, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, c, s, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, c, s, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(c, s, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(c, s, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, c, s, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(c, s), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(c, s, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(c, s, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(c, s, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(c, s, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, c, s, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>
As an instance of the `rv_continuous` class, `powernorm` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `powernorm` is:

\[ f(x, c) = c \phi(x)(\Phi(-x))^{c-1} \]

where \( \phi \) is the normal pdf, and \( \Phi \) is the normal cdf, and \( x > 0, c > 0 \).

`powernorm` takes \( c \) as a shape parameter for \( c \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the \( \text{loc} \) and \( \text{scale} \) parameters. Specifically, `powernorm.pdf(x, c, \text{loc}, \text{scale})` is identically equivalent to `powernorm.pdf(y, c) / scale` with \( y = (x - \text{loc}) / \text{scale} \).

**Examples**
```python
>>> from scipy.stats import powernorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```
Calculate a few first moments:
```python
>>> c = 4.45
>>> mean, var, skew, kurt = powernorm.stats(c, moments='mvsk')
```
Display the probability density function (pdf):
```python
>>> x = np.linspace(powernorm.ppf(0.01, c), ...
... powernorm.ppf(0.99, c), 100)
>>> ax.plot(x, powernorm.pdf(x, c), ...
... 'r-', lw=5, alpha=0.6, label='powernorm pdf')
```
Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:
```python
>>> rv = powernorm(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```
Check accuracy of cdf and ppf:
```python
>>> vals = powernorm.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], powernorm.cdf(vals, c))
True
```
Generate random numbers:
```python
>>> r = powernorm.rvs(c, size=1000)
```
And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

<table>
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</tr>
</thead>
<tbody>
<tr>
<td>rvs(c, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, c, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, c, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, c, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, c, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, c, loc=0, scale=1)</td>
<td>Survival function (also defined as $1 - cdf$, but $sf$ is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, c, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, c, loc=0, scale=1)</td>
<td>Percent point function (inverse of $cdf$ — percentiles).</td>
</tr>
<tr>
<td>isf(q, c, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of $sf$).</td>
</tr>
<tr>
<td>moment(n, c, loc=0, scale=1)</td>
<td>Non-central moment of order $n$</td>
</tr>
<tr>
<td>stats(c, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(c, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, c, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(c, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(c, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(c, loc=0, scale=1)</td>
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</tr>
<tr>
<td>std(c, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, c, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

scipy.stats.rdist

scipy.stats.rdist = <scipy.stats._continuous_distns.rdist_gen object>

An R-distributed continuous random variable.
As an instance of the `rv_continuous` class, `rdist` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `rdist` is:

\[ f(x, c) = \frac{(1 - x^2)^{c/2-1}}{B(1/2, c/2)} \]

for \(-1 \leq x \leq 1, c > 0\).

`rdist` takes \(c\) as a shape parameter for \(c\).

This distribution includes the following distribution kernels as special cases:

<table>
<thead>
<tr>
<th>(c)</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>uniform</td>
</tr>
<tr>
<td>4</td>
<td>Epanechnikov (parabolic)</td>
</tr>
<tr>
<td>6</td>
<td>quartic (biweight)</td>
</tr>
<tr>
<td>8</td>
<td>triweight</td>
</tr>
</tbody>
</table>

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `rdist.pdf(x, c, loc, scale)` is identically equivalent to `rdist.pdf(y, c) / scale` with \(y = (x - loc) / scale\).

**Examples**

```python
>>> from scipy.stats import rdist
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> c = 0.9
>>> mean, var, skew, kurt = rdist.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(rdist.ppf(0.01, c),
...                  rdist.ppf(0.99, c), 100)
>>> ax.plot(x, rdist.pdf(x, c),
...          'r-', lw=5, alpha=0.6, label='rdist pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = rdist(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

```python
>>> vals = rdist.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], rdist.cdf(vals, c))
```

Generate random numbers:
>>> r = rdist.rvs(c, size=1000)

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
## Methods

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<td>rvs(c, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, c, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, c, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, c, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, c, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, c, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
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<tr>
<td>logsf(x, c, loc=0, scale=1)</td>
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</tr>
<tr>
<td>ppf(q, c, loc=0, scale=1)</td>
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<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, c, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(c, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(c, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, c, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
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<td>var(c, loc=0, scale=1)</td>
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<tr>
<td>std(c, loc=0, scale=1)</td>
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</tr>
<tr>
<td>interval(alpha, c, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

### scipy.stats.reciprocal

**scipy.stats.reciprocal** = <scipy.stats._continuous_distns.reciprocal_gen object>

A reciprocal continuous random variable.

As an instance of the *rv_continuous* class, *reciprocal* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for *reciprocal* is:

\[
f(x, a, b) = \frac{1}{x \log(b/a)}
\]

for \(a \leq x \leq b, \ b > a > 0\).

*reciprocal* takes \(a\) and \(b\) as shape parameters.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the *loc* and *scale* parameters. Specifically, *reciprocal.pdf*(x, a, b, loc, scale) is identically equivalent to *reciprocal.pdf*(y, a, b) / scale with y = (x - loc) / scale.

**Examples**

```python
>>> from scipy.stats import reciprocal
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```
Calculate a few first moments:

```python
>>> a, b = 0.00623, 1.01
>>> mean, var, skew, kurt = reciprocal.stats(a, b, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(reciprocal.ppf(0.01, a, b),
...                  reciprocal.ppf(0.99, a, b), 100)
>>> ax.plot(x, reciprocal.pdf(x, a, b),
...         'r-', lw=5, alpha=0.6, label='reciprocal pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = reciprocal(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = reciprocal.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], reciprocal.cdf(vals, a, b))
True
```

Generate random numbers:

```python
>>> r = reciprocal.rvs(a, b, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

<table>
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<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rvs(a, b, loc=0, scale=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, a, b, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, a, b, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, a, b, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, a, b, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, a, b, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, a, b, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, a, b, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, a, b, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, a, b, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(a, b, loc=0, scale=1, moments='mv')</td>
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</tr>
<tr>
<td>entropy(a, b, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, a, b, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(a, b), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(a, b, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(a, b, loc=0, scale=1)</td>
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<td>var(a, b, loc=0, scale=1)</td>
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<td>std(a, b, loc=0, scale=1)</td>
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</tr>
<tr>
<td>interval(alpha, a, b, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

**scipy.stats.rayleigh**

scipy.stats.rayleigh = <scipy.stats._continuous_distns.rayleigh_gen object>

A Rayleigh continuous random variable.

As an instance of the `rv_continuous` class, rayleigh object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `rayleigh` is:

\[
f(x) = x \exp(-x^2/2)
\]

for \(x \geq 0\).

`rayleigh` is a special case of `chi` with \(df=2\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `rayleigh.pdf(x, loc, scale)` is identically equivalent to `rayleigh.pdf(y) / scale` with \(y = (x - loc) / scale\).

**Examples**

```python
>>> from scipy.stats import rayleigh
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```
Calculate a few first moments:

```python
>>> mean, var, skew, kurt = rayleigh.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(rayleigh.ppf(0.01),
...                   rayleigh.ppf(0.99), 100)
>>> ax.plot(x, rayleigh.pdf(x),
...          'r-', lw=5, alpha=0.6, label='rayleigh pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = rayleigh()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = rayleigh.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], rayleigh.cdf(vals))
True
```

Generate random numbers:

```python
>>> r = rayleigh.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

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</tr>
<tr>
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<tr>
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</tr>
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</tr>
<tr>
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<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
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</tr>
<tr>
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<td>Percent point function (inverse of cdf — percentiles).</td>
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</tr>
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<td>fit(data, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
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<td>expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
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</tr>
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<td>interval(alpha, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
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</table>

`scipy.stats.rice`

`scipy.stats.rice = <scipy.stats._continuous_distns.rice_gen object>`

A Rice continuous random variable.

As an instance of the `rv_continuous` class, `rice` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for `rice` is:

\[ f(x, b) = x \exp \left( -\frac{x^2 + b^2}{2} \right) I_0(xb) \]

for \( x > 0, b > 0 \). \( I_0 \) is the modified Bessel function of order zero (`scipy.special.i0`).

`rice` takes \( b \) as a shape parameter for \( b \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `rice.pdf(x, b, loc, scale)` is identically equivalent to `rice.pdf(y, b) / scale` with \( y = (x - loc) / scale \).

The Rice distribution describes the length, \( r \), of a 2-D vector with components \((U + u, V + v)\), where \( U, V \) are constant, \( u, v \) are independent Gaussian random variables with standard deviation \( s \). Let \( R = \sqrt{U^2 + V^2} \). Then the pdf of \( r \) is `rice.pdf(x, R/s, scale=s)`.
Examples

```python
>>> from scipy.stats import rice
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> b = 0.775
>>> mean, var, skew, kurt = rice.stats(b, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(rice.ppf(0.01, b),
...                 rice.ppf(0.99, b), 100)
>>> ax.plot(x, rice.pdf(x, b),
...         'r-', lw=5, alpha=0.6, label='rice pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = rice(b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = rice.ppf([0.001, 0.5, 0.999], b)
>>> np.allclose([0.001, 0.5, 0.999], rice.cdf(vals, b))
True
```

Generate random numbers:

```python
>>> r = rice.rvs(b, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

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<td><code>fit(data, b, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, args=(b,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
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<td><code>interval(alpha, b, loc=0, scale=1)</code></td>
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**scipy.stats.recipinvgauss**

```python
scipy.stats.recipinvgauss = <scipy.stats._continuous_distns.recipinvgauss_gen object>
```

A reciprocal inverse Gaussian continuous random variable.
As an instance of the `rv_continuous` class, `recipinvgauss` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `recipinvgauss` is:

\[ f(x, \mu) = \frac{1}{\sqrt{2\pi x}} \exp\left(-\frac{(1 - \mu x)^2}{2\mu^2 x}\right) \]

for \( x \geq 0 \).

`recipinvgauss` takes \( \mu \) as a shape parameter for \( \mu \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `recipinvgauss.pdf(x, \mu, loc, scale)` is identically equivalent to `recipinvgauss.pdf(y, \mu) / scale` with \( y = (x - \text{loc}) / \text{scale} \).

**Examples**

```python
>>> from scipy.stats import recipinvgauss
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> mu = 0.63
>>> mean, var, skew, kurt = recipinvgauss.stats(mu, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(recipinvgauss.ppf(0.01, mu), ...
...                   recipinvgauss.ppf(0.99, mu), 100)
>>> ax.plot(x, recipinvgauss.pdf(x, mu), ...
...          'r-', lw=5, alpha=0.6, label='recipinvgauss pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = recipinvgauss(mu)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = recipinvgauss.ppf([0.001, 0.5, 0.999], mu)
>>> np.allclose([0.001, 0.5, 0.999], recipinvgauss.cdf(vals, mu))
True
```

Generate random numbers:

```python
>>> r = recipinvgauss.rvs(mu, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

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<td><code>sf(x, mu, loc=0, scale=1)</code></td>
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<td><code>logsf(x, mu, loc=0, scale=1)</code></td>
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<td><code>ppf(q, mu, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
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<tr>
<td><code>moment(n, mu, loc=0, scale=1)</code></td>
<td>Non-central moment of order n</td>
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<tr>
<td><code>stats(mu, loc=0, scale=1, moments='mv')</code></td>
<td>Mean(‘m’), variance(‘v’), skew(‘s’), and/or kurtosis(‘k’).</td>
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<td><code>entropy(mu, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
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<td><code>fit(data, mu, loc=0, scale=1)</code></td>
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<tr>
<td><code>interval(alpha, mu, loc=0, scale=1)</code></td>
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**scipy.stats.semicircular**

`scipy.stats.semicircular = <scipy.stats._continuous_distns.semicircular_gen object>`

A semicircular continuous random variable.
As an instance of the `rv_continuous` class, `semicircular` object inherits from it a collection of
generic methods (see below for the full list), and completes them with details specific for this particular
distribution.

**Notes**
The probability density function for `semicircular` is:

\[ f(x) = \frac{2}{\pi} \sqrt{1 - x^2} \]

for \(-1 \leq x \leq 1\).

The probability density above is defined in the “standardized” form. To shift and/or scale the dis-
tribution use the `loc` and `scale` parameters. Specifically, `semicircular.pdf(x, loc, scale)` is
identically equivalent to `semicircular.pdf(y) / scale` with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
>>> from scipy.stats import semicircular
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> mean, var, skew, kurt = semicircular.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(semicircular.ppf(0.01),
...                 semicircular.ppf(0.99), 100)
>>> ax.plot(x, semicircular.pdf(x),
...          'r-', lw=5, alpha=0.6, label='semicircular pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale
parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = semicircular()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = semicircular.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], semicircular.cdf(vals))
```

Generate random numbers:

```python
>>> r = semicircular.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

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scipy.stats.skewnorm

scipy.stats.skewnorm = <scipy.stats._continuous_distns.skew_norm_gen object>

A skew-normal random variable.
As an instance of the `rv_continuous` class, `skewnorm` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The pdf is:

```python
skewnorm.pdf(x, a) = 2 * norm.pdf(x) * norm.cdf(a*x)
```

`skewnorm` takes a real number `a` as a skewness parameter When `a = 0` the distribution is identical to a normal distribution (`norm`). `rvs` implements the method of [1].

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `skewnorm.pdf(x, a, loc, scale)` is identically equivalent to `skewnorm.pdf(y, a) / scale` with `y = (x - loc) / scale`.

**References**
[1]

**Examples**
```python
>>> from scipy.stats import skewnorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:
```a = 4
>>> mean, var, skew, kurt = skewnorm.stats(a, moments='mvsk')

Display the probability density function (pdf):
```x = np.linspace(skewnorm.ppf(0.01, a),
                  skewnorm.ppf(0.99, a), 100)
>>> ax.plot(x, skewnorm.pdf(x, a),
          lw=5, alpha=0.6, label='skewnorm pdf')

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:
```rv = skewnorm(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')

Check accuracy of cdf and ppf:
```vals = skewnorm.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], skewnorm.cdf(vals, a))
True

Generate random numbers:
```r = skewnorm.rvs(a, size=1000)

And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Skewnorm PDF and Frozen PDF]

**Methods**

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<td><code>ppf(q, a, loc=0, scale=1)</code></td>
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<td><code>expect(func, args=(a,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</code></td>
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<tr>
<td><code>median(a, loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(a, loc=0, scale=1)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(a, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(a, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, a, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
</tr>
</tbody>
</table>
scipy.stats.t

scipy.stats.t = <scipy.stats._continuous_distns.t_gen object>

A Student's t continuous random variable.

As an instance of the rv_continuous class, t object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for t is:

\[ f(x, \nu) = \frac{\Gamma((\nu + 1)/2)}{\sqrt{\pi \nu} \Gamma(\nu)} \left(1 + \frac{x^2}{\nu}\right)^{-(\nu+1)/2} \]

where \( x \) is a real number and the degrees of freedom parameter \( \nu \) (denoted df in the implementation) satisfies \( \nu > 0 \). \( \Gamma \) is the gamma function (scipy.special.gamma).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, \( t.pdf(x, \nu, \text{loc}, \text{scale}) \) is identically equivalent to \( t.pdf(y, \nu) / \text{scale} \) with \( y = (x - \text{loc}) / \text{scale} \).

Examples

```python
>>> from scipy.stats import t
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> df = 2.74
>>> mean, var, skew, kurt = t.stats(df, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(t.ppf(0.01, df), t.ppf(0.99, df), 100)
>>> ax.plot(x, t.pdf(x, df), 'r-', lw=5, alpha=0.6, label='t pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = t(df)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = t.ppf([0.001, 0.5, 0.999], df)
>>> np.allclose([0.001, 0.5, 0.999], t.cdf(vals, df))
True
```

Generate random numbers:

```python
>>> r = t.rvs(df, size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

**Methods**

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</tr>
</thead>
<tbody>
<tr>
<td>rvs(df, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, df, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, df, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, df, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, df, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, df, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 – cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, df, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, df, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, df, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, df, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(df, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(df, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, df, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(df,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(df, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(df, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(df, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(df, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, df, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>
scipy.stats.trapz

scipy.stats.trapz = <scipy.stats._continuous_distns.trapz_gen object>

A trapezoidal continuous random variable.

As an instance of the rv_continuous class, trapz object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The trapezoidal distribution can be represented with an up-sloping line from loc to \((\text{loc} + c \times \text{scale})\), then constant to \((\text{loc} + d \times \text{scale})\) and then downsloping from \((\text{loc} + d \times \text{scale})\) to \((\text{loc} + \text{scale})\).

\(\text{trapz}\) takes \(c\) and \(d\) as shape parameters.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the \(\text{loc}\) and \(\text{scale}\) parameters. Specifically, \(\text{trapz.pdf}(x, c, d, \text{loc}, \text{scale})\) is identically equivalent to \(\text{trapz.pdf}(y, c, d) / \text{scale}\) with \(y = (x - \text{loc}) / \text{scale}\).

The standard form is in the range \([0, 1]\) with \(c\) the mode. The location parameter shifts the start to \(\text{loc}\). The scale parameter changes the width from 1 to \(\text{scale}\).

Examples

```python
>>> from scipy.stats import trapz
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> c, d = 0.2, 0.8
>>> mean, var, skew, kurt = trapz.stats(c, d, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(trapz.ppf(0.01, c, d), ...
... trapz.ppf(0.99, c, d), 100)
>>> ax.plot(x, trapz.pdf(x, c, d), ...
... 'r-', lw=5, alpha=0.6, label='trapz pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = trapz(c, d)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = trapz.ppf([0.001, 0.5, 0.999], c, d)
>>> np.allclose([0.001, 0.5, 0.999], trapz.cdf(vals, c, d))
True
```

Generate random numbers:

```python
>>> r = trapz.rvs(c, d, size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

**Methods**

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<tr>
<td><code>rvs(c, d, loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, c, d, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, c, d, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, c, d, loc=0, scale=1)</code></td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td><code>logcdf(x, c, d, loc=0, scale=1)</code></td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td><code>sf(x, c, d, loc=0, scale=1)</code></td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, c, d, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, c, d, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, c, d, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>moment(n, c, d, loc=0, scale=1)</code></td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td><code>stats(c, d, loc=0, scale=1, moments='mv')</code></td>
<td>Mean(‘m’), variance(‘v’), skew(‘s’), and/or kurtosis(‘k’).</td>
</tr>
<tr>
<td><code>entropy(c, d, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
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<tr>
<td><code>fit(data, c, d, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, args=(c, d), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
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<td><code>median(c, d, loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
</tr>
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<td><code>mean(c, d, loc=0, scale=1)</code></td>
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<td><code>var(c, d, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(c, d, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, c, d, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>
scipy.stats.triang

scipy.stats.triang = <scipy.stats._continuous_distns.triang_gen object>

A triangular continuous random variable.

As an instance of the `rv_continuous` class, `triang` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The triangular distribution can be represented with an up-sloping line from `loc` to `(loc + c*scale)` and then downsloping for `(loc + c*scale)` to `(loc + scale)`.

`triang` takes `c` as a shape parameter for `c`.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `triang.pdf(x, c, loc, scale)` is identically equivalent to `triang.pdf(y, c) / scale` with `y = (x - loc) / scale`.

The standard form is in the range [0, 1] with `c` the mode. The location parameter shifts the start to `loc`. The scale parameter changes the width from 1 to `scale`.

Examples

```python
>>> from scipy.stats import triang
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> c = 0.158
>>> mean, var, skew, kurt = triang.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(triang.ppf(0.01, c), ... triang.ppf(0.99, c), 100)
>>> ax.plot(x, triang.pdf(x, c), ... 'r-', lw=5, alpha=0.6, label='triang pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = triang(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = triang.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], triang.cdf(vals, c))
```

Generate random numbers:

```python
>>> r = triang.rvs(c, size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

### Methods

<table>
<thead>
<tr>
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</tr>
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<tbody>
<tr>
<td>rvs(c, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, c, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, c, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, c, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, c, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, c, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, c, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, c, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, c, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
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<tr>
<td>moment(n, c, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
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<tr>
<td>stats(c, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
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<tr>
<td>entropy(c, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
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<tr>
<td>fit(data, c, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
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<tr>
<td>expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(c, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
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<td>mean(c, loc=0, scale=1)</td>
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<td>var(c, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
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<tr>
<td>std(c, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, c, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
</tr>
</tbody>
</table>
**scipy.stats.truncexpon**

**scipy.stats.truncexpon = <scipy.stats._continuous_distns.truncexpon_gen object>**

A truncated exponential continuous random variable.

As an instance of the `rv_continuous` class, `truncexpon` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `truncexpon` is:

\[
f(x, b) = \frac{\exp(-x)}{1 - \exp(-b)}
\]

for \(0 < x < b\).

`truncexpon` takes \(b\) as a shape parameter for \(b\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `truncexpon.pdf(x, b, loc, scale)` is identically equivalent to `truncexpon.pdf(y, b) / scale` with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
>>> from scipy.stats import truncexpon
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> b = 4.69
>>> mean, var, skew, kurt = truncexpon.stats(b, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(truncexpon.ppf(0.01, b), ...
                        truncexpon.ppf(0.99, b), 100)
>>> ax.plot(x, truncexpon.pdf(x, b), ...
                'r-', lw=5, alpha=0.6, label='truncexpon pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = truncexpon(b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = truncexpon.ppf([0.001, 0.5, 0.999], b)
>>> np.allclose([0.001, 0.5, 0.999], truncexpon.cdf(vals, b))
```

Generate random numbers:

```python
>>> r = truncexpon.rvs(b, size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Graph of truncated exponential distribution](image)

**Methods**

- `rvs(b, loc=0, scale=1, size=1, random_state=None)`
  - Random variates.

- `pdf(x, b, loc=0, scale=1)`
  - Probability density function.

- `logpdf(x, b, loc=0, scale=1)`
  - Log of the probability density function.

- `cdf(x, b, loc=0, scale=1)`
  - Cumulative distribution function.

- `logcdf(x, b, loc=0, scale=1)`
  - Log of the cumulative distribution function.

- `sf(x, b, loc=0, scale=1)`
  - Survival function (also defined as $1 - cdf$, but $sf$ is sometimes more accurate).

- `logsf(x, b, loc=0, scale=1)`
  - Log of the survival function.

- `ppf(q, b, loc=0, scale=1)`
  - Percent point function (inverse of cdf — percentiles).

- `isf(q, b, loc=0, scale=1)`
  - Inverse survival function (inverse of sf).

- `moment(n, b, loc=0, scale=1)`
  - Non-central moment of order n.

- `stats(b, loc=0, scale=1, moments='mv')`
  - Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').

- `entropy(b, loc=0, scale=1)`
  - (Differential) entropy of the RV.

- `fit(data, b, loc=0, scale=1)`
  - Parameter estimates for generic data.

- `expect(func, args=(b,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)`
  - Expected value of a function (of one argument) with respect to the distribution.

- `median(b, loc=0, scale=1)`
  - Median of the distribution.

- `mean(b, loc=0, scale=1)`
  - Mean of the distribution.

- `var(b, loc=0, scale=1)`
  - Variance of the distribution.

- `std(b, loc=0, scale=1)`
  - Standard deviation of the distribution.

- `interval(alpha, b, loc=0, scale=1)`
  - Endpoints of the range that contains alpha percent of the distribution.
scipy.stats.truncnorm

scipy.stats.truncnorm = <scipy.stats._continuous_distns.truncnorm_gen object>

A truncated normal continuous random variable.

As an instance of the rv_continuous class, truncnorm object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The standard form of this distribution is a standard normal truncated to the range [a, b] — notice that a and b are defined over the domain of the standard normal. To convert clip values for a specific mean and standard deviation, use:

\[
a, b = (\text{myclip}_a - \text{my}\_\text{mean}) / \text{my}\_\text{std}, (\text{myclip}_b - \text{my}\_\text{mean}) / \text{my}\_\text{std}
\]

truncnorm takes a and b as shape parameters.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, \( \text{truncnorm.pdf}(x, a, b) / \text{scale} \) is identically equivalent to \( \text{truncnorm.pdf}(y, a, b) / \text{scale} \) with \( y = (x - \text{loc}) / \text{scale} \).

Examples

```python
>>> from scipy.stats import truncnorm
>>> import matplotlib.pyplot as plt

fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> a, b = 0.1, 2
>>> mean, var, skew, kurt = truncnorm.stats(a, b, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(truncnorm.ppf(0.01, a, b),
...                 truncnorm.ppf(0.99, a, b), 100)
>>> ax.plot(x, truncnorm.pdf(x, a, b),
...          'r-', lw=5, alpha=0.6, label='truncnorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = truncnorm(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = truncnorm.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], truncnorm.cdf(vals, a, b))
True
```

Generate random numbers:

```python
>>> r = truncnorm.rvs(a, b, size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Graph showing the difference between `truncnorm pdf` and `frozen pdf`]

### Methods

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<thead>
<tr>
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</tr>
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<tbody>
<tr>
<td><code>rvs(a, b, loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, a, b, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, a, b, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, a, b, loc=0, scale=1)</code></td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td><code>logcdf(x, a, b, loc=0, scale=1)</code></td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td><code>sf(x, a, b, loc=0, scale=1)</code></td>
<td>Survival function (also defined as $1 - cdf$, but $sf$ is sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, a, b, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, a, b, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, a, b, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of $sf$).</td>
</tr>
<tr>
<td><code>moment(n, a, b, loc=0, scale=1)</code></td>
<td>Non-central moment of order $n$.</td>
</tr>
<tr>
<td><code>stats(a, b, loc=0, scale=1, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy(a, b, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, a, b, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, args=(a, b), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
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<td><code>median(a, b, loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
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<td><code>std(a, b, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, a, b, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>
Scipy Reference Guide, Release 1.2.0

scipy.stats.tukeylambda

scipy.stats.tukeylambda = <scipy.stats._continuous_distns.tukeylambda_gen object>

A Tukey-Lamdba continuous random variable.

As an instance of the rv_continuous class, tukeylambda object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

A flexible distribution, able to represent and interpolate between the following distributions:

- Cauchy (\( \lambda = -1 \))
- logistic (\( \lambda = 0 \))
- approx Normal (\( \lambda = 0.14 \))
- uniform from -1 to 1 (\( \lambda = 1 \))

\texttt{tukeylambda} takes a real number \( \lambda \) (denoted \( \text{lam} \) in the implementation) as a shape parameter.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the \texttt{loc} and \texttt{scale} parameters. Specifically, \( \text{tukeylambda.pdf}(x, \lambda, \text{loc}, \text{scale}) \) is identically equivalent to \( \text{tukeylambda.pdf}(y, \lambda) / \text{scale} \) with \( y = (x - \text{loc}) / \text{scale} \).

Examples

```python
>>> from scipy.stats import tukeylambda
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> lam = 3.13
>>> mean, var, skew, kurt = tukeylambda.stats(lam, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(tukeylambda.ppf(0.01, lam),
... tukeylambda.ppf(0.99, lam), 100)
>>> ax.plot(x, tukeylambda.pdf(x, lam),
... 'r-', lw=5, alpha=0.6, label='tukeylambda pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = tukeylambda(lam)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of \texttt{cdf} and \texttt{ppf}:

```python
>>> vals = tukeylambda.ppf([0.001, 0.5, 0.999], lam)
>>> np.allclose([0.001, 0.5, 0.999], tukeylambda.cdf(vals, lam))
```

Generate random numbers:
>>> r = tukeylambda.rvs(lam, size=1000)

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

<table>
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<th>Description</th>
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<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, lam, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, lam, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
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<td>cdf(x, lam, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
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<td>sf(x, lam, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
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<td>isf(q, lam, loc=0, scale=1)</td>
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<td>moment(n, lam, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
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<tr>
<td>stats(lam, loc=0, scale=1, moments='mv')</td>
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<td>entropy(lam, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, lam, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(lam,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(lam, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
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<tr>
<td>mean(lam, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
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<td>var(lam, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(lam, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, lam, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

scipy.stats.uniform

scipy.stats.uniform = <scipy.stats._continuous_distns.uniform_gen object>

A uniform continuous random variable.

In the standard form, the distribution is uniform on [0, 1]. Using the parameters loc and scale, one obtains the uniform distribution on [loc, loc + scale].

As an instance of the rv_continuous class, uniform object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Examples

```python
>>> from scipy.stats import uniform
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> mean, var, skew, kurt = uniform.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(uniform.ppf(0.01),
                   uniform.ppf(0.99), 100)
```

(continues on next page)
Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = uniform()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = uniform.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], uniform.cdf(vals))
True
```

Generate random numbers:

```python
>>> r = uniform.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

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<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, loc=0, scale=1)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(x, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
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<td>logsf(x, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
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<td>ppf(q, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
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<td>isf(q, loc=0, scale=1)</td>
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<td>moment(n, loc=0, scale=1)</td>
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<td>stats(loc=0, scale=1, moments='mv')</td>
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<td>entropy(loc=0, scale=1)</td>
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</tr>
<tr>
<td>fit(data, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(loc=0, scale=1)</td>
<td>Median of the distribution.</td>
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<tr>
<td>interval(alpha, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
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</table>

#### scipy.stats.vonmises

**scipy.stats.vonmises = <scipy.stats._continuous_distns.vonmises_gen object>**

A Von Mises continuous random variable.

As an instance of the `rv_continuous` class, `vonmises` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability density function for `vonmises` and `vonmises_line` is:

\[
f(x, \kappa) = \frac{\exp(\kappa \cos(x))}{2\pi I_0(\kappa)}
\]

for \(-\pi \leq x \leq \pi, \kappa > 0\). \(I_0\) is the modified Bessel function of order zero (`scipy.special.i0`).

`vonmises` is a circular distribution which does not restrict the distribution to a fixed interval. Currently, there is no circular distribution framework in scipy. The `cdf` is implemented such that `cdf(x + 2*np.pi) = cdf(x) + 1`.

`vonmises_line` is the same distribution, defined on \([-\pi, \pi]\) on the real line. This is a regular (i.e. non-circular) distribution.

`vonmises` and `vonmises_line` take `kappa` as a shape parameter.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `vonmises.pdf(x, kappa, loc, scale)` is
identically equivalent to 
\[ \text{vonmises.pdf}(y, \kappa) / \text{scale} \] 
with 
\[ y = (x - \text{loc}) / \text{scale} \].

**Examples**

```python
>>> from scipy.stats import vonmises
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> kappa = 3.99
>>> mean, var, skew, kurt = vonmises.stats(kappa, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(vonmises.ppf(0.01, kappa), ...
...                 vonmises.ppf(0.99, kappa), 100)
>>> ax.plot(x, vonmises.pdf(x, kappa), ...
...         'r-', lw=5, alpha=0.6, label='vonmises pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = vonmises(kappa)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = vonmises.ppf([0.001, 0.5, 0.999], kappa)
>>> np.allclose([0.001, 0.5, 0.999], vonmises.cdf(vals, kappa))
True
```

Generate random numbers:

```python
>>> r = vonmises.rvs(kappa, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

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<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, kappa, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, kappa, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
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<tr>
<td><code>cdf(x, kappa, loc=0, scale=1)</code></td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td><code>logcdf(x, kappa, loc=0, scale=1)</code></td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td><code>sf(x, kappa, loc=0, scale=1)</code></td>
<td>Survival function (also defined as <code>1 - cdf</code>, but <code>sf</code> is sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, kappa, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, kappa, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of <code>cdf</code> — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, kappa, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of <code>sf</code>).</td>
</tr>
<tr>
<td><code>moment(n, kappa, loc=0, scale=1)</code></td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td><code>stats(kappa, loc=0, scale=1, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
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<tr>
<td><code>entropy(kappa, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, kappa, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, args=(kappa,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td><code>median(kappa, loc=0, scale=1)</code></td>
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<td><code>std(kappa, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
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<tr>
<td><code>interval(alpha, kappa, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
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</tbody>
</table>

```python
scipy.stats.vonmises_line

scipy.stats.vonmises_line = <scipy.stats._continuous_distns.vonmises_gen object>
```

A Von Mises continuous random variable.
As an instance of the `rv_continuous` class, `vonmises_line` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability density function for `vonmises` and `vonmises_line` is:

\[ f(x, \kappa) = \frac{\exp(\kappa \cos(x))}{2\pi I_0(\kappa)} \]

for \(-\pi \leq x \leq \pi, \kappa > 0\). \(I_0\) is the modified Bessel function of order zero (scipy.special.i0).

`vonmises` is a circular distribution which does not restrict the distribution to a fixed interval. Currently, there is no circular distribution framework in scipy. The cdf is implemented such that cdf(x + 2*np.pi) == cdf(x) + 1.

`vonmises_line` is the same distribution, defined on \([-\pi, \pi]\) on the real line. This is a regular (i.e. non-circular) distribution.

`vonmises` and `vonmises_line` take \(\kappa\) as a shape parameter.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the \(\text{loc}\) and \(\text{scale}\) parameters. Specifically, `vonmises_line.pdf(x, \kappa, \text{loc}, \text{scale})` is identically equivalent to `vonmises_line.pdf(y, \kappa) / \text{scale}` with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
>>> from scipy.stats import vonmises_line
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> kappa = 3.99
>>> mean, var, skew, kurt = vonmises_line.stats(kappa, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(vonmises_line.ppf(0.01, kappa),
...                  vonmises_line.ppf(0.99, kappa), 100)
>>> ax.plot(x, vonmises_line.pdf(x, kappa),
...         'r-', lw=5, alpha=0.6, label='vonmises_line pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = vonmises_line(kappa)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = vonmises_line.ppf([0.001, 0.5, 0.999], kappa)
>>> np.allclose([0.001, 0.5, 0.999], vonmises_line.cdf(vals, kappa))
True
```

Generate random numbers:
>>> r = vonmises_line.rvs(kappa, size=1000)

And compare the histogram:

>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
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</tr>
<tr>
<td>interval(alpha, kappa, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

scipy.stats.wald

scipy.stats.wald = <scipy.stats._continuous_distns.wald_gen object>

A Wald continuous random variable.

As an instance of the rv_continuous class, wald object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for wald is:

\[
f(x) = \frac{1}{\sqrt{2\pi x^3}} \exp\left(- \frac{(x - 1)^2}{2x}\right)
\]

for \( x > 0 \).

wald is a special case of invgauss with mu=1.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, wald.pdf(x, loc, scale) is identically equivalent to wald.pdf(y) / scale with y = (x - loc) / scale.

Examples

```python
>>> from scipy.stats import wald
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```
Calculate a few first moments:

```python
>>> mean, var, skew, kurt = wald.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(wald.ppf(0.01), ...
...                 wald.ppf(0.99), 100)
>>> ax.plot(x, wald.pdf(x), ...
...          'r-', lw=5, alpha=0.6, label='wald pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = wald()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = wald.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], wald.cdf(vals))
True
```

Generate random numbers:

```python
>>> r = wald.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

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<tbody>
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</tr>
<tr>
<td><code>pdf(x, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, loc=0, scale=1)</code></td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td><code>logcdf(x, loc=0, scale=1)</code></td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td><code>sf(x, loc=0, scale=1)</code></td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>moment(n, loc=0, scale=1)</code></td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td><code>stats(loc=0, scale=1, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy(loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td><code>median(loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(loc=0, scale=1)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
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</table>

scipy.stats.weibull_min

`scipy.stats.weibull_min = <scipy.stats._continuous_distns.weibull_min_gen object>`

Weibull minimum continuous random variable.

As an instance of the `rv_continuous` class, `weibull_min` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

weibull_max

Notes

The probability density function for `weibull_min` is:

\[ f(x, c) = cx^{c-1} \exp(-x^c) \]

for \(x > 0, c > 0\).

`weibull_min` takes \(c\) as a shape parameter for \(c\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `weibull_min.pdf(x, c, loc, scale)` is identically equivalent to `weibull_min.pdf(y, c) / scale` with \(y = (x - loc) / scale\).
Examples

```python
>>> from scipy.stats import weibull_min
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> c = 1.79
>>> mean, var, skew, kurt = weibull_min.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(weibull_min.ppf(0.01, c),
...                 weibull_min.ppf(0.99, c), 100)
>>> ax.plot(x, weibull_min.pdf(x, c),
...          'r-', lw=5, alpha=0.6, label='weibull_min pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = weibull_min(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = weibull_min.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], weibull_min.cdf(vals, c))
True
```

Generate random numbers:

```python
>>> r = weibull_min.rvs(c, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
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</thead>
<tbody>
<tr>
<td><code>rvs(c, loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, c, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, c, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, c, loc=0, scale=1)</code></td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td><code>logcdf(x, c, loc=0, scale=1)</code></td>
<td>Log of the cumulative distribution function.</td>
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<td>Survival function (also defined as $1 - \text{cdf}$, but $\text{sf}$ is sometimes more accurate).</td>
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<td><code>logsf(x, c, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
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<td>Percent point function (inverse of cdf — percentiles).</td>
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<td>Inverse survival function (inverse of sf).</td>
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<tr>
<td><code>moment(n, c, loc=0, scale=1)</code></td>
<td>Non-central moment of order $n$</td>
</tr>
<tr>
<td><code>stats(c, loc=0, scale=1, moments='mv')</code></td>
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<td><code>entropy(c, loc=0, scale=1)</code></td>
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<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
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</table>

### scipy.stats.weibull_max

`scipy.stats.weibull_max = <scipy.stats._continuous_distns.weibull_max_gen object>`

Weibull maximum continuous random variable.
As an instance of the `rv_continuous` class, `weibull_max` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:
`weibull_min`

Notes
The probability density function for `weibull_max` is:

\[ f(x, c) = c (-x)^{c-1} \exp(-(-x)^c) \]

for \( x < 0 \), \( c > 0 \).

`weibull_max` takes \( c \) as a shape parameter for \( c \).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `weibull_max.pdf(x, c, loc, scale)` is identically equivalent to `weibull_max.pdf(y, c) / scale` with \( y = (x - loc) / scale \).

Examples
```python
>>> from scipy.stats import weibull_max
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:
```n
```python
>>> c = 2.87
>>> mean, var, skew, kurt = weibull_max.stats(c, moments='mvsk')
```

Display the probability density function (pdf):
```python
>>> x = np.linspace(weibull_max.ppf(0.01, c), ...
...                weibull_max.ppf(0.99, c), 100)
>>> ax.plot(x, weibull_max.pdf(x, c), ...
...         'r-', lw=5, alpha=0.6, label='weibull_max pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:
```python
>>> rv = weibull_max(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:
```python
>>> vals = weibull_max.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], weibull_max.cdf(vals, c))
True
```

Generate random numbers:
```python
>>> r = weibull_max.rvs(c, size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

2.0
1.5
1.0
0.5
0.0
0.0
0.2
0.4
0.6
0.8
1.0
1.2
weibull_max pdf
frozen pdf

### Methods

<table>
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<tr>
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</tr>
</thead>
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<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, c, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
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<td>Log of the probability density function.</td>
</tr>
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</tr>
<tr>
<td>logcdf(x, c, loc=0, scale=1)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(x, c, loc=0, scale=1)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, c, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, c, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, c, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, c, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(c, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(c, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
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<td>fit(data, c, loc=0, scale=1)</td>
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<td>var(c, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
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<tr>
<td>std(c, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, c, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>
scipy.stats.wrapcauchy

scipy.stats.wrapcauchy = <scipy.stats._continuous_distns.wrapcauchy_gen object>
A wrapped Cauchy continuous random variable.

As an instance of the rv_continuous class, wrapcauchy object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes
The probability density function for wrapcauchy is:

\[ f(x, c) = \frac{1 - c^2}{2\pi(1 + c^2 - 2c\cos(x))} \]

for \(0 \leq x \leq 2\pi, 0 < c < 1\).

wrapcauchy takes \(c\) as a shape parameter for \(c\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, wrapcauchy.pdf(x, c, loc, scale) is identically equivalent to wrapcauchy.pdf(y, c) / scale with y = (x - loc) / scale.

Examples

```python
>>> from scipy.stats import wrapcauchy
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> c = 0.0311
>>> mean, var, skew, kurt = wrapcauchy.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(wrapcauchy.ppf(0.01, c), ...
... wrapcauchy.ppf(0.99, c), 100)
>>> ax.plot(x, wrapcauchy.pdf(x, c), ...
... 'r-', lw=5, alpha=0.6, label='wrapcauchy pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```python
>>> rv = wrapcauchy(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = wrapcauchy.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], wrapcauchy.cdf(vals, c))
True
```

Generate random numbers:

```python
>>> r = wrapcauchy.rvs(c, size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

### Methods

- **rvs(c, loc=0, scale=1, size=1, random_state=None)**: Random variates.
- **pdf(x, c, loc=0, scale=1)**: Probability density function.
- **logpdf(x, c, loc=0, scale=1)**: Log of the probability density function.
- **cdf(x, c, loc=0, scale=1)**: Cumulative distribution function.
- **logcdf(x, c, loc=0, scale=1)**: Log of the cumulative distribution function.
- **sf(x, c, loc=0, scale=1)**: Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).
- **logsf(x, c, loc=0, scale=1)**: Log of the survival function.
- **ppf(q, c, loc=0, scale=1)**: Percent point function (inverse of cdf — percentiles).
- **isf(q, c, loc=0, scale=1)**: Inverse survival function (inverse of sf).
- **moment(n, c, loc=0, scale=1)**: Non-central moment of order n
- **stats(c, loc=0, scale=1, moments='mv')**: Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
- **entropy(c, loc=0, scale=1)**: (Differential) entropy of the RV.
- **fit(data, c, loc=0, scale=1)**: Parameter estimates for generic data.
- **expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)**: Expected value of a function (of one argument) with respect to the distribution.
- **median(c, loc=0, scale=1)**: Median of the distribution.
- **mean(c, loc=0, scale=1)**: Mean of the distribution.
- **var(c, loc=0, scale=1)**: Variance of the distribution.
- **std(c, loc=0, scale=1)**: Standard deviation of the distribution.
- **interval(alpha, c, loc=0, scale=1)**: Endpoints of the range that contains alpha percent of the distribution.
6.27.5 Multivariate distributions

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<td>A multivariate normal random variable.</td>
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<tr>
<td>matrix_normal</td>
<td>A matrix normal random variable.</td>
</tr>
<tr>
<td>dirichlet</td>
<td>A Dirichlet random variable.</td>
</tr>
<tr>
<td>wishart</td>
<td>A Wishart random variable.</td>
</tr>
<tr>
<td>invwishart</td>
<td>An inverse Wishart random variable.</td>
</tr>
<tr>
<td>multinomial</td>
<td>A multinomial random variable.</td>
</tr>
<tr>
<td>special_ortho_group</td>
<td>A matrix-valued SO(N) random variable.</td>
</tr>
<tr>
<td>ortho_group</td>
<td>A matrix-valued O(N) random variable.</td>
</tr>
<tr>
<td>unitary_group</td>
<td>A matrix-valued U(N) random variable.</td>
</tr>
<tr>
<td>random_correlation</td>
<td>A random correlation matrix.</td>
</tr>
</tbody>
</table>

**scipy.stats.multivariate_normal**

scipy.stats.multivariate_normal = <scipy.stats._multivariate.multivariate_normal_gen object>

A multivariate normal random variable.

The `mean` keyword specifies the mean. The `cov` keyword specifies the covariance matrix.

**Parameters**

- **x** : [array_like] Quantiles, with the last axis of `x` denoting the components.
- **mean** : [array_like, optional] Mean of the distribution (default zero)
- **cov** : [array_like, optional] Covariance matrix of the distribution (default one)
- **allow_singular** : [bool, optional] Whether to allow a singular covariance matrix. (Default: False)
- **random_state** : [None or int or np.random.RandomState instance, optional] If int or RandomState, use it for drawing the random variates. If None (or np.random), the global np.random state is used. Default is None.

Alternatively, the object may be called (as a function) to fix the mean and covariance parameters, returning a “frozen” multivariate normal random variable:

```python
rv = multivariate_normal(mean=None, cov=1, allow_singular=False)
```

- Frozen object with the same methods but holding the given mean and covariance fixed.

**Notes**

*Setting the parameter mean to None is equivalent to having mean be* the zero-vector. The parameter `cov` can be a scalar, in which case the covariance matrix is the identity times that value, a vector of diagonal entries for the covariance matrix, or a two-dimensional array_like.

The covariance matrix `cov` must be a (symmetric) positive semi-definite matrix. The determinant and inverse of `cov` are computed as the pseudo-determinant and pseudo-inverse, respectively, so that `cov` does not need to have full rank.

The probability density function for `multivariate_normal` is

\[
f(x) = \frac{1}{\sqrt{(2\pi)^k \det \Sigma}} \exp \left( -\frac{1}{2} (x - \mu)^T \Sigma^{-1} (x - \mu) \right),
\]

where \( \mu \) is the mean, \( \Sigma \) the covariance matrix, and \( k \) is the dimension of the space where \( x \) takes values.

New in version 0.14.0.
Examples

```python
>>> import matplotlib.pyplot as plt
>>> from scipy.stats import multivariate_normal

>>> x = np.linspace(0, 5, 10, endpoint=False)
>>> y = multivariate_normal.pdf(x, mean=2.5, cov=0.5); y
array([0.00108914, 0.01033349, 0.05946514, 0.20755375, 0.43939129,
       0.56418958, 0.43939129, 0.20755375, 0.05946514, 0.01033349])
>>> fig1 = plt.figure()
>>> ax = fig1.add_subplot(111)
>>> ax.plot(x, y)
```

The input quantiles can be any shape of array, as long as the last axis labels the components. This allows us for instance to display the frozen pdf for a non-isotropic random variable in 2D as follows:

```python
>>> x, y = np.mgrid[-1:1:.01, -1:1:.01]
>>> pos = np.dstack((x, y))
>>> rv = multivariate_normal([0.5, -0.2], [[2.0, 0.3], [0.3, 0.5]])
>>> fig2 = plt.figure()
>>> ax2 = fig2.add_subplot(111)
>>> ax2.contourf(x, y, rv.pdf(pos))
```

Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>pdf(x, mean=None, cov=1, allow_singular=False)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, mean=None, cov=1, allow_singular=False)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, mean=None, cov=1, allow_singular=False, maxpts=100000*dim, abseps=1e-5, releps=1e-5)</code></td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td><code>logcdf(x, mean=None, cov=1, allow_singular=False, maxpts=100000*dim, abseps=1e-5, releps=1e-5)</code></td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td><code>rvs(mean=None, cov=1, size=1, random_state=None)</code></td>
<td>Draw random samples from a multivariate normal distribution.</td>
</tr>
<tr>
<td><code>entropy()</code></td>
<td>Compute the differential entropy of the multivariate normal.</td>
</tr>
</tbody>
</table>
scipy.stats.matrix_normal

scipy.stats.matrix_normal = <scipy.stats._multivariate.matrix_normal_gen object>

A matrix normal random variable.

The *mean* keyword specifies the mean. The *rowcov* keyword specifies the among-row covariance matrix. The ‘colcov’ keyword specifies the among-column covariance matrix.

**Parameters**

- **X** [array_like] Quantiles, with the last two axes of *X* denoting the components.
- **mean** [array_like, optional] Mean of the distribution (default: *None*).
- **rowcov** [array_like, optional] Among-row covariance matrix of the distribution (default: *I*).
- **colcov** [array_like, optional] Among-column covariance matrix of the distribution (default: *I*).
- **random_state** [None or int or np.random.RandomState instance, optional] If int or RandomState, use it for drawing the random variates. If None (or np.random), the global np.random state is used. Default is None.

Alternatively, the object may be called (as a function) to fix the mean and covariance parameters, returning a “frozen” matrix normal random variable:

```python
rv = matrix_normal(mean=None, rowcov=1, colcov=1)
```

- Frozen object with the same methods but holding the given mean and covariance fixed.

**Notes**

*If mean is set to None then a matrix of zeros is used for the mean.*

The dimensions of this matrix are inferred from the shape of *rowcov* and *colcov*, if these are provided, or set to *I* if ambiguous.

*rowcov* and *colcov* can be two-dimensional array_likes specifying the covariance matrices directly. Alternatively, a one-dimensional array will be be interpreted as the entries of a diagonal matrix, and a scalar or zero-dimensional array will be interpreted as this value times the identity matrix.
The covariance matrices specified by `rowcov` and `colcov` must be (symmetric) positive definite. If the samples in `X` are \(m \times n\), then `rowcov` must be \(m \times m\) and `colcov` must be \(n \times n\). `mean` must be the same shape as `X`.

The probability density function for `matrix_normal` is

\[
    f(X) = (2\pi)^{-mn/2} |U|^{-\frac{m}{2}} |V|^{-\frac{n}{2}} \exp \left( -\frac{1}{2} \text{Tr} \left[ U^{-1} (X - M) V^{-1} (X - M)^T \right] \right),
\]

where \(M\) is the mean, \(U\) the among-row covariance matrix, \(V\) the among-column covariance matrix.

The `allow_singular` behaviour of the `multivariate_normal` distribution is not currently supported. Covariance matrices must be full rank.

The `matrix_normal` distribution is closely related to the `multivariate_normal` distribution. Specifically, \(\text{Vec}(X)\) (the vector formed by concatenating the columns of \(X\)) has a multivariate normal distribution with mean \(\text{Vec}(M)\) and covariance \(V \otimes U\) (where \(\otimes\) is the Kronecker product). Sampling and pdf evaluation are \(O(m^3 + n^3 + m^2 n + mn^2)\) for the matrix normal, but \(O(m^3 n^3)\) for the equivalent multivariate normal, making this equivalent form algorithmically inefficient.

New in version 0.17.0.

**Examples**

```python
>>> from scipy.stats import matrix_normal

>>> M = np.arange(6).reshape(3,2); M
array([[0, 1],
       [2, 3],
       [4, 5]])

>>> U = np.diag([1,2,3]); U
array([[1, 0, 0],
       [0, 2, 0],
       [0, 0, 3]])

>>> V = 0.3*np.identity(2); V
array([[ 0.3, 0. ],
       [ 0. , 0.3]])

>>> X = M + 0.1; X
array([[0.1, 1.1],
       [2.1, 3.1],
       [4.1, 5.1]])

>>> matrix_normal.pdf(X, mean=M, rowcov=U, colcov=V)
0.023410202050005054

>>> # Equivalent multivariate normal
>>> from scipy.stats import multivariate_normal
>>> vectorised_X = X.T.flatten()
>>> equiv_mean = M.T.flatten()
>>> equiv_cov = np.kron(V,U)

>>> multivariate_normal.pdf(vectorised_X, mean=equiv_mean, cov=equiv_cov)
0.023410202050005054
```

**Methods**

```
```

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>&quot;pdf(X, mean=None, rowcov=1, colcov=1)&quot;</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>&quot;logpdf(X, mean=None, rowcov=1, colcov=1)&quot;</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>&quot;rvs(mean=None, rowcov=1, colcov=1, size=1, random_state=None)&quot;</td>
<td>Draw random samples.</td>
</tr>
</tbody>
</table>
scipy.stats.dirichlet

scipy.stats.dirichlet = <scipy.stats._multivariate.dirichlet_gen object>
A Dirichlet random variable.

The alpha keyword specifies the concentration parameters of the distribution.
New in version 0.15.0.

Parameters
x [array_like] Quantiles, with the last axis of x denoting the components.
alpha [array_like] The concentration parameters. The number of entries determines the
dimensionality of the distribution.

random_state
[None or int or np.random.RandomState instance, optional] If int or RandomState, use it for drawing the random variates. If None (or np.random), the global
np.random state is used. Default is None.

Alternatively, the object may be called (as a function) to fix
concentration parameters, returning a “frozen” Dirichlet
random variable:
rv = dirichlet(alpha)

- Frozen object with the same methods but holding the given concentration pa-
rameters fixed.

Notes
Each α entry must be positive. The distribution has only support on the simplex defined by

\[ \sum_{i=1}^{K} x_i \leq 1 \]

The probability density function for dirichlet is

\[ f(x) = \frac{1}{B(\alpha)} \prod_{i=1}^{K} x_i^{\alpha_i - 1} \]

where

\[ B(\alpha) = \frac{\prod_{i=1}^{K} \Gamma(\alpha_i)}{\Gamma(\sum_{i=1}^{K} \alpha_i)} \]

and \( \alpha = (\alpha_1, \ldots, \alpha_K) \), the concentration parameters and \( K \) is the dimension of the space where \( x \) takes values.

Note that the dirichlet interface is somewhat inconsistent. The array returned by the rvs function is
transposed with respect to the format expected by the pdf and logpdf.

Examples

```python
>>> from scipy.stats import dirichlet

Generate a dirichlet random variable
```

```python
>>> quantiles = np.array([0.2, 0.2, 0.6]) # specify quantiles
>>> alpha = np.array([0.4, 5, 15]) # specify concentration parameters
>>> dirichlet.pdf(quantiles, alpha)
```

The same PDF but following a log scale

0.2843831684937255
Once we specify the dirichlet distribution we can then calculate quantities of interest.

```python
dirichlet.logpdf(quantiles, alpha)
```

-1.2574327653159187

We can also return random samples from the distribution.

```python
dirichlet.rvs(alpha, size=1, random_state=1)
```

```
array([[0.00766178, 0.24670518, 0.74563305]])
```

```python
dirichlet.rvs(alpha, size=2, random_state=2)
```

```
array([[0.01639427, 0.12922730, 0.85437844],
       [0.00156917, 0.19033695, 0.80809388]])
```

Methods

- **pdf(x, alpha)**
  Probability density function.

- **logpdf(x, alpha)**
  Log of the probability density function.

- **rvs(alpha, size=1, random_state=None)**
  Draw random samples from a Dirichlet distribution.

- **mean(alpha)**
  The mean of the Dirichlet distribution.

- **var(alpha)**
  The variance of the Dirichlet distribution.

- **entropy(alpha)**
  Compute the differential entropy of the Dirichlet distribution.

scipy.stats.wishart

```
scipy.stats.wishart = <scipy.stats._multivariate.wishart_gen object>
```

A Wishart random variable.

The `df` keyword specifies the degrees of freedom. The `scale` keyword specifies the scale matrix, which must be symmetric and positive definite. In this context, the scale matrix is often interpreted in terms of a multivariate normal precision matrix (the inverse of the covariance matrix).

**Parameters**

- `x` [array_like] Quantiles, with the last axis of `x` denoting the components.
- `df` [int] Degrees of freedom, must be greater than or equal to dimension of the scale matrix.
- `scale` [array_like] Symmetric positive definite scale matrix of the distribution.
- `random_state` [None or int or np.random.RandomState instance, optional] If int or RandomState, use it for drawing the random variates. If None (or np.random), the global np.random.state is used. Default is None.

Alternatively, the object may be called (as a function) to fix the degrees of freedom and scale parameters, returning a “frozen” Wishart random variable:

```
rv = wishart(df=1, scale=1)
```
Frozen object with the same methods but holding the given degrees of freedom and scale fixed.

See also:

\texttt{invwishart}, \texttt{chi2}

Notes
The scale matrix \texttt{scale} must be a symmetric positive definite matrix. Singular matrices, including the symmetric positive semi-definite case, are not supported.

The Wishart distribution is often denoted

\[ W_p(\nu, \Sigma) \]

where \( \nu \) is the degrees of freedom and \( \Sigma \) is the \( p \times p \) scale matrix.

The probability density function for \texttt{wishart} has support over positive definite matrices \( S \); if \( S \sim W_p(\nu, \Sigma) \), then its PDF is given by:

\[
    f(S) = \frac{|S|^{\nu-p-\frac{1}{2}}}{2^{\frac{p^2}{2}}|\Sigma|^{\frac{p}{2}} \Gamma_p \left( \frac{\nu}{2} \right)} \exp \left( -\text{tr}(\Sigma^{-1}S)/2 \right)
\]

If \( S \sim W_p(\nu, \Sigma) \) (Wishart) then \( S^{-1} \sim W_p^{-1}(\nu, \Sigma^{-1}) \) (inverse Wishart).

If the scale matrix is 1-dimensional and equal to one, then the Wishart distribution \( W_1(\nu, 1) \) collapses to the \( \chi^2(\nu) \) distribution.

New in version 0.16.0.

References
[1], [2]

Examples

```python
>>> import matplotlib.pyplot as plt
>>> from scipy.stats import wishart, chi2
>>> x = np.linspace(1e-5, 8, 100)
>>> w = wishart.pdf(x, df=3, scale=1); w[:5]
array([ 0.00126156, 0.10892176, 0.14793434, 0.17400548, 0.1929669 ])
>>> c = chi2.pdf(x, 3); c[:5]
array([ 0.00126156, 0.10892176, 0.14793434, 0.17400548, 0.1929669 ])
>>> plt.plot(x, w)
```

The input quantiles can be any shape of array, as long as the last axis labels the components.

Methods

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>\texttt{pdf(x, df, scale)}</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>\texttt{logpdf(x, df, scale)}</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>\texttt{rvs(df, scale, size=1, random_state=None)}</td>
<td>Draw random samples from a Wishart distribution.</td>
</tr>
<tr>
<td>\texttt{entropy()}</td>
<td>Compute the differential entropy of the Wishart distribution.</td>
</tr>
</tbody>
</table>

\texttt{scipy.stats.invwishart}

\texttt{scipy.stats.invwishart} = <\texttt{scipy.stats._multivariate.invwishart_gen object}>

An inverse Wishart random variable.

The \texttt{df} keyword specifies the degrees of freedom. The \texttt{scale} keyword specifies the scale matrix, which must be symmetric and positive definite. In this context, the scale matrix is often interpreted in terms of a multivariate normal covariance matrix.
Parameters

- **x** [array_like] Quantiles, with the last axis of x denoting the components.
- **df** [int] Degrees of freedom, must be greater than or equal to dimension of the scale matrix.
- **scale** [array_like] Symmetric positive definite scale matrix of the distribution.
- **random_state** [None or int or np.random.RandomState instance, optional] If int or RandomState, use it for drawing the random variates. If None (or np.random), the global np.random state is used. Default is None.

Alternatively, the object may be called (as a function) to fix the degrees of freedom and scale parameters, returning a “frozen” inverse Wishart random variable:

```python
rv = invwishart(df=1, scale=1)
```

- Frozen object with the same methods but holding the given degrees of freedom and scale fixed.

See also:

- **wishart**

Notes

The scale matrix `scale` must be a symmetric positive definite matrix. Singular matrices, including the symmetric positive semi-definite case, are not supported.

The inverse Wishart distribution is often denoted

\[ W_p^{-1}(\nu, \Psi) \]

where \( \nu \) is the degrees of freedom and \( \Psi \) is the \( p \times p \) scale matrix.

The probability density function for `invwishart` has support over positive definite matrices \( S \); if \( S \sim W_p^{-1}(\nu, \Sigma) \), then its PDF is given by:

\[
f(S) = \frac{|\Sigma|^\frac{\nu}{2}}{2^\frac{\nu p}{2} |S|^{\frac{\nu + p + 1}{2}}} \Gamma_p \left( \frac{\nu}{2} \right) \exp \left( -tr(\Sigma S^{-1}) / 2 \right)
\]

If \( S \sim W_p^{-1}(\nu, \Psi) \) (inverse Wishart) then \( S^{-1} \sim W_p(\nu, \Psi^{-1}) \) (Wishart).
If the scale matrix is 1-dimensional and equal to one, then the inverse Wishart distribution $W_1(\nu, 1)$ collapses to the inverse Gamma distribution with parameters $\text{shape} = \frac{\nu}{2}$ and $\text{scale} = \frac{1}{2}$.

New in version 0.16.0.

References
[1], [2]

Examples

```python
>>> import matplotlib.pyplot as plt
>>> from scipy.stats import invwishart, invgamma
>>> x = np.linspace(0.01, 1, 100)
>>> iw = invwishart.pdf(x, df=6, scale=1)
>>> iw[:3]
array([1.20546865e-15, 5.42497807e-06, 4.45813929e-03])
>>> ig = invgamma.pdf(x, 6/2., scale=1/2)
>>> ig[:3]
array([1.20546865e-15, 5.42497807e-06, 4.45813929e-03])
>>> plt.plot(x, iw)
```

The input quantiles can be any shape of array, as long as the last axis labels the components.

```
0.0 0.2 0.4 0.6 0.8 1.0
0 1 2 3 4
```

Methods

```
`pdf(x, df, scale)` Probability density function.

`logpdf(x, df, scale)` Log of the probability density function.

`rvs(df, scale, size=1, random_state=None)` Draw random samples from an inverse Wishart distribution.

```
```

scipy.stats.multinomial

```python
scipy.stats.multinomial = <scipy.stats._multivariate.multinomial_gen object>
```
A multinomial random variable.

**Parameters**

- x | [array_like] Quantiles, with the last axis of $x$ denoting the components.
- n | [int] Number of trials
**SciPy Reference Guide, Release 1.2.0**

**random_state**

[None or int or np.random.RandomState instance, optional] If int or RandomState, use it for drawing the random variates. If None (or np.random), the global np.random state is used. Default is None.

**See also:**

* scipy.stats.binom
  The binomial distribution.

* numpy.random.multinomial
  Sampling from the multinomial distribution.

**Notes**

n should be a positive integer. Each element of p should be in the interval [0, 1] and the elements should sum to 1. If they do not sum to 1, the last element of the p array is not used and is replaced with the remaining probability left over from the earlier elements.

Alternatively, the object may be called (as a function) to fix the n and p parameters, returning a “frozen” multinomial random variable:

The probability mass function for multinomial is

\[
    f(x) = \frac{n!}{x_1! \cdots x_k!} p_1^{x_1} \cdots p_k^{x_k},
\]

supported on \( x = (x_1, \ldots, x_k) \) where each \( x_i \) is a nonnegative integer and their sum is n.

New in version 0.19.0.

**Examples**

```python
>>> from scipy.stats import multinomial
>>> rv = multinomial(8, [0.3, 0.2, 0.5])
>>> rv.pmf([1, 3, 4])
0.04200000000000072
```

The multinomial distribution for \( k = 2 \) is identical to the corresponding binomial distribution (tiny numerical differences notwithstanding):

```python
>>> from scipy.stats import binom
>>> multinomial.pmf([3, 4], n=7, p=[0.4, 0.6])
0.29030399999999973
>>> binom.pmf(3, 7, 0.4)
0.29030400000000012
```

The functions pmf, logpmf, entropy, and cov support broadcasting, under the convention that the vector parameters (x and p) are interpreted as if each row along the last axis is a single object. For instance:

```python
>>> multinomial.pmf([[3, 4], [3, 5]], n=[7, 8], p=[.3, .7])
array([0.2268945, 0.25412184])
```

Here, x.shape == (2, 2), n.shape == (2,), and p.shape == (2,), but following the rules mentioned above they behave as if the rows [3, 4] and [3, 5] in x and [.3, .7] in p were a single object, and as if we had x.shape == (2,), n.shape == (2,), and p.shape == (). To obtain the individual elements without broadcasting, we would do this:
This broadcasting also works for `cov`, where the output objects are square matrices of size `p.shape[−1]`. For example:

```python
>>> multinomial.cov([4, 5], [[.3, .7], [.4, .6]])
array([[[ 0.84, -0.84],
       [-0.84,  0.84]],
       [[ 1.2 , -1.2 ],
       [-1.2 ,  1.2 ]]])
```

In this example, `n.shape == (2,)` and `p.shape == (2, 2)`, and following the rules above, these broadcast as if `p.shape == (2,)`. Thus the result should also be of shape `(2,)`, but since each output is a $2 \times 2$ matrix, the result in fact has shape `(2, 2, 2)`, where `result[0]` is equal to `multinomial.cov(n=4, p=[.3, .7])` and `result[1]` is equal to `multinomial.cov(n=5, p=[.4, .6])`.

### Methods

- **`pmf(x, n, p)`** — Probability mass function.
- **`logpmf(x, n, p)`** — Log of the probability mass function.
- **`rvs(n, p, size=1, random_state=None)`** — Draw random samples from a multinomial distribution.
- **`entropy(n, p)`** — Compute the entropy of the multinomial distribution.
- **`cov(n, p)`** — Compute the covariance matrix of the multinomial distribution.

### scipy.stats.special_ortho_group

`scipy.stats.special_ortho_group = <scipy.stats._multivariate.special_ortho_group_gen object>`

A matrix-valued SO(N) random variable.

Return a random rotation matrix, drawn from the Haar distribution (the only uniform distribution on SO(n)).

The `dim` keyword specifies the dimension N.

#### Parameters

- **`dim`** — [scalar] Dimension of matrices

#### Notes

This class is wrapping the random_rot code from the MDP Toolkit, [https://github.com/mdp-toolkit/mdp-toolkit](https://github.com/mdp-toolkit/mdp-toolkit)

Return a random rotation matrix, drawn from the Haar distribution (the only uniform distribution on SO(n)). The algorithm is described in the paper Stewart, G.W., “The efficient generation of random orthogonal matrices with an application to condition estimators”, SIAM Journal on Numerical Analysis, 17(3), pp. 403-409, 1980. For more information see [https://en.wikipedia.org/wiki/Orthogonal_matrix#Randomization](https://en.wikipedia.org/wiki/Orthogonal_matrix#Randomization)

See also the similar `ortho_group`.

#### Examples

```python
>>> from scipy.stats import special_ortho_group
>>> x = special_ortho_group.rvs(3)
```
This generates one random matrix from SO(3). It is orthogonal and has a determinant of 1.

Methods

```
"rvs(dim=None, size=1, random_state=None)" | Draw random samples from SO(N).
```

`scipy.stats.ortho_group`

A matrix-valued O(N) random variable.

Return a random orthogonal matrix, drawn from the O(N) Haar distribution (the only uniform distribution on O(N)).

The `dim` keyword specifies the dimension N.

Parameters

- `dim` [scalar] Dimension of matrices

Notes

This class is closely related to `special_ortho_group`.

Some care is taken to avoid numerical error, as per the paper by Mezzadri.

References

[1]

Examples

```
from scipy.stats import ortho_group
x = ortho_group.rvs(3)
```

This generates one random matrix from O(3). It is orthogonal and has a determinant of +1 or -1.

Methods

```
"rvs(dim=None, size=1, random_state=None)" | Draw random samples from O(N).
```
scipy.stats.unitary_group

scipy.stats.unitary_group = <scipy.stats._multivariate.unitary_group_gen object>
A matrix-valued U(N) random variable.
Return a random unitary matrix.
The `dim` keyword specifies the dimension N.

**Parameters**
- **dim** [scalar] Dimension of matrices

**Notes**
This class is similar to ortho_group.

**References**
[1]

**Examples**

```python
>>> from scipy.stats import unitary_group
>>> x = unitary_group.rvs(3)
```

```python
def dot(x, x.conj().T):
    return np.array([[ 1.00000000e+00, 1.13231364e-17, -2.86852790e-16],
                     [ 1.13231364e-17, 1.00000000e+00, -1.46845020e-16],
                     [-2.86852790e-16, -1.46845020e-16, 1.00000000e+00]])
```

This generates one random matrix from U(3). The dot product confirms that it is unitary up to machine precision.

**Methods**
- **`rvs(dim=None, size=1, random_state=None)`** Draw random samples from U(N).

scipy.stats.random_correlation

scipy.stats.random_correlation = <scipy.stats._multivariate.random_correlation_gen object>
A random correlation matrix.
Return a random correlation matrix, given a vector of eigenvalues.
The `eigs` keyword specifies the eigenvalues of the correlation matrix, and implies the dimension.

**Parameters**
- **eigs** [1d ndarray] Eigenvalues of correlation matrix.

**Notes**
Generates a random correlation matrix following a numerically stable algorithm spelled out by Davies & Higham. This algorithm uses a single O(N) similarity transformation to construct a symmetric positive semi-definite matrix, and applies a series of Givens rotations to scale it to have ones on the diagonal.

**References**
[1]

**Examples**

```python
>>> from scipy.stats import random_correlation
>>> np.random.seed(514)
>>> x = random_correlation.rvs((.5, .8, 1.2, 1.5))
```
```python
>>> x
array([[ 1.        , -0.20387311, 0.18366501, -0.04953711],
       [-0.20387311, 1.        , -0.24351129, 0.06703474],
       [ 0.18366501, -0.24351129, 1.        , 0.38530195],
       [-0.04953711, 0.06703474, 0.38530195, 1.        ]])
```

```python
>>> import scipy.linalg
>>> e, v = scipy.linalg.eigh(x)
>>> e
array([ 0.5, 0.8, 1.2, 1.5])
```

### Methods

<table>
<thead>
<tr>
<th>Description</th>
<th>Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>“rvs(eigs=None, random_state=None)”</td>
<td>Draw random correlation matrices, all with eigenvalues eigs.</td>
</tr>
</tbody>
</table>

## 6.27.6 Discrete distributions

- **beroulli**: A Bernoulli discrete random variable.
- **binom**: A binomial discrete random variable.
- **boltzmann**: A Boltzmann (Truncated Discrete Exponential) random variable.
- **dlaplace**: A Laplacian discrete random variable.
- **geom**: A geometric discrete random variable.
- **hypergeom**: A hypergeometric discrete random variable.
- **logser**: A Logarithmic (Log-Series, Series) discrete random variable.
- **nbinom**: A negative binomial discrete random variable.
- **planck**: A Planck discrete exponential random variable.
- **poisson**: A Poisson discrete random variable.
- **randint**: A uniform discrete random variable.
- **skellam**: A Skellam discrete random variable.
- **zipf**: A Zipf discrete random variable.
- **yulesimon**: A Yule-Simon discrete random variable.

### scipy.stats.bernoulli

**scipy.stats.bernoulli = <scipy.stats._discrete_distns.bernoulli_gen object>**

A Bernoulli discrete random variable.

As an instance of the `rv_discrete` class, `bernoulli` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

### Notes

The probability mass function for `bernoulli` is:

\[
f(k) = \begin{cases} 
1 - p & \text{if } k = 0 \\
p & \text{if } k = 1 
\end{cases}
\]

for \(k\) in \(\{0, 1\}\).

`bernoulli` takes \(p\) as shape parameter.

The probability mass function above is defined in the “standardized” form. To shift distribution use the
loc parameter. Specifically, `bernoulli.pmf(k, p, loc)` is identically equivalent to `bernoulli.pmf(k - loc, p)`.

**Examples**

```python
>>> from scipy.stats import bernoulli
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> p = 0.3
>>> mean, var, skew, kurt = bernoulli.stats(p, moments='mvsk')
```

Display the probability mass function (pmf):

```python
>>> x = np.arange(bernoulli.ppf(0.01, p),
...               bernoulli.ppf(0.99, p))
>>> ax.plot(x, bernoulli.pmf(x, p), 'bo', ms=8, label='bernoulli pmf')
>>> ax.vlines(x, 0, bernoulli.pmf(x, p), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pmf:

```python
>>> rv = bernoulli(p)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...           label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Check accuracy of cdf and ppf:

```python
>>> prob = bernoulli.cdf(x, p)
>>> np.allclose(x, bernoulli.ppf(prob, p))
True
```
Generate random numbers:

```python
>>> r = bernoulli.rvs(p, size=1000)
```

**Methods**

<table>
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<tbody>
<tr>
<td>rvs(p, loc=0, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pmf(k, p, loc=0)</td>
<td>Probability mass function.</td>
</tr>
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<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(k, p, loc=0)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, p, loc=0)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, p, loc=0)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
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<td>stats(p, loc=0, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
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<td>entropy(p, loc=0)</td>
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</tr>
<tr>
<td>expect(func, args=(p,), loc=0, lb=0, ub=None, conditional=False)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
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<td>interval(alpha, p, loc=0)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

**scipy.stats.binom**

`scipy.stats.binom = <scipy.stats._discrete_distns.binom_gen object>`

A binomial discrete random variable.

As an instance of the `rv_discrete` class, `binom` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability mass function for `binom` is:

\[
f(k) = \binom{n}{k} p^k (1-p)^{n-k}\]

for k in \{0, 1, ..., n\}.

`binom` takes n and p as shape parameters.

The probability mass function above is defined in the “standardized” form. To shift distribution use the `loc` parameter. Specifically, `binom.pmf(k, n, p, loc)` is identically equivalent to `binom.pmf(k - loc, n, p)`.

**Examples**

```python
>>> from scipy.stats import binom
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```
Calculate a few first moments:

```python
>>> n, p = 5, 0.4
>>> mean, var, skew, kurt = binom.stats(n, p, moments='mvsk')
```

Display the probability mass function (pmf):

```python
>>> x = np.arange(binom.ppf(0.01, n, p),
...                binom.ppf(0.99, n, p))
>>> ax.plot(x, binom.pmf(x, n, p), 'bo', ms=8, label='binom pmf')
>>> ax.vlines(x, 0, binom.pmf(x, n, p), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pmf:

```python
>>> rv = binom(n, p)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1, 
...           label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Check accuracy of `cdf` and `ppf`:

```python
>>> prob = binom.cdf(x, n, p)
>>> np.allclose(x, binom.ppf(prob, n, p))
```

Generate random numbers:

```python
>>> r = binom.rvs(n, p, size=1000)
```
Methods

<table>
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<tr>
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</tr>
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<tr>
<td>rvs(n, p, loc=0, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pmf(k, n, p, loc=0)</td>
<td>Probability mass function.</td>
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<td>sf(k, n, p, loc=0)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
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</tr>
<tr>
<td>ppf(q, n, p, loc=0)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, n, p, loc=0)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>stats(n, p, loc=0, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(n, p, loc=0)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>expect(func, args=(n, p), loc=0, lb=None, ub=None, conditional=False)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
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<tr>
<td>median(n, p, loc=0)</td>
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<td>var(n, p, loc=0)</td>
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<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, n, p, loc=0)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

```
scipy.stats.boltzmann
```

As an instance of the `rv_discrete` class, `boltzmann` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes
The probability mass function for `boltzmann` is:

\[ f(k) = \frac{(1 - \exp(-\lambda)) \exp(-\lambda k)}{(1 - \exp(-\lambda N))} \]

for \( k = 0, ..., N - 1 \).

`boltzmann` takes \( \lambda > 0 \) and \( N > 0 \) as shape parameters.

The probability mass function above is defined in the “standardized” form. To shift distribution use the `loc` parameter. Specifically, `boltzmann.pmf(k, lambda_, N, loc)` is identically equivalent to `boltzmann.pmf(k - loc, lambda_, N)`.

Examples
```
>>> from scipy.stats import boltzmann
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:
```
>>> lambda_, N = 1.4, 19
>>> mean, var, skew, kurt = boltzmann.stats(lambda_, N, moments='mvsk')
```

Display the probability mass function (pmf):
```
>>> x = np.arange(boltzmann.ppf(0.01, lambda_, N), ...
    ...    boltzmann.ppf(0.99, lambda_, N))
>>> ax.plot(x, boltzmann.pmf(x, lambda_, N), 'bo', ms=8, label='boltzmann pmf')
>>> ax.vlines(x, 0, boltzmann.pmf(x, lambda_, N), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pmf:
```
>>> rv = boltzmann(lambda_, N)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1, ...
    ...    label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Check accuracy of cdf and ppf:
```
>>> prob = boltzmann.cdf(x, lambda_, N)
>>> np.allclose(x, boltzmann.ppf(prob, lambda_, N))
True
```

Generate random numbers:
```
>>> r = boltzmann.rvs(lambda_, N, size=1000)
```
Methods

<table>
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<th>Description</th>
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<tr>
<td>rvs(lambda__, N, loc=0, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pmf(k, lambda__, N, loc=0)</td>
<td>Probability mass function.</td>
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<td>logpmf(k, lambda__, N, loc=0)</td>
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<td>cdf(k, lambda__, N, loc=0)</td>
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<td>logcdf(k, lambda__, N, loc=0)</td>
<td>Log of the cumulative distribution function.</td>
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<td>sf(k, lambda__, N, loc=0)</td>
<td>Survival function (also defined as (1 - \text{cdf}), but (sf) is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(k, lambda__, N, loc=0)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, lambda__, N, loc=0)</td>
<td>Percent point function (inverse of (\text{cdf}) — percentiles).</td>
</tr>
<tr>
<td>isf(q, lambda__, N, loc=0)</td>
<td>Inverse survival function (inverse of (sf)).</td>
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<tr>
<td>stats(lambda__, N, loc=0, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(lambda__, N, loc=0)</td>
<td>(Differential) entropy of the RV.</td>
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<tr>
<td>expect(func, args=(lambda__, N), loc=0, lb=None, ub=None, conditional=False)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
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<tr>
<td>median(lambda__, N, loc=0)</td>
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<tr>
<td>interval(alpha, lambda__, N, loc=0)</td>
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</table>

scipy.stats.dlaplace

**scipy.stats.dlaplace = <scipy.stats._discrete_distns.dlaplace_gen object>**

A Laplacian discrete random variable.

As an instance of the `rv_discrete` class, `dlaplace` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability mass function for `dlaplace` is:

\[
f(k) = \frac{\tanh(\alpha/2) \exp(-\alpha|k|)}{2}
\]

for integers \(k\) and \(\alpha > 0\).

`dlaplace` takes \(\alpha\) as shape parameter.

The probability mass function above is defined in the “standardized” form. To shift distribution use the `loc` parameter. Specifically, `dlaplace.pmf(k, \alpha, \text{loc})` is identically equivalent to `dlaplace.pmf(k - \text{loc}, \alpha)`.

**Examples**

```python
>>> from scipy.stats import dlaplace
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:
```python
>>> a = 0.8
>>> mean, var, skew, kurt = dlaplace.stats(a, moments='mvsk')

Display the probability mass function (pmf):

```python
>>> x = np.arange(dlaplace.ppf(0.01, a),
...                dlaplace.ppf(0.99, a))
>>> ax.plot(x, dlaplace.pmf(x, a), 'bo', ms=8, label='dlaplace pmf')
>>> ax.vlines(x, 0, dlaplace.pmf(x, a), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pmf:

```python
>>> rv = dlaplace(a)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...           label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Check accuracy of cdf and ppf:

```python
>>> prob = dlaplace.cdf(x, a)
>>> np.allclose(x, dlaplace.ppf(prob, a))
True
```

Generate random numbers:

```python
>>> r = dlaplace.rvs(a, size=1000)
```
### Methods

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<td>rvs(a, loc=0, size=1, random_state=None)</td>
<td>Random variates.</td>
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<td>pmf(k, a, loc=0)</td>
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<td>sf(k, a, loc=0)</td>
<td>Survival function (also defined as $1 - \text{cdf}$, but \text{sf} is sometimes more accurate).</td>
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<td>ppf(q, a, loc=0)</td>
<td>Percent point function (inverse of \text{cdf} — percentiles).</td>
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<tr>
<td>isf(q, a, loc=0)</td>
<td>Inverse survival function (inverse of \text{sf}).</td>
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<tr>
<td>stats(a, loc=0, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
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<td>entropy(a, loc=0)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>expect(func, args=(a,), loc=0, lb=None, ub=None, conditional=False)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
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<tr>
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</tr>
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<td>interval(alpha, a, loc=0)</td>
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</table>

**scipy.stats.geom**

scipy.stats.geom = <scipy.stats._discrete_distns.geom_gen object>

A geometric discrete random variable.

As an instance of the \texttt{rv\_discrete} class, \texttt{geom} object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability mass function for \texttt{geom} is:

$$f(k) = (1 - p)^{k-1} p$$

for $k \geq 1$.

\texttt{geom} takes $p$ as shape parameter.

The probability mass function above is defined in the “standardized” form. To shift distribution use the \texttt{loc} parameter. Specifically, \texttt{geom.pmf(k, p, loc)} is identically equivalent to \texttt{geom.pmf(k - loc, p)}.

**Examples**

```python
>>> from scipy.stats import geom
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

>>> p = 0.5
>>> mean, var, skew, kurt = geom.stats(p, moments='mvsk')
```
Display the probability mass function (pmf):

```python
>>> x = np.arange(geom.ppf(0.01, p), 
                  geom.ppf(0.99, p))
>>> ax.plot(x, geom.pmf(x, p), 'bo', ms=8, label='geom pmf')
>>> ax.vlines(x, 0, geom.pmf(x, p), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pmf:

```python
>>> rv = geom(p)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
                      label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Check accuracy of cdf and ppf:

```python
>>> prob = geom.cdf(x, p)
>>> np.allclose(x, geom.ppf(prob, p))
True
```

Generate random numbers:

```python
>>> r = geom.rvs(p, size=1000)
```
Methods

<table>
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<tr>
<td>ppf(q, p, loc=0)</td>
<td>Percent point function (inverse of (cdf) — percentiles).</td>
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<tr>
<td>isf(q, p, loc=0)</td>
<td>Inverse survival function (inverse of (sf)).</td>
</tr>
<tr>
<td>stats(p, loc=0, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(p, loc=0)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>expect(func, args=(p,), loc=0, lb=None, ub=None, conditional=False)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
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<tr>
<td>median(p, loc=0)</td>
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</tr>
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<td>interval(alpha, p, loc=0)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

**scipy.stats.hypergeom**

`scipy.stats.hypergeom = <scipy.stats._discrete_distns.hypergeom_gen object>`

A hypergeometric discrete random variable.

The hypergeometric distribution models drawing objects from a bin. \(M\) is the total number of objects, \(n\) is total number of Type I objects. The random variate represents the number of Type I objects in \(N\) drawn without replacement from the total population.

As an instance of the `rv_discrete` class, `hypergeom` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The symbols used to denote the shape parameters \((M, n, \text{ and } N)\) are not universally accepted. See the Examples for a clarification of the definitions used here.

The probability mass function is defined as,

\[
p(k, M, n, N) = \frac{\binom{k}{n} \binom{M-n}{N-k}}{\binom{M}{N}}
\]

for \(k \in \text{[max(0, }N - M + n), \min(n, N)]\), where the binomial coefficients are defined as,

\[
\binom{n}{k} = \frac{n!}{k!(n-k)!}.
\]

The probability mass function above is defined in the “standardized” form. To shift distribution use the `loc` parameter. Specifically, `hypergeom.pmf(k, M, n, N, loc)` is identically equivalent to `hypergeom.pmf(k - loc, M, n, N)`.
Examples

```python
>>> from scipy.stats import hypergeom
>>> import matplotlib.pyplot as plt
```

Suppose we have a collection of 20 animals, of which 7 are dogs. Then if we want to know the probability of finding a given number of dogs if we choose at random 12 of the 20 animals, we can initialize a frozen distribution and plot the probability mass function:

```python
>>> [M, n, N] = [20, 7, 12]
>>> rv = hypergeom(M, n, N)
>>> x = np.arange(0, n+1)
>>> pmf_dogs = rv.pmf(x)

```python
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(x, pmf_dogs, 'bo')
>>> ax.vlines(x, 0, pmf_dogs, lw=2)
>>> ax.set_xlabel('# of dogs in our group of chosen animals')
>>> ax.set_ylabel('hypergeom PMF')
>>> plt.show()
```

Instead of using a frozen distribution we can also use `hypergeom` methods directly. To for example obtain the cumulative distribution function, use:

```python
>>> prb = hypergeom.cdf(x, M, n, N)
```

And to generate random numbers:

```python
>>> R = hypergeom.rvs(M, n, N, size=10)
```
### Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rvs(M, n, N, loc=0, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pmf(k, M, n, N, loc=0)</code></td>
<td>Probability mass function.</td>
</tr>
<tr>
<td><code>logpmf(k, M, n, N, loc=0)</code></td>
<td>Log of the probability mass function.</td>
</tr>
<tr>
<td><code>cdf(k, M, n, N, loc=0)</code></td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td><code>logcdf(k, M, n, N, loc=0)</code></td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td><code>sf(k, M, n, N, loc=0)</code></td>
<td>Survival function (also defined as $1 - \text{cdf}$, but $sf$ is sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(k, M, n, N, loc=0)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, M, n, N, loc=0)</code></td>
<td>Percent point function (inverse of $\text{cdf}$ — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, M, n, N, loc=0)</code></td>
<td>Inverse survival function (inverse of $\text{sf}$).</td>
</tr>
<tr>
<td><code>stats(M, n, N, loc=0, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy(M, n, N, loc=0)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>expect(func, args=(M, n, N), loc=0, lb=None, ub=None, conditional=False)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td><code>median(M, n, N, loc=0)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(M, n, N, loc=0)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(M, n, N, loc=0)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(M, n, N, loc=0)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, M, n, N, loc=0)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

---

**scipy.stats.logser**

`scipy.stats.logser = <scipy.stats._discrete_distns.logser_gen object>`

A Logarithmic (Log-Series, Series) discrete random variable.

As an instance of the `rv_discrete` class, `logser` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability mass function for `logser` is:

$$f(k) = \frac{p^k}{k \log(1 - p)}$$

for $k \geq 1$.

`logser` takes $p$ as shape parameter.

The probability mass function above is defined in the “standardized” form. To shift distribution use the `loc` parameter. Specifically, `logser.pmf(k, p, loc)` is identically equivalent to `logser.pmf(k - loc, p).

**Examples**

```python
>>> from scipy.stats import logser
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> p = 0.6
>>> mean, var, skew, kurt = logser.stats(p, moments='mvsk')
```
Display the probability mass function (pmf):

```python
>>> x = np.arange(logser.ppf(0.01, p),
                 logser.ppf(0.99, p))
>>> ax.plot(x, logser.pmf(x, p), 'bo', ms=8, label='logser pmf')
>>> ax.vlines(x, 0, logser.pmf(x, p), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pmf:

```python
>>> rv = logser(p)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
            label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Check accuracy of cdf and ppf:

```python
>>> prob = logser.cdf(x, p)
>>> np.allclose(x, logser.ppf(prob, p))
```

Generate random numbers:

```python
>>> r = logser.rvs(p, size=1000)
```
Methods

- `rvs(p, loc=0, size=1, random_state=None)`: Random variates.
- `pmf(k, p, loc=0)`: Probability mass function.
- `logpmf(k, p, loc=0)`: Log of the probability mass function.
- `cdf(k, p, loc=0)`: Cumulative distribution function.
- `logcdf(k, p, loc=0)`: Log of the cumulative distribution function.
- `sf(k, p, loc=0)`: Survival function (also defined as $1 - cdf$, but $sf$ is sometimes more accurate).
- `logsf(k, p, loc=0)`: Log of the survival function.
- `ppf(q, p, loc=0)`: Percent point function (inverse of $cdf$ — percentiles).
- `isf(q, p, loc=0)`: Inverse survival function (inverse of $sf$).
- `stats(p, loc=0, moments='mv')`: Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
- `entropy(p, loc=0)`: (Differential) entropy of the RV.
- `expect(func, args=(p,), loc=0, lb=None, ub=None, conditional=False)`: Expected value of a function (of one argument) with respect to the distribution.
- `median(p, loc=0)`: Median of the distribution.
- `mean(p, loc=0)`: Mean of the distribution.
- `var(p, loc=0)`: Variance of the distribution.
- `std(p, loc=0)`: Standard deviation of the distribution.
- `interval(alpha, p, loc=0)`: Endpoints of the range that contains alpha percent of the distribution.

**scipy.stats.nbinom**

`scipy.stats.nbinom = <scipy.stats._discrete_distns.nbinom_gen object>`

A negative binomial discrete random variable.

As an instance of the `rv_discrete` class, `nbinom` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

Negative binomial distribution describes a sequence of i.i.d. Bernoulli trials, repeated until a predefined, non-random number of successes occurs.

The probability mass function of the number of failures for `nbinom` is:

$$f(k) = \binom{k + n - 1}{n - 1} p^n (1-p)^k$$

for $k \geq 0$.

`nbinom` takes $n$ and $p$ as shape parameters where $n$ is the number of successes, whereas $p$ is the probability of a single success.

The probability mass function above is defined in the “standardized” form. To shift distribution use the `loc` parameter. Specifically, `nbinom.pmf(k, n, p, loc)` is identically equivalent to `nbinom.pmf(k - loc, n, p)`.

**Examples**

```python
>>> from scipy.stats import nbinom
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:
```python
>>> n, p = 0.4, 0.4
>>> mean, var, skew, kurt = nbinom.stats(n, p, moments='mvsk')

Display the probability mass function (pmf):

```python
>>> x = np.arange(nbinom.ppf(0.01, n, p), ...
... nbinom.ppf(0.99, n, p))
>>> ax.plot(x, nbinom.pmf(x, n, p), 'bo', ms=8, label='nbinom pmf')
>>> ax.vlines(x, 0, nbinom.pmf(x, n, p), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pmf:

```python
>>> rv = nbinom(n, p)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1, ...
... label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Check accuracy of cdf and ppf:

```python
>>> prob = nbinom.cdf(x, n, p)
>>> np.allclose(x, nbinom.ppf(prob, n, p))
True
```

Generate random numbers:

```python
>>> r = nbinom.rvs(n, p, size=1000)
```
Methods

<table>
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<th>Description</th>
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</thead>
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<tr>
<td>rvs(n, p, loc=0, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pmf(k, n, p, loc=0)</td>
<td>Probability mass function.</td>
</tr>
<tr>
<td>logpmf(k, n, p, loc=0)</td>
<td>Log of the probability mass function.</td>
</tr>
<tr>
<td>cdf(k, n, p, loc=0)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(k, n, p, loc=0)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(k, n, p, loc=0)</td>
<td>Survival function (also defined as $1 - \text{cdf}$, but $sf$ is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(k, n, p, loc=0)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, n, p, loc=0)</td>
<td>Percent point function (inverse of \text{cdf} — percentiles).</td>
</tr>
<tr>
<td>isf(q, n, p, loc=0)</td>
<td>Inverse survival function (inverse of \text{sf}).</td>
</tr>
<tr>
<td>stats(n, p, loc=0, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(n, p, loc=0)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>expect(func, args=(n, p), loc=0=0, lb=None, ub=None, conditional=False)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(n, p, loc=0)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(n, p, loc=0)</td>
<td>Mean of the distribution.</td>
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<tr>
<td>var(n, p, loc=0)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(n, p, loc=0)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, n, p, loc=0)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

scipy.stats.planck

scipy.stats.planck = <scipy.stats._discrete_distns.planck_gen object>

A Planck discrete exponential random variable.

As an instance of the \text{rv_discrete} class, planck object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes
The probability mass function for planck is:

$$f(k) = (1 - \exp(-\lambda)) \exp(-\lambda k)$$

for $k \geq 0$ and $\lambda > 0$.

planck takes \lambda as shape parameter.

The probability mass function above is defined in the “standardized” form. To shift distribution use the loc parameter. Specifically, planck.pmf(k, lambda_, loc) is identically equivalent to planck.pmf(k - loc, lambda_).

Examples

```python
>>> from scipy.stats import planck
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> lambda_ = 0.51
>>> mean, var, skew, kurt = planck.stats(lambda_, moments='mvsk')
```
Display the probability mass function (pmf):

```python
>>> x = np.arange(planck.ppf(0.01, lambda_),
                 planck.ppf(0.99, lambda_))
>>> ax.plot(x, planck.pmf(x, lambda_), 'bo', ms=8, label='planck pmf')
>>> ax.vlines(x, 0, planck.pmf(x, lambda_), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called as a function to fix the shape and location. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pmf:

```python
>>> rv = planck(lambda_)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
            label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Check accuracy of cdf and ppf:

```python
>>> prob = planck.cdf(x, lambda_)
>>> np.allclose(x, planck.ppf(prob, lambda_))
True
```

Generate random numbers:

```python
>>> r = planck.rvs(lambda_, size=1000)
```
Methods

<table>
<thead>
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<th>Description</th>
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<tr>
<td>rvs(lambda_, loc=0, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pmf(k, lambda_, loc=0)</td>
<td>Probability mass function.</td>
</tr>
<tr>
<td>logpmf(k, lambda_, loc=0)</td>
<td>Log of the probability mass function.</td>
</tr>
<tr>
<td>cdf(k, lambda_, loc=0)</td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td>logcdf(k, lambda_, loc=0)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(k, lambda_, loc=0)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(k, lambda_, loc=0)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, lambda_, loc=0)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, lambda_, loc=0)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>stats(lambda_, loc=0, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(lambda_, loc=0)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>expect(func, args=(lambda_,), loc=0, lb=None, ub=None, conditional=False)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(lambda_, loc=0)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(lambda_, loc=0)</td>
<td>Mean of the distribution.</td>
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<tr>
<td>var(lambda_, loc=0)</td>
<td>Variance of the distribution.</td>
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<tr>
<td>std(lambda_, loc=0)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, lambda_, loc=0)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

`scipy.stats.poisson`

`scipy.stats.poisson = <scipy.stats._discrete_distns.poisson_gen object>`

A Poisson discrete random variable.

As an instance of the `rv_discrete` class, `poisson` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

The probability mass function for `poisson` is:

\[ f(k) = \exp(-\mu) \frac{\mu^k}{k!} \]

for \( k \geq 0 \).

`poisson` takes \( \mu \) as shape parameter.

The probability mass function above is defined in the “standardized” form. To shift distribution use the `loc` parameter. Specifically, `poisson.pmf(k, mu, loc)` is identically equivalent to `poisson.pmf(k - loc, mu)`.

**Examples**

```python
>>> from scipy.stats import poisson
>>> import matplotlib.pyplot as plt
>>> ax = plt.subplots(1, 1)

Calculate a few first moments:

```
Display the probability mass function (pmf):

```python
>>> x = np.arange(poisson.ppf(0.01, mu), ... poisson.ppf(0.99, mu))
>>> ax.plot(x, poisson.pmf(x, mu), 'bo', ms=8, label='poisson pmf')
>>> ax.vlines(x, 0, poisson.pmf(x, mu), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pmf:

```python
>>> rv = poisson(mu)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1, ... label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Check accuracy of cdf and ppf:

```python
>>> prob = poisson.cdf(x, mu)
>>> np.allclose(x, poisson.ppf(prob, mu))
True
```

Generate random numbers:

```python
>>> r = poisson.rvs(mu, size=1000)
```
Methods

<table>
<thead>
<tr>
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<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rvs(mu, loc=0, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pmf(k, mu, loc=0)</td>
<td>Probability mass function.</td>
</tr>
<tr>
<td>logpmf(k, mu, loc=0)</td>
<td>Log of the probability mass function.</td>
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<tr>
<td>cdf(k, mu, loc=0)</td>
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<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(k, mu, loc=0)</td>
<td>Survival function (also defined as $1 - \text{cdf}$, but $sf$ is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(k, mu, loc=0)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, mu, loc=0)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, mu, loc=0)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>stats(mu, loc=0, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(mu, loc=0)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>expect(func, args=(mu,), loc=0, lb=None, ub=None, conditional=False)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(mu, loc=0)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(mu, loc=0)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(mu, loc=0)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(mu, loc=0)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, mu, loc=0)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

**scipy.stats.randint**

*scipy.stats.randint = <scipy.stats._discrete_distns.randint_gen object>*

A uniform discrete random variable.

As an instance of the `rv_discrete` class, `randint` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**
The probability mass function for `randint` is:

$$f(k) = \frac{1}{\text{high} - \text{low}}$$

for \(k = \text{low}, \ldots, \text{high} - 1\).

`randint` takes `low` and `high` as shape parameters.

The probability mass function above is defined in the “standardized” form. To shift distribution use the `loc` parameter. Specifically, `randint.pmf(k, low, high, loc)` is identically equivalent to `randint.pmf(k - loc, low, high)`.

**Examples**

```python
>>> from scipy.stats import randint
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> low, high = 7, 31
>>> mean, var, skew, kurt = randint.stats(low, high, moments='mvsk')
```
Display the probability mass function (pmf):

```python
>>> x = np.arange(randint.ppf(0.01, low, high),
                 randint.ppf(0.99, low, high))
>>> ax.plot(x, randint.pmf(x, low, high), 'bo', ms=8, label='randint pmf')
>>> ax.vlines(x, 0, randint.pmf(x, low, high), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pmf:

```python
>>> rv = randint(low, high)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
            label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Check accuracy of cdf and ppf:

```python
>>> prob = randint.cdf(x, low, high)
>>> np.allclose(x, randint.ppf(prob, low, high))
True
```

Generate random numbers:

```python
>>> r = randint.rvs(low, high, size=1000)
```
### Methods

<table>
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<tr>
<th>Method</th>
<th>Description</th>
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<tr>
<td>rvs(low, high, loc=0, size=1, random_state= None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pmf(k, low, high, loc=0)</td>
<td>Probability mass function.</td>
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<td>logpmf(k, low, high, loc=0)</td>
<td>Log of the probability mass function.</td>
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<td>cdf(k, low, high, loc=0)</td>
<td>Cumulative distribution function.</td>
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<td>Log of the cumulative distribution function.</td>
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<td>sf(k, low, high, loc=0)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
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<td>logsf(k, low, high, loc=0)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, low, high, loc=0)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, low, high, loc=0)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>stats(low, high, loc=0, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(low, high, loc=0)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>expect(func, args=(low, high), loc=0, lb=None, ub=None, conditional=False)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(low, high, loc=0)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(low, high, loc=0)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(low, high, loc=0)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(low, high, loc=0)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, low, high, loc=0)</td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
</tr>
</tbody>
</table>

**scipy.stats.skellam**

`scipy.stats.skellam = <scipy.stats._discrete_distns.skellam_gen object>`

A Skellam discrete random variable.

As an instance of the `rv_discrete` class, `skellam` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

**Notes**

Probability distribution of the difference of two correlated or uncorrelated Poisson random variables.

Let $k_1$ and $k_2$ be two Poisson-distributed r.v. with expected values $\lambda_1$ and $\lambda_2$. Then, $k_1 - k_2$ follows a Skellam distribution with parameters $\mu_1 = \lambda_1 - \rho\sqrt{\lambda_1 \lambda_2}$ and $\mu_2 = \lambda_2 - \rho\sqrt{\lambda_1 \lambda_2}$, where $\rho$ is the correlation coefficient between $k_1$ and $k_2$. If the two Poisson-distributed r.v. are independent then $\rho = 0$.

Parameters $\mu_1$ and $\mu_2$ must be strictly positive.

For details see: [https://en.wikipedia.org/wiki/Skellam_distribution](https://en.wikipedia.org/wiki/Skellam_distribution)

The probability mass function above is defined in the “standardized” form. To shift distribution use the loc parameter. Specifically, `skellam.pmf(k, mu1, mu2, loc)` is identically equivalent to `skellam.pmf(k - loc, mu1, mu2)`.

**Examples**

```python
>>> from scipy.stats import skellam
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:
Display the probability mass function (pmf):

```python
>>> x = np.arange(skellam.ppf(0.01, mu1, mu2),
                  ... skellam.ppf(0.99, mu1, mu2))
>>> ax.plot(x, skellam.pmf(x, mu1, mu2), 'bo', ms=8, label='skellam pmf')
>>> ax.vlines(x, 0, skellam.pmf(x, mu1, mu2), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pmf:

```python
>>> rv = skellam(mu1, mu2)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
            ... label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Check accuracy of cdf and ppf:

```python
>>> prob = skellam.cdf(x, mu1, mu2)
>>> np.allclose(x, skellam.ppf(prob, mu1, mu2))
True
```

Generate random numbers:

```python
>>> r = skellam.rvs(mu1, mu2, size=1000)
```
### Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rvs(mu1, mu2, loc=0, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pmf(k, mu1, mu2, loc=0)</code></td>
<td>Probability mass function.</td>
</tr>
<tr>
<td><code>logpmf(k, mu1, mu2, loc=0)</code></td>
<td>Log of the probability mass function.</td>
</tr>
<tr>
<td><code>cdf(k, mu1, mu2, loc=0)</code></td>
<td>Cumulative distribution function.</td>
</tr>
<tr>
<td><code>logcdf(k, mu1, mu2, loc=0)</code></td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td><code>sf(k, mu1, mu2, loc=0)</code></td>
<td>Survival function (also defined as $1 - \text{cdf}$, but $sf$ is sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(k, mu1, mu2, loc=0)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, mu1, mu2, loc=0)</code></td>
<td>Percent point function (inverse of $\text{cdf}$ — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, mu1, mu2, loc=0)</code></td>
<td>Inverse survival function (inverse of $sf$).</td>
</tr>
<tr>
<td><code>stats(mu1, mu2, loc=0, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy(mu1, mu2, loc=0)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>expect(func, args=(mu1, mu2), loc=0, lb=None, ub=None, conditional=False)</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td><code>median(mu1, mu2, loc=0)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(mu1, mu2, loc=0)</code></td>
<td>Mean of the distribution.</td>
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<tr>
<td><code>var(mu1, mu2, loc=0)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(mu1, mu2, loc=0)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, mu1, mu2, loc=0)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
</tr>
</tbody>
</table>

### scipy.stats.zipf

`scipy.stats.zipf = <scipy.stats._discrete_distns.zipf_gen object>`

A Zipf discrete random variable.

As an instance of the `rv_discrete` class, `zipf` object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

### Notes

The probability mass function for `zipf` is:

$$f(k, a) = \frac{1}{\zeta(a)k^a}$$

for $k \geq 1$.

`zipf` takes `a` as shape parameter. $\zeta$ is the Riemann zeta function (`scipy.special.zeta`)

The probability mass function above is defined in the “standardized” form. To shift distribution use the `loc` parameter. Specifically, `zipf.pmf(k, a, loc)` is identically equivalent to `zipf.pmf(k - loc, a)`.

### Examples

```python
>>> from scipy.stats import zipf
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> a = 6.5
>>> mean, var, skew, kurt = zipf.stats(a, moments='mvsk')
```
Display the probability mass function (pmf):

```python
>>> x = np.arange(zipf.ppf(0.01, a),
                 ...     zipf.ppf(0.99, a))
>>> ax.plot(x, zipf.pmf(x, a), 'bo', ms=8, label='zipf pmf')
>>> ax.vlines(x, 0, zipf.pmf(x, a), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pmf:

```python
>>> rv = zipf(a)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
               ...        label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Check accuracy of cdf and ppf:

```python
>>> prob = zipf.cdf(x, a)
>>> np.allclose(x, zipf.ppf(prob, a))
True
```

Generate random numbers:

```python
>>> r = zipf.rvs(a, size=1000)
```
Methods

<table>
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<tr>
<th>Function</th>
<th>Description</th>
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</thead>
<tbody>
<tr>
<td>rvs(a, loc=0, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pmf(k, a, loc=0)</td>
<td>Probability mass function.</td>
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<td>logpmf(k, a, loc=0)</td>
<td>Log of the probability mass function.</td>
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<td>cdf(k, a, loc=0)</td>
<td>Cumulative distribution function.</td>
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<td>logcdf(k, a, loc=0)</td>
<td>Log of the cumulative distribution function.</td>
</tr>
<tr>
<td>sf(k, a, loc=0)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(k, a, loc=0)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, a, loc=0)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, a, loc=0)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>stats(a, loc=0, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(a, loc=0)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>expect(func, args=(a,), loc=0, lb=None, ub=None, conditional=False)</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median(a, loc=0)</td>
<td>Median of the distribution.</td>
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<td>mean(a, loc=0)</td>
<td>Mean of the distribution.</td>
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<td>Variance of the distribution.</td>
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<tr>
<td>std(a, loc=0)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, a, loc=0)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

scipy.stats.yulesimon

scipy.stats.yulesimon = <scipy.stats._discrete_distns.yulesimon_gen object>

A Yule-Simon discrete random variable.

As an instance of the rv_discrete class, yulesimon object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for the yulesimon is:

\[ f(k) = \alpha B(k, \alpha + 1) \]

for \( k = 1, 2, 3, \ldots \), where \( \alpha > 0 \). Here \( B \) refers to the scipy.special.beta function.

The sampling of random variates is based on pg 553, Section 6.3 of [1]. Our notation maps to the referenced logic via \( a = \alpha - 1 \).

For details see the wikipedia entry [2].

References

The probability mass function above is defined in the “standardized” form. To shift distribution use the loc parameter. Specifically, yulesimon.pmf(k, alpha, loc) is identically equivalent to yulesimon.pmf(k - loc, alpha).

[1], [2]

Examples

```python
>>> from scipy.stats import yulesimon
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```
Calculate a few first moments:

```python
>>> alpha = 11
>>> mean, var, skew, kurt = yulesimon.stats(alpha, moments='mvsk')
```

Display the probability mass function (pmf):

```python
>>> x = np.arange(yulesimon.ppf(0.01, alpha), ... yulesimon.ppf(0.99, alpha))
>>> ax.plot(x, yulesimon.pmf(x, alpha), 'bo', ms=8, label='yulesimon pmf')
>>> ax.vlines(x, 0, yulesimon.pmf(x, alpha), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pmf:

```python
>>> rv = yulesimon(alpha)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1, ... label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Check accuracy of cdf and ppf:

```python
>>> prob = yulesimon.cdf(x, alpha)
>>> np.allclose(x, yulesimon.ppf(prob, alpha))
True
```

Generate random numbers:

```python
>>> r = yulesimon.rvs(alpha, size=1000)
```
### Methods

<table>
<thead>
<tr>
<th>Method</th>
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<tbody>
<tr>
<td>rvs(alpha, loc=0, size=1, random_state=None)</td>
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<tr>
<td>pmf(k, alpha, loc=0)</td>
<td>Probability mass function.</td>
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<td>Log of the probability mass function.</td>
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<td>cdf(k, alpha, loc=0)</td>
<td>Cumulative distribution function.</td>
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<td>logcdf(k, alpha, loc=0)</td>
<td>Log of the cumulative distribution function.</td>
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<tr>
<td>sf(k, alpha, loc=0)</td>
<td>Survival function (also defined as 1 - cdf, but sf is sometimes more accurate).</td>
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<td>ppf(q, alpha, loc=0)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
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<td>stats(alpha, loc=0, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
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<tr>
<td>entropy(alpha, loc=0)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>expect(func, args=(alpha,), loc=0, lb=None, ub=None, conditional=False)</td>
<td>Expected value of a function of one argument with respect to the distribution.</td>
</tr>
<tr>
<td>median(alpha, loc=0)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(alpha, loc=0)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(alpha, loc=0)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(alpha, loc=0)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, alpha, loc=0)</td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
</tr>
</tbody>
</table>

An overview of statistical functions is given below. Several of these functions have a similar version in `scipy.stats.mstats` which work for masked arrays.

#### 6.27.7 Summary statistics

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>describe(a[, axis, ddof, bias, nan_policy])</td>
<td>Compute several descriptive statistics of the passed array.</td>
</tr>
<tr>
<td>gmean(a[, axis, dtype])</td>
<td>Compute the geometric mean along the specified axis.</td>
</tr>
<tr>
<td>hmean(a[, axis, dtype])</td>
<td>Calculate the harmonic mean along the specified axis.</td>
</tr>
<tr>
<td>kurtosis(a[, axis, fisher, bias, nan_policy])</td>
<td>Compute the kurtosis (Fisher or Pearson) of a dataset.</td>
</tr>
<tr>
<td>mode(a[, axis, nan_policy])</td>
<td>Return an array of the modal (most common) value in the passed array.</td>
</tr>
<tr>
<td>moment(a[, moment, axis, nan_policy])</td>
<td>Calculate the nth moment about the mean for a sample.</td>
</tr>
<tr>
<td>skew(a[, axis, bias, nan_policy])</td>
<td>Compute the skewness of a data set.</td>
</tr>
<tr>
<td>kstat(data[, n])</td>
<td>Return the nth k-statistic (1&lt;=n&lt;=4 so far).</td>
</tr>
<tr>
<td>kstatvar(data[, n])</td>
<td>Returns an unbiased estimator of the variance of the k-statistic.</td>
</tr>
<tr>
<td>tmean(a[, limits, inclusive, axis])</td>
<td>Compute the trimmed mean.</td>
</tr>
<tr>
<td>tvar(a[, limits, inclusive, axis, ddof])</td>
<td>Compute the trimmed variance.</td>
</tr>
<tr>
<td>tmin(a[, lowerlimit, axis, inclusive, ...])</td>
<td>Compute the trimmed minimum.</td>
</tr>
<tr>
<td>tmax(a[, upperlimit, axis, inclusive, ...])</td>
<td>Compute the trimmed maximum.</td>
</tr>
</tbody>
</table>
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- `tstd(a, limits, inclusive, axis, ddof)`: Compute the trimmed sample standard deviation.
- `tsem(a, limits, inclusive, axis, ddof)`: Compute the trimmed standard error of the mean.
- `variation(a, axis, nan_policy)`: Compute the coefficient of variation, the ratio of the biased standard deviation to the mean.
- `find_repeats(arr)`: Find repeats and repeat counts.
- `trim_mean(a, proportiontocut, axis)`: Return mean of array after trimming distribution from both tails.
- `iqr(x, axis, rng, scale, nan_policy, ...)`: Compute the interquartile range of the data along the specified axis.
- `sem(a, axis, ddof, nan_policy)`: Calculate the standard error of the mean (or standard error of measurement) of the values in the input array.
- `bayes_mvs(data, alpha)`: Bayesian confidence intervals for the mean, var, and std.
- `mvsdist(data)`: ‘Frozen’ distributions for mean, variance, and standard deviation of data.
- `entropy(pk, qk, base)`: Calculate the entropy of a distribution for given probability values.

**scipy.stats.describe**

**scipy.stats.describe(a, axis=0, ddof=1, bias=True, nan_policy='propagate')**

Compute several descriptive statistics of the passed array.

**Parameters**

- `a` [array_like] Input data.
- `axis` [int or None, optional] Axis along which statistics are calculated. Default is 0. If None, compute over the whole array `a`.
- `ddof` [int, optional] Delta degrees of freedom (only for variance). Default is 1.
- `bias` [bool, optional] If False, then the skewness and kurtosis calculations are corrected for statistical bias.

**Returns**

- `nobs` [int or ndarray of ints] Number of observations (length of data along axis). When ‘omit’ is chosen as nan_policy, each column is counted separately.
- `minmax`: tuple of ndarrays or floats Minimum and maximum value of data array.
- `mean` [ndarray or float] Arithmetic mean of data along axis.
- `variance` [ndarray or float] Unbiased variance of the data along axis, denominator is number of observations minus one.
- `skewness` [ndarray or float] Skewness, based on moment calculations with denominator equal to the number of observations, i.e. no degrees of freedom correction.
- `kurtosis` [ndarray or float] Kurtosis (Fisher). The kurtosis is normalized so that it is zero for the normal distribution. No degrees of freedom are used.

**See also:**

- `skew`, `kurtosis`
Examples

```python
>>> from scipy import stats
>>> a = np.arange(10)
>>> stats.describe(a)
DescribeResult(nobs=10, minmax=(0, 9), mean=4.5, variance=9.166666666666666,
               skewness=0.0, kurtosis=-1.2242424242424244)
>>> b = [[1, 2], [3, 4]]
>>> stats.describe(b)
DescribeResult(nobs=2, minmax=(array([1, 2]), array([3, 4]))),
               mean=array([2., 3.]), variance=array([2., 2.]),
               skewness=array([0., 0.]), kurtosis=array([-2., -2.]))
```

scipy.stats.gmean

```
scipy.stats.gmean(a, axis=0, dtype=None)

Compute the geometric mean along the specified axis.

Return the geometric average of the array elements. That is: n-th root of (x1 * x2 * ... * xn)

Parameters

- a [array_like] Input array or object that can be converted to an array.
- axis [int or None, optional] Axis along which the geometric mean is computed. Default is 0. If None, compute over the whole array a.
- dtype [dtype, optional] Type of the returned array and of the accumulator in which the elements are summed. If dtype is not specified, it defaults to the dtype of a, unless a has an integer dtype with a precision less than that of the default platform integer. In that case, the default platform integer is used.

Returns

- gmean [ndarray] see dtype parameter above

See also:

- numpy.mean
  - Arithmetic average
- numpy.average
  - Weighted average
- hmean
  - Harmonic mean

Notes

The geometric average is computed over a single dimension of the input array, axis=0 by default, or all values in the array if axis=None. float64 intermediate and return values are used for integer inputs.

Use masked arrays to ignore any non-finite values in the input or that arise in the calculations such as Not a Number and infinity because masked arrays automatically mask any non-finite values.

Examples

```python
>>> from scipy.stats import gmean
>>> gmean([1, 4])
2.0
>>> gmean([1, 2, 3, 4, 5, 6, 7])
3.3800151591412964
```
**scipy.stats.hmean**

**scipy.stats.hmean**\( (a, \text{axis}=0, \text{dtype}=\text{None}) \)

Calculate the harmonic mean along the specified axis.

That is: \( n / (1/x_1 + 1/x_2 + \ldots + 1/x_n) \)

**Parameters**

- **a** [array_like] Input array, masked array or object that can be converted to an array.
- **axis** [int or None, optional] Axis along which the harmonic mean is computed. Default is 0. If None, compute over the whole array \( a \).
- **dtype** [dtype, optional] Type of the returned array and of the accumulator in which the elements are summed. If \( \text{dtype} \) is not specified, it defaults to the dtype of \( a \), unless \( a \) has an integer \( \text{dtype} \) with a precision less than that of the default platform integer. In that case, the default platform integer is used.

**Returns**

- **hmean** [ndarray] see \( \text{dtype} \) parameter above

**See also:**

- **numpy.mean**
  - Arithmetic average
- **numpy.average**
  - Weighted average
- **gmean**
  - Geometric mean

**Notes**

The harmonic mean is computed over a single dimension of the input array, axis=0 by default, or all values in the array if axis=None. float64 intermediate and return values are used for integer inputs.

Use masked arrays to ignore any non-finite values in the input or that arise in the calculations such as Not a Number and infinity.

**Examples**

```python
>>> from scipy.stats import hmean
>>> hmean([1, 4])
1.6000000000000001
>>> hmean([1, 2, 3, 4, 5, 6, 7])
2.6997245179063363
```

**scipy.stats.kurtosis**

**scipy.stats.kurtosis**\( (a, \text{axis}=0, \text{fisher=\text{True}}, \text{bias=\text{True}}, \text{nan_policy=’propagate’}) \)

Compute the kurtosis (Fisher or Pearson) of a dataset.

Kurtosis is the fourth central moment divided by the square of the variance. If Fisher’s definition is used, then 3.0 is subtracted from the result to give 0.0 for a normal distribution.

If bias is False then the kurtosis is calculated using k statistics to eliminate bias coming from biased moment estimators.

Use **kurtosistest** to see if result is close enough to normal.

**Parameters**
**SciPy Reference Guide, Release 1.2.0**

**kurtosis**

**a** [array] data for which the kurtosis is calculated

**axis** [int or None, optional] Axis along which the kurtosis is calculated. Default is 0. If None, compute over the whole array a.

**fisher** [bool, optional] If True, Fisher’s definition is used (normal ==> 0.0). If False, Pearson’s definition is used (normal ==> 3.0).

**bias** [bool, optional] If False, then the calculations are corrected for statistical bias.


**Returns**

**kurtosis** [array] The kurtosis of values along an axis. If all values are equal, return -3 for Fisher’s definition and 0 for Pearson’s definition.

**References**

[1]

**Examples**

```python
>>> from scipy.stats import kurtosis
>>> kurtosis([1, 2, 3, 4, 5])
-1.3
```

**scipy.stats.mode**

**scipy.stats.mode**(*a*, *axis=0*, *nan_policy=’propagate’*)

Return an array of the modal (most common) value in the passed array.

If there is more than one such value, only the smallest is returned. The bin-count for the modal bins is also returned.

**Parameters**

**a** [array_like] n-dimensional array of which to find mode(s).

**axis** [int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array a.


**Returns**

**mode** [ndarray] Array of modal values.

**count** [ndarray] Array of counts for each mode.

**Examples**

```python
>>> a = np.array([[6, 8, 3, 0],
...               [3, 2, 1, 7],
...               [8, 1, 6, 4],
...               [5, 3, 0, 5],
...               [4, 7, 5, 9]])
>>> from scipy import stats
>>> stats.mode(a)
(array([[3, 1, 0, 0]]), array([[1, 1, 1, 1]])
```

To get mode of whole array, specify axis=None:
scipy.stats.mode

`scipy.stats.mode(a, axis=None)`

Calculate the mode(s) of the data along the specified axis.

Parameters

- `a` ([array_like] data)
- `axis` ([int or None, optional] Axis along which the mode is computed. Default is 0. If None, compute over the whole array `a`.
- `nan_policy` ([{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. ‘propagate’ returns nan, ‘raise’ throws an error, ‘omit’ performs the calculations ignoring nan values. Default is ‘propagate’.

Returns

- `Mode(s)` [ndarray or float] The mode(s) along the given axis or over all values if axis is None. The denominator for the moment calculation is the number of observations, no degrees of freedom correction is done.

See also:

`kurtosis, skew, describe`

Notes

The k-th central moment of a data sample is:

\[ m_k = \frac{1}{n} \sum_{i=1}^{n} (x_i - \bar{x})^k \]

Where n is the number of samples and \( \bar{x} \) is the mean. This function uses exponentiation by squares [1] for efficiency.

References

[1]

Examples

```python
>>> from scipy.stats import moment
>>> moment([1, 2, 3, 4, 5], moment=1)
0.0
>>> moment([1, 2, 3, 4, 5], moment=2)
2.0
```
For normally distributed data, the skewness should be about 0. For unimodal continuous distributions, a skewness value > 0 means that there is more weight in the right tail of the distribution. The function `skewtest` can be used to determine if the skewness value is close enough to 0, statistically speaking.

**Parameters**

- **a** [ndarray] data
- **axis** [int or None, optional] Axis along which skewness is calculated. Default is 0. If None, compute over the whole array a.
- **bias** [bool, optional] If False, then the calculations are corrected for statistical bias.

**Returns**

- **skewness** [ndarray] The skewness of values along an axis, returning 0 where all values are equal.

**References**

[1]

**Examples**

```python
>>> from scipy.stats import skew
>>> skew([1, 2, 3, 4, 5])
0.0
>>> skew([2, 8, 0, 4, 1, 9, 9])
0.2650554122698573
```

**scipy.stats.kstat**

`scipy.stats.kstat(data, n=2)`

Return the nth k-statistic (1<=n<=4 so far).

The nth k-statistic k_n is the unique symmetric unbiased estimator of the nth cumulant kappa_n.

**Parameters**

- **data** [array_like] Input array. Note that n-D input gets flattened.
- **n** [int, {1, 2, 3, 4}, optional] Default is equal to 2.

**Returns**

- **kstat** [float] The nth k-statistic.

**See also:**

- **kstatvar**
  Returns an unbiased estimator of the variance of the k-statistic.
- **moment**
  Returns the n-th central moment about the mean for a sample.

**Notes**

For a sample size n, the first few k-statistics are given by:

\[
k_1 = \mu k_2 = \frac{n}{n-1} m_2 k_3 = \frac{n^2}{(n-1)(n-2)} m_3 k_4 = \frac{n^2[(n+1)m_4 - 3(n-1)m_2^2]}{(n-1)(n-2)(n-3)}
\]

where \(\mu\) is the sample mean, \(m_2\) is the sample variance, and \(m_i\) is the i-th sample central moment.
References
http://mathworld.wolfram.com/k-Statistic.html
http://mathworld.wolfram.com/Cumulant.html

Examples

```python
>>> from scipy import stats
>>> rndm = np.random.RandomState(1234)
```

As sample size increases, n-th moment and n-th k-statistic converge to the same number (although they aren’t identical). In the case of the normal distribution, they converge to zero.

```python
>>> for n in [2, 3, 4, 5, 6, 7]:
...     x = rndm.normal(size=10**n)
...     m, k = stats.moment(x, 3), stats.kstat(x, 3)
...     print("%.3g %.3g %.3g % (m, k, m-k)"
...     -0.631 -0.651 0.0194
0.0282 0.0283 -8.49e-05
-0.0454 -0.0454 1.36e-05
7.53e-05 7.53e-05 -2.26e-09
0.00166 0.00166 -4.99e-09
-2.88e-06 -2.88e-06 8.63e-13
```

**scipy.stats.kstatvar**

**scipy.stats.kstatvar(data, n=2)**

Returns an unbiased estimator of the variance of the k-statistic.

See kstat for more details of the k-statistic.

**Parameters**

- **data** [array_like] Input array. Note that n-D input gets flattened.
- **n** [int, {1, 2}, optional] Default is equal to 2.

**Returns**

- **kstatvar** [float] The nth k-statistic variance.

See also:

- **kstat**
  - Returns the n-th k-statistic.
- **moment**
  - Returns the n-th central moment about the mean for a sample.

**Notes**

The variances of the first few k-statistics are given by:

\[
\begin{align*}
\text{var}(k_1) &= \frac{\kappa^2}{n} \\
\text{var}(k_2) &= \frac{\kappa^4}{n} + \frac{2\kappa^2}{n-1} \\
\text{var}(k_3) &= \frac{\kappa^6}{n} + \frac{9\kappa^2\kappa_4}{n-1} + \frac{9\kappa_3^2}{n-1} + \frac{6n\kappa_3^2}{(n-1)(n-2)} \\
\text{var}(k_4) &= \frac{\kappa^8}{n} + \frac{16\kappa_2\kappa_6}{n-1} + \frac{48\kappa_3\kappa_5}{n-1}
\end{align*}
\]

**scipy.stats.tmean**

**scipy.stats.tmean(a, limits=None, inclusive=(True, True), axis=None)**

Compute the trimmed mean.

This function finds the arithmetic mean of given values, ignoring values outside the given limits.

6.27. Statistical functions (scipy.stats)
Parameters

- **a** [array_like] Array of values.
- **limits** [None or (lower limit, upper limit), optional] Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None (default), then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval.
- **inclusive** [(bool, bool), optional] A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).
- **axis** [int or None, optional] Axis along which to compute test. Default is None.

Returns

- **tmean** [float]

See also:

- **trim_mean** returns mean after trimming a proportion from both tails.

Examples

```python
>>> from scipy import stats
>>> x = np.arange(20)
>>> stats.tmean(x)
9.5
>>> stats.tmean(x, (3,17))
10.0
```

**scipy.stats.tvar**

**scipy.stats.tvar**(*a*, **limits=None**, **inclusive=(True, True)**, **axis=0**, **ddof=1**)

This function computes the sample variance of an array of values, while ignoring values which are outside of given limits.

Parameters

- **a** [array_like] Array of values.
- **limits** [None or (lower limit, upper limit), optional] Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None, then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval. The default value is None.
- **inclusive** [(bool, bool), optional] A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).
- **axis** [int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array a.
- **ddof** [int, optional] Delta degrees of freedom. Default is 1.

Returns

- **tvar** [float] Trimmed variance.

Notes

- **tvar** computes the unbiased sample variance, i.e. it uses a correction factor \( n / (n - 1) \).
Examples

```python
>>> from scipy import stats
>>> x = np.arange(20)
>>> stats.tvar(x)
35.0
>>> stats.tvar(x, (3,17))
20.0
```

**scipy.stats.tmin**

scipy.stats.tmin(*a*, lowerlimit=None, axis=0, inclusive=True, nan_policy='propagate')

Compute the trimmed minimum.

This function finds the minimum value of an array *a* along the specified axis, but only considering values greater than a specified lower limit.

**Parameters**

* a ([array_like] array of values)
* lowerlimit ([None or float, optional] Values in the input array less than the given limit will be ignored. When lowerlimit is None, then all values are used. The default value is None.)
* axis ([int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array *a*.)
* inclusive ([{True, False}, optional] This flag determines whether values exactly equal to the lower limit are included. The default value is True.)
* nan_policy ([{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. ‘propagate’ returns nan, ‘raise’ throws an error, ‘omit’ performs the calculations ignoring nan values. Default is ‘propagate’.)

**Returns**

* tmin ([float, int or ndarray])

Examples

```python
>>> from scipy import stats
>>> x = np.arange(20)
>>> stats.tmin(x)
0
>>> stats.tmin(x, 13)
13
>>> stats.tmin(x, 13, inclusive=False)
14
```

**scipy.stats.tmax**

scipy.stats.tmax(*a*, upperlimit=None, axis=0, inclusive=True, nan_policy='propagate')

Compute the trimmed maximum.

This function computes the maximum value of an array along a given axis, while ignoring values larger than a specified upper limit.

**Parameters**
a [array_like] array of values
upperlimit [None or float, optional] Values in the input array greater than the given limit will be ignored. When upperlimit is None, then all values are used. The default value is None.
axis [int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array a.
inclusive [(True, False), optional] This flag determines whether values exactly equal to the upper limit are included. The default value is True.
nan_policy [({'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. ‘propagate’ returns nan, ‘raise’ throws an error, ‘omit’ performs the calculations ignoring nan values. Default is ‘propagate’.

Returns
tmax [float, int or ndarray]

Examples
tmax

```python
>>> from scipy import stats
>>> x = np.arange(20)
>>> stats.tmax(x)
19

>>> stats.tmax(x, 13)
13

>>> stats.tmax(x, 13, inclusive=False)
12
```

scipy.stats.tstd

scipy.stats.tstd(a, limits=None, inclusive=(True, True), axis=0, ddof=1)

Compute the trimmed sample standard deviation.

This function finds the sample standard deviation of given values, ignoring values outside the given limits.

Parameters

a [array_like] array of values
limits [None or (lower limit, upper limit), optional] Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None, then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval. The default value is None.
inclusive [(bool, bool), optional] A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).
axis [int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array a.
ddof [int, optional] Delta degrees of freedom. Default is 1.

Returns
tstd [float]

Notes
tstd computes the unbiased sample standard deviation, i.e. it uses a correction factor \( n / (n - 1) \).
Examples

```python
>>> from scipy import stats
>>> x = np.arange(20)
>>> stats.tstd(x)
5.9160797830996161
>>> stats.tstd(x, (3,17))
4.4721359549995796
```

**scipy.stats.tsem**

`scipy.stats.tsem(a, limits=None, inclusive=(True, True), axis=0, ddof=1)`

Compute the trimmed standard error of the mean.

This function finds the standard error of the mean for given values, ignoring values outside the given limits.

**Parameters**

- `a` : array_like
  Array of values.
- `limits` : None or (lower limit, upper limit), optional
  Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None, then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval. The default value is None.
- `inclusive` : (bool, bool), optional
  A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).
- `axis` : int or None, optional
  Axis along which to operate. Default is 0. If None, compute over the whole array `a`.
- `ddof` : int, optional
  Delta degrees of freedom. Default is 1.

**Returns**

- `tsem` : float

**Notes**

`tsem` uses unbiased sample standard deviation, i.e. it uses a correction factor $n / (n - 1)$.

**Examples**

```python
>>> from scipy import stats
>>> x = np.arange(20)
>>> stats.tsem(x)
1.3228756555322954
>>> stats.tsem(x, (3,17))
1.1547005383792515
```

**scipy.stats.variation**

`scipy.stats.variation(a, axis=0, nan_policy='propagate')`

Compute the coefficient of variation, the ratio of the biased standard deviation to the mean.

**Parameters**

- `a` : array_like
  Input array.
- `axis` : int or None, optional
  Axis along which to calculate the coefficient of variation. Default is 0. If None, compute over the whole array `a`.
- `nan_policy` : str, optional
  Policy for dealing with NaNs. By default, returns NaN.
Defines how to handle when input contains nan. ‘propagate’ returns nan, ‘raise’ throws an error, ‘omit’ performs the calculations ignoring nan values. Default is ‘propagate’.

Returns
variation [ndarray] The calculated variation along the requested axis.

References
[1]

Examples
```python
>>> from scipy.stats import variation
>>> variation([1, 2, 3, 4, 5])
0.47140452079103173
```

scipy.stats.find_repeats

Parameters
arr [array_like] Input array. This is cast to float64.

Returns
values [ndarray] The unique values from the (flattened) input that are repeated.
counts [ndarray] Number of times the corresponding ‘value’ is repeated.

Notes
In numpy >= 1.9 numpy.unique provides similar functionality. The main difference is that find_repeats only returns repeated values.

Examples
```python
>>> from scipy import stats
>>> stats.find_repeats([2, 1, 2, 3, 2, 2, 5])
RepeatedResults(values=array([2.]), counts=array([4]))

>>> stats.find_repeats([[10, 20, 1, 2], [5, 5, 4, 4]])
RepeatedResults(values=array([4., 5.]), counts=array([2, 2]))
```

scipy.stats.trim_mean

Parameters

a [array_like] Input array
proportiontocut [float] Fraction to cut off of both tails of the distribution
axis [int or None, optional] Axis along which the trimmed means are computed. Default is 0. If None, compute over the whole array a.

Returns
trim_mean

[ndarray] Mean of trimmed array.

See also:
trimboth
tmean

compute the trimmed mean ignoring values outside given limits.

Examples

>>> from scipy import stats
>>> x = np.arange(20)
>>> stats.trim_mean(x, 0.1)
9.5
>>> x2 = x.reshape(5, 4)
>>> x2
array([[ 0, 1, 2, 3],
       [ 4, 5, 6, 7],
       [ 8, 9, 10, 11],
       [12, 13, 14, 15],
       [16, 17, 18, 19]])
>>> stats.trim_mean(x2, 0.25)
array([ 8., 9., 10., 11.])
>>> stats.trim_mean(x2, 0.25, axis=1)
array([ 1.5, 5.5, 9.5, 13.5, 17.5])

scipy.stats.iqr

scipy.stats.iqr(x, axis=None, rng=(25, 75), scale='raw', nan_policy='propagate', interpolation='linear', keepdims=False)

Compute the interquartile range of the data along the specified axis.

The interquartile range (IQR) is the difference between the 75th and 25th percentile of the data. It is a measure of the dispersion similar to standard deviation or variance, but is much more robust against outliers [2].

The rng parameter allows this function to compute other percentile ranges than the actual IQR. For example, setting rng=(0, 100) is equivalent to numpy.ptp.

The IQR of an empty array is np.nan.

New in version 0.18.0.

Parameters

x [array_like] Input array or object that can be converted to an array.
axis [int or sequence of int, optional] Axis along which the range is computed. The default is to compute the IQR for the entire array.
rng [Two-element sequence containing floats in range of [0,100] optional] Percentiles over which to compute the range. Each must be between 0 and 100, inclusive. The default is the true IQR: (25, 75). The order of the elements is not important.
scale [scalar or str, optional] The numerical value of scale will be divided out of the final result. The following string values are recognized:
   ‘raw’: No scaling, just return the raw IQR. ‘normal’: Scale by \(2\sqrt{2\pi}f^{-1}\left(\frac{1}{2}\right) \approx 1.349\).
The default is ‘raw’. Array-like scale is also allowed, as long as it broadcasts correctly to the output such that \(\text{out} / \text{scale}\) is a valid operation. The output dimensions depend on the input array, \(x\), the \(\text{axis}\) argument, and the \(\text{keepdims}\) flag.

**nan_policy**

[{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. ‘propagate’ returns nan, ‘raise’ throws an error, ‘omit’ performs the calculations ignoring nan values. Default is ‘propagate’.

**interpolation**

[{'linear', 'lower', 'higher', 'midpoint', 'nearest'}, optional] Specifies the interpolation method to use when the percentile boundaries lie between two data points \(i\) and \(j\):

- **‘linear’** \([i + (j - i) \times \text{fraction}]\), where \(\text{fraction}\) is the fractional part of the index surrounded by \(i\) and \(j\).
- **‘lower’** : \(i\).
- **‘higher’** : \(j\).
- **‘nearest’** : \(i\) or \(j\) whichever is nearest.
- **‘midpoint’** : \((i + j) / 2\).

Default is ‘linear’.

**keepdims**

[bool, optional] If this is set to \(\text{True}\), the reduced axes are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original array \(x\).

**Returns**

**iqr**

[scalar or ndarray] If \(\text{axis} = \text{None}\), a scalar is returned. If the input contains integers or floats of smaller precision than \(\text{np.float64}\), then the output data-type is \(\text{np.float64}\). Otherwise, the output data-type is the same as that of the input.

See also:

- numpy.std, numpy.var

Notes

This function is heavily dependent on the version of numpy that is installed. Versions greater than 1.11.0b3 are highly recommended, as they include a number of enhancements and fixes to numpy.percentile and numpy.nanpercentile that affect the operation of this function. The following modifications apply:

**Below 1.10.0**

[\(\text{nan_policy}\) is poorly defined.] The default behavior of numpy.percentile is used for ‘propagate’. This is a hybrid of ‘omit’ and ‘propagate’ that mostly yields a skewed version of ‘omit’ since NaNs are sorted to the end of the data. A warning is raised if there are NaNs in the data.

**Below 1.9.0:** numpy.nanpercentile does not exist.

This means that numpy.percentile is used regardless of \(\text{nan_policy}\) and a warning is issued. See previous item for a description of the behavior.

**Below 1.9.0:** keepdims and interpolation are not supported.

The keywords get ignored with a warning if supplied with non-default values. However, multiple axes are still supported.

References

[1], [2], [3]
Examples

```python
>>> from scipy.stats import iqr
>>> x = np.array([[10, 7, 4], [3, 2, 1]])
>>> x
array([[10, 7, 4],
       [3, 2, 1]])
>>> iqr(x)
4.0
>>> iqr(x, axis=0)
array([ 3.5,  2.5,  1.5])
>>> iqr(x, axis=1)
array([ 3.,  1.])
>>> iqr(x, axis=1, keepdims=True)
array([[[ 3.],
       [ 1.]]])
```

**scipy.stats.sem**

`scipy.stats.sem(a, axis=0, ddof=1, nan_policy='propagate')`

Calculate the standard error of the mean (or standard error of measurement) of the values in the input array.

**Parameters**

- `a` : array_like
  An array containing the values for which the standard error is returned.
- `axis` : int or None, optional
  Axis along which to operate. Default is 0. If None, compute over the whole array `a`.
- `ddof` : int, optional
  Delta degrees-of-freedom. How many degrees of freedom to adjust for bias in limited samples relative to the population estimate of variance. Defaults to 1.
- `nan_policy` : {'propagate', 'raise', 'omit'}, optional
  Defines how to handle when input contains nan. ‘propagate’ returns nan, ‘raise’ throws an error, ‘omit’ performs the calculations ignoring nan values. Default is ‘propagate’.

**Returns**

- `s` : ndarray or float
  The standard error of the mean in the sample(s), along the input axis.

**Notes**

The default value for `ddof` is different to the default (0) used by other ddof containing routines, such as np.std and np.nanstd.

**Examples**

Find standard error along the first axis:

```python
>>> from scipy import stats
>>> a = np.arange(20).reshape(5, 4)
>>> stats.sem(a)
array([ 2.8284,  2.8284,  2.8284,  2.8284])
```

Find standard error across the whole array, using n degrees of freedom:

```python
>>> stats.sem(a, axis=None, ddof=0)
1.2893796958227628
```
scipy.stats.bayes_mvs

scipy.stats.bayes_mvs(data, alpha=0.9)
Bayesian confidence intervals for the mean, var, and std.

Parameters

- data: array_like. Input data, if multi-dimensional it is flattened to 1-D by bayes_mvs. Requires 2 or more data points.
- alpha: float, optional. Probability that the returned confidence interval contains the true parameter.

Returns

- mean_cntr, var_cntr, std_cntr: tuple. The three results are for the mean, variance and standard deviation, respectively. Each result is a tuple of the form:

  (center, (lower, upper))

  with center the mean of the conditional pdf of the value given the data, and (lower, upper) a confidence interval, centered on the median, containing the estimate to a probability alpha.

See also:

mvsdist

Notes

Each tuple of mean, variance, and standard deviation estimates represent the (center, (lower, upper)) with center the mean of the conditional pdf of the value given the data and (lower, upper) is a confidence interval centered on the median, containing the estimate to a probability alpha.

Converts data to 1-D and assumes all data has the same mean and variance. Uses Jeffrey’s prior for variance and std.

Equivalent to tuple((x.mean(), x.interval(alpha)) for x in mvsdist(dat))

References


Examples

First a basic example to demonstrate the outputs:

```python
>>> from scipy import stats
>>> data = [6, 9, 12, 7, 8, 8, 13]
>>> mean, var, std = stats.bayes_mvs(data)
>>> mean
Mean(statistic=9.0, minmax=(7.103650222612533, 10.896349777387467))
>>> var
Variance(statistic=10.0, minmax=(3.176724206..., 24.45910382...))
>>> std
Std_dev(statistic=2.9724954732045084, minmax=(1.7823367265645143, 4.
  →945614605014631))
```

Now we generate some normally distributed random data, and get estimates of mean and standard deviation with 95% confidence intervals for those estimates:
```python
>>> n_samples = 100000
>>> data = stats.norm.rvs(size=n_samples)
>>> res_mean, res_var, res_std = stats.bayes_mvs(data, alpha=0.95)

>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.hist(data, bins=100, density=True, label='Histogram of data')
>>> ax.vlines(res_mean.statistic, 0, 0.5, colors='r', label='Estimated mean')
>>> ... ax.vlines(res_mean.minmax[0],res_mean.minmax[1], facecolor='r',
>>> ... alpha=0.2, label=r'Estimated mean (95\% limits)')
>>> ax.vlines(res_std.statistic, 0, 0.5, colors='g', label='Estimated scale')
>>> ax.axvspan(res_mean.minmax[0],res_mean.minmax[1], facecolor='g', alpha=0.2,
>>> ... label=r'Estimated scale (95\% limits)')

>>> ax.legend(fontsize=10)
>>> ax.set_xlim([-4, 4])
>>> ax.set_ylim([0, 0.5])
>>> plt.show()
```

---

**scipy.stats.mvsdist**

`scipy.stats.mvsdist(data)`

‘Frozen’ distributions for mean, variance, and standard deviation of data.

**Parameters**

- `data` [array_like] Input array. Converted to 1-D using ravel. Requires 2 or more datapoints.

**Returns**

- `mdist` [“frozen” distribution object] Distribution object representing the mean of the data
- `vdist` [“frozen” distribution object] Distribution object representing the variance of the data
sdist "frozen" distribution object

Distribution object representing the standard deviation of the data

See also:
bayes_mvs

Notes
The return values from bayes_mvs(data) is equivalent to tuple((x.mean(), x.interval(0.90))
for x in mvsdist(data)).

In other words, calling <dist>.mean() and <dist>.interval(0.90) on the three distribution objects
returned from this function will give the same results that are returned from bayes_mvs.

References
T.E. Oliphant, “A Bayesian perspective on estimating mean, variance, and standard-deviation from

Examples
>>> from scipy import stats
>>> data = [8, 9, 12, 7, 8, 8, 13]
>>> mean, var, std = stats.mvsdist(data)

We now have frozen distribution objects “mean”, “var” and “std” that we can examine:

>>> mean.mean()
9.0
>>> mean.interval(0.95)
(6.6120585482655692, 11.387941451734431)
>>> mean.std()
1.1952286093343936

scipy.stats.entropy

scipy.stats.entropy(pk=None, qk=None, base=None)

Calculate the entropy of a distribution for given probability values.

If only probabilities pk are given, the entropy is calculated as \( S = -\sum pk * \log(pk), \text{ axis=0} \).

If qk is not None, then compute the Kullback-Leibler divergence \( S = \sum pk * \log(pk / qk), \text{ axis=0} \).

This routine will normalize pk and qk if they don’t sum to 1.

Parameters

- pk [sequence] Defines the (discrete) distribution. pk[i] is the (possibly unnormalized) probability of event i.
- qk [sequence, optional] Sequence against which the relative entropy is computed. Should be in the same format as pk.
- base [float, optional] The logarithmic base to use, defaults to e (natural logarithm).

Returns

- S [float] The calculated entropy.

6.27.8 Frequency statistics
### cumfreq

**cumfreq(a[, numbins, defaultreallimits, weights])**

Return a cumulative frequency histogram, using the histogram function.

### itemfreq

**itemfreq(*args, **kwds)**

**itemfreq** is deprecated! **itemfreq** is deprecated and will be removed in a future version.

### percentileofscore

**percentileofscore(a, score[, kind])**

The percentile rank of a score relative to a list of scores.

### scoreatpercentile

**scoreatpercentile(a, per[, limit, ...])**

Calculate the score at a given percentile of the input sequence.

### relfreq

**relfreq(a[, numbins, defaultreallimits, weights])**

Return a relative frequency histogram, using the histogram function.

---

**scipy.stats.cumfreq**

**scipy.stats.cumfreq(a, numbins=10, defaultreallimits=None, weights=None)**

Return a cumulative frequency histogram, using the histogram function.

A cumulative histogram is a mapping that counts the cumulative number of observations in all of the bins up to the specified bin.

**Parameters**

- **a** [array_like] Input array.
- **numbins** [int, optional] The number of bins to use for the histogram. Default is 10.
- **defaultreallimits** [tuple (lower, upper), optional] The lower and upper values for the range of the histogram. If no value is given, a range slightly larger than the range of the values in `a` is used. Specifically 
  \[(a.min() - s, a.max() + s),\]
  where \(s = (1/2)(a.max() - a.min()) / (numbins - 1)\).
- **weights** [array_like, optional] The weights for each value in `a`. Default is None, which gives each value a weight of 1.0

**Returns**

- **cumcount** [ndarray] Binned values of cumulative frequency.
- **lowerlimit** [float] Lower real limit
- **binsize** [float] Width of each bin.
- **extrapoints** [int] Extra points.

**Examples**

```python
>>> import matplotlib.pyplot as plt
>>> from scipy import stats
>>> x = [1, 4, 2, 1, 3, 1]
>>> res = stats.cumfreq(x, numbins=4, defaultreallimits=(1.5, 5))
>>> res.cumcount
array([ 1.,  2.,  3.,  3.])
>>> res.extrapoints
3
```

Create a normal distribution with 1000 random values

```python
>>> rng = np.random.RandomState(seed=12345)
>>> samples = stats.norm.rvs(size=1000, random_state=rng)
```
Calculate cumulative frequencies

```python
>>> res = stats.cumfreq(samples, numbins=25)
```

Calculate space of values for x

```python
>>> x = res.lowerlimit + np.linspace(0, res.binsize*res.cumcount.size, ...
                     res.cumcount.size)
```

Plot histogram and cumulative histogram

```python
>>> fig = plt.figure(figsize=(10, 4))
>>> ax1 = fig.add_subplot(1, 2, 1)
>>> ax2 = fig.add_subplot(1, 2, 2)
>>> ax1.hist(samples, bins=25)
>>> ax1.set_title('Histogram')
>>> ax2.bar(x, res.cumcount, width=res.binsize)
>>> ax2.set_title('Cumulative histogram')
>>> ax2.set_xlim([x.min(), x.max()])
```

```python
>>> plt.show()
```

**scipy.stats.itemfreq**

scipy.stats.itemfreq(*args, **kwds)

itemfreq is deprecated! itemfreq is deprecated and will be removed in a future version. Use instead np.unique(…, return_counts=True)

Return a 2-D array of item frequencies.

**Parameters**

- `a` ([N, ) array_like] Input array.

**Returns**

- `itemfreq` [(K, 2) ndarray] A 2-D frequency table. Column 1 contains sorted, unique values from a, column 2 contains their respective counts.
Examples

```python
>>> from scipy import stats
>>> a = np.array([1, 1, 5, 0, 1, 2, 0, 1, 4])
>>> stats.itemfreq(a)
array([[ 0.,  2.],
       [ 1.,  4.],
       [ 2.,  2.],
       [ 4.,  1.],
       [ 5.,  1.]])
>>> np.bincount(a)
array([2, 4, 2, 0, 1, 1])
>>> stats.itemfreq(a/10.)
array([[ 0. ,  2. ],
       [ 0.1,  4. ],
       [ 0.2,  2. ],
       [ 0.4,  1. ],
       [ 0.5,  1. ]])
```

scipy.stats.percentileofscore

scipy.stats.percentileofscore(a, score, kind='rank')

The percentile rank of a score relative to a list of scores.

A percentileofscore of, for example, 80% means that 80% of the scores in `a` are below the given score. In the case of gaps or ties, the exact definition depends on the optional keyword, `kind`.

**Parameters**

- **a** [array_like] Array of scores to which `score` is compared.
- **score** [int or float] Score that is compared to the elements in `a`.
- **kind** [{‘rank’, ‘weak’, ‘strict’, ‘mean’}, optional] This optional parameter specifies the interpretation of the resulting score:
  - **“rank”**: Average percentage ranking of score. In case of multiple matches, average the percentage rankings of all matching scores.
  - **“weak”**: This kind corresponds to the definition of a cumulative distribution function. A percentileofscore of 80% means that 80% of values are less than or equal to the provided score.
  - **“strict”**: Similar to “weak”, except that only values that are strictly less than the given score are counted.
  - **“mean”**: The average of the “weak” and “strict” scores, often used in testing. See https://en.wikipedia.org/wiki/Percentile_rank

**Returns**

- **pcos** [float] Percentile-position of score (0-100) relative to `a`.

See also:

numpy.percentile

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Examples

Three-quarters of the given values lie below a given score:

```python
>>> from scipy import stats
>>> stats.percentileofscore([1, 2, 3, 4], 3)
75.0
```

With multiple matches, note how the scores of the two matches, 0.6 and 0.8 respectively, are averaged:

```python
>>> stats.percentileofscore([1, 2, 3, 3, 4], 3)
70.0
```

Only 2/5 values are strictly less than 3:

```python
>>> stats.percentileofscore([1, 2, 3, 3, 4], 3, kind='strict')
40.0
```

But 4/5 values are less than or equal to 3:

```python
>>> stats.percentileofscore([1, 2, 3, 3, 4], 3, kind='weak')
80.0
```

The average between the weak and the strict scores is

```python
>>> stats.percentileofscore([1, 2, 3, 3, 4], 3, kind='mean')
60.0
```

`scipy.stats.scoreatpercentile`

`scipy.stats.scoreatpercentile(a, per, limit=(), interpolation_method='fraction', axis=None)`

Calculate the score at a given percentile of the input sequence.

For example, the score at `per=50` is the median. If the desired quantile lies between two data points, we interpolate between them, according to the value of `interpolation`. If the parameter `limit` is provided, it should be a tuple (lower, upper) of two values.

**Parameters**

- `a` [array_like] A 1-D array of values from which to extract score.
- `per` [array_like] Percentile(s) at which to extract score. Values should be in range [0,100].
- `limit` [tuple, optional] Tuple of two scalars, the lower and upper limits within which to compute the percentile. Values of `a` outside this (closed) interval will be ignored.
- `interpolation_method` [‘fraction’, ‘lower’, ‘higher’], optional This optional parameter specifies the interpolation method to use, when the desired quantile lies between two data points `i` and `j`:
  - fraction: `i + (j - i) * fraction` where `fraction` is the fractional part of the index surrounded by `i` and `j`.
  - lower: `i`.
  - higher: `j`.
- `axis` [int, optional] Axis along which the percentiles are computed. Default is None. If None, compute over the whole array `a`.

**Returns**

- `score` [float or ndarray] Score at percentile(s).
See also:

`percentileofscore`, `numpy.percentile`

Notes
This function will become obsolete in the future. For Numpy 1.9 and higher, `numpy.percentile` provides all the functionality that `scoreatpercentile` provides. And it’s significantly faster. Therefore it’s recommended to use `numpy.percentile` for users that have numpy $\geq 1.9$.

Examples

```python
>>> from scipy import stats
>>> a = np.arange(100)
>>> stats.scoreatpercentile(a, 50)
49.5
```
>>> rng = np.random.RandomState(seed=12345)
>>> samples = stats.norm.rvs(size=1000, random_state=rng)

Calculate relative frequencies

>>> res = stats.relfreq(samples, numbins=25)

Calculate space of values for x

>>> x = res.lowerlimit + np.linspace(0, res.binsize*res.frequency.size, ...
... res.frequency.size)

Plot relative frequency histogram

>>> fig = plt.figure(figsize=(5, 4))
>>> ax = fig.add_subplot(1, 1, 1)
>>> ax.bar(x, res.frequency, width=res.binsize)
>>> ax.set_title('Relative frequency histogram')
>>> ax.set_xlim([x.min(), x.max()])

>>> plt.show()

```
<table>
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<th>Function</th>
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<td>binned_statistic(x, values[, statistic, ...])</td>
<td>Compute a binned statistic for one or more sets of data.</td>
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<td>binned_statistic_2d(x, y, values[, ...])</td>
<td>Compute a bidimensional binned statistic for one or more sets of data.</td>
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```
scipy.stats.binned_statistic

scipy.stats.binned_statistic(x, values, statistic='mean', bins=10, range=None)

Compute a binned statistic for one or more sets of data.

This is a generalization of a histogram function. A histogram divides the space into bins, and returns the count of the number of points in each bin. This function allows the computation of the sum, mean, median, or other statistic of the values (or set of values) within each bin.

Parameters

- **x** : [(N,) array_like] A sequence of values to be binned.
- **values** : [(N,) array_like or list of (N,) array_like] The data on which the statistic will be computed. This must be the same shape as x, or a set of sequences - each the same shape as x. If values is a set of sequences, the statistic will be computed on each independently.
- **statistic** : [string or callable, optional] The statistic to compute (default is 'mean'). The following statistics are available:
  - 'mean' : compute the mean of values for points within each bin. Empty bins will be represented by NaN.
  - 'median' : compute the median of values for points within each bin. Empty bins will be represented by NaN.
  - 'count' : compute the count of points within each bin. This is identical to an unweighted histogram. values array is not referenced.
  - 'sum' : compute the sum of values for points within each bin. This is identical to a weighted histogram.
  - 'min' : compute the minimum of values for points within each bin. Empty bins will be represented by NaN.
  - 'max' : compute the maximum of values for point within each bin. Empty bins will be represented by NaN.
  - function : a user-defined function which takes a 1D array of values, and outputs a single numerical statistic. This function will be called on the values in each bin. Empty bins will be represented by function([]), or NaN if this returns an error.
- **bins** : [int or sequence of scalars, optional] If bins is an int, it defines the number of equal-width bins in the given range (10 by default). If bins is a sequence, it defines the bin edges, including the rightmost edge, allowing for non-uniform bin widths. Values in x that are smaller than lowest bin edge are assigned to bin number 0, values beyond the highest bin are assigned to bins[-1]. If the bin edges are specified, the number of bins will be, nx = len(bins)-1.
- **range** : [(float, float) or [(float, float)], optional] The lower and upper range of the bins. If not provided, range is simply (x.min(), x.max()). Values outside the range are ignored.

Returns

- **statistic** : [array] The values of the selected statistic in each bin.
- **bin_edges** : [array of dtype float] Return the bin edges (length(statistic)+1).
- **binnumber** : 1-D ndarray of ints
  Indices of the bins (corresponding to bin_edges) in which each value of x belongs. Same length as values. A binnumber of i means the corresponding value is between (bin_edges[i-1], bin_edges[i]).
See also:

numpy.digitize, numpy.histogram, binned_statistic_2d, binned_statistic_dd

Notes
All but the last (righthand-most) bin is half-open. In other words, if bins is [1, 2, 3, 4], then the first bin is [1, 2) (including 1, but excluding 2) and the second [2, 3). The last bin, however, is [3, 4], which includes 4.

New in version 0.11.0.

Examples

```python
from scipy import stats
import matplotlib.pyplot as plt

First some basic examples:

Create two evenly spaced bins in the range of the given sample, and sum the corresponding values in each of those bins:

```python
values = [1.0, 1.0, 2.0, 1.5, 3.0]
stats.binned_statistic([1, 1, 2, 5, 7], values, 'sum', bins=2)
(array([ 4. , 4.5]), array([ 1., 4., 7.]), array([1, 1, 1, 2, 2]))
```

Multiple arrays of values can also be passed. The statistic is calculated on each set independently:

```python
values = [[1.0, 1.0, 2.0, 1.5, 3.0], [2.0, 2.0, 4.0, 3.0, 6.0]]
stats.binned_statistic([1, 1, 2, 5, 7], values, 'sum', bins=2)
(array([[ 4. , 4.5], [ 8., 9. ]]), array([ 1., 4., 7.]), array([1, 1, 1, 2, 2]))
```

```python
stats.binned_statistic([1, 2, 1, 2, 4], np.arange(5), statistic='mean', ... bins=3)
(array([1., 2., 4.]), array([ 1., 2., 3., 4.]), array([1, 2, 1, 2, 3]))
```

As a second example, we now generate some random data of sailing boat speed as a function of wind speed, and then determine how fast our boat is for certain wind speeds:

```python
windspeed = 8 * np.random.rand(500)
boatspeed = .3 * windspeed**.5 + .2 * np.random.rand(500)
bin_means, bin_edges, binnumber = stats.binned_statistic(windspeed, ... boatspeed, statistic='median', bins=[1,2,3,4,5,6,7])
plt.figure()
plt.plot(windspeed, boatspeed, 'b.', label='raw data')
plt.hlines(bin_means, bin_edges[:-1], bin_edges[1:], colors='g', lw=5, ... label='binned statistic of data')
plt.legend()
```

Now we can use binnumber to select all datapoints with a windspeed below 1:

```python
low_boatspeed = boatspeed[binnumber == 0]
```

As a final example, we will use bin_edges and binnumber to make a plot of a distribution that shows the mean and distribution around that mean per bin, on top of a regular histogram and the probability distribution function:
```python
>>> x = np.linspace(0, 5, num=500)
>>> x_pdf = stats.maxwell.pdf(x)
>>> samples = stats.maxwell.rvs(size=10000)

>>> bin_means, bin_edges, binnumber = stats.binned_statistic(x, x_pdf,
... statistic='mean', bins=25)
>>> bin_width = (bin_edges[1] - bin_edges[0])
>>> bin_centers = bin_edges[1:] - bin_width/2

>>> plt.figure()
>>> plt.hist(samples, bins=50, density=True, histtype='stepfilled',
... alpha=0.2, label='histogram of data')
>>> plt.plot(x, x_pdf, 'r-', label='analytical pdf')
>>> plt.hlines(bin_means, bin_edges[:-1], bin_edges[1:], colors='g', lw=2,
... label='binned statistic of data')
>>> plt.plot((binnumber - 0.5) * bin_width, x_pdf, 'g.', alpha=0.5)
>>> plt.legend(fontsize=10)
>>> plt.show()
```

### scipy.stats.binned_statistic_2d

**scipy.stats.binned_statistic_2d**

`scipy.stats.binned_statistic_2d(x, y, values, statistic='mean', bins=10, range=None, expand_binnumbers=False)`

Compute a bidimensional binned statistic for one or more sets of data.

This is a generalization of a histogram2d function. A histogram divides the space into bins, and returns the count of the number of points in each bin. This function allows the computation of the sum, mean, median, or other statistic of the values (or set of values) within each bin.

**Parameters**

- **x** : [(N,)] array_like
  A sequence of values to be binned along the first dimension.
- **y** : [(N,)] array_like
  A sequence of values to be binned along the second dimension.
- **values** : [(N,)] array_like or list of (N,) array_like
  The data on which the statistic will be computed. This must be the same shape as x, or a list of sequences - each with
the same shape as `x`. If `values` is such a list, the statistic will be computed on each independently.

**statistic** [string or callable, optional] The statistic to compute (default is ‘mean’). The following statistics are available:
- ‘mean’ : compute the mean of values for points within each bin. Empty bins will be represented by NaN.
- ‘median’ : compute the median of values for points within each bin. Empty bins will be represented by NaN.
- ‘count’ : compute the count of points within each bin. This is identical to an unweighted histogram. `values` array is not referenced.
- ‘sum’ : compute the sum of values for points within each bin. This is identical to a weighted histogram.
- ‘min’ : compute the minimum of values for points within each bin. Empty bins will be represented by NaN.
- ‘max’ : compute the maximum of values for point within each bin. Empty bins will be represented by NaN.
- function : a user-defined function which takes a 1D array of values, and outputs a single numerical statistic. This function will be called on the values in each bin. Empty bins will be represented by `function([])`, or NaN if this returns an error.

**bins** [int or [int, int] or array_like or [array, array], optional] The bin specification:
- the number of bins for the two dimensions (nx = ny = bins),
- the number of bins in each dimension (nx, ny = bins),
- the bin edges for the two dimensions (x_edge = y_edge = bins),
- the bin edges in each dimension (x_edge, y_edge = bins).
If the bin edges are specified, the number of bins will be, (nx = len(x_edge)-1, ny = len(y_edge)-1).

**range** [(2,2) array_like, optional] The leftmost and rightmost edges of the bins along each dimension (if not specified explicitly in the `bins` parameters): [xmin, xmax], [ymin, ymax]]. All values outside of this range will be considered outliers and not tallied in the histogram.

**expand_binnumbers** [bool, optional] ‘False’ (default): the returned `binnumber` is a shape (N,) array of linearized bin indices. ‘True’: the returned `binnumber` is ‘unraveled’ into a
shape (2,N) ndarray, where each row gives the bin numbers in the corresponding dimension. See the binnumber returned value, and the Examples section. New in version 0.17.0.

Returns

- **statistic** [(nx, ny) ndarray] The values of the selected statistic in each two-dimensional bin.
- **x_edge** [(nx + 1) ndarray] The bin edges along the first dimension.
- **y_edge** [(ny + 1) ndarray] The bin edges along the second dimension.
- **binnumber** [(N,) array of ints or (2,N) ndarray of ints] This assigns to each element of sample an integer that represents the bin in which this observation falls. The representation depends on the expand_binnumbers argument. See Notes for details.

See also:

numpy.digitize, numpy.histogram2d, binned_statistic, binned_statistic_dd

Notes

Binedges: All but the last (righthand-most) bin is half-open. In other words, if bins is [1, 2, 3, 4], then the first bin is [1, 2) (including 1, but excluding 2) and the second [2, 3). The last bin, however, is [3, 4], which includes 4.

binnumber: This returned argument assigns to each element of sample an integer that represents the bin in which it belongs. The representation depends on the expand_binnumbers argument. If ‘False’ (default): The returned binnumber is a shape (N,) array of linearized indices mapping each element of sample to its corresponding bin (using row-major ordering). If ‘True’: The returned binnumber is a shape (2,N) ndarray where each row indicates bin placements for each dimension respectively. In each dimension, a binnumber of i means the corresponding value is between (D_edge[i-1], D_edge[i]), where ‘D’ is either ‘x’ or ‘y’.

New in version 0.11.0.

Examples

```python
>>> from scipy import stats

Calculate the counts with explicit bin-edges:

```python
>>> x = [0.1, 0.1, 0.1, 0.6]
>>> y = [2.1, 2.6, 2.1, 2.1]
>>> binx = [0.0, 0.5, 1.0]
>>> biny = [2.0, 2.5, 3.0]
>>> ret = stats.binned_statistic_2d(x, y, None, 'count', bins=[binx,biny])
>>> ret.statistic
array([[ 2.,  1.],
       [ 1.,  0.]])
```

The bin in which each sample is placed is given by the binnumber returned parameter. By default, these are the linearized bin indices:

```python
>>> ret.binnumber
array([5, 6, 5, 9])
```

The bin indices can also be expanded into separate entries for each dimension using the expand_binnumbers parameter:

```python
>>> ret = stats.binned_statistic_2d(x, y, None, 'count', bins=[binx,biny], expand_binnumbers=True)
```

(continues on next page)
Which shows that the first three elements belong in the xbin 1, and the fourth into xbin 2; and so on for y.

**scipy.stats.binned_statistic_dd**

`scipy.stats.binned_statistic_dd(sample, values, statistic='mean', bins=10, range=None, expand_binnumbers=False)`

Compute a multidimensional binned statistic for a set of data.

This is a generalization of a histogramdd function. A histogram divides the space into bins, and returns the count of the number of points in each bin. This function allows the computation of the sum, mean, median, or other statistic of the values within each bin.

**Parameters**

- **sample** [array_like] Data to histogram passed as a sequence of D arrays of length N, or as an (N,D) array.
- **values** [(N,) array_like or list of (N,) array_like] The data on which the statistic will be computed. This must be the same shape as `sample`, or a list of sequences - each with the same shape as `sample`. If `values` is such a list, the statistic will be computed on each independently.
- **statistic** [string or callable, optional] The statistic to compute (default is ‘mean’). The following statistics are available:
  - ‘mean’ : compute the mean of values for points within each bin. Empty bins will be represented by NaN.
  - ‘median’ : compute the median of values for points within each bin. Empty bins will be represented by NaN.
  - ‘count’ : compute the count of points within each bin. This is identical to an unweighted histogram. `values` array is not referenced.
  - ‘sum’ : compute the sum of values for points within each bin. This is identical to a weighted histogram.
  - ‘min’ : compute the minimum of values for points within each bin. Empty bins will be represented by NaN.
  - ‘max’ : compute the maximum of values for point within each bin. Empty bins will be represented by NaN.
  - `function` : a user-defined function which takes a 1D array of values, and outputs a single numerical statistic. This function will be called on the values in each bin. Empty bins will be represented by `function([])`, or NaN if this returns an error.
- **bins** [sequence or int, optional] The bin specification must be in one of the following forms:
  - A sequence of arrays describing the bin edges along each dimension.
  - The number of bins for each dimension (nx, ny, ... = bins).
  - The number of bins for all dimensions (nx = ny = ... = bins).
- **range** [sequence, optional] A sequence of lower and upper bin edges to be used if the edges are not given explicitly in `bins`. Defaults to the minimum and maximum values along each dimension.
- **expand_binnumbers** [bool, optional] ‘False’ (default): the returned `binnumber` is a shape (N,) array of linearized bin indices. ‘True’: the returned `binnumber` is ‘unraveled’ into a
shape (D,N) ndarray, where each row gives the bin numbers in the corresponding dimension. See the binnumber returned value, and the Examples section of binned_statistic_2d.

New in version 0.17.0.

**Returns**

- **statistic**
  [ndarray, shape(nx1, nx2, nx3,...)] The values of the selected statistic in each two-dimensional bin.

- **bin_edges**
  list of ndarrays A list of D arrays describing the (nxi + 1) bin edges for each dimension.

- **binnumber**
  [(N,) array of ints or (D,N) ndarray of ints] This assigns to each element of sample an integer that represents the bin in which this observation falls. The representation depends on the expand_binnumbers argument. See Notes for details.

See also:
numpy.digitize, numpy.histogramdd, binned_statistic, binned_statistic_2d

**Notes**

Bin edges: All but the last (righthand-most) bin is half-open in each dimension. In other words, if bins is [1, 2, 3, 4], then the first bin is [1, 2) (including 1, but excluding 2) and the second [2, 3).

The last bin, however, is [3, 4], which includes 4.

Bin number: This returned argument assigns to each element of sample an integer that represents the bin in which it belongs. The representation depends on the expand_binnumbers argument. If ‘False’ (default): The returned binnumber is a shape (N,) array of linearized indices mapping each element of sample to its corresponding bin (using row-major ordering). If ‘True’: The returned binnumber is a shape (D,N) ndarray where each row indicates bin placements for each dimension respectively. In each dimension, a binnumber of i means the corresponding value is between (bin_edges[D][i-1], bin_edges[D][i]), for each dimension ‘D’.

New in version 0.11.0.

### 6.27.9 Correlation functions

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<td>f_oneway(*args)</td>
<td>Performs a 1-way ANOVA.</td>
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<tr>
<td>pearsonr(x, y)</td>
<td>Calculate a Pearson correlation coefficient and the p-value for testing non-correlation.</td>
</tr>
<tr>
<td>spearmanr(a[, b, axis, nan_policy])</td>
<td>Calculate a Spearman rank-order correlation coefficient and the p-value to test for non-correlation.</td>
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<tr>
<td>siegelslopes(y[, x, method])</td>
<td>Computes the Siegel estimator for a set of points (x, y).</td>
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<td>Computes the Theil-Sen estimator for a set of points (x, y).</td>
</tr>
</tbody>
</table>
`scipy.stats.f_oneway`

`scipy.stats.f_oneway(*args)`

Performs a 1-way ANOVA.

The one-way ANOVA tests the null hypothesis that two or more groups have the same population mean. The test is applied to samples from two or more groups, possibly with differing sizes.

**Parameters**

- `sample1, sample2, ...`
  - `array_like` The sample measurements for each group.

**Returns**

- `statistic` [float] The computed F-value of the test.
- `pvalue` [float] The associated p-value from the F-distribution.

**Notes**

The ANOVA test has important assumptions that must be satisfied in order for the associated p-value to be valid.

1. The samples are independent.
2. Each sample is from a normally distributed population.
3. The population standard deviations of the groups are all equal. This property is known as homoscedasticity.

If these assumptions are not true for a given set of data, it may still be possible to use the Kruskal-Wallis H-test (`scipy.stats.kruskal`) although with some loss of power.

The algorithm is from Heiman[2], pp.394-7.

**References**

[1], [2], [3]

**Examples**

```python
>>> import scipy.stats as stats
```

[3] Here are some data on a shell measurement (the length of the anterior adductor muscle scar, standardized by dividing by length) in the mussel Mytilus trossulus from five locations: Tillamook, Oregon; Newport, Oregon; Petersburg, Alaska; Magadan, Russia; and Tvarminne, Finland, taken from a much larger data set used in McDonald et al. (1991).

```python
>>> tillamook = [0.0571, 0.0813, 0.0831, 0.0976, 0.0817, 0.0859, 0.0735, ...
               0.0659, 0.0836]
>>> newport = [0.0873, 0.0662, 0.0672, 0.0819, 0.0749, 0.0649, 0.0835, ...
              0.0725]
>>> petersburg = [0.0974, 0.1352, 0.0817, 0.1016, 0.0968, 0.1064, 0.105]
>>> magadan = [0.1033, 0.0915, 0.0781, 0.0685, 0.0677, 0.0697, 0.0764,
              0.0689]
>>> tvarminne = [0.0703, 0.1026, 0.0956, 0.0973, 0.1039, 0.1045]
>>> stats.f_oneway(tillamook, newport, petersburg, magadan, tvarminne)
(7.1210194716424473, 0.00028122423145345439)
```

`scipy.stats.pearsonr`

`scipy.stats.pearsonr(x, y)`

Calculate a Pearson correlation coefficient and the p-value for testing non-correlation.
The Pearson correlation coefficient measures the linear relationship between two datasets. Strictly speaking, Pearson's correlation requires that each dataset be normally distributed, and not necessarily zero-mean. Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply an exact linear relationship. Positive correlations imply that as x increases, so does y. Negative correlations imply that as x increases, y decreases.

The p-value roughly indicates the probability of an uncorrelated system producing datasets that have a Pearson correlation at least as extreme as the one computed from these datasets. The p-values are not entirely reliable but are probably reasonable for datasets larger than 500 or so.

**Parameters**

- `x` : [(N,) array_like] Input
- `y` : [(N,) array_like] Input

**Returns**

- `r` : [float] Pearson's correlation coefficient
- `p-value` : [float] 2-tailed p-value

**Notes**

The correlation coefficient is calculated as follows:

\[
   r_{pb} = \frac{\sum (x - m_x)(y - m_y)}{\sqrt{\sum (x - m_x)^2 \sum (y - m_y)^2}}
\]

where \( m_x \) is the mean of the vector \( x \) and \( m_y \) is the mean of the vector \( y \).

**References**

http://www.statsoft.com/textbook/glosp.html#Pearson%20Correlation

**Examples**

```python
>>> from scipy import stats
>>> a = np.array([0, 0, 0, 1, 1, 1, 1])
>>> b = np.arange(7)
>>> stats.pearsonr(a, b)
(0.8660254037844386, 0.011724811003954654)
```

```python
>>> stats.pearsonr([1,2,3,4,5], [5,6,7,8,7])
(0.83205029433784372, 0.080509573298498519)
```

**scipy.stats.spearmanr**

Calculate a Spearman rank-order correlation coefficient and the p-value to test for non-correlation.

The Spearman correlation is a nonparametric measure of the monotonicity of the relationship between two datasets. Unlike the Pearson correlation, the Spearman correlation does not assume that both datasets are normally distributed. Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply an exact monotonic relationship. Positive correlations imply that as x increases, so does y. Negative correlations imply that as x increases, y decreases.

The p-value roughly indicates the probability of an uncorrelated system producing datasets that have a Spearman correlation at least as extreme as the one computed from these datasets. The p-values are not entirely reliable but are probably reasonable for datasets larger than 500 or so.

**Parameters**
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a, b  [1D or 2D array_like, b is optional] One or two 1-D or 2-D arrays containing multiple variables and observations. When these are 1-D, each represents a vector of observations of a single variable. For the behavior in the 2-D case, see under axis, below. Both arrays need to have the same length in the axis dimension.

axis  [int or None, optional] If axis=0 (default), then each column represents a variable, with observations in the rows. If axis=1, the relationship is transposed: each row represents a variable, while the columns contain observations. If axis=None, then both arrays will be raveled.


Returns
correlation  [float or ndarray (2-D square)] Spearman correlation matrix or correlation coefficient (if only 2 variables are given as parameters. Correlation matrix is square with length equal to total number of variables (columns or rows) in a and b combined.
pvalue  [float] The two-sided p-value for a hypothesis test whose null hypothesis is that two sets of data are uncorrelated, has same dimension as rho.

References
[1]

Examples

```python
>>> from scipy import stats
>>> stats.spearmanr([1,2,3,4,5], [5,6,7,8,7])
(0.82078268166812329, 0.088587005313543798)
>>> np.random.seed(1234321)
>>> x2n = np.random.randn(100, 2)
>>> y2n = np.random.randn(100, 2)
>>> stats.spearmanr(x2n)
(0.059969996999699973, 0.55338590803773591)
>>> stats.spearmanr(x2n[:,0], x2n[:,1])
(0.059969996999699973, 0.55338590803773591)
>>> rho, pval = stats.spearmanr(x2n, y2n)
>>> rho
array([[ 1. , 0.05997 , 0.18569457, 0.06258626],
       [ 0.05997 , 1. , 0.110003 , 0.02534653],
       [ 0.18569457, 0.110003 , 1. , 0.03488749],
       [ 0.06258626, 0.02534653, 0.03488749, 1. ]])
>>> pval
array([[ 0. , 0.55338591, 0.06430364, 0.53617935],
       [ 0.55338591, 0. , 0.27592895, 0.80234077],
       [ 0.06430364, 0.27592895, 0. , 0.73039992],
       [ 0.53617935, 0.80234077, 0.73039992, 0. ]])
>>> rho, pval = stats.spearmanr(x2n.T, y2n.T, axis=1)
>>> rho
array([[ 1. , 0.05997 , 0.18569457, 0.06258626],
       [ 0.05997 , 1. , 0.110003 , 0.02534653],
       [ 0.18569457, 0.110003 , 1. , 0.03488749],
       [ 0.06258626, 0.02534653, 0.03488749, 1. ]])
>>> stats.spearmanr(x2n, y2n, axis=None)
(0.10816770419260482, 0.1273562188027364)
```
scipy.stats.pointbiserialr

scipy.stats.pointbiserialr(x, y)

Calculate a point biserial correlation coefficient and its p-value.

The point biserial correlation is used to measure the relationship between a binary variable, x, and a continuous variable, y. Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply a determinative relationship.

This function uses a shortcut formula but produces the same result as pearsonr.

Parameters

x [array_like of bools] Input array.
y [array_like] Input array.

Returns

correlation [float] R value
pvalue [float] 2-tailed p-value

Notes

pointbiserialr uses a t-test with n-1 degrees of freedom. It is equivalent to pearsonr.

The value of the point-biserial correlation can be calculated from:

\[ r_{pb} = \frac{Y_1 - Y_0}{s_y} \sqrt{\frac{N_1 N_2}{N(N-1)}} \]

Where \( Y_0 \) and \( Y_1 \) are means of the metric observations coded 0 and 1 respectively; \( N_0 \) and \( N_1 \) are number of observations coded 0 and 1 respectively; \( N \) is the total number of observations and \( s_y \) is the standard deviation of all the metric observations.

A value of \( r_{pb} \) that is significantly different from zero is completely equivalent to a significant difference in means between the two groups. Thus, an independent groups t Test with \( N - 2 \) degrees of freedom may be used to test whether \( r_{pb} \) is nonzero. The relation between the t-statistic for comparing two independent groups and \( r_{pb} \) is given by:

\[ t = \sqrt{N - 2} \frac{r_{pb}}{\sqrt{1 - r_{pb}^2}} \]

References

[1], [2], [3]

Examples

```python
>>> from scipy import stats
>>> a = np.array([0, 0, 0, 1, 1, 1])
>>> b = np.array([0, 1, 2, 3, 4, 5])
```

(continues on next page)
scipy.stats.kendalltau

scipy.stats.kendalltau(x, y, initial_lexsort=None, nan_policy='propagate', method='auto')

Calculate Kendall’s tau, a correlation measure for ordinal data.

Kendall’s tau is a measure of the correspondence between two rankings. Values close to 1 indicate strong agreement, values close to -1 indicate strong disagreement. This is the 1945 “tau-b” version of Kendall’s tau [2], which can account for ties and which reduces to the 1938 “tau-a” version [1] in absence of ties.

**Parameters**

- `x, y` [array_like] Arrays of rankings, of the same shape. If arrays are not 1-D, they will be flattened to 1-D.
- `initial_lexsort` [bool, optional] Unused (deprecated).
- `nan_policy` [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. ‘propagate’ returns nan, ‘raise’ throws an error, ‘omit’ performs the calculations ignoring nan values. Default is ‘propagate’. Note that if the input contains nan ‘omit’ delegates to mstats_basic.kendalltau(), which has a different implementation.
- `method`: {'auto', 'asymptotic', 'exact'}, optional
  Defines which method is used to calculate the p-value [5]. ‘asymptotic’ uses a normal approximation valid for large samples. ‘exact’ computes the exact p-value, but can only be used if no ties are present. ‘auto’ is the default and selects the appropriate method based on a trade-off between speed and accuracy.

**Returns**

- `correlation` [float] The tau statistic.
- `pvalue` [float] The two-sided p-value for a hypothesis test whose null hypothesis is an absence of association, tau = 0.

See also:

- `spearmanr`
  Calculates a Spearman rank-order correlation coefficient.
- `theilslopes`
  Computes the Theil-Sen estimator for a set of points (x, y).
- `weightedtau`
  Computes a weighted version of Kendall’s tau.
Notes
The definition of Kendall’s tau that is used is [2]:

$$\tau = \frac{(P - Q)}{\sqrt{(P + Q + T) \cdot (P + Q + U)}}$$

where P is the number of concordant pairs, Q the number of discordant pairs, T the number of ties only in x, and U the number of ties only in y. If a tie occurs for the same pair in both x and y, it is not added to either T or U.

References
[1], [2], [3], [4], [5]

Examples
```python
>>> from scipy import stats
>>> x1 = [12, 2, 1, 12, 2]
>>> x2 = [1, 4, 7, 1, 0]
>>> tau, p_value = stats.kendalltau(x1, x2)
>>> tau
-0.47140452079103173
>>> p_value
0.2827454599327748
```
**weigher** [callable, optional] The weigher function. Must map nonnegative integers (zero representing the most important element) to a nonnegative weight. The default, None, provides hyperbolic weighing, that is, rank \( r \) is mapped to weight \( 1/(r+1) \).

**additive** [bool, optional] If True, the weight of an exchange is computed by adding the weights of the ranks of the exchanged elements; otherwise, the weights are multiplied. The default is True.

**Returns**

- **correlation** [float] The weighted \( \tau \) correlation index.
- **pvalue** [float] Presently np.nan, as the null statistics is unknown (even in the additive hyperbolic case).

**See also:**

- **kendalltau**
  Calculates Kendall’s tau.
- **spearmanr**
  Calculates a Spearman rank-order correlation coefficient.
- **theilslopes**
  Computes the Theil-Sen estimator for a set of points \((x, y)\).

**Notes**

This function uses an \( O(n \log n) \), mergesort-based algorithm [1] that is a weighted extension of Knight’s algorithm for Kendall’s \( \tau \) [2]. It can compute Shieh’s weighted \( \tau \) [3] between rankings without ties (i.e., permutations) by setting **additive** and **rank** to False, as the definition given in [1] is a generalization of Shieh’s.

NaNs are considered the smallest possible score.

New in version 0.19.0.

**References**

[1], [2], [3]

**Examples**

```python
>>> from scipy import stats
>>> x = [12, 2, 1, 12, 2]
>>> y = [1, 4, 7, 1, np.nan]
>>> tau, p_value = stats.weightedtau(x, y, additive=False)
>>> tau
-0.62205716951801038
```

NaNs are considered the smallest possible score:

```python
>>> x = [12, 2, 1, 12, 2]
>>> y = [1, 4, 7, 1, np.nan]
>>> tau, _ = stats.weightedtau(x, y)
```

(continues on next page)
This is exactly Kendall’s tau:

```python
>>> x = [12, 2, 1, 12, 2]
>>> y = [1, 4, 7, 1, 0]
>>> tau, _ = stats.weightedtau(x, y, weigher=lambda x: 1)
>>> tau
-0.47140452079103173
```

```python
>>> x = [12, 2, 1, 12, 2]
>>> y = [1, 4, 7, 1, 0]
>>> stats.weightedtau(x, y, rank=None)
WeightedTauResult(correlation=-0.4157652301037516, pvalue=nan)
>>> stats.weightedtau(y, x, rank=None)
WeightedTauResult(correlation=-0.7181341329699028, pvalue=nan)
```

### scipy.stats.linregress

**scipy.stats.linregress**

*scipy.stats.linregress*(x, y=None)*

Calculate a linear least-squares regression for two sets of measurements.

**Parameters**

- **x**, **y**  
  [array_like] Two sets of measurements. Both arrays should have the same length. If only x is given (and y=None), then it must be a two-dimensional array where one dimension has length 2. The two sets of measurements are then found by splitting the array along the length-2 dimension.

**Returns**

- **slope**  
  [float] slope of the regression line
- **intercept**  
  [float] intercept of the regression line
- **rvalue**  
  [float] correlation coefficient
- **pvalue**  
  [float] two-sided p-value for a hypothesis test whose null hypothesis is that the slope is zero, using Wald Test with t-distribution of the test statistic.
- **stderr**  
  [float] Standard error of the estimated gradient.

**See also:**

- **scipy.optimize.curve_fit**
  Use non-linear least squares to fit a function to data.
- **scipy.optimize.leastsq**
  Minimize the sum of squares of a set of equations.

**Examples**

```python
>>> import matplotlib.pyplot as plt
>>> from scipy import stats
```

Generate some data:
>>> np.random.seed(12345678)
>>> x = np.random.random(10)
>>> y = 1.6*x + np.random.random(10)

Perform the linear regression:

```python
>>> slope, intercept, r_value, p_value, std_err = stats.linregress(x, y)
>>> print("slope: \%f  intercept: \%f \
       (slope, intercept))
```

```python
slope: 1.944864  intercept: 0.268578
```

To get coefficient of determination (r_squared):

```python
>>> print("r-squared: \%f \
       r_value**2")
```

```python
r-squared: 0.735498
```

Plot the data along with the fitted line:

```python
>>> plt.plot(x, y, 'o', label='original data')
>>> plt.plot(x, intercept + slope*x, 'r', label='fitted line')
>>> plt.legend()
>>> plt.show()
```

---

**scipy.stats.siegelslopes**

`scipy.stats.siegelslopes(y, x=None, method='hierarchical')`

Computes the Siegel estimator for a set of points \((x, y)\).

`siegelslopes` implements a method for robust linear regression using repeated medians (see [1]) to fit a line to the points \((x, y)\). The method is robust to outliers with an asymptotic breakdown point of 50%.

**Parameters**

- **y** [array_like] Dependent variable.
- **x** [array_like or None, optional] Independent variable. If None, use `arange(len(y))` instead.
method [{‘hierarchical’, ‘separate’}] If ‘hierarchical’, estimate the intercept using the estimated slope \( \text{medslope} \) (default option). If ‘separate’, estimate the intercept independent of the estimated slope. See Notes for details.

Returns

medslope [float] Estimate of the slope of the regression line.
medintercept [float] Estimate of the intercept of the regression line.

See also:

\text{theilslopes}

a similar technique without repeated medians

Notes

With \( n = \text{len}(y) \), compute \( m_j \) as the median of the slopes from the point \((x[j], y[j])\) to all other \( n-1 \) points. \( \text{medslope} \) is then the median of all slopes \( m_j \). Two ways are given to estimate the intercept in [1] which can be chosen via the parameter method. The hierarchical approach uses the estimated slope \( \text{medslope} \) and computes \( \text{medintercept} \) as the median of \( y - \text{medslope} \times x \). The other approach estimates the intercept separately as follows: for each point \((x[j], y[j])\), compute the intercepts of all the \( n-1 \) lines through the remaining points and take the median \( i_{j} \). \( \text{medintercept} \) is the median of the \( i_{j} \).

The implementation computes \( n \) times the median of a vector of size \( n \) which can be slow for large vectors. There are more efficient algorithms (see [2]) which are not implemented here.

References

[1], [2]

Examples

```python
>>> from scipy import stats
>>> import matplotlib.pyplot as plt

>>> x = np.linspace(-5, 5, num=150)
>>> y = x + np.random.normal(size=x.size)
>>> y[11:15] += 10  # add outliers
>>> y[-5:] -= 7

Compute the slope and intercept. For comparison, also compute the least-squares fit with \text{linregress}:

```python
>>> res = stats.siegelslopes(y, x)
>>> lsq_res = stats.linregress(x, y)
```

Plot the results. The Siegel regression line is shown in red. The green line shows the least-squares fit for comparison.

```python
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(x, y, 'b. ')
>>> ax.plot(x, res[1] + res[0] * x, 'r- ')
>>> ax.plot(x, lsq_res[1] + lsq_res[0] * x, 'g- ')
>>> plt.show()
```
scipy.stats.theilslopes

scipy.stats.theilslopes(y, x=None, alpha=0.95)

Computes the Theil-Sen estimator for a set of points (x, y).

theilslopes implements a method for robust linear regression. It computes the slope as the median of all slopes between paired values.

Parameters

- y: [array_like] Dependent variable.
- x: [array_like or None, optional] Independent variable. If None, use \texttt{arange(len(y))} instead.
- alpha: [float, optional] Confidence degree between 0 and 1. Default is 95\% confidence. Note that \texttt{alpha} is symmetric around 0.5, i.e. both 0.1 and 0.9 are interpreted as “find the 90\% confidence interval”.

Returns

- medslope: [float] Theil slope.
- medintercept: [float] Intercept of the Theil line, as median(y) - medslope*median(x).
- lo_slope: [float] Lower bound of the confidence interval on medslope.
- up_slope: [float] Upper bound of the confidence interval on medslope.

See also:

siegelslopes

a similar technique using repeated medians

Notes

The implementation of \texttt{theilslopes} follows [1]. The intercept is not defined in [1], and here it is defined as median(y) - medslope*median(x), which is given in [3]. Other definitions of the intercept exist in the literature. A confidence interval for the intercept is not given as this question is not addressed in [1].
References
[1], [2], [3]

Examples

```python
>>> from scipy import stats
>>> import matplotlib.pyplot as plt

>>> x = np.linspace(-5, 5, num=150)
>>> y = x + np.random.normal(size=x.size)
>>> y[11:15] += 10  # add outliers
>>> y[-5:] -= 7

Compute the slope, intercept and 90% confidence interval. For comparison, also compute the least-squares fit with `linregress`:

```python
>>> res = stats.theilslopes(y, x, 0.90)
>>> lsq_res = stats.linregress(x, y)
```

Plot the results. The Theil-Sen regression line is shown in red, with the dashed red lines illustrating the confidence interval of the slope (note that the dashed red lines are not the confidence interval of the regression as the confidence interval of the intercept is not included). The green line shows the least-squares fit for comparison.

```python
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(x, y, 'b.'
>>> ax.plot(x, res[1] + res[0] * x, 'r-')
>>> ax.plot(x, lsq_res[1] + lsq_res[0] * x, 'g-')
>>> plt.show()
```

6.27.10 Statistical tests
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<td>Calculate the T-test for the mean of ONE group of scores.</td>
</tr>
<tr>
<td><code>ttest_ind(a, b[, axis, equal_var, nan_policy])</code></td>
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<tr>
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</tr>
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<tr>
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<td><code>brunnermunzel(x, y[, alternative, …])</code></td>
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<tr>
<td><code>jarque_bera(x)</code></td>
<td>Perform the Jarque-Bera goodness of fit test on sample data.</td>
</tr>
</tbody>
</table>

**scipy.stats.ttest_1samp**

The `ttest_1samp(a, popmean, axis=0, nan_policy='propagate')` function calculates the T-test for the mean of ONE group of scores. This is a two-sided test for the null hypothesis that the expected value (mean) of a sample of independent observations `a` is equal to the given population mean, `popmean`.

**Parameters**

- **a** [array_like] sample observation
- **popmean** [float or array_like] expected value in null hypothesis. If array_like, then it must have the same shape as `a` excluding the axis dimension
- **axis** [int or None, optional] Axis along which to compute test. If None, compute over the whole array `a`.
- **nan_policy** [{‘propagate’, ‘raise’, ‘omit’}, optional] Defines how to handle when input contains nan. ‘propagate’ returns nan, ‘raise’ throws an error, ‘omit’ performs the
calculations ignoring nan values. Default is 'propagate'.

**Returns**

- **statistic**: [float or array] t-statistic
- **pvalue**: [float or array] two-tailed p-value

**Examples**

```python
>>> from scipy import stats

>>> np.random.seed(7654567)  # fix seed to get the same result
>>> rvs = stats.norm.rvs(loc=5, scale=10, size=(50,2))
```

Test if mean of random sample is equal to true mean, and different mean. We reject the null hypothesis in the second case and don’t reject it in the first case.

```python
>>> stats.ttest_1samp(rvs, 5.0)
(array([-0.68014479, -0.04323899]), array([ 0.49961383, 0.96568674]))
>>> stats.ttest_1samp(rvs, 0.0)
(array([ 2.77025808, 4.11038784]), array([ 0.00789095, 0.00014999]))
```

Examples using axis and non-scalar dimension for population mean.

```python
>>> stats.ttest_1samp(rvs, [5.0, 0.0])
(array([-0.68014479, 4.11038784]), array([ 4.99613833e-01, 1.49961383e-04]))
>>> stats.ttest_1samp(rvs, [5.0, 0.0], axis=1)
(array([-0.68014479, 4.11038784]), array([ 4.99613833e-01, 1.49961383e-04]))
>>> stats.ttest_1samp(rvs, [[5.0],[0.0]])
(array([-0.68014479, -0.04323899],
    [ 2.77025808, 4.11038784]), array([[ 4.99613833e-01, 9.65686743e-01],
        [ 7.89094663e-03, 1.49986458e-04]]))
```

**scipy.stats.ttest_ind**

`scipy.stats.ttest_ind(a, b, axis=0, equal_var=True, nan_policy='propagate')`

Calculate the T-test for the means of two independent samples of scores.

This is a two-sided test for the null hypothesis that 2 independent samples have identical average (expected) values. This test assumes that the populations have identical variances by default.

**Parameters**

- **a, b** : [array_like] The arrays must have the same shape, except in the dimension corresponding to `axis` (the first, by default).
- **axis** : [int or None, optional] Axis along which to compute test. If None, compute over the whole arrays, `a`, and `b`.
- **equal_var** : [bool, optional] If True (default), perform a standard independent 2 sample test that assumes equal population variances [1]. If False, perform Welch’s t-test, which does not assume equal population variance [2]. New in version 0.11.0.

**Returns**
statistic  [float or array] The calculated t-statistic.
pvalue    [float or array] The two-tailed p-value.

Notes
We can use this test, if we observe two independent samples from the same or different population,
e.g. exam scores of boys and girls or of two ethnic groups. The test measures whether the average
(expected) value differs significantly across samples. If we observe a large p-value, for example larger
than 0.05 or 0.1, then we cannot reject the null hypothesis of identical average scores. If the p-value is
smaller than the threshold, e.g. 1%, 5% or 10%, then we reject the null hypothesis of equal averages.

References
[1], [2]

Examples
>>> from scipy import stats
>>> np.random.seed(12345678)

Test with sample with identical means:

>>> rvs1 = stats.norm.rvs(loc=5, scale=10, size=500)
>>> rvs2 = stats.norm.rvs(loc=5, scale=10, size=500)
>>> stats.ttest_ind(rvs1, rvs2)
(0.26833823296239279, 0.78849443369564776)
>>> stats.ttest_ind(rvs1, rvs2, equal_var=False)
(0.26833823296239279, 0.78849452749500748)

ttest_ind underestimates p for unequal variances:

>>> rvs3 = stats.norm.rvs(loc=5, scale=20, size=500)
>>> stats.ttest_ind(rvs1, rvs3)
(-0.46580283298287162, 0.64149646246569292)
>>> stats.ttest_ind(rvs1, rvs3, equal_var=False)
(-0.46580283298287162, 0.64149646246569292)

When n1 != n2, the equal variance t-statistic is no longer equal to the unequal variance t-statistic:

>>> rvs4 = stats.norm.rvs(loc=5, scale=20, size=100)
>>> stats.ttest_ind(rvs1, rvs4)
(-0.99882539442782481, 0.3182832709103896)
>>> stats.ttest_ind(rvs1, rvs4, equal_var=False)
(-0.99882539442782481, 0.3182832709103896)

T-test with different means, variance, and n:

>>> rvs5 = stats.norm.rvs(loc=8, scale=20, size=100)
>>> stats.ttest_ind(rvs1, rvs5)
(-1.4679669884490653, 0.14263895620529152)
>>> stats.ttest_ind(rvs1, rvs5, equal_var=False)
(-1.4679669884490653, 0.14263895620529152)

scipy.stats.ttest_ind_from_stats

scipy.stats.ttest_ind_from_stats(mean1, std1, nobs1, mean2, std2, nobs2, equal_var=True)
T-test for means of two independent samples from descriptive statistics.
This is a two-sided test for the null hypothesis that two independent samples have identical average
(expected) values.
Parameters

- **mean1** [array_like] The mean(s) of sample 1.
- **std1** [array_like] The standard deviation(s) of sample 1.
- **nobs1** [array_like] The number(s) of observations of sample 1.
- **mean2** [array_like] The mean(s) of sample 2.
- **std2** [array_like] The standard deviations(s) of sample 2.
- **nobs2** [array_like] The number(s) of observations of sample 2.
- **equal_var** [bool, optional] If True (default), perform a standard independent 2 sample test that assumes equal population variances [1]. If False, perform Welch's t-test, which does not assume equal population variance [2].

Returns

- **statistic** [float or array] The calculated t-statistics
- **pvalue** [float or array] The two-tailed p-value.

See also:

- `scipy.stats.ttest_ind`

Notes

New in version 0.16.0.

References

[1], [2]

Examples

Suppose we have the summary data for two samples, as follows:

<table>
<thead>
<tr>
<th>Sample</th>
<th>Size</th>
<th>Mean</th>
<th>Variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sample 1</td>
<td>13</td>
<td>15.0</td>
<td>87.5</td>
</tr>
<tr>
<td>Sample 2</td>
<td>11</td>
<td>12.0</td>
<td>39.0</td>
</tr>
</tbody>
</table>

Apply the t-test to this data (with the assumption that the population variances are equal):

```python
>>> from scipy.stats import ttest_ind_from_stats
>>> ttest_ind_from_stats(mean1=15.0, std1=np.sqrt(87.5), nobs1=13,
...                        mean2=12.0, std2=np.sqrt(39.0), nobs2=11)
Ttest_indResult(statistic=0.9051358093310269, pvalue=0.3751996797581487)
```

For comparison, here is the data from which those summary statistics were taken. With this data, we can compute the same result using `scipy.stats.ttest_ind`:

```python
>>> a = np.array([1, 3, 4, 6, 11, 13, 15, 19, 22, 24, 25, 26, 26])
>>> b = np.array([2, 4, 6, 9, 11, 13, 14, 15, 18, 19, 21])
>>> from scipy.stats import ttest_ind
>>> ttest_ind(a, b)
Ttest_indResult(statistic=0.905135809331027, pvalue=0.3751996797581486)
```

`scipy.stats.ttest_rel`

- **scipy.stats.ttest_rel(a, b, axis=0, nan_policy='propagate')**
  - Calculate the T-test on TWO RELATED samples of scores, a and b.
  - This is a two-sided test for the null hypothesis that 2 related or repeated samples have identical average (expected) values.

---

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Parameters

- **a, b** [array_like] The arrays must have the same shape.
- **axis** [int or None, optional] Axis along which to compute test. If None, compute over the whole arrays, a, and b.
- **nan_policy** [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. ‘propagate’ returns nan, ‘raise’ throws an error, ‘omit’ performs the calculations ignoring nan values. Default is ‘propagate’.

Returns

- **statistic** [float or array] t-statistic
- **pvalue** [float or array] two-tailed p-value

Notes

Examples for the use are scores of the same set of student in different exams, or repeated sampling from the same units. The test measures whether the average score differs significantly across samples (e.g. exams). If we observe a large p-value, for example greater than 0.05 or 0.1 then we cannot reject the null hypothesis of identical average scores. If the p-value is smaller than the threshold, e.g. 1%, 5% or 10%, then we reject the null hypothesis of equal averages. Small p-values are associated with large t-statistics.

References

https://en.wikipedia.org/wiki/T-test#Dependent_t-test_for_paired_samples

Examples

```python
>>> from scipy import stats
>>> np.random.seed(12345678)  # fix random seed to get same numbers

>>> rvs1 = stats.norm.rvs(loc=5, scale=10, size=500)
>>> rvs2 = (stats.norm.rvs(loc=5, scale=10, size=500) +
...    stats.norm.rvs(scale=0.2, size=500))
>>> stats.ttest_rel(rvs1, rvs2)
(0.24101764965300962, 0.80964043445811562)

>>> rvs3 = (stats.norm.rvs(loc=8, scale=10, size=500) +
...    stats.norm.rvs(scale=0.2, size=500))
>>> stats.ttest_rel(rvs1, rvs3)
(-3.9995108708727933, 7.3082402191726459e-005)
```

**scipy.stats.kstest**

**scipy.stats.kstest**(rvs, cdf, args=(), N=20, alternative='two-sided', mode='approx')

Perform the Kolmogorov-Smirnov test for goodness of fit.

This performs a test of the distribution G(x) of an observed random variable against a given distribution F(x). Under the null hypothesis the two distributions are identical, G(x)=F(x). The alternative hypothesis can be either ‘two-sided’ (default), ‘less’ or ‘greater’. The KS test is only valid for continuous distributions.

Parameters

- **rvs** [str, array or callable] If a string, it should be the name of a distribution in scipy.stats. If an array, it should be a 1-D array of observations of random variables. If a callable, it should be a function to generate random variables; it is required to have a keyword argument size.
**cdf**  
[str or callable] If a string, it should be the name of a distribution in `scipy.stats`. If `rvs` is a string then `cdf` can be False or the same as `rvs`. If a callable, that callable is used to calculate the cdf.

**args**  
[tuple, sequence, optional] Distribution parameters, used if `rvs` or `cdf` are strings.

**N**  
[int, optional] Sample size if `rvs` is string or callable. Default is 20.

**alternative**  
[{'two-sided', 'less', 'greater'}, optional] Defines the alternative hypothesis (see explanation above). Default is ‘two-sided’.

**mode**  
['approx' (default) or 'asymp', optional] Defines the distribution used for calculating the p-value.  
- ‘approx’: use approximation to exact distribution of test statistic  
- ‘asymp’: use asymptotic distribution of test statistic

**Returns**

**statistic**  
[float] KS test statistic, either D, D+ or D-.

**pvalue**  
[float] One-tailed or two-tailed p-value.

**Notes**

In the one-sided test, the alternative is that the empirical cumulative distribution function of the random variable is “less” or “greater” than the cumulative distribution function $F(x)$ of the hypothesis, $G(x) \leq F(x)$, resp. $G(x) \geq F(x)$.

**Examples**

```python
>>> from scipy import stats

>>> x = np.linspace(-15, 15, 9)
>>> stats.kstest(x, 'norm')
(0.44435602715924361, 0.038850142705171065)

>>> np.random.seed(987654321)  # set random seed to get the same result
>>> stats.kstest('norm', False, N=100)
(0.058352892479417884, 0.88531190944151261)
```

The above lines are equivalent to:

```python
>>> np.random.seed(987654321)
>>> stats.kstest(stats.norm.rvs(size=100), 'norm')
(0.058352892479417884, 0.88531190944151261)
```

**Test against one-sided alternative hypothesis**

Shift distribution to larger values, so that $cdf_{dgp}(x) < \text{norm}.cdf(x)$:

```python
>>> np.random.seed(987654321)
>>> x = stats.norm.rvs(loc=0.2, size=100)
>>> stats.kstest(x, 'norm', alternative = 'less')
(0.12464329735846891, 0.040989164077641749)
```

Reject equal distribution against alternative hypothesis: less

```python
>>> stats.kstest(x, 'norm', alternative = 'greater')
(0.007211523216311081, 0.98531158590396395)
```

Don’t reject equal distribution against alternative hypothesis: greater
Testing t distributed random variables against normal distribution

With 100 degrees of freedom the t distribution looks close to the normal distribution, and the K-S test does not reject the hypothesis that the sample came from the normal distribution:

```python
>>> np.random.seed(987654321)
>>> stats.kstest(stats.t.rvs(100, size=100), 'norm')
(0.072018929165471257, 0.67630062862479168)
```

With 3 degrees of freedom the t distribution looks sufficiently different from the normal distribution, that we can reject the hypothesis that the sample came from the normal distribution at the 10% level:

```python
>>> np.random.seed(987654321)
>>> stats.kstest(stats.t.rvs(3, size=100), 'norm')
(0.131016895759829, 0.058826222555312224)
```

**scipy.stats.chisquare**

```python
scipy.stats.chisquare(f_obs, f_exp=None, ddof=0, axis=0)
```

Calculate a one-way chi square test.

The chi square test tests the null hypothesis that the categorical data has the given frequencies.

**Parameters**

- `f_obs` [array_like] Observed frequencies in each category.
- `f_exp` [array_like, optional] Expected frequencies in each category. By default the categories are assumed to be equally likely.
- `ddof` [int, optional] “Delta degrees of freedom”: adjustment to the degrees of freedom for the p-value. The p-value is computed using a chi-squared distribution with \( k - 1 - \text{ddof} \) degrees of freedom, where \( k \) is the number of observed frequencies. The default value of \( \text{ddof} \) is 0.
- `axis` [int or None, optional] The axis of the broadcast result of `f_obs` and `f_exp` along which to apply the test. If axis is None, all values in `f_obs` are treated as a single data set. Default is 0.

**Returns**

- `chisq` [float or ndarray] The chi-squared test statistic. The value is a float if `axis` is None or `f_obs` and `f_exp` are 1-D.
- `p` [float or ndarray] The p-value of the test. The value is a float if `ddof` and the return value `chisq` are scalars.

**See also:**

`power_divergence`, `mstats.chisquare`

**Notes**

This test is invalid when the observed or expected frequencies in each category are too small. A typical rule is that all of the observed and expected frequencies should be at least 5.

The default degrees of freedom, \( k-1 \), are for the case when no parameters of the distribution are estimated. If \( p \) parameters are estimated by efficient maximum likelihood then the correct degrees of freedom are \( k-1-p \). If the parameters are estimated in a different way, then the dof can be between \( k-1-p \) and \( k-1 \). However, it is also possible that the asymptotic distribution is not a chi-square, in which case this test is not appropriate.
References
[1], [2]

Examples
When just \( f_{\text{obs}} \) is given, it is assumed that the expected frequencies are uniform and given by the mean of the observed frequencies.

```python
>>> from scipy.stats import chisquare
>>> chisquare([16, 18, 16, 14, 12, 12])
(2.0, 0.8491450360846096)
```

With \( f_{\text{exp}} \) the expected frequencies can be given.

```python
>>> chisquare([16, 18, 16, 14, 12, 12], f_exp=[16, 16, 16, 16, 16, 8])
(3.5, 0.6233876277495822)
```

When \( f_{\text{obs}} \) is 2-D, by default the test is applied to each column.

```python
>>> obs = np.array([[16, 18, 16, 14, 12, 12], [32, 24, 16, 28, 20, 24]]).T
>>> obs.shape
(6, 2)
>>> chisquare(obs)
(array([ 2. , 6.66666667]), array([ 0.84914504, 0.24663415]))
```

By setting \texttt{axis=\texttt{None}}, the test is applied to all data in the array, which is equivalent to applying the test to the flattened array.

```python
>>> chisquare(obs, axis=\texttt{None})
(23.31034482758621, 0.015975692534127565)
```

\texttt{ddof} is the change to make to the default degrees of freedom.

```python
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=1)
(2.0, 0.7357588823428847)
```

The calculation of the p-values is done by broadcasting the chi-squared statistic with \texttt{ddof}.

```python
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=[0,1,2])
(2.0, array([ 0.84914504, 0.73575888, 0.5724067 ]))
```

\( f_{\text{obs}} \) and \( f_{\text{exp}} \) are also broadcast. In the following, \( f_{\text{obs}} \) has shape (6,) and \( f_{\text{exp}} \) has shape (2, 6), so the result of broadcasting \( f_{\text{obs}} \) and \( f_{\text{exp}} \) has shape (2, 6). To compute the desired chi-squared statistics, we use \texttt{axis=1}:

```python
>>> chisquare([16, 18, 16, 14, 12, 12],
... f_exp=[[16, 16, 16, 16, 16, 8], [8, 20, 20, 16, 12, 12]],
... axis=1)
(array([ 3.5 , 9.25]), array([ 0.62338763, 0.09949846]))
```

\texttt{scipy.stats.power\_divergence}

\texttt{scipy.stats.power\_divergence}(f_{\text{obs}}, f_{\text{exp}}=\texttt{None}, ddof=0, axis=0, lambda_=\texttt{None})

Cressie-Read power divergence statistic and goodness of fit test.

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This function tests the null hypothesis that the categorical data has the given frequencies, using the Cressie-Read power divergence statistic.

**Parameters**

- `f_obs` [array_like] Observed frequencies in each category.
- `f_exp` [array_like, optional] Expected frequencies in each category. By default the categories are assumed to be equally likely.
- `ddof` [int, optional] “Delta degrees of freedom”: adjustment to the degrees of freedom for the p-value. The p-value is computed using a chi-squared distribution with \( k - 1 - ddof \) degrees of freedom, where \( k \) is the number of observed frequencies. The default value of `ddof` is 0.
- `axis` [int or None, optional] The axis of the broadcast result of `f_obs` and `f_exp` along which to apply the test. If axis is None, all values in `f_obs` are treated as a single data set. Default is 0.
- `lambda_` [float or str, optional] `lambda_` gives the power in the Cressie-Read power divergence statistic. The default is 1. For convenience, `lambda_` may be assigned one of the following strings, in which case the corresponding numerical value is used:

<table>
<thead>
<tr>
<th>String</th>
<th>Value</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>&quot;pearson&quot;</td>
<td>1</td>
<td>Pearson's chi-squared statistic. In this case, the function is equivalent to 'stats.chisquare'.</td>
</tr>
<tr>
<td>&quot;log-likelihood&quot;</td>
<td>0</td>
<td>Log-likelihood ratio. Also known as the G-test [Rf6c2a1ea428c-3].</td>
</tr>
<tr>
<td>&quot;freeman-tukey&quot;</td>
<td>-1/2</td>
<td>Freeman-Tukey statistic.</td>
</tr>
<tr>
<td>&quot;mod-log-likelihood&quot;</td>
<td>-1</td>
<td>Modified log-likelihood ratio.</td>
</tr>
<tr>
<td>&quot;neyman&quot;</td>
<td>-2</td>
<td>Neyman's statistic.</td>
</tr>
<tr>
<td>&quot;cressie-read&quot;</td>
<td>2/3</td>
<td>The power recommended in [Rf6c2a1ea428c-5].</td>
</tr>
</tbody>
</table>

**Returns**

- `statistic` [float or ndarray] The Cressie-Read power divergence test statistic. The value is a float if `axis` is None or if \( f_{obs} \) and \( f_{exp} \) are 1-D.
- `pvalue` [float or ndarray] The p-value of the test. The value is a float if `ddof` and the return value `stat` are scalars.

**See also:**

`chisquare`

**Notes**

This test is invalid when the observed or expected frequencies in each category are too small. A typical rule is that all of the observed and expected frequencies should be at least 5.

When `lambda_` is less than zero, the formula for the statistic involves dividing by \( f_{obs} \), so a warning or error may be generated if any value in `f_obs` is 0.

Similarly, a warning or error may be generated if any value in `f_exp` is zero when `lambda_` >= 0.

The default degrees of freedom, k-1, are for the case when no parameters of the distribution are estimated. If \( p \) parameters are estimated by efficient maximum likelihood then the correct degrees of freedom are k-1-\( p \). If the parameters are estimated in a different way, then the dof can be between k-1-\( p \) and k-1. However, it is also possible that the asymptotic distribution is not a chi-square, in which case this test is not appropriate.
This function handles masked arrays. If an element of \( f_{\text{obs}} \) or \( f_{\text{exp}} \) is masked, then data at that position is ignored, and does not count towards the size of the data set.

New in version 0.13.0.

References
[1], [2], [3], [4], [5]

Examples
(See \texttt{chisquare} for more examples.)

When just \( f_{\text{obs}} \) is given, it is assumed that the expected frequencies are uniform and given by the mean of the observed frequencies. Here we perform a G-test (i.e. use the log-likelihood ratio statistic):

```python
>>> from scipy.stats import power_divergence
>>> power_divergence([16, 18, 16, 14, 12, 12], lambda_='log-likelihood')
(2.006573162632538, 0.84823476779463769)
```

The expected frequencies can be given with the \( f_{\text{exp}} \) argument:

```python
>>> power_divergence([16, 18, 16, 14, 12, 12], lambda_='log-likelihood',
                      f_exp=[16, 16, 16, 16, 16, 8])
(3.3281031458963746, 0.6495419288047497)
```

When \( f_{\text{obs}} \) is 2-D, by default the test is applied to each column.

```python
>>> obs = np.array([[16, 18, 16, 14, 12, 12], [32, 24, 16, 28, 20, 24]]).T
>>> obs.shape
(6, 2)
>>> power_divergence(obs, lambda_="log-likelihood")
(array([2.00657316, 6.77634498]), array([0.84823477, 0.23781225]))
```

By setting \texttt{axis=None}, the test is applied to all data in the array, which is equivalent to applying the test to the flattened array.

```python
>>> power_divergence(obs, axis=None)
(23.31034482758621, 0.015975692534127565)
>>> power_divergence(obs.ravel())
(23.31034482758621, 0.015975692534127565)
```

\texttt{ddof} is the change to make to the default degrees of freedom.

```python
>>> power_divergence([16, 18, 16, 14, 12, 12], ddof=1)
(2.0, 0.73575888234288467)
```

The calculation of the p-values is done by broadcasting the test statistic with \texttt{ddof}.

```python
>>> power_divergence([16, 18, 16, 14, 12, 12], ddof=[0,1,2])
(2.0, array([0.84914504, 0.73575888, 0.5724067 ]))
```

\( f_{\text{obs}} \) and \( f_{\text{exp}} \) are also broadcast. In the following, \( f_{\text{obs}} \) has shape (6,) and \( f_{\text{exp}} \) has shape (2, 6), so the result of broadcasting \( f_{\text{obs}} \) and \( f_{\text{exp}} \) has shape (2, 6). To compute the desired chi-squared statistics, we must use \texttt{axis=1}:

```python
>>> power_divergence([16, 18, 16, 14, 12, 12],
                   f_exp=[[16, 16, 16, 16, 16, 8]],
                   axis=1)
(continues on next page)
scipy.stats.ks_2samp

`scipy.stats.ks_2samp(data1, data2)`

Compute the Kolmogorov-Smirnov statistic on 2 samples.

This is a two-sided test for the null hypothesis that 2 independent samples are drawn from the same continuous distribution.

**Parameters**

- `data1, data2` [sequence of 1-D ndarrays] two arrays of sample observations assumed to be drawn from a continuous distribution, sample sizes can be different

**Returns**

- `statistic` [float] KS statistic
- `pvalue` [float] two-tailed p-value

**Notes**

This tests whether 2 samples are drawn from the same distribution. Note that, like in the case of the one-sample K-S test, the distribution is assumed to be continuous.

This is the two-sided test, one-sided tests are not implemented. The test uses the two-sided asymptotic Kolmogorov-Smirnov distribution.

If the K-S statistic is small or the p-value is high, then we cannot reject the hypothesis that the distributions of the two samples are the same.

**Examples**

```python
>>> from scipy import stats
>>> np.random.seed(12345678)  # fix random seed to get the same result
>>> n1 = 200  # size of first sample
>>> n2 = 300  # size of second sample
```

For a different distribution, we can reject the null hypothesis since the pvalue is below 1%:

```python
>>> rvs1 = stats.norm.rvs(size=n1, loc=0., scale=1)
>>> rvs2 = stats.norm.rvs(size=n2, loc=0.5, scale=1.5)
>>> stats.ks_2samp(rvs1, rvs2)
(0.20833333333333337, 4.6674975515806989e-005)
```

For a slightly different distribution, we cannot reject the null hypothesis at a 10% or lower alpha since the p-value at 0.144 is higher than 10%:

```python
>>> rvs3 = stats.norm.rvs(size=n2, loc=0.01, scale=1.0)
>>> stats.ks_2samp(rvs1, rvs3)
(0.1033333333333333, 0.14498781825751686)
```

For an identical distribution, we cannot reject the null hypothesis since the p-value is high, 41%:
```python
generate_n = stats.norm.rvs(size=n2, loc=0.0, scale=1.0)
ww_stat, pvalue = stats.ks_2samp(generate_n, rvs4)
```

**scipy.stats.mannwhitneyu**

### scipy.stats.mannwhitneyu(x, y, use_continuity=True, alternative=None)

Compute the Mann-Whitney rank test on samples x and y.

**Parameters**

- **x, y** [array_like] Array of samples, should be one-dimensional.
- **use_continuity** [bool, optional] Whether a continuity correction (1/2.) should be taken into account. Default is True.
- **alternative** [None (deprecated), 'less', 'two-sided', or 'greater'] Whether to get the p-value for the one-sided hypothesis ('less' or 'greater') or for the two-sided hypothesis ('two-sided'). Defaults to None, which results in a p-value half the size of the 'two-sided' p-value and a different U statistic. The default behavior is not the same as using 'less' or 'greater': it only exists for backward compatibility and is deprecated.

**Returns**

- **statistic** [float] The Mann-Whitney U statistic, equal to min(U for x, U for y) if alternative is equal to None (deprecated; exists for backward compatibility), and U for y otherwise.
- **pvalue** [float] p-value assuming an asymptotic normal distribution. One-sided or two-sided, depending on the choice of alternative.

**Notes**

Use only when the number of observation in each sample is > 20 and you have 2 independent samples of ranks. Mann-Whitney U is significant if the u-obtained is LESS THAN or equal to the critical value of U.

This test corrects for ties and by default uses a continuity correction.

**References**

[1], [2]

**scipy.stats.tiecorrect**

### scipy.stats.tiecorrect(rankvals)

Tie correction factor for ties in the Mann-Whitney U and Kruskal-Wallis H tests.

**Parameters**

- **rankvals** [array_like] A 1-D sequence of ranks. Typically this will be the array returned by stats.rankdata.

**Returns**

- **factor** [float] Correction factor for U or H.

See also:

- rankdata

  Assign ranks to the data
mannwhitneyu

Mann-Whitney rank test

kruskal

Kruskal-Wallis H test

References
[1]

Examples

```python
>>> from scipy.stats import tiecorrect, rankdata
>>> tiecorrect([1, 2.5, 2.5, 4])
0.9
>>> ranks = rankdata([1, 3, 2, 4, 5, 7, 2, 8, 4])
>>> ranks
array([1., 4., 2.5, 5.5, 7., 8., 2.5, 9., 5.5])
>>> tiecorrect(ranks)
0.9833333333333333
```

c scipy.stats.rankdata

scipy.stats.rankdata(a, method='average')

Assign ranks to data, dealing with ties appropriately.

Ranks begin at 1. The method argument controls how ranks are assigned to equal values. See [1] for further discussion of ranking methods.

Parameters

- `a` [array_like] The array of values to be ranked. The array is first flattened.
- `method` [str, optional] The method used to assign ranks to tied elements. The options are 'average', 'min', 'max', 'dense' and 'ordinal'.
  - 'average': The average of the ranks that would have been assigned to all the tied values is assigned to each value.
  - 'min': The minimum of the ranks that would have been assigned to all the tied values is assigned to each value. (This is also referred to as "competition" ranking.)
  - 'max': The maximum of the ranks that would have been assigned to all the tied values is assigned to each value.
  - 'dense': Like 'min', but the rank of the next highest element is assigned the rank immediately after those assigned to the tied elements.
  - 'ordinal': All values are given a distinct rank, corresponding to the order that the values occur in a.

The default is 'average'.

Returns

- `ranks` [ndarray] An array of length equal to the size of `a`, containing rank scores.

References
[1]

Examples

```python
>>> from scipy.stats import rankdata
>>> rankdata([0, 2, 3, 2])
(continues on next page)
```
```python
array([ 1., 2.5, 4., 2.5])
>>> rankdata([0, 2, 3, 2], method='min')
array([ 1, 2, 4, 2])
>>> rankdata([0, 2, 3, 2], method='max')
array([ 1, 3, 4, 3])
>>> rankdata([0, 2, 3, 2], method='dense')
array([ 1, 2, 3, 2])
>>> rankdata([0, 2, 3, 2], method='ordinal')
array([ 1, 2, 4, 3])
```

**scipy.stats.ranksums**

**scipy.stats.ranksums(x, y)**

Compute the Wilcoxon rank-sum statistic for two samples.

The Wilcoxon rank-sum test tests the null hypothesis that two sets of measurements are drawn from the same distribution. The alternative hypothesis is that values in one sample are more likely to be larger than the values in the other sample.

This test should be used to compare two samples from continuous distributions. It does not handle ties between measurements in x and y. For tie-handling and an optional continuity correction see `scipy.stats.mannwhitneyu`.

**Parameters**

- **x, y** [array_like] The data from the two samples

**Returns**

- **statistic** [float] The test statistic under the large-sample approximation that the rank sum statistic is normally distributed
- **pvalue** [float] The two-sided p-value of the test

**References**

[1]

**scipy.stats.wilcoxon**

**scipy.stats.wilcoxon(x, y=None, zero_method='wilcox', correction=False)**

Calculate the Wilcoxon signed-rank test.

The Wilcoxon signed-rank test tests the null hypothesis that two related paired samples come from the same distribution. In particular, it tests whether the distribution of the differences x - y is symmetric about zero. It is a non-parametric version of the paired T-test.

**Parameters**

- **x** [array_like] The first set of measurements.
- **y** [array_like, optional] The second set of measurements. If y is not given, then the x array is considered to be the differences between the two sets of measurements.
- **zero_method** [string, {“pratt”, “wilcox”, “zsplits”}, optional]
  - “pratt”: Pratt treatment: includes zero-differences in the ranking process (more conservative)
  - “wilcox”: Wilcoxon treatment: discards all zero-differences
  - “zsplits”: Zero rank split: just like Pratt, but splitting the zero rank between positive and negative ones
**correction**

[bool, optional] If True, apply continuity correction by adjusting the Wilcoxon rank statistic by 0.5 towards the mean value when computing the z-statistic. Default is False.

**Returns**

**statistic** [float] The sum of the ranks of the differences above or below zero, whichever is smaller.

**pvalue** [float] The two-sided p-value for the test.

**Notes**

Because the normal approximation is used for the calculations, the samples used should be large. A typical rule is to require that n > 20.

**References**

[1]

**scipy.stats.kruskal**

**scipy.stats.kruskal(*args, **kwargs)**

Compute the Kruskal-Wallis H-test for independent samples

The Kruskal-Wallis H-test tests the null hypothesis that the population median of all of the groups are equal. It is a non-parametric version of ANOVA. The test works on 2 or more independent samples, which may have different sizes. Note that rejecting the null hypothesis does not indicate which of the groups differs. Post-hoc comparisons between groups are required to determine which groups are different.

**Parameters**

**sample1, sample2, ...**

[array_like] Two or more arrays with the sample measurements can be given as arguments.

**nan_policy**

[{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

**Returns**

**statistic** [float] The Kruskal-Wallis H statistic, corrected for ties

**pvalue** [float] The p-value for the test using the assumption that H has a chi square distribution

**See also:**

**f_oneway**

1-way ANOVA

**mannwhitneyu**

Mann-Whitney rank test on two samples.

**friedmanchisquare**

Friedman test for repeated measurements

**Notes**

Due to the assumption that H has a chi square distribution, the number of samples in each group must not be too small. A typical rule is that each sample must have at least 5 measurements.
References

[1], [2]

Examples

```python
>>> from scipy import stats
>>> x = [1, 3, 5, 7, 9]
>>> y = [2, 4, 6, 8, 10]
>>> stats.kruskal(x, y)
KruskalResult(statistic=0.2727272727272734, pvalue=0.6015081344405895)

>>> x = [1, 1, 1]
>>> y = [2, 2, 2]
>>> z = [2, 2]
>>> stats.kruskal(x, y, z)
KruskalResult(statistic=7.0, pvalue=0.0301973834223185)
```

scipy.stats.friedmanchisquare

```python
scipy.stats.friedmanchisquare(*args)
```

Compute the Friedman test for repeated measurements

The Friedman test tests the null hypothesis that repeated measurements of the same individuals have the same distribution. It is often used to test for consistency among measurements obtained in different ways. For example, if two measurement techniques are used on the same set of individuals, the Friedman test can be used to determine if the two measurement techniques are consistent.

Parameters

- `measurements1, measurements2, measurements3...` [array_like] Arrays of measurements. All of the arrays must have the same number of elements. At least 3 sets of measurements must be given.

Returns

- `statistic` [float] the test statistic, correcting for ties
- `pvalue` [float] the associated p-value assuming that the test statistic has a chi squared distribution

Notes

Due to the assumption that the test statistic has a chi squared distribution, the p-value is only reliable for n > 10 and more than 6 repeated measurements.

References

[1]

scipy.stats.brunnermunzel

```python
scipy.stats.brunnermunzel(x, y, alternative='two-sided', distribution='t', nan_policy='propagate')
```

Computes the Brunner-Munzel test on samples x and y

The Brunner-Munzel test is a nonparametric test of the null hypothesis that when values are taken one by one from each group, the probabilities of getting large values in both groups are equal. Unlike the Wilcoxon-Mann-Whitney’s U test, this does not require the assumption of equivariance of two groups. Note that this does not assume the distributions are same. This test works on two independent samples, which may have different sizes.

Parameters

- `x, y` [array_like] Array of samples, should be one-dimensional.
alternative
    ['less', 'two-sided', or 'greater', optional] Whether to get the p-value for the one-
    sided hypothesis ('less' or 'greater') or for the two-sided hypothesis ('two-sided').
    Defaults value is 'two-sided'.

distribution: 't' or 'normal', optional
    Whether to get the p-value by t-distribution or by standard normal distribution.
    Defaults value is 't'.

nan_policy
    [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input con-
    tains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the
    calculations ignoring nan values. Default is 'propagate'.

Returns

pvalue [float] p-value assuming an t distribution. One-sided or two-sided, depending on
    the choice of alternative and distribution.

See also:

mannwhitneyu

Mann-Whitney rank test on two samples.

Notes
Brunner and Munzel recommended to estimate the p-value by t-distribution when the size of data is
50 or less. If the size is lower than 10, it would be better to use permuted Brunner Munzel test (see
[2]).

References
[1], [2]

Examples

```python
>>> from scipy import stats
>>> x1 = [1,2,1,1,1,1,1,1,2,4,1,1]
>>> x2 = [3,3,4,3,1,2,3,1,1,5,4]
>>> w, p_value = stats.brunnermunzel(x1, x2)
>>> w
3.1374674823029505
>>> p_value
0.0057862086661515377
```

scipy.stats.combine_pvalues

Methods for combining the p-values of independent tests bearing upon the same hypothesis.

Parameters

pvalues [array_like, 1-D] Array of p-values assumed to come from independent tests.
method [{‘fisher’, ‘stouffer’}, optional] Name of method to use to combine p-values. The
    following methods are available:
    • “fisher”: Fisher’s method (Fisher’s combined probability test), the default.
    • “stouffer”: Stouffer’s Z-score method.
weights [array_like, 1-D, optional] Optional array of weights used only for Stouffer’s Z-score
    method.

Returns

statistic: float
The statistic calculated by the specified method: - “fisher”: The chi-squared statistic - “stouffer”: The Z-score

pval: float
The combined p-value.

Notes
Fisher’s method (also known as Fisher’s combined probability test) \cite{1} uses a chi-squared statistic to compute a combined p-value. The closely related Stouffer’s Z-score method \cite{2} uses Z-scores rather than p-values. The advantage of Stouffer’s method is that it is straightforward to introduce weights, which can make Stouffer’s method more powerful than Fisher’s method when the p-values are from studies of different size \cite{3} \cite{4}.

Fisher’s method may be extended to combine p-values from dependent tests \cite{5}. Extensions such as Brown’s method and Kost’s method are not currently implemented.

New in version 0.15.0.

References
\cite{1}, \cite{2}, \cite{3}, \cite{4}, \cite{5}

scipy.stats.jarque_bera

scipy.stats.jarque_bera(x)
Perform the Jarque-Bera goodness of fit test on sample data.

The Jarque-Bera test tests whether the sample data has the skewness and kurtosis matching a normal distribution.

Note that this test only works for a large enough number of data samples (>2000) as the test statistic asymptotically has a Chi-squared distribution with 2 degrees of freedom.

Parameters
x [array_like] Observations of a random variable.

Returns
jb_value [float] The test statistic.
p [float] The p-value for the hypothesis test.

References
\cite{1}

Examples

```python
>>> from scipy import stats
>>> np.random.seed(987654321)
>>> x = np.random.normal(0, 1, 100000)
>>> y = np.random.rayleigh(1, 100000)
>>> stats.jarque_bera(x)
(4.7165707989581342, 0.09458225503041906)
>>> stats.jarque_bera(y)
(6713.7098548143422, 0.0)
```

| ansari(x, y) | Perform the Ansari-Bradley test for equal scale parameters |
| bartlett(*args) | Perform Bartlett’s test for equal variances |
| levene(*args, **kwds) | Perform Levene test for equal variances. |
| shapiro(x) | Perform the Shapiro-Wilk test for normality. |

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scipy.stats.ansari

**scipy.stats.ansari(x, y)**

Perform the Ansari-Bradley test for equal scale parameters

The Ansari-Bradley test is a non-parametric test for the equality of the scale parameter of the distributions from which two samples were drawn.

**Parameters**

- `x, y` : [array_like] arrays of sample data

**Returns**

- `statistic` : [float] The Ansari-Bradley test statistic
- `pvalue` : [float] The p-value of the hypothesis test

**See also:**

fligner

A non-parametric test for the equality of k variances

mood

A non-parametric test for the equality of two scale parameters

**Notes**

The p-value given is exact when the sample sizes are both less than 55 and there are no ties, otherwise a normal approximation for the p-value is used.

**References**

[1]

scipy.stats.bartlett

**scipy.stats.bartlett(*args)**

Perform Bartlett’s test for equal variances

Bartlett’s test tests the null hypothesis that all input samples are from populations with equal variances. For samples from significantly non-normal populations, Levene’s test `levene` is more robust.

**Parameters**
sample1, sample2, ...
[array_like] arrays of sample data. Only 1d arrays are accepted, they may have different lengths.

Returns

statistic [float] The test statistic.
pvalue [float] The p-value of the test.

See also:

fligner
A non-parametric test for the equality of k variances

levene
A robust parametric test for equality of k variances

Notes
Conover et al. (1981) examine many of the existing parametric and nonparametric tests by extensive simulations and they conclude that the tests proposed by Fligner and Killeen (1976) and Levene (1960) appear to be superior in terms of robustness of departures from normality and power (1/3).

References
[1], [2], [3], [4]

scipy.stats.levene

scipy.stats.levene(*args, **kwds)
Perform Levene test for equal variances.

The Levene test tests the null hypothesis that all input samples are from populations with equal variances. Levene’s test is an alternative to Bartlett’s test bartlett in the case where there are significant deviations from normality.

Parameters

sample1, sample2, ...
[array_like] The sample data, possibly with different lengths. Only one-dimensional samples are accepted.
proportiontocut [float, optional] When center is ‘trimmed’, this gives the proportion of data points to cut from each end. (See scipy.stats.trim_mean.) Default is 0.05.

Returns

statistic [float] The test statistic.
pvalue [float] The p-value for the test.

Notes
Three variations of Levene’s test are possible. The possibilities and their recommended usages are:

- ‘median’: Recommended for skewed (non-normal) distributions.
- ‘mean’: Recommended for symmetric, moderate-tailed distributions.
- ‘trimmed’: Recommended for heavy-tailed distributions.
The test version using the mean was proposed in the original article of Levene ([2]) while the median and trimmed mean have been studied by Brown and Forsythe ([3]), sometimes also referred to as Brown-Forsythe test.

References
[1], [2], [3]

scipy.stats.shapiro

scipy.stats.shapiro(x)
Perform the Shapiro-Wilk test for normality.

The Shapiro-Wilk test tests the null hypothesis that the data was drawn from a normal distribution.

Parameters
x [array_like] Array of sample data.

Returns
W [float] The test statistic.
p-value [float] The p-value for the hypothesis test.

See also:
anderson
The Anderson-Darling test for normality
kstest
The Kolmogorov-Smirnov test for goodness of fit.

Notes
The algorithm used is described in [4] but censoring parameters as described are not implemented. For N > 5000 the W test statistic is accurate but the p-value may not be.

The chance of rejecting the null hypothesis when it is true is close to 5% regardless of sample size.

References
[1], [2], [3], [4]

Examples

```python
>>> from scipy import stats
>>> np.random.seed(12345678)
>>> x = stats.norm.rvs(loc=5, scale=3, size=100)
>>> stats.shapiro(x)
(0.9772805571556091, 0.08144091814756393)
```

scipy.stats.anderson

scipy.stats.anderson(x, dist='norm')
Anderson-Darling test for data coming from a particular distribution

The Anderson-Darling tests the null hypothesis that a sample is drawn from a population that follows a particular distribution. For the Anderson-Darling test, the critical values depend on which distribution is being tested against. This function works for normal, exponential, logistic, or Gumbel (Extreme Value Type I) distributions.

Parameters
x [array_like] array of sample data
The Anderson-Darling test statistic

critical_values

A2

significance_level

see also

kstest

The Kolmogorov-Smirnov test for goodness-of-fit.

Notes

Critical values provided are for the following significance levels:

normal/exponential

15%, 10%, 5%, 2.5%, 1%

logistic

25%, 10%, 5%, 2.5%, 1%, 0.5%

Gumbel

25%, 10%, 5%, 2.5%, 1%

If the returned statistic is larger than these critical values then for the corresponding significance level, the null hypothesis that the data come from the chosen distribution can be rejected. The returned statistic is referred to as ‘A2’ in the references.

References

[1], [2], [3], [4], [5], [6]

scipy.stats.anderson_ksamp

scipy.stats.anderson_ksamp(samples, midrank=True)

The k-sample Anderson-Darling test for k-samples.

Parameters

samples [sequence of 1-D array_like] Array of sample data in arrays.

midrank [bool, optional] Type of Anderson-Darling test which is computed. Default (True) is the midrank test applicable to continuous and discrete populations. If False, the right side empirical distribution is used.

Returns

statistic [float] Normalized k-sample Anderson-Darling test statistic.

critical_values [array] The critical values for significance levels 25%, 10%, 5%, 2.5%, 1%.
significance_level

[float] An approximate significance level at which the null hypothesis for the provided samples can be rejected. The value is floored / capped at 1% / 25%.

Raises

ValueError

If less than 2 samples are provided, a sample is empty, or no distinct observations are in the samples.

See also:

ks_2samp

2 sample Kolmogorov-Smirnov test

anderson

1 sample Anderson-Darling test

Notes

[1] defines three versions of the k-sample Anderson-Darling test: one for continuous distributions and two for discrete distributions, in which ties between samples may occur. The default of this routine is to compute the version based on the midrank empirical distribution function. This test is applicable to continuous and discrete data. If midrank is set to False, the right side empirical distribution is used for a test for discrete data. According to [1], the two discrete test statistics differ only slightly if a few collisions due to round-off errors occur in the test not adjusted for ties between samples.

The critical values corresponding to the significance levels from 0.01 to 0.25 are taken from [1]. p-values are floored / capped at 0.1% / 25%. Since the range of critical values might be extended in future releases, it is recommended not to test \( p = 0.25 \), but rather \( p \geq 0.25 \) (analogously for the lower bound).

New in version 0.14.0.

References

[1]

Examples

```python
>>> from scipy import stats
>>> np.random.seed(314159)
```

The null hypothesis that the two random samples come from the same distribution can be rejected at the 5% level because the returned test value is greater than the critical value for 5% (1.961) but not at the 2.5% level. The interpolation gives an approximate significance level of 3.2%:

```python
>>> stats.anderson_ksamp([np.random.normal(size=50), ...
                      np.random.normal(loc=0.5, size=30)])
(2.4615796189876105,
 array([ 0.325, 1.226, 1.961, 2.718, 3.752, 4.592, 6.546]),
 0.03176687568842282)
```

The null hypothesis cannot be rejected for three samples from an identical distribution. The reported p-value (25%) has been capped and may not be very accurate (since it corresponds to the value 0.449 whereas the statistic is -0.731):

```python
>>> stats.anderson_ksamp([np.random.normal(size=50), ...
                      np.random.normal(size=30), np.random.normal(size=20)])
(-0.73091722665244196,
 0.03176687568842282)
```

(continues on next page)
array([ 0.44925884, 1.3052767 , 1.9434184 , 2.57696569, 3.41634856, 
4.07210043, 5.56419101]),
0.25)

**scipy.stats.binom_test**

**scipy.stats.binom_test**(*x*, *n=None*, *p=0.5*, *alternative='two-sided'*)

Perform a test that the probability of success is *p*.

This is an exact, two-sided test of the null hypothesis that the probability of success in a Bernoulli experiment is *p*.

**Parameters**

- **x**  
  [integer or array_like] the number of successes, or if *x* has length 2, it is the number of successes and the number of failures.

- **n**  
  [integer] the number of trials. This is ignored if *x* gives both the number of successes and failures

- **p**  
  [float, optional] The hypothesized probability of success. 0 <= *p* <= 1. The default value is *p* = 0.5

- **alternative**  
  [{}‘two-sided’, ‘greater’, ‘less’}, optional] Indicates the alternative hypothesis. The default value is ‘two-sided’.

**Returns**

- **p-value**  
  [float] The p-value of the hypothesis test

**References**

[1]

**Examples**

```python
>>> from scipy import stats

A car manufacturer claims that no more than 10% of their cars are unsafe. 15 cars are inspected for safety, 3 were found to be unsafe. Test the manufacturer’s claim:

```python
>>> stats.binom_test(3, n=15, p=0.1, alternative='greater')
0.18406106910639114
```

The null hypothesis cannot be rejected at the 5% level of significance because the returned p-value is greater than the critical value of 5%.

**scipy.stats.fligner**

**scipy.stats.fligner**(*args, **kwds*)

Perform Fligner-Killeen test for equality of variance.

Fligner’s test tests the null hypothesis that all input samples are from populations with equal variances. Fligner-Killeen’s test is distribution free when populations are identical [2].

**Parameters**

- **sample1, sample2, ...**  
  [array_like] Arrays of sample data. Need not be the same length.

- **center**  
  [‘mean’, ‘median’, ‘trimmed’], optional] Keyword argument controlling which function of the data is used in computing the test statistic. The default is ‘median’.
proportiontocut

[float, optional] When center is ‘trimmed’, this gives the proportion of data points to cut from each end. (See scipy.stats.trim_mean.) Default is 0.05.

Returns

statistic [float] The test statistic.

pvalue [float] The p-value for the hypothesis test.

See also:

bartlett

A parametric test for equality of k variances in normal samples

levene

A robust parametric test for equality of k variances

Notes

As with Levene’s test there are three variants of Fligner’s test that differ by the measure of central tendency used in the test. See levene for more information.

Conover et al. (1981) examine many of the existing parametric and nonparametric tests by extensive simulations and they conclude that the tests proposed by Fligner and Killeen (1976) and Levene (1960) appear to be superior in terms of robustness of departures from normality and power [3].

References

[1], [2], [3], [4]

scipy.stats.median_test

scipy.stats.median_test(*args, **kwds)

Mood’s median test.

Test that two or more samples come from populations with the same median.

Let n = len(args) be the number of samples. The “grand median” of all the data is computed, and a contingency table is formed by classifying the values in each sample as being above or below the grand median. The contingency table, along with correction and lambda_, are passed to scipy.stats.chi2_contingency to compute the test statistic and p-value.

Parameters

sample1, sample2, ...

[array_like] The set of samples. There must be at least two samples. Each sample must be a one-dimensional sequence containing at least one value. The samples are not required to have the same length.

ties [str, optional] Determines how values equal to the grand median are classified in the contingency table. The string must be one of:

"below":
  Values equal to the grand median are counted as "below".
"above":
  Values equal to the grand median are counted as "above".
"ignore":
  Values equal to the grand median are not counted.

The default is “below”.

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correction
[bool, optional] If True, and there are just two samples, apply Yates’ correction for continuity when computing the test statistic associated with the contingency table. Default is True.

lambda_
[float or str, optional.] By default, the statistic computed in this test is Pearson’s chi-squared statistic. lambda_ allows a statistic from the Cressie-Read power divergence family to be used instead. See power_divergence for details. Default is 1 (Pearson’s chi-squared statistic).

nan_policy
[{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. ‘propagate’ returns nan, ‘raise’ throws an error, ‘omit’ performs the calculations ignoring nan values. Default is ‘propagate’.

Returns
stat [float] The test statistic. The statistic that is returned is determined by lambda_. The default is Pearson’s chi-squared statistic.
p [float] The p-value of the test.
m [float] The grand median.
table [ndarray] The contingency table. The shape of the table is (2, n), where n is the number of samples. The first row holds the counts of the values above the grand median, and the second row holds the counts of the values below the grand median. The table allows further analysis with, for example, scipy.stats.chi2_contingency, or with scipy.stats.fisher_exact if there are two samples, without having to recompute the table. If nan_policy is “propagate” and there are nans in the input, the return value for table is None.

See also:
kruskal
Compute the Kruskal-Wallis H-test for independent samples.
mannwhitneyu
Computes the Mann-Whitney rank test on samples x and y.

Notes
New in version 0.15.0.

References
[1], [2]

Examples
A biologist runs an experiment in which there are three groups of plants. Group 1 has 16 plants, group 2 has 15 plants, and group 3 has 17 plants. Each plant produces a number of seeds. The seed counts for each group are:

<table>
<thead>
<tr>
<th>Group</th>
<th>1: 10 14 14 18 20 22 24 25 31 31 32 39 43 43 48 49</th>
</tr>
</thead>
<tbody>
<tr>
<td>Group</td>
<td>2: 28 30 31 33 34 35 36 40 44 55 57 61 91 92 99</td>
</tr>
<tr>
<td>Group</td>
<td>3: 0 3 9 22 23 25 25 33 34 40 45 46 62 67 84</td>
</tr>
</tbody>
</table>

The following code applies Mood’s median test to these samples.

```python
>>> g1 = [10, 14, 14, 18, 20, 22, 24, 25, 31, 31, 32, 39, 43, 43, 48, 49]
>>> g2 = [28, 30, 31, 33, 34, 35, 36, 40, 44, 55, 57, 61, 91, 92, 99]
>>> g3 = [0, 3, 9, 22, 23, 25, 25, 33, 34, 40, 45, 46, 48, 62, 67, 84]
```
>>> from scipy.stats import median_test
>>> stat, p, med, tbl = median_test(g1, g2, g3)

The median is

```python
>>> med
34.0
```

and the contingency table is

```python
>>> tbl
array([[ 5, 10,  7],
       [11,  5, 10]])
```

$p$ is too large to conclude that the medians are not the same:

```python
>>> p
0.12609082774093244
```

The “G-test” can be performed by passing `lambda_="log-likelihood"` to `median_test`.

```python
>>> g, p, med, tbl = median_test(g1, g2, g3, lambda_="log-likelihood")
>>> p
0.12224779737117837
```

The median occurs several times in the data, so we’ll get a different result if, for example, `ties="above"` is used:

```python
>>> stat, p, med, tbl = median_test(g1, g2, g3, ties="above")
>>> p
0.063873276069553273
```

```python
>>> tbl
array([[ 5, 11,  9],
       [11,  4,  8]])
```

This example demonstrates that if the data set is not large and there are values equal to the median, the p-value can be sensitive to the choice of `ties`.

**scipy.stats.mood**

**scipy.stats.mood(x, y, axis=0)**

Perform Mood’s test for equal scale parameters.

Mood’s two-sample test for scale parameters is a non-parametric test for the null hypothesis that two samples are drawn from the same distribution with the same scale parameter.

**Parameters**

- `x, y` [array_like] Arrays of sample data.
- `axis` [int, optional] The axis along which the samples are tested. $x$ and $y$ can be of different length along `axis`. If `axis` is None, $x$ and $y$ are flattened and the test is done on all values in the flattened arrays.

**Returns**
z [scalar or ndarray] The z-score for the hypothesis test. For 1-D inputs a scalar is returned.
p-value [scalar ndarray] The p-value for the hypothesis test.

See also:
fligner
A non-parametric test for the equality of k variances
ansari
A non-parametric test for the equality of 2 variances
bartlett
A parametric test for equality of k variances in normal samples
levene
A parametric test for equality of k variances

Notes
The data are assumed to be drawn from probability distributions \( f(x) \) and \( f(x/s) / s \) respectively, for some probability density function \( f \). The null hypothesis is that \( s == 1 \).

For multi-dimensional arrays, if the inputs are of shapes \((n0, n1, n2, n3)\) and \((n0, m1, n2, n3)\), then if \(axis=1\), the resulting \(z\) and \(p\) values will have shape \((n0, n2, n3)\). Note that \(n1\) and \(m1\) don’t have to be equal, but the other dimensions do.

Examples

```python
>>> from scipy import stats
>>> np.random.seed(1234)
>>> x2 = np.random.randn(2, 45, 6, 7)
>>> x1 = np.random.randn(2, 30, 6, 7)
>>> z, p = stats.mood(x1, x2, axis=1)
>>> p.shape
(2, 6, 7)
```

Find the number of points where the difference in scale is not significant:

```python
>>> (p > 0.1).sum()
74
```

Perform the test with different scales:

```python
>>> x1 = np.random.randn(2, 30)
>>> x2 = np.random.randn(2, 35) * 10.0
>>> stats.mood(x1, x2, axis=1)
(array([-5.7178125 , -5.25342163]), array([ 1.07904114e-08, 1.49299218e-07]))
```

scipy.stats.skewtest

scipy.stats.skewtest(a, axis=0, nan_policy=’propagate’)
Test whether the skew is different from the normal distribution.

This function tests the null hypothesis that the skewness of the population that the sample was drawn from is the same as that of a corresponding normal distribution.

Parameters
SciPy Reference Guide, Release 1.2.0

**skewtest**

`skewtest(a, axis=0, nan_policy='propagate')`

Test whether a dataset has normal skew.

This function tests the null hypothesis that the skewness of the population from which the sample was drawn is that of the normal distribution: skewness = 1/(n+1).

**Parameters**

- `a` : array [array] The data to be tested
- `axis` : int or None, optional [int or None, optional] Axis along which statistics are calculated. Default is 0. If None, compute over the whole array a.

**Returns**

- `statistic` : float [float] The computed z-score for this test.
- `pvalue` : float [float] a 2-sided p-value for the hypothesis test

**Notes**

The sample size must be at least 8.

**References**

[1]

**Examples**

```python
>>> from scipy.stats import skewtest
>>> skewtest([1, 2, 3, 4, 5, 6, 7, 8])
SkewtestResult(statistic=1.0108048609177787, pvalue=0.3121098361421897)
>>> skewtest([2, 8, 0, 4, 1, 9, 9, 0])
SkewtestResult(statistic=0.44626385374196975, pvalue=0.6554066631275459)
>>> skewtest([1, 2, 3, 4, 5, 6, 7, 8000])
SkewtestResult(statistic=0.44626385374196975, pvalue=0.6554066631275459)
>>> skewtest([100, 100, 100, 100, 100, 100, 100, 101])
SkewtestResult(statistic=3.5717766638478072, pvalue=0.000354567720281634)
```

**kurtosistest**

`scipy.stats.kurtosistest(a, axis=0, nan_policy='propagate')`

Test whether a dataset has normal kurtosis.

This function tests the null hypothesis that the kurtosis of the population from which the sample was drawn is that of the normal distribution: kurtosis = 3(n-1)/(n+1).

**Parameters**

- `a` : array [array] array of the sample data
- `axis` : int or None, optional [int or None, optional] Axis along which to compute test. Default is 0. If None, compute over the whole array a.

**Returns**

- `statistic` : float [float] The computed z-score for this test.
- `pvalue` : float [float] The 2-sided p-value for the hypothesis test

**Notes**

Valid only for n>20. This function uses the method described in [1].

**References**

[1]
Examples

```python
>>> from scipy.stats import kurtosistest
>>> kurtosistest(list(range(20)))
KurtosistestResult(statistic=-1.7058104152122062, pvalue=0.08804338332528348)
```

```python
>>> np.random.seed(28041990)
>>> s = np.random.normal(0, 1, 1000)
>>> kurtosistest(s)
KurtosistestResult(statistic=1.2317590987707365, pvalue=0.21803908613450895)
```

`scipy.stats.normaltest`

`scipy.stats.normaltest(a, axis=0, nan_policy='propagate')`

Test whether a sample differs from a normal distribution.

This function tests the null hypothesis that a sample comes from a normal distribution. It is based on D’Agostino and Pearson’s [1], [2] test that combines skew and kurtosis to produce an omnibus test of normality.

**Parameters**

- `a` `[array_like]` The array containing the sample to be tested.
- `axis` `[int or None, optional]` Axis along which to compute test. Default is 0. If None, compute over the whole array `a`.
- `nan_policy` `[{'propagate', 'raise', 'omit'}, optional]` Defines how to handle when input contains nan. ‘propagate’ returns nan, ‘raise’ throws an error, ‘omit’ performs the calculations ignoring nan values. Default is ‘propagate’.

**Returns**

- `statistic` `[float or array]` $s^2 + k^2$, where $s$ is the z-score returned by `skewtest` and $k$ is the z-score returned by `kurtosistest`.
- `pvalue` `[float or array]` A 2-sided chi squared probability for the hypothesis test.

**References**

[1], [2]

**Examples**

```python
>>> from scipy import stats
>>> pts = 1000
>>> np.random.seed(28041990)
>>> a = np.random.normal(0, 1, size=pts)
>>> b = np.random.normal(2, 1, size=pts)
>>> x = np.concatenate((a, b))
>>> k2, p = stats.normaltest(x)
>>> alpha = 1e-3
>>> print("p = {:g}".format(p))
p = 3.27207e-11
>>> if p < alpha:  # null hypothesis: x comes from a normal distribution
...     print("The null hypothesis can be rejected")
... else:
...     print("The null hypothesis cannot be rejected")
```

The null hypothesis can be rejected
6.27.11 Transformations

- **boxcox**\((x[, \text{lmbda}, \text{alpha}])\) Return a positive dataset transformed by a Box-Cox power transformation.
- **boxcox_normmax**\((x[, \text{brack}, \text{method}])\) Compute optimal Box-Cox transform parameter for input data.
- **boxcox_llf**\((\text{lmb}, \text{data})\) The boxcox log-likelihood function.
- **y eosjoh**\((x[, \text{lmbda}])\) Return a dataset transformed by a Yeo-Johnson power transformation.
- **y eosjoh**\((x[, \text{brack}])\) Compute optimal Yeo-Johnson transform parameter for input data, using maximum likelihood estimation.
- **y eosjoh**\((\text{lmb}, \text{data})\) The yeojohnson log-likelihood function.
- **obrientransform**\((*\text{args})\) Compute the O’Brien transform on input data (any number of arrays).
- **sigmaclip**\((a[, \text{low}, \text{high}])\) Iterative sigma-clipping of array elements.
- **trimboth**\((a, \text{proportiontocut}[, \text{axis}])\) Slices off a proportion of items from both ends of an array.
- **trim1**\((a, \text{proportiontocut}[, \text{tail}, \text{axis}])\) Slices off a proportion from ONE end of the passed array distribution.
- **zmap**\((\text{scores}, \text{compare}[, \text{axis}, \text{ddof}])\) Calculate the relative z-scores.
- **zscore**\((a[, \text{axis}, \text{ddof}])\) Calculate the z score of each value in the sample, relative to the sample mean and standard deviation.

### scipy.stats.boxcox

**scipy.stats.boxcox**\((x, \text{lmbda=}\text{None}, \text{alpha=}\text{None})\)

Return a positive dataset transformed by a Box-Cox power transformation.

**Parameters**

- **x** [ndarray] Input array. Should be 1-dimensional.
- **lmbda** {[None, scalar], optional} If \(lmbda\) is not None, do the transformation for that value. If \(lmbda\) is None, find the lambda that maximizes the log-likelihood function and return it as the second output argument.
- **alpha** {[None, float], optional} If \(alpha\) is not None, return the \(100 \times (1-\text{alpha})\%\) confidence interval for \(lmbda\) as the third output argument. Must be between 0.0 and 1.0.

**Returns**

- **boxcox** [ndarray] Box-Cox power transformed array.
- **maxlog** [float, optional] If the \(lmbda\) parameter is None, the second returned argument is the lambda that maximizes the log-likelihood function.
- **(min_ci, max_ci)** [tuple of float, optional] If \(lmbda\) parameter is None and \(alpha\) is not None, this returned tuple of floats represents the minimum and maximum confidence limits given \(alpha\).

See also:

- **probplot**, **boxcox_normplot**, **boxcox_normmax**, **boxcox_llf**

**Notes**

The Box-Cox transform is given by:

\[
\lambda(x) = \begin{cases} 
\frac{x^{\lambda} - 1}{\lambda} & \text{if } \lambda \neq 0 \\
\log(x) & \text{if } \lambda = 0
\end{cases}
\]
\[ y = \begin{cases} \frac{x^{*\lambda} - 1}{\lambda} & \text{for } \lambda > 0 \\ \log(x) & \text{for } \lambda = 0 \end{cases} \]

`boxcox` requires the input data to be positive. Sometimes a Box-Cox transformation provides a shift parameter to achieve this; `boxcox` does not. Such a shift parameter is equivalent to adding a positive constant to \( x \) before calling `boxcox`.

The confidence limits returned when `alpha` is provided give the interval where:

\[ llf(\hat{\lambda}) - llf(\lambda) < \frac{1}{2} \chi^2(1 - \alpha, 1), \]

with \( llf \) the log-likelihood function and \( \chi^2 \) the chi-squared function.

**References**

**Examples**
```python
>>> from scipy import stats
>>> import matplotlib.pyplot as plt

We generate some random variates from a non-normal distribution and make a probability plot for it, to show it is non-normal in the tails:

```python
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(211)
>>> x = stats.loggamma.rvs(5, size=500) + 5
>>> prob = stats.probplot(x, dist=stats.norm, plot=ax1)
>>> ax1.set_xlabel('')
>>> ax1.set_title('Probplot against normal distribution')
```

We now use `boxcox` to transform the data so it’s closest to normal:

```python
>>> ax2 = fig.add_subplot(212)
>>> xt, _ = stats.boxcox(x)
>>> prob = stats.probplot(xt, dist=stats.norm, plot=ax2)
>>> ax2.set_title('Probplot after Box-Cox transformation')
```

```python
>>> plt.show()
```

**scipy.stats.boxcox_normmax**

Compute optimal Box-Cox transform parameter for input data.

**Parameters**

- `x` [array_like] Input array.
- `brack` [2-tuple, optional] The starting interval for a downhill bracket search with `optimize.brent`. Note that this is in most cases not critical; the final result is allowed to be outside this bracket.
- `method` [str, optional] The method to determine the optimal transform parameter (`boxcox lmbda` parameter). Options are:
  - `pearsonr` (default) Maximizes the Pearson correlation coefficient between \( y = \text{boxcox}(x) \) and the expected values for \( y \) if \( x \) would be normally-distributed.
Ordered Values

Probplot against normal distribution

Ordered Values

Theoretical quantiles

Ordered Values

Probplot after Box-Cox transformation

Ordered Values

Theoretical quantiles

'mle' Minimizes the log-likelihood `boxcox_llf`. This is the method used in `boxcox`.

'all' Use all optimization methods available, and return all results. Useful to compare different methods.

Returns

maxlog [float or ndarray] The optimal transform parameter found. An array instead of a scalar for method='all'.

See also:

`boxcox`, `boxcox_llf`, `boxcox_normplot`

Examples

```python
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
>>> np.random.seed(1234)  # make this example reproducible

Generate some data and determine optimal lmbda in various ways:

```n
```python
>>> x = stats.loggamma.rvs(5, size=30) + 5
>>> y, lmax_mle = stats.boxcox(x)
>>> lmax_pearsonr = stats.boxcox_normmax(x)
```

```python
>>> lmax_mle
7.177...
>>> lmax_pearsonr
7.916...
```

```python
>>> stats.boxcox_normmax(x, method='all')
array([ 7.91667384, 7.17718692])
```

```python
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> prob = stats.boxcox_normplot(x, -10, 10, plot=ax)
```

(continues on next page)
```python
>>> ax.axvline(lmax_mle, color='r')
>>> ax.axvline(lmax_pearsonr, color='g', ls='--')

>>> plt.show()
```

![Box-Cox Normality Plot](image)

**scipy.stats.boxcox_llf**

The boxcox log-likelihood function.

**Parameters**

- `lmb` [scalar] Parameter for Box-Cox transformation. See `boxcox` for details.
- `data` [array_like] Data to calculate Box-Cox log-likelihood for. If `data` is multi-dimensional, the log-likelihood is calculated along the first axis.

**Returns**

- `llf` [float or ndarray] Box-Cox log-likelihood of `data` given `lmb`. A float for 1-D `data`, an array otherwise.

**See also:**

- `boxcox`, `probplot`, `boxcox_normplot`, `boxcox_normmax`

**Notes**

The Box-Cox log-likelihood function is defined here as

\[
llf = (\lambda - 1) \sum (\log(x_i)) - N/2 \log(\sum(y_i - \bar{y})^2/N),
\]

where \( y \) is the Box-Cox transformed input data \( x \).

**Examples**

```python
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
>>> from mpl_toolkits.axes_grid1.inset_locator import inset_axes
>>> np.random.seed(1245)
```
Generate some random variates and calculate Box-Cox log-likelihood values for them for a range of \( \lambda \) values:

```python
>>> x = stats.loggamma.rvs(5, loc=10, size=1000)
>>> llf = np.zeros(lmbdas.shape, dtype=float)
>>> for ii, lmbda in enumerate(lmbdas):
...    llf[ii] = stats.boxcox_llf(lmbda, x)
```

Also find the optimal \( \lambda \) value with `boxcox`:

```python
>>> x_most_normal, lmbda_optimal = stats.boxcox(x)
```

Plot the log-likelihood as function of \( \lambda \). Add the optimal \( \lambda \) as a horizontal line to check that that’s really the optimum:

```python
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(lmbdas, llf, 'b-')
>>> ax.axhline(stats.boxcox_llf(lmbda_optimal, x), color='r')
>>> ax.set_xlabel('\( \lambda \) parameter')
>>> ax.set_ylabel('Box-Cox log-likelihood')
```

Now add some probability plots to show that where the log-likelihood is maximized the data transformed with `boxcox` looks closest to normal:

```python
>>> locs = [3, 10, 4]  # 'lower left', 'center', 'lower right'
>>> for lmbda, loc in zip([-1, lmbda_optimal, 9], locs):
...    xt = stats.boxcox(x, lmbda=lmbda)
...    (osm, osr), (slope, intercept, r_sq) = stats.probplot(xt)
...    ax_inset = inset_axes(ax, width="20\%", height="20\%", loc=loc)
...    ax_inset.plot(osm, osr, 'c.', osm, slope=osm + intercept, 'k-')
...    ax_inset.set_xticklabels([])
...    ax_inset.set_yticklabels([])
...    ax_inset.set_title('\( \lambda=\%1.2f\) \% lmbda')
```

**scipy.stats.yeojohnson**

`scipy.stats.yeojohnson(x, lmbda=None)`  
Return a dataset transformed by a Yeo-Johnson power transformation.

**Parameters**

- **x** [ndarray] Input array. Should be 1-dimensional.
- **lmbda** [float, optional] If \( \lambda \) is None, find the lambda that maximizes the log-likelihood function and return it as the second output argument. Otherwise the transformation is done for the given value.

**Returns**

- **yeojohnson**: ndarray  
  Yeo-Johnson power transformed array.
- **maxlog** [float, optional] If the \( \lambda \) parameter is None, the second returned argument is the lambda that maximizes the log-likelihood function.
See also:

`probplot`, `yeojohnson_normplot`, `yeojohnson_normmax`, `yeojohnson_llf`, `boxcox`

Notes

The Yeo-Johnson transform is given by:

\[
\begin{align*}
y &= \frac{((x + 1)^*\lambda - 1)}{\lambda}, & \text{for } x \geq 0, \lambda \neq 0 \\
\log(x + 1), & \text{for } x > 0, \lambda = 0 \\
-\frac{(-x + 1)^*(2 - \lambda) - 1}{(2 - \lambda)}, & \text{for } x < 0, \lambda \neq 2 \\
-\log(-x + 1), & \text{for } x < 0, \lambda = 2
\end{align*}
\]

Unlike `boxcox`, `yeojohnson` does not require the input data to be positive.

New in version 1.2.0.

References


Examples

```python
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

We generate some random variates from a non-normal distribution and make a probability plot for it, to show it is non-normal in the tails:

```python
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(211)
>>> x = stats.loggamma.rvs(5, size=500) + 5
>>> prob = stats.probplot(x, dist=stats.norm, plot=ax1)
>>> ax1.set_xlabel('')
>>> ax1.set_title('Probplot against normal distribution')
```

We now use `yeojohnson` to transform the data so it’s closest to normal:
```python
>>> ax2 = fig.add_subplot(212)
>>> xt, lmbda = stats.yeojohnson(x)
>>> prob = stats.probplot(xt, dist=stats.norm, plot=ax2)
>>> ax2.set_title('Probplot after Yeo-Johnson transformation')

>>> plt.show()
```

![Probplot against normal distribution](image)

**scipy.stats.yeojohnson_normmax**

*scipy.stats.yeojohnson_normmax*(*x*, *brack=(-2, 2)*)

Compute optimal Yeo-Johnson transform parameter for input data, using maximum likelihood estimation.

**Parameters**

- **x** [array_like] Input array.
- **brack** [2-tuple, optional] The starting interval for a downhill bracket search with *optimize.brent*. Note that this is in most cases not critical; the final result is allowed to be outside this bracket.

**Returns**

- **maxlog** [float] The optimal transform parameter found.

See also:

*yeojohnson*, *yeojohnson_llf*, *yeojohnson_normplot*

**Notes**

New in version 1.2.0.

**Examples**

```python
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
>>> np.random.seed(1234)  # make this example reproducible
```

Generate some data and determine optimal *lmbda*. 
```python
>>> x = stats.loggamma.rvs(5, size=30) + 5
>>> lmax = stats.yeojohnson_normmax(x)

>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> prob = stats.yeojohnson_normplot(x, -10, 10, plot=ax)
>>> ax.axvline(lmax, color='r')

>>> plt.show()
```

**scipy.stats.yeojohnson_llf**

`scipy.stats.yeojohnson_llf(lmb, data)`  
The yeojohnson log-likelihood function.

**Parameters**

- `lmb`  
  [scalar] Parameter for Yeo-Johnson transformation. See `yeojohnson` for details.
- `data`  
  [array_like] Data to calculate Yeo-Johnson log-likelihood for. If `data` is multi-dimensional, the log-likelihood is calculated along the first axis.

**Returns**

- `llf`  
  [float] Yeo-Johnson log-likelihood of `data` given `lmb`.

See also:

- `yeojohnson`, `probplot`, `yeojohnson_normplot`, `yeojohnson_normmax`

**Notes**

The Yeo-Johnson log-likelihood function is defined here as

\[
llf = N/2 \log(\hat{\sigma}^2) + (\lambda - 1) \sum_i \text{sign}(x_i) \log(|x_i| + 1)
\]

where \(\hat{\sigma}^2\) is estimated variance of the the Yeo-Johnson transformed input data \(x\).

New in version 1.2.0.
Examples

```python
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
>>> from mpl_toolkits.axes_grid1.inset_locator import inset_axes

Generate some random variates and calculate Yeo-Johnson log-likelihood values for them for a range
of `lmbda` values:

```plaintext
>>> x = stats.loggamma.rvs(5, loc=10, size=1000)
>>> lmbdas = np.linspace(-2, 10)
>>> llf = np.zeros(lmbdas.shape, dtype=float)
>>> for ii, lmbda in enumerate(lmbdas):
...     llf[ii] = stats.yeojohnson_llf(lmbda, x)

Also find the optimal `lmbda` value with `yeojohnson`:

```plaintext
>>> x_most_normal, lmbda_optimal = stats.yeojohnson(x)

Plot the log-likelihood as function of `lmbda`. Add the optimal `lmbda` as a horizontal line to check that
that's really the optimum:

```plaintext
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(lmbdas, llf, 'b.-')
>>> ax.axhline(stats.yeojohnson_llf(lmbda_optimal, x), color='r')
>>> ax.set_xlabel('lmbda parameter')
>>> ax.set_ylabel('Yeo-Johnson log-likelihood')

Now add some probability plots to show that where the log-likelihood is maximized the data trans-
formed with `yeojohnson` looks closest to normal:

```plaintext
>>> locs = [3, 10, 4] # 'lower left', 'center', 'lower right'
>>> for lmbda, loc in zip([-1, lmbda_optimal, 9], locs):
...     xt = stats.yeojohnson(x, lmbda=lmbda)
...     (osm, osr), (slope, intercept, r_sq) = stats.probplot(xt)
...     ax_inset = inset_axes(ax, width="20%", height="20%", loc=loc)
...     ax_inset.plot(osm, osr, 'c.', osm, slope=osm + intercept, 'k-')
...     ax_inset.set_xticklabels([])
...     ax_inset.set_yticklabels([])
...     ax_inset.set_title('$\lambda=%1.2f$' % lmbda)

scipy.stats.obrientransform

`scipy.stats.obrientransform(*args)`

Compute the O’Brien transform on input data (any number of arrays).

Used to test for homogeneity of variance prior to running one-way stats. Each array in *args is one
level of a factor. If `f_oneway` is run on the transformed data and found significant, the variances are
unequal. From Maxwell and Delaney [1], p.112.

Parameters

- `args` [tuple of array_like] Any number of arrays.
Returns

obrientransform

[ndarray] Transformed data for use in an ANOVA. The first dimension of the result corresponds to the sequence of transformed arrays. If the arrays given are all 1-D of the same length, the return value is a 2-D array; otherwise it is a 1-D array of type object, with each element being an ndarray.

References

[1]

Examples

We’ll test the following data sets for differences in their variance.

```python
>>> x = [10, 11, 13, 9, 7, 12, 12, 9, 10]
>>> y = [13, 21, 5, 10, 8, 14, 10, 12, 7, 15]
```

Apply the O’Brien transform to the data.

```python
>>> from scipy.stats import obrientransform
>>> tx, ty = obrientransform(x, y)
```

Use `scipy.stats.f_oneway` to apply a one-way ANOVA test to the transformed data.

```python
>>> from scipy.stats import f_oneway
>>> F, p = f_oneway(tx, ty)
>>> p
0.1314139477040335
```

If we require that `p < 0.05` for significance, we cannot conclude that the variances are different.

scipy.stats.sigmaclip

scipy.stats.sigmaclip(a, low=4.0, high=4.0)

Iterative sigma-clipping of array elements.

Starting from the full sample, all elements outside the critical range are removed, i.e. all elements of the input array `c` that satisfy either of the following conditions
c < mean(c) - std(c) * low

The iteration continues with the updated sample until no elements are outside the (updated) range.

Parameters

- **a** [array_like] Data array, will be raveled if not 1-D.
- **low** [float, optional] Lower bound factor of sigma clipping. Default is 4.
- **high** [float, optional] Upper bound factor of sigma clipping. Default is 4.

Returns

- **clipped** [ndarray] Input array with clipped elements removed.
- **lower** [float] Lower threshold value use for clipping.
- **upper** [float] Upper threshold value use for clipping.

Examples

```python
>>> from scipy.stats import sigmaclip
>>> a = np.concatenate((np.linspace(9.5, 10.5, 31), ...
                       np.linspace(0, 20, 5)))
>>> fact = 1.5
>>> c, low, upp = sigmaclip(a, fact, fact)
>>> c
array([ 9.96666667, 10. , 10.03333333, 10. ])
>>> c.var(), c.std()
(0.00055555555555555165, 0.023570226039551501)
>>> low, c.mean() - fact*c.std(), c.min()
(9.9646446609406727, 9.9646446609406727, 9.9666666666666668)
>>> upp, c.mean() + fact*c.std(), c.max()
(10.035355339059327, 10.035355339059327, 10.033333333333333)
```

```python
>>> a = np.concatenate((np.linspace(9.5, 10.5, 11), ...
                       np.linspace(-100, -50, 3)))
>>> c, low, upp = sigmaclip(a, 1.8, 1.8)
>>> (c == np.linspace(9.5, 10.5, 11)).all()
True
```

**scipy.stats.trimboth**

**scipy.stats.trimboth(a, proportiontocut, axis=0)**

Slices off a proportion of items from both ends of an array.

Slices off the passed proportion of items from both ends of the passed array (i.e., with `proportiontocut` = 0.1, slices leftmost 10% and rightmost 10% of scores). The trimmed values are the lowest and highest ones. Slices off less if proportion results in a non-integer slice index (i.e., conservatively slices off 'proportiontocut').

Parameters

- **a** [array_like] Data to trim.
- **proportiontocut** [float] Proportion (in range 0-1) of total data set to trim of each end.
- **axis** [int or None, optional] Axis along which to trim data. Default is 0. If None, compute over the whole array `a`.

Returns
**out**  [ndarray] Trimmed version of array \(a\). The order of the trimmed content is undefined.

See also:

*trim_mean*

**Examples**

```python
g from scipy import stats
g a = np.arange(20)
g b = stats.trimboth(a, 0.1)
g b.shape
(16,)
```

---

**scipy.stats.trim1**

`scipy.stats.trim1(a, proportiontocut, tail='right', axis=0)`

Slices off a proportion from ONE end of the passed array distribution.

If `proportiontocut = 0.1`, slices off ‘leftmost’ or ‘rightmost’ 10% of scores. The lowest or highest values are trimmed (depending on the tail). Slices off less if proportion results in a non-integer slice index (i.e., conservatively slices off `proportiontocut`).

**Parameters**

- **a** 
  [array_like] Input array
- **proportiontocut** 
  [float] Fraction to cut off of ‘left’ or ‘right’ of distribution
- **tail** 
  [{'left', 'right'}, optional] Defaults to ‘right’.
- **axis** 
  [int or None, optional] Axis along which to trim data. Default is 0. If None, compute over the whole array \(a\).

**Returns**

- **trim1** 
  [ndarray] Trimmed version of array \(a\). The order of the trimmed content is undefined.

---

**scipy.stats.zmap**

`scipy.stats.zmap(scores, compare, axis=0, ddof=0)`

Calculate the relative z-scores.

Return an array of z-scores, i.e., scores that are standardized to zero mean and unit variance, where mean and variance are calculated from the comparison array.

**Parameters**

- **scores** 
  [array_like] The input for which z-scores are calculated.
- **compare** 
  [array_like] The input from which the mean and standard deviation of the normalization are taken; assumed to have the same dimension as `scores`.
- **axis** 
  [int or None, optional] Axis over which mean and variance of `compare` are calculated. Default is 0. If None, compute over the whole array `scores`.
- **ddof** 
  [int, optional] Degrees of freedom correction in the calculation of the standard deviation. Default is 0.

**Returns**

- **zscores** 
  [array_like] Z-scores, in the same shape as `scores`. 
Notes
This function preserves ndarray subclasses, and works also with matrices and masked arrays (it uses
`asanyarray` instead of `asarray` for parameters).

Examples
```python
>>> from scipy.stats import zmap
>>> a = [0.5, 2.0, 2.5, 3]
>>> b = [0, 1, 2, 3, 4]
>>> zmap(a, b)
array([-1.06066017, 0. , 0.35355339, 0.70710678])
```

scipy.stats.zscore

scipy.stats.zscore(a, axis=0, ddof=0)

Calculate the z-score of each value in the sample, relative to the sample mean and standard deviation.

Parameters
- `a` [array_like] An array like object containing the sample data.
- `axis` [int or None, optional] Axis along which to operate. Default is 0. If None, compute
  over the whole array `a`.
- `ddof` [int, optional] Degrees of freedom correction in the calculation of the standard
deviation. Default is 0.

Returns
- `zscore` [array_like] The z-scores, standardized by mean and standard deviation of input
  array `a`.

Notes
This function preserves ndarray subclasses, and works also with matrices and masked arrays (it uses
`asanyarray` instead of `asarray` for parameters).

Examples
```python
>>> a = np.array([ 0.7972, 0.0767, 0.4383, 0.7866, 0.8091,
...                 0.1954, 0.6307, 0.6599, 0.1065, 0.0508])
>>> from scipy import stats
>>> stats.zscore(a)
array([ 1.1273, -1.247 , -0.0552, 1.0923, 1.1664, -0.8559, 0.5786,
...        0.6748, -1.1488, -1.3324])
```

Computing along a specified axis, using n-1 degrees of freedom (`ddof=1`) to calculate the standard
deviation:
```python
>>> b = np.array([[ 0.3148, 0.0478, 0.6243, 0.4608],
...               [ 0.7149, 0.0775, 0.6072, 0.9656],
...               [ 0.6341, 0.1403, 0.9759, 0.4064],
...               [ 0.5918, 0.6948, 0.904 , 0.3721],
...               [ 0.0921, 0.2481, 0.1188, 0.1366]])
>>> stats.zscore(b, axis=1, ddof=1)
array([[-0.19264823, -1.28415119, 1.0729584, 0.40420358],
...       [ 0.33048416, -1.37380874, 0.04251374, 1.00081084],
...       [ 0.26796377, -1.12598418, 1.23283094, -0.37481053],
...       [-0.22095197, 0.24468594, 1.19042819, -1.21416216],
...       [-0.82780366, 1.4457416 , -0.43867764, -0.1792603 ]])
```
6.27.12 Statistical distances

**wasserstein_distance(u_values, v_values[, ...])**  
Compute the first Wasserstein distance between two 1D distributions.

**energy_distance(u_values, v_values[, ...])**  
Compute the energy distance between two 1D distributions.

```python
scipy.stats.wasserstein_distance
```

**scipy.stats.wasserstein_distance(u_values, v_values, u_weights=None, v_weights=None)**  
Compute the first Wasserstein distance between two 1D distributions.

This distance is also known as the earth mover’s distance, since it can be seen as the minimum amount of “work” required to transform \( u \) into \( v \), where “work” is measured as the amount of distribution weight that must be moved, multiplied by the distance it has to be moved.

New in version 1.0.0.

**Parameters**

- **u_values, v_values**  
  [array_like] Values observed in the (empirical) distribution.

- **u_weights, v_weights**  
  [array_like, optional] Weight for each value. If unspecified, each value is assigned the same weight. \( u \) weights (resp. \( v \) weights) must have the same length as \( u \) values (resp. \( v \) values). If the weight sum differs from 1, it must still be positive and finite so that the weights can be normalized to sum to 1.

**Returns**

- **distance**  
  [float] The computed distance between the distributions.

**Notes**

The first Wasserstein distance between the distributions \( u \) and \( v \) is:

\[
l_1(u, v) = \inf_{\pi \in \Gamma(u, v)} \int_{\mathbb{R} \times \mathbb{R}} |x - y| d\pi(x, y)
\]

where \( \Gamma(u, v) \) is the set of (probability) distributions on \( \mathbb{R} \times \mathbb{R} \) whose marginals are \( u \) and \( v \) on the first and second factors respectively.

If \( U \) and \( V \) are the respective CDFs of \( u \) and \( v \), this distance also equals to:

\[
l_1(u, v) = \int_{-\infty}^{+\infty} |U - V|
\]

See [2] for a proof of the equivalence of both definitions.

The input distributions can be empirical, therefore coming from samples whose values are effectively inputs of the function, or they can be seen as generalized functions, in which case they are weighted sums of Dirac delta functions located at the specified values.

**References**

[1], [2]

**Examples**

```python
>>> from scipy.stats import wasserstein_distance
>>> wasserstein_distance([0, 1, 3], [5, 6, 8])
5.0
>>> wasserstein_distance([0, 1], [0, 1], [3, 1], [2, 2])
```

(continues on next page)
```python
>>> wasserstein_distance([3.4, 3.9, 7.5, 7.8], [4.5, 1.4], ...
... [1.4, 0.9, 3.1, 7.2], [3.2, 3.5])
4.0781331438047861
```

**scipy.stats.energy_distance**

`scipy.stats.energy_distance(u_values, v_values, u_weights=None, v_weights=None)`  
Compute the energy distance between two 1D distributions.

New in version 1.0.0.

**Parameters**

- `u_values, v_values`  
  [array_like] Values observed in the (empirical) distribution.

- `u_weights, v_weights`  
  [array_like, optional] Weight for each value. If unspecified, each value is assigned the same weight. `u_weights` (resp. `v_weights`) must have the same length as `u_values` (resp. `v_values`). If the weight sum differs from 1, it must still be positive and finite so that the weights can be normalized to sum to 1.

**Returns**

- `distance`  
  [float] The computed distance between the distributions.

**Notes**

The energy distance between two distributions $u$ and $v$, whose respective CDFs are $U$ and $V$, equals to:

$$D(u, v) = \left(2\mathbb{E}|X - Y| - \mathbb{E}|X - X'| - \mathbb{E}|Y - Y'|\right)^{1/2}$$

where $X$ and $X'$ (resp. $Y$ and $Y'$) are independent random variables whose probability distribution is $u$ (resp. $v$).

As shown in [2], for one-dimensional real-valued variables, the energy distance is linked to the non-distribution-free version of the Cramer-von Mises distance:

$$D(u, v) = \sqrt{2l_2(u, v)} = \left(2 \int_{-\infty}^{+\infty} (U - V)^2 \right)^{1/2}$$

Note that the common Cramer-von Mises criterion uses the distribution-free version of the distance. See [2] (section 2), for more details about both versions of the distance.

The input distributions can be empirical, therefore coming from samples whose values are effectively inputs of the function, or they can be seen as generalized functions, in which case they are weighted sums of Dirac delta functions located at the specified values.

**References**

[1], [2], [3], [4]

**Examples**

```python
from scipy.stats import energy_distance
energy_distance([0], [2])
2.0000000000000004
>>> energy_distance([0, 8], [0, 8], [3, 1], [2, 2])
1.0000000000000002
```
energy_distance([0.7, 7.4, 2.4, 6.8], [1.4, 8.], ... [2.1, 4.2, 7.4, 8.], [7.6, 8.8])
0.88003340976158217

6.27.13 Random variate generation

rvs_ratio_uniforms(pdf, umax, vmin, vmax[, ...]) Generate random samples from a probability density function using the ratio-of-uniforms method.

scipy.stats.rvs_ratio_uniforms(pdf, umax, vmin, vmax, size=1, c=0, random_state=None)
Generate random samples from a probability density function using the ratio-of-uniforms method.

Parameters

- **pdf**: [callable] A function with signature `pdf(x)` that is the probability density function of the distribution.
- **umax**: [float] The upper bound of the bounding rectangle in the u-direction.
- **vmin**: [float] The lower bound of the bounding rectangle in the v-direction.
- **vmax**: [float] The upper bound of the bounding rectangle in the v-direction.
- **size**: [int or tuple of ints, optional] Defining number of random variates (default is 1).
- **c**: [float, optional] Shift parameter of ratio-of-uniforms method, see Notes. Default is 0.
- **random_state**: [int or np.random.RandomState instance, optional] If already a RandomState instance, use it. If seed is an int, return a new RandomState instance seeded with seed. If None, use np.random.RandomState. Default is None.

Returns

- **rvs**: [ndarray] The random variates distributed according to the probability distribution defined by the pdf.

Notes

Given a univariate probability density function `pdf` and a constant `c`, define the set

\[ A = \{(u, v) : 0 < u \leq \sqrt{pdf(v/u + c)}\} \]

If `(U, V)` is a random vector uniformly distributed over `A`, then `V/U + c` follows a distribution according to `pdf`.

The above result (see `[1]`, `[2]`) can be used to sample random variables using only the pdf, i.e. no inversion of the cdf is required. Typical choices of `c` are zero or the mode of `pdf`. The set `A` is a subset of the rectangle `R = [0, umax] x [vmin, vmax]` where

- \( \text{umax} = \sup \sqrt{pdf(x)} \)
- \( \text{vmin} = \inf (x - c) \sqrt{pdf(x)} \)
- \( \text{vmax} = \sup (x - c) \sqrt{pdf(x)} \)

In particular, these values are finite if `pdf` is bounded and \( x \geq 2 \cdot \sqrt{pdf(x)} \) is bounded (i.e. subquadratic tails). One can generate `(U, V)` uniformly on `R` and return `V/U + c` if `(U, V)` are also in `A` which can be directly verified.

Intuitively, the method works well if `A` fills up most of the enclosing rectangle such that the probability is high that `(U, V)` lies in `A` whenever it lies in `R` as the number of required iterations becomes too large otherwise. To be more precise, note that the expected number of iterations to draw `(U, V)` uniformly distributed on `R` such that `(U, V)` is also in `A` is given by the ratio \( \text{area}(R) / \text{area}(A) = 2 \cdot \text{umax} \)
* (vmax - vmin), using the fact that the area of A is equal to 1/2 (Theorem 7.1 in [1]). A warning
is displayed if this ratio is larger than 20. Moreover, if the sampling fails to generate a single random
variate after 50000 iterations (i.e. not a single draw is in A), an exception is raised.

If the bounding rectangle is not correctly specified (i.e. if it does not contain A), the algorithm samples
from a distribution different from the one given by pdf. It is therefore recommended to perform a test
such as stats.kstest as a check.

References
[1], [2], [3]

Examples
```python
>>> from scipy import stats
```

Simulate normally distributed random variables. It is easy to compute the bounding rectangle explicitly
in that case.

```python
>>> f = stats.norm.pdf
>>> v_bound = np.sqrt(f(np.sqrt(2))) * np.sqrt(2)
>>> umax, vmin, vmax = np.sqrt(f(0)), -v_bound, v_bound
>>> np.random.seed(12345)
>>> rvs = stats.rvs_ratio_uniforms(f, umax, vmin, vmax, size=2500)
```

The K-S test confirms that the random variates are indeed normally distributed (normality is not
rejected at 5% significance level):

```python
>>> stats.kstest(rvs, 'norm')[1]
0.3420173467307603
```

The exponential distribution provides another example where the bounding rectangle can be deter-
mined explicitly.

```python
>>> np.random.seed(12345)
>>> rvs = stats.rvs_ratio_uniforms(lambda x: np.exp(-x), umax=1,
... vmin=0, vmax=2*np.exp(-1), size=1000)
>>> stats.kstest(rvs, 'expon')[1]
0.928454552559516
```

Sometimes it can be helpful to use a non-zero shift parameter c, see e.g. [2] above in the case of the
generalized inverse Gaussian distribution.

### 6.27.14 Circular statistical functions

<table>
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<tr>
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<th>Description</th>
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<td>circmean</td>
<td>Compute the circular mean for samples in a range.</td>
</tr>
<tr>
<td>circvar</td>
<td>Compute the circular variance for samples assumed to be in a range.</td>
</tr>
<tr>
<td>circstd</td>
<td>Compute the circular standard deviation for samples assumed to be in the range [low to high].</td>
</tr>
</tbody>
</table>

```python
scipy.stats.circmean

scipy.stats.circmean(samples, high=6.283185307179586, low=0, axis=None)
```

Compute the circular mean for samples in a range.

**Parameters**
SciPy Reference Guide, Release 1.2.0

```
samples [array_like] Input array.
high [float or int, optional] High boundary for circular mean range. Default is 2*pi.
low [float or int, optional] Low boundary for circular mean range. Default is 0.
axis [int, optional] Axis along which means are computed. The default is to compute the mean of the flattened array.

Returns
circmean [float] Circular mean.
```

```
Examples
>>> from scipy.stats import circmean
>>> circmean([0.1, 2*np.pi+0.2, 6*np.pi+0.3])
0.2

>>> from scipy.stats import circmean
>>> circmean([0.2, 1.4, 2.6], high = 1, low = 0)
0.4
```

```
samples [array_like] Input array.
low [float or int, optional] Low boundary for circular variance range. Default is 0.
high [float or int, optional] High boundary for circular variance range. Default is 2*pi.
axis [int, optional] Axis along which variances are computed. The default is to compute the variance of the flattened array.

Returns
circvar [float] Circular variance.
```

```
Examples
>>> from scipy.stats import circvar
>>> circvar([0, 2*np.pi/3, 5*np.pi/3])
2.19722457734
```

```
samples [array_like] Input array.
low [float or int, optional] Low boundary for circular standard deviation range. Default is 0.
high [float or int, optional] High boundary for circular standard deviation range. Default is 2*pi.
axis [int, optional] Axis along which standard deviations are computed. The default is to compute the standard deviation of the flattened array.

Returns
circstd [float] Circular standard deviation.
```

```
Examples
>>> from scipy.stats import circstd
>>> circstd([0, 2*np.pi/3, 5*np.pi/3])
2.19722457734
```

6.27. Statistical functions (scipy.stats)
**Returns**

circstd  [float] Circular standard deviation.

**Notes**

This uses a definition of circular standard deviation that in the limit of small angles returns a number close to the ‘linear’ standard deviation.

**Examples**

```python
>>> from scipy.stats import circstd
>>> circstd([0, 0.1*np.pi/2, 0.001*np.pi, 0.03*np.pi/2])
0.063564063306
```

## 6.27.15 Contingency table functions

<table>
<thead>
<tr>
<th>Function</th>
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<tbody>
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<td>Chi-square test of independence of variables in a contingency table.</td>
</tr>
<tr>
<td><code>contingency.expected_freq</code></td>
<td>Compute the expected frequencies from a contingency table.</td>
</tr>
<tr>
<td><code>contingency.margins</code></td>
<td>Return a list of the marginal sums of the array <code>a</code>.</td>
</tr>
<tr>
<td><code>fisher_exact</code></td>
<td>Performs a Fisher exact test on a 2x2 contingency table.</td>
</tr>
</tbody>
</table>

**scipy.stats.chi2_contingency**

```python
scipy.stats.chi2_contingency( observed[, correction=True, lambda_=None])
```

Chi-square test of independence of variables in a contingency table.

This function computes the chi-square statistic and p-value for the hypothesis test of independence of the observed frequencies in the contingency table. The expected frequencies are computed based on the marginal sums under the assumption of independence; see `scipy.stats.contingency.expected_freq`. The number of degrees of freedom is (expressed using numpy functions and attributes):

\[
dof = observed.size - \text{sum}(\text{observed.shape}) + \text{observed.ndim} - 1
\]

**Parameters**

- **observed** [array_like] The contingency table. The table contains the observed frequencies (i.e., number of occurrences) in each category. In the two-dimensional case, the table is often described as an “R x C table”.
- **correction** [bool, optional] If True, and the degrees of freedom is 1, apply Yates’ correction for continuity. The effect of the correction is to adjust each observed value by 0.5 towards the corresponding expected value.
- **lambda_** [float or str, optional] By default, the statistic computed in this test is Pearson’s chi-squared statistic. `lambda_` allows a statistic from the Cressie-Read power divergence family to be used instead. See `power_divergence` for details.

**Returns**

- **chi2** [float] The test statistic.
- **p** [float] The p-value of the test
- **dof** [int] Degrees of freedom
expected [ndarray, same shape as observed] The expected frequencies, based on the marginal sums of the table.

See also:
contingency.expected_freq, fisher_exact, chisquare, power_divergence

Notes
An often quoted guideline for the validity of this calculation is that the test should be used only if the observed and expected frequencies in each cell are at least 5.

This is a test for the independence of different categories of a population. The test is only meaningful when the dimension of observed is two or more. Applying the test to a one-dimensional table will always result in expected equal to observed and a chi-square statistic equal to 0.

This function does not handle masked arrays, because the calculation does not make sense with missing values.

Like stats.chisquare, this function computes a chi-square statistic; the convenience this function provides is to figure out the expected frequencies and degrees of freedom from the given contingency table. If these were already known, and if the Yates’ correction was not required, one could use stats.chisquare. That is, if one calls:

```python
chi2, p, dof, ex = chi2_contingency(obs, correction=False)
```

then the following is true:

```python
(chi2, p) == stats.chisquare(obs.ravel(), f_exp=ex.ravel(), ddof=obs.size - 1 - dof)
```

The lambda_ argument was added in version 0.13.0 of scipy.

References
[1], [2], [3]

Examples
A two-way example (2 x 3):

```python
>>> from scipy.stats import chi2_contingency
>>> obs = np.array([[10, 10, 20], [20, 20, 20]])
>>> chi2_contingency(obs)
(2.7777777777777777, 0.24935220877729619, 2, array([[ 12., 12., 16.], [ 18., 18., 24.]]))
```

Perform the test using the log-likelihood ratio (i.e. the “G-test”) instead of Pearson’s chi-squared statistic.

```python
>>> g, p, dof, expctd = chi2_contingency(obs, lambda_="log-likelihood")
>>> g, p
(2.7688587616781319, 0.25046668010954165)
```

A four-way example (2 x 2 x 2 x 2):

```python
>>> obs = np.array(...

[[[[12, 17],
```
scipy.stats.contingency.expected_freq

**scipy.stats.contingency.expected_freq(observed)**

Compute the expected frequencies from a contingency table.

Given an n-dimensional contingency table of observed frequencies, compute the expected frequencies for the table based on the marginal sums under the assumption that the groups associated with each dimension are independent.

**Parameters**

- **observed** [array_like] The table of observed frequencies. (While this function can handle a 1-D array, that case is trivial. Generally observed is at least 2-D.)

**Returns**

- **expected** [ndarray of float64] The expected frequencies, based on the marginal sums of the table. Same shape as observed.

**Examples**

```python
>>> observed = np.array([[10, 10, 20], [20, 20, 20]])
>>> from scipy.stats import expected_freq
>>> expected_freq(observed)
array([[ 12.,  12.,  16.],
       [ 18.,  18.,  24.]])
```

scipy.stats.contingency.margins

**scipy.stats.contingency.margins(a)**

Return a list of the marginal sums of the array a.

**Parameters**

- **a** [ndarray] The array for which to compute the marginal sums.

**Returns**
margsums

A list of length $a.ndim$. margsums[k] is the result of summing $a$ over all axes except $k$; it has the same number of dimensions as $a$, but the length of each axis except axis $k$ will be 1.

**Examples**

```python
generate examples here
```

`scipy.stats.fisher_exact`

`scipy.stats.fisher_exact(table, alternative='two-sided')`

Performs a Fisher exact test on a 2x2 contingency table.

**Parameters**

- `table` [array_like of ints] A 2x2 contingency table. Elements should be non-negative integers.
- `alternative` [‘two-sided’, ‘less’, ‘greater’], optional Which alternative hypothesis to the null hypothesis the test uses. Default is ‘two-sided’.

**Returns**

- `oddsratio` [float] This is prior odds ratio and not a posterior estimate.
- `p_value` [float] P-value, the probability of obtaining a distribution at least as extreme as the one that was actually observed, assuming that the null hypothesis is true.

**See also:**

chi2_contingency

Chi-square test of independence of variables in a contingency table.
Notes
The calculated odds ratio is different from the one R uses. This scipy implementation returns the (more common) “unconditional Maximum Likelihood Estimate”, while R uses the “conditional Maximum Likelihood Estimate”.

For tables with large numbers, the (inexact) chi-square test implemented in the function `chi2_contingency` can also be used.

Examples
Say we spend a few days counting whales and sharks in the Atlantic and Indian oceans. In the Atlantic ocean we find 8 whales and 1 shark, in the Indian ocean 2 whales and 5 sharks. Then our contingency table is:

<table>
<thead>
<tr>
<th></th>
<th>Atlantic</th>
<th>Indian</th>
</tr>
</thead>
<tbody>
<tr>
<td>whales</td>
<td>8</td>
<td>2</td>
</tr>
<tr>
<td>sharks</td>
<td>1</td>
<td>5</td>
</tr>
</tbody>
</table>

We use this table to find the p-value:

```python
>>> import scipy.stats as stats
>>> oddsratio, pvalue = stats.fisher_exact([[8, 2], [1, 5]])
>>> pvalue
0.0349...
```

The probability that we would observe this or an even more imbalanced ratio by chance is about 3.5%. A commonly used significance level is 5%–if we adopt that, we can therefore conclude that our observed imbalance is statistically significant; whales prefer the Atlantic while sharks prefer the Indian ocean.

6.27.16 Plot-tests

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>ppcc_max(x[, brack, dist])</code></td>
<td>Calculate the shape parameter that maximizes the PPCC</td>
</tr>
<tr>
<td><code>ppcc_plot(x, a, b[, dist, plot, N])</code></td>
<td>Calculate and optionally plot probability plot correlation coefficient.</td>
</tr>
<tr>
<td><code>probplot(x[, sparams, dist, fit, plot, rvalue])</code></td>
<td>Calculate quantiles for a probability plot, and optionally show the plot.</td>
</tr>
<tr>
<td><code>boxcox_normplot(x, la, lb[, plot, N])</code></td>
<td>Compute parameters for a Box-Cox normality plot, optionally show it.</td>
</tr>
<tr>
<td><code>yeojohnson_normplot(x, la, lb[, plot, N])</code></td>
<td>Compute parameters for a Yeo-Johnson normality plot, optionally show it.</td>
</tr>
</tbody>
</table>

`scipy.stats.ppcc_max`

`scipy.stats.ppcc_max(x, brack=(0.0, 1.0), dist='tuckeylambda')`

Calculate the shape parameter that maximizes the PPCC

The probability plot correlation coefficient (PPCC) plot can be used to determine the optimal shape parameter for a one-parameter family of distributions. `ppcc_max` returns the shape parameter that would maximize the probability plot correlation coefficient for the given data to a one-parameter family of distributions.

**Parameters**

- `x` [array_like] Input array.
- `brack` [tuple, optional] Triple (a,b,c) where (a<b<c). If bracket consists of two numbers (a, c) then they are assumed to be a starting interval for a downhill bracket search.
dist: [str or stats.distributions instance, optional] Distribution or distribution function
name. Objects that look enough like a stats.distributions instance (i.e. they have a
`ppf` method) are also accepted. The default is 'tukeylambda'.

Returns:

shape_value: [float] The shape parameter at which the probability plot correlation
coefficient reaches its max value.

See also:

`ppcc_plot`, `probplot`, `boxcox`

Notes
The brack keyword serves as a starting point which is useful in corner cases. One can use a plot to
obtain a rough visual estimate of the location for the maximum to start the search near it.

References
[1], [2]

Examples

First we generate some random data from a Tukey-Lambda distribution, with shape parameter -0.7:

```python
>>> from scipy import stats
>>> x = stats.tukeylambda.rvs(-0.7, loc=2, scale=0.5, size=10000,
...                           random_state=1234567) + 1e4
```

Now we explore this data with a PPCC plot as well as the related probability plot and Box-Cox
normplot. A red line is drawn where we expect the PPCC value to be maximal (at the shape parameter
-0.7 used above):

```python
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure(figsize=(8, 6))
>>> ax = fig.add_subplot(111)
>>> res = stats.ppcc_plot(x, -5, 5, plot=ax)
```

We calculate the value where the shape should reach its maximum and a red line is drawn there. The
line should coincide with the highest point in the `ppcc_plot`.

```python
>>> max = stats.ppcc_max(x)
>>> ax.vlines(max, 0, 1, colors='r', label='Expected shape value')
```

```python
>>> plt.show()
```

`scipy.stats.ppcc_plot`

`scipy.stats.ppcc_plot(x, a, b, dist='tukeylambda', plot=None, N=80)`
Calcule and optionally plot probability plot correlation coefficient.

The probability plot correlation coefficient (PPCC) plot can be used to determine the optimal shape
parameter for a one-parameter family of distributions. It cannot be used for distributions without
shape parameters (like the normal distribution) or with multiple shape parameters.

By default a Tukey-Lambda distribution (`stats.tukeylambda`) is used. A Tukey-Lambda PPCC plot
interpolates from long-tailed to short-tailed distributions via an approximately normal one, and is
therefore particularly useful in practice.

Parameters

(see `scipy.optimize.brent`).

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[369x748]

x  
[array_like] Input array.

a, b: scalar

Lower and upper bounds of the shape parameter to use.

dist  
[str or stats.distributions instance, optional] Distribution or distribution function name. Objects that look enough like a stats.distributions instance (i.e. they have a ppf method) are also accepted. The default is 'tukeylambda'.

plot  
[object, optional] If given, plots PPCC against the shape parameter. plot is an object that has to have methods “plot” and “text”. The matplotlib.pyplot module or a Matplotlib Axes object can be used, or a custom object with the same methods. Default is None, which means that no plot is created.

N  
[int, optional] Number of points on the horizontal axis (equally distributed from a to b).

Returns

svals  
[ndarray] The shape values for which ppcc was calculated.

ppcc  
[ndarray] The calculated probability plot correlation coefficient values.

See also:

ppcc_max, probplot, boxcox_normplot, tukeylambda

References


Examples

First we generate some random data from a Tukey-Lambda distribution, with shape parameter -0.7:

```python
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
>>> np.random.seed(1234567)
>>> x = stats.tukeylambda.rvs(-0.7, loc=2, scale=0.5, size=10000) + 1e4
```

Now we explore this data with a PPCC plot as well as the related probability plot and Box-Cox normplot. A red line is drawn where we expect the PPCC value to be maximal (at the shape parameter -0.7 used above):

```python
>>> fig = plt.figure(figsize=(12, 4))
>>> ax1 = fig.add_subplot(131)
>>> ax2 = fig.add_subplot(132)
>>> ax3 = fig.add_subplot(133)
>>> res = stats.probplot(x, plot=ax1)
>>> res = stats.boxcox_normplot(x, -5, 5, plot=ax2)
>>> res = stats.ppcc_plot(x, -5, 5, plot=ax3)
>>> ax3.vlines(-0.7, 0, 1, colors='r', label='Expected shape value')
>>> plt.show()
```

scipy.stats.probplot

Calculate quantiles for a probability plot, and optionally show the plot.

Generates a probability plot of sample data against the quantiles of a specified theoretical distribution (the normal distribution by default). probplot optionally calculates a best-fit line for the data and plots the results using Matplotlib or a given plot function.

Parameters
Theoretical quantiles

```
x  [array_like] Sample/response data from which `probplot` creates the plot.
sparams  [tuple, optional] Distribution-specific shape parameters (shape parameters plus location and scale).
dist  [str or stats.distributions instance, optional] Distribution or distribution function name. The default is ‘norm’ for a normal probability plot. Objects that look enough like a stats.distributions instance (i.e. they have a `ppf` method) are also accepted.
fit  [bool, optional] Fit a least-squares regression (best-fit) line to the sample data if True (default).
plot  [object, optional] If given, plots the quantiles and least squares fit. `plot` is an object that has to have methods “plot” and “text”. The `matplotlib.pyplot` module or a Matplotlib Axes object can be used, or a custom object with the same methods. Default is None, which means that no plot is created.

Returns

( osm, osr )  [tuple of ndarrays] Tuple of theoretical quantiles (osm, or order statistic medians) and ordered responses (osr). `osr` is simply sorted input `x`. For details on how `osm` is calculated see the Notes section.

(slope, intercept, r)  [tuple of floats, optional] Tuple containing the result of the least-squares fit, if that is performed by `probplot`. `r` is the square root of the coefficient of determination. If fit=False and plot=None, this tuple is not returned.
```

Notes

Even if `plot` is given, the figure is not shown or saved by `probplot`; `plt.show()` or `plt.savefig('fignname.png')` should be used after calling `probplot`.

`probplot` generates a probability plot, which should not be confused with a Q-Q or a P-P plot. Statsmodels has more extensive functionality of this type, see `statsmodels.api.ProbPlot`.

The formula used for the theoretical quantiles (horizontal axis of the probability plot) is Filliben’s estimate:

```
quantiles = dist.ppf(val), for

0.5**(1/n), for i = n
val = (i - 0.3175) / (n + 0.365), for i = 2, ..., n-1
1 - 0.5**(1/n), for i = 1
```

where `i` indicates the i-th ordered value and `n` is the total number of values.
Examples

```python
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
>>> nsample = 100
>>> np.random.seed(7654321)

A t distribution with small degrees of freedom:
```n

```python
>>> ax1 = plt.subplot(221)
>>> x = stats.t.rvs(3, size=nsample)
>>> res = stats.probplot(x, plot=plt)
```

A t distribution with larger degrees of freedom:
```python
>>> ax2 = plt.subplot(222)
>>> x = stats.t.rvs(25, size=nsample)
>>> res = stats.probplot(x, plot=plt)
```

A mixture of two normal distributions with broadcasting:
```python
>>> ax3 = plt.subplot(223)
>>> x = stats.norm.rvs(loc=[0, 5], scale=[1, 1.5],
                     ...                     size=(nsample//2, 2)).ravel()
>>> res = stats.probplot(x, plot=plt)
```

A standard normal distribution:
```python
>>> ax4 = plt.subplot(224)
>>> x = stats.norm.rvs(loc=0, scale=1, size=nsample)
>>> res = stats.probplot(x, plot=plt)
```

Produce a new figure with a loggamma distribution, using the `dist` and `sparams` keywords:
```python
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> x = stats.loggamma.rvs(c=2.5, size=500)
>>> res = stats.probplot(x, dist=stats.loggamma, sparams=(2.5,), plot=ax)
>>> ax.set_title("Probplot for loggamma dist with shape parameter 2.5")
```

Show the results with Matplotlib:
```python
>>> plt.show()
```

`scipy.stats.boxcox_normplot`

`scipy.stats.boxcox_normplot(x, la, lb, plot=None, N=80)`

Compute parameters for a Box-Cox normality plot, optionally show it.

A Box-Cox normality plot shows graphically what the best transformation parameter is to use in `boxcox` to obtain a distribution that is close to normal.

**Parameters**

- `x` [array_like] Input array.
- `la`, `lb` [scalar] The lower and upper bounds for the \( \lambda \) values to pass to `boxcox` for Box-Cox transformations. These are also the limits of the horizontal axis of the plot if that is generated.
Theoretical quantiles

Ordered Values

Probability Plot

Proplot for loggamma dist with shape parameter 2.5

Theoretical quantiles

Ordered Values

Probability Plot

Theoretical quantiles

Ordered Values

Theoretical quantiles

Probability Plot

Theoretical quantiles

Ordered Values

Probability Plot

Theoretical quantiles

Ordered Values

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Theoretical quantiles

Ordered Values

Probability Plot

Theoretical quantiles

OrderedValues
boxcox_normplot

`scipy.stats.boxcox_normplot(x, la, lb, plot=None, N=80)`

Compute parameters for a Yeo-Johnson normality plot, optionally show it.

A Yeo-Johnson normality plot shows graphically what the best transformation parameter is to use in `yeojohnson` to obtain a distribution that is close to normal.

**Parameters**

- `x` [array_like] Input array.
- `la, lb` [scalar] The lower and upper bounds for the `lmbda` values to pass to `yeojohnson` for Yeo-Johnson transformations. These are also the limits of the horizontal axis of the plot if that is generated.
- `plot` [object, optional] If given, plots the quantiles and least squares fit. `plot` is an object that has to have methods “plot” and “text”. The `matplotlib.pyplot` module or a Matplotlib Axes object can be used, or a custom object with the same methods. Default is None, which means that no plot is created.
- `N` [int, optional] Number of points on the horizontal axis (equally distributed from `la` to `lb`).

**Returns**

- `lmbdas` [ndarray] The `lmbda` values for which a Box-Cox transform was done.
- `ppcc` [ndarray] Probability Plot Correlelation Coefficient, as obtained from `probplot` when fitting the Box-Cox transformed input `x` against a normal distribution.

**Examples**

```python
>>> from scipy import stats
>>> import matplotlib.pyplot as plt

Generate some non-normally distributed data, and create a Box-Cox plot:

```python
code_snippet:
```
N

[int, optional] Number of points on the horizontal axis (equally distributed from \( la \) to \( lb \)).

Returns

lmbdas [ndarray] The \( \lambda \) values for which a Yeo-Johnson transform was done.

ppcc [ndarray] Probability Plot Correlation Coefficient, as obtained from probplot when fitting the Box-Cox transformed input \( x \) against a normal distribution.

See also:

probplot, yeojohnson, yeojohnson_normmax, yeojohnson_llf, ppcc_max

Notes

Even if \( plot \) is given, the figure is not shown or saved by boxcox_normplot; plt.show() or plt.savefig('figname.png') should be used after calling probplot.

New in version 1.2.0.

Examples

```python
>>> from scipy import stats
>>> import matplotlib.pyplot as plt

generate some non-normally distributed data, and create a Yeo-Johnson plot:
```
```python
>>> x = stats.loggamma.rvs(5, size=500) + 5
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> prob = stats.yeojohnson_normplot(x, -20, 20, plot=ax)

Determine and plot the optimal \( \lambda \) to transform \( x \) and plot it in the same plot:
```
```python
>>> _, maxlog = stats.yeojohnson(x)
>>> ax.axvline(maxlog, color='r')

>>> plt.show()
```
6.27.17 Masked statistics functions

Statistical functions for masked arrays (scipy.stats.mstats)

This module contains a large number of statistical functions that can be used with masked arrays.

Most of these functions are similar to those in scipy.stats but might have small differences in the API or in the algorithm used. Since this is a relatively new package, some API changes are still possible.

Summary statistics

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<tr>
<th>Function</th>
<th>Description</th>
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</thead>
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<td>Computes several descriptive statistics of the passed array.</td>
</tr>
<tr>
<td><code>gmean(a[, axis, dtype])</code></td>
<td>Compute the geometric mean along the specified axis.</td>
</tr>
<tr>
<td><code>hmean(a[, axis, dtype])</code></td>
<td>Calculate the harmonic mean along the specified axis.</td>
</tr>
<tr>
<td><code>kurtosis(a[, axis, fisher, bias])</code></td>
<td>Computes the kurtosis (Fisher or Pearson) of a dataset.</td>
</tr>
<tr>
<td><code>mode(a[, axis])</code></td>
<td>Returns an array of the modal (most common) value in the passed array.</td>
</tr>
<tr>
<td><code>gquantiles(a[, prob, alphap, betap, axis, limit])</code></td>
<td>Computes empirical quantiles for a data array.</td>
</tr>
<tr>
<td><code>hdmedian(data[, axis, var])</code></td>
<td>Returns the Harrell-Davis estimate of the median along the given axis.</td>
</tr>
<tr>
<td><code>hdquantiles(data[, prob, axis, var])</code></td>
<td>Computes quantile estimates with the Harrell-Davis method.</td>
</tr>
<tr>
<td><code>hdquantiles_sd(data[, prob, axis])</code></td>
<td>The standard error of the Harrell-Davis quantile estimates by jackknife.</td>
</tr>
<tr>
<td><code>idealfourths(data[, axis])</code></td>
<td>Returns an estimate of the lower and upper quartiles.</td>
</tr>
<tr>
<td><code>plotting_positions(data[, alpha, beta])</code></td>
<td>Returns plotting positions (or empirical percentile points) for the data.</td>
</tr>
<tr>
<td><code>meppf(data[, alpha, beta])</code></td>
<td>Returns plotting positions (or empirical percentile points) for the data.</td>
</tr>
</tbody>
</table>
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<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>moment(a[, moment, axis])</td>
<td>Calculates the nth moment about the mean for a sample.</td>
</tr>
<tr>
<td>skew(a[, axis, bias])</td>
<td>Computes the skewness of a data set.</td>
</tr>
<tr>
<td>tmean(a[, limits, inclusive, axis])</td>
<td>Compute the trimmed mean.</td>
</tr>
<tr>
<td>tvar(a[, limits, inclusive, axis, ddof])</td>
<td>Compute the trimmed variance</td>
</tr>
<tr>
<td>tmin(a[, lowerlimit, axis, inclusive])</td>
<td>Compute the trimmed minimum</td>
</tr>
<tr>
<td>tmax(a[, upperlimit, axis, inclusive])</td>
<td>Compute the trimmed maximum</td>
</tr>
<tr>
<td>tsem(a[, limits, inclusive, axis, ddof])</td>
<td>Compute the trimmed standard error of the mean.</td>
</tr>
<tr>
<td>variation(a[, axis])</td>
<td>Computes the coefficient of variation, the ratio of the biased standard deviation to the mean.</td>
</tr>
<tr>
<td>find_repeats(arr)</td>
<td>Find repeats in arr and return a tuple (repeats, repeat_count).</td>
</tr>
<tr>
<td>sem(a[, axis, ddof])</td>
<td>Calculates the standard error of the mean of the input array.</td>
</tr>
<tr>
<td>trimmed_mean(a[, limits, inclusive, ...])</td>
<td>Selected confidence interval of the trimmed mean along the given axis.</td>
</tr>
<tr>
<td>trimmed_mean_ci(data[, limits, inclusive, ...])</td>
<td>Selected confidence interval of the trimmed mean along the given axis.</td>
</tr>
<tr>
<td>trimmed_std(a[, limits, inclusive, ...])</td>
<td>Selected confidence interval of the trimmed mean along the given axis.</td>
</tr>
<tr>
<td>trimmed_var(a[, limits, inclusive, ...])</td>
<td>Selected confidence interval of the trimmed mean along the given axis.</td>
</tr>
</tbody>
</table>

scipy.stats.mstats.describe

scipy.stats.mstats.describe(a, axis=0, ddof=0, bias=True)

Computes several descriptive statistics of the passed array.

**Parameters**

- **a** : [array_like] Data array
- **axis** : [int or None, optional] Axis along which to calculate statistics. Default 0. If None, compute over the whole array a.
- **ddof** : [int, optional] degree of freedom (default 0); note that default ddof is different from the same routine in stats.describe
- **bias** : [bool, optional] If False, then the skewness and kurtosis calculations are corrected for statistical bias.

**Returns**

- **nobs** : [int] (size of the data (discarding missing values)
- **minmax** : [(int, int)] min, max
- **mean** : [float] arithmetic mean
- **variance** : [float] unbiased variance
- **skewness** : [float] biased skewness
- **kurtosis** : [float] biased kurtosis

**Examples**

```python
>>> from scipy.stats.mstats import describe
>>> ma = np.ma.array(range(6), mask=[0, 0, 0, 1, 1, 1])
>>> describe(ma)
DescribeResult(nobs=3, minmax=(masked_array(data=0,
    mask=False,
    fill_value=999999), masked_array(data=2,
    mask=False,
    fill_value=999999)), mean=1.0, variance=0.6666666666666666, (continues on next page)
```
scipy.stats.mstats.gmean

scipy.stats.mstats.gmean(a, axis=0, dtype=None)

Compute the geometric mean along the specified axis.

Return the geometric average of the array elements. That is: n-th root of (x1 * x2 * ... * xn)

Parameters

- **a** [array_like] Input array or object that can be converted to an array.
- **axis** [int or None, optional] Axis along which the geometric mean is computed. Default is 0. If None, compute over the whole array a.
- **dtype** [dtype, optional] Type of the returned array and of the accumulator in which the elements are summed. If dtype is not specified, it defaults to the dtype of a, unless a has an integer dtype with a precision less than that of the default platform integer. In that case, the default platform integer is used.

Returns

- **gmean** [ndarray] see dtype parameter above

See also:

- **numpy.mean**
  Arithmetic average
- **numpy.average**
  Weighted average
- **hmean**
  Harmonic mean

Notes

The geometric average is computed over a single dimension of the input array, axis=0 by default, or all values in the array if axis=None. float64 intermediate and return values are used for integer inputs.

Use masked arrays to ignore any non-finite values in the input or that arise in the calculations such as Not a Number and infinity because masked arrays automatically mask any non-finite values.

Examples

```python
>>> from scipy.stats import gmean
>>> gmean([1, 4])
2.0
>>> gmean([1, 2, 3, 4, 5, 6, 7])
3.3800151591412964
```

scipy.stats.mstats.hmean

scipy.stats.mstats.hmean(a, axis=0, dtype=None)

Calculate the harmonic mean along the specified axis.

That is: n / (1/x1 + 1/x2 + ... + 1/xn)
Parameters

- **a**  
  [array_like] Input array, masked array or object that can be converted to an array.
- **axis**  
  [int or None, optional] Axis along which the harmonic mean is computed. Default is 0. If None, compute over the whole array a.
- **dtype**  
  [dtype, optional] Type of the returned array and of the accumulator in which the elements are summed. If `dtype` is not specified, it defaults to the `dtype` of `a`, unless `a` has an integer `dtype` with a precision less than that of the default platform integer. In that case, the default platform integer is used.

Returns

- **hmean**  
  [ndarray] see `dtype` parameter above

See also:

- `numpy.mean`
  Arithmetic average
- `numpy.average`
  Weighted average
- `gmean`
  Geometric mean

Notes

The harmonic mean is computed over a single dimension of the input array, axis=0 by default, or all values in the array if axis=None. float64 intermediate and return values are used for integer inputs.

Use masked arrays to ignore any non-finite values in the input or that arise in the calculations such as Not a Number and infinity.

Examples

```python
>>> from scipy.stats import hmean
>>> hmean([1, 4])
1.6000000000000001
>>> hmean([1, 2, 3, 4, 5, 6, 7])
2.6997245179063363
```

`scipy.stats.mstats.kurtosis`

`scipy.stats.mstats.kurtosis(a, axis=0, fisher=True, bias=True)`  
Computes the kurtosis (Fisher or Pearson) of a dataset.

- Kurtosis is the fourth central moment divided by the square of the variance. If Fisher’s definition is used, then 3.0 is subtracted from the result to give 0.0 for a normal distribution.
- If bias is False then the kurtosis is calculated using k statistics to eliminate bias coming from biased moment estimators
- Use `kurtosistest` to see if result is close enough to normal.

Parameters

- **a**  
  [array] data for which the kurtosis is calculated
- **axis**  
  [int or None, optional] Axis along which the kurtosis is calculated. Default is 0. If None, compute over the whole array a.
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fisher  [bool, optional] If True, Fisher’s definition is used (normal ==> 0.0). If False, Pearson’s definition is used (normal ==> 3.0).

bias    [bool, optional] If False, then the calculations are corrected for statistical bias.

Returns
kurtosis [array] The kurtosis of values along an axis. If all values are equal, return -3 for Fisher’s definition and 0 for Pearson’s definition.

Notes
For more details about kurtosis, see stats.kurtosis.

scipy.stats.mstats.mode

scipy.stats.mstats.mode(a, axis=0)
Returns an array of the modal (most common) value in the passed array.

Parameters
a  [array_like] n-dimensional array of which to find mode(s).
axis [int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array a.

Returns
mode [ndarray] Array of modal values.
count [ndarray] Array of counts for each mode.

Notes
For more details, see stats.mode.

Examples
>>> from scipy import stats
>>> from scipy.stats import mstats
>>> m_arr = np.ma.array([1, 1, 0, 0, 0, 0], mask=[0, 0, 1, 1, 1, 0])
>>> stats.mode(m_arr)
ModeResult(mode=array([0]), count=array([4]))
>>> mstats.mode(m_arr)
ModeResult(mode=array([1.]), count=array([2.]))

scipy.stats.mstats.mquantiles

scipy.stats.mstats.mquantiles(a, prob=[0.25, 0.5, 0.75], alphap=0.4, betap=0.4, axis=None, limit=())
Computes empirical quantiles for a data array.

Samples quantile are defined by Q(p) = (1-gamma)*x[j] + gamma*x[j+1], where x[j] is the j-th order statistic, and gamma is a function of j = floor(n*p + m), m = alphap + p*(1 - alphap - betap) and g = n*p + m - j.

Reinterpreting the above equations to compare to R lead to the equation: p(k) = (k - alphap)/(n + 1 - alphap - betap)

Typical values of (alphap,betap) are:
- (0,1) : p(k) = k/n : linear interpolation of cdf (R type 4)
- (.5,.5) : p(k) = (k - 1/2.)/n : piecewise linear function (R type 5)
- (0,0) : p(k) = k/(n+1) : (R type 6)
• \((1,1)\): \(p(k) = \frac{(k-1)}{(n-1)}\): \(p(k) = \text{mode}[F(x[k])]\). (R type 7, R default)
• \((1/3,1/3)\): \(p(k) = \frac{(k-1/3)}{(n+1/3)}\): Then \(p(k) \sim \text{median}[F(x[k])]\). The resulting quantile estimates are approximately median-unbiased regardless of the distribution of \(x\). (R type 8)
• \((3/8,3/8)\): \(p(k) = \frac{(k-3/8)}{(n+1/4)}\): Blom. The resulting quantile estimates are approximately unbiased if \(x\) is normally distributed (R type 9)
• \((.4,.4)\): approximately quantile unbiased (Cunnane)
• \((.35,.35)\): APL, used with PWM

Parameters

\(a\) [array_like] Input data, as a sequence or array of dimension at most 2.

\(prob\) [array_like, optional] List of quantiles to compute.

\(alphap\) [float, optional] Plotting positions parameter, default is 0.4.

\(betap\) [float, optional] Plotting positions parameter, default is 0.4.

\(axis\) [int, optional] Axis along which to perform the trimming. If None (default), the input array is first flattened.

\(limit\) [tuple, optional] Tuple of (lower, upper) values. Values of \(a\) outside this open interval are ignored.

Returns

\(mquantiles\) [MaskedArray] An array containing the calculated quantiles.

Notes

This formulation is very similar to R except the calculation of \(m\) from \(alphap\) and \(betap\), where in R \(m\) is defined with each type.

References

[1], [2]

Examples

```python
>>> from scipy.stats.mstats import mquantiles
>>> a = np.array([6., 47., 15., 42., 41., 7., 39., 43., 40., 36.])
>>> mquantiles(a)
array([ 19.2, 40. , 42.8])
```

Using a 2D array, specifying axis and limit.

```python
>>> data = np.array([[ 6., 7., 1.],
... [ 47., 15., 2.],
... [ 49., 36., 3.],
... [ 15., 39., 4.],
... [ 42., 40., -999.],
... [ 41., 41., -999.],
... [ 7., -999., -999.],
... [ 39., -999., -999.],
... [ 43., -999., -999.],
... [ 40., -999., -999.],
... [ 36., -999., -999.]])
>>> print(mquantiles(data, axis=0, limit=(0, 50)))
[[19.2 14.6 1.45]
 [40. 37.5 2.5 ]
 [42.8 40.06 3.55]]
```
```python
>>> data[:, 2] = -999.
>>> print(mquantiles(data, axis=0, limit=(0, 50)))
[[19.200000000000003 14.6 --]
 [40.0 37.5 --]
 [42.800000000000004 40.05 --]]
```

**scipy.stats.mstats.hdmedian**

**scipy.stats.mstats.hdmedian**(data, axis=-1, var=False)

Returns the Harrell-Davis estimate of the median along the given axis.

Parameters:
- **data**: [ndarray] Data array.
- **axis**: [int, optional] Axis along which to compute the quantiles. If None, use a flattened array.
- **var**: [bool, optional] Whether to return the variance of the estimate.

Returns:
- **hdmedian**: [MaskedArray] The median values. If var=True, the variance is returned inside the masked array. E.g. for a 1-D array the shape change from (1,) to (2,).

**scipy.stats.mstats.hdquantiles**

**scipy.stats.mstats.hdquantiles**(data, prob=[0.25, 0.5, 0.75], axis=None, var=False)

Computes quantile estimates with the Harrell-Davis method.

The quantile estimates are calculated as a weighted linear combination of order statistics.

Parameters:
- **data**: [array_like] Data array.
- **prob**: [sequence, optional] Sequence of quantiles to compute.
- **axis**: [int or None, optional] Axis along which to compute the quantiles. If None, use a flattened array.
- **var**: [bool, optional] Whether to return the variance of the estimate.

Returns:
- **hdquantiles**: [MaskedArray] A (p,) array of quantiles (if var is False), or a (2,p) array of quantiles and variances (if var is True), where p is the number of quantiles.

See also:
- hdquantiles_sd

**scipy.stats.mstats.hdquantiles_sd**

**scipy.stats.mstats.hdquantiles_sd**(data, prob=[0.25, 0.5, 0.75], axis=None)

The standard error of the Harrell-Davis quantile estimates by jackknife.

Parameters:
- **data**: [array_like] Data array.
- **prob**: [sequence, optional] Sequence of quantiles to compute.
axis  [int, optional] Axis along which to compute the quantiles. If None, use a flattened array.

Returns

hdquantiles_sd  [MaskedArray] Standard error of the Harrell-Davis quantile estimates.

See also:

hdquantiles

scipy.stats.mstats.idealfourths

scipy.stats.mstats.idealfourths(data, axis=None)

Returns an estimate of the lower and upper quartiles.

Uses the ideal fourths algorithm.

Parameters

- data  [array_like] Input array.
- axis  [int, optional] Axis along which the quartiles are estimated. If None, the arrays are flattened.

Returns

idealfourths  [[list of floats, masked array]] Returns the two internal values that divide data into four parts using the ideal fourths algorithm either along the flattened array (if axis is None) or along axis of data.

scipy.stats.mstats.plotting_positions

scipy.stats.mstats.plotting_positions(data, alpha=0.4, beta=0.4)

Returns plotting positions (or empirical percentile points) for the data.

**Plotting positions are defined as** *(i-alpha)/(n+1-alpha-beta)*, **where:**

- i is the rank order statistics
- n is the number of unmasked values along the given axis
- alpha and beta are two parameters.

**Typical values for alpha and beta are:**

- (0,1) : p(k) = k/n, linear interpolation of cdf (R, type 4)
- (.5,.5) : p(k) = (k-1/2.)/n, piecewise linear function (R, type 5)
- (0.0) : p(k) = k/(n+1), Weibull (R type 6)
- (1,1) : p(k) = (k-1)/(n-1), in this case, p(k) = mode[F(x[k])]. That’s R default (R type 7)
- (1/3,1/3): p(k) = (k-1/3)/(n+1/3), then p(k) = median[F(x[k])]. The resulting quantile estimates are approximately median-unbiased regardless of the distribution of x. (R type 8)
- (3/8,3/8): p(k) = (k-3/8)/(n+1/4), Blom. The resulting quantile estimates are approximately unbiased if x is normally distributed (R type 9)
- (.4,.4) : approximately quantile unbiased (Cunnane)
• (.35,.35): APL, used with PWM
• (.3175, .3175): used in scipy.stats.probplot

**Parameters**

- **data** [array_like] Input data, as a sequence or array of dimension at most 2.
- **alpha** [float, optional] Plotting positions parameter. Default is 0.4.
- **beta** [float, optional] Plotting positions parameter. Default is 0.4.

**Returns**

- **positions** [MaskedArray] The calculated plotting positions.

**scipy.stats.mstats.meppf**

`scipy.stats.mstats.meppf(data, alpha=0.4, beta=0.4)`

Returns plotting positions (or empirical percentile points) for the data.

*Plotting positions are defined as* \((i-\alpha)/(n+1-\alpha-\beta)\), *where:*

- \(i\) is the rank order statistics
- \(n\) is the number of unmasked values along the given axis
- \(\alpha\) and \(\beta\) are two parameters.

**Typical values for alpha and beta are:**

- \((0,1)\) : \(p(k) = k/n\), linear interpolation of cdf (R, type 4)
- \((.5,.5)\) : \(p(k) = (k-1/2.)/n\), piecewise linear function (R, type 5)
- \((0,0)\) : \(p(k) = k/(n+1)\), Weibull (R type 6)
- \((1,1)\) : \(p(k) = (k-1)/(n-1)\), in this case, \(p(k) = \text{mode}[F(x[k])]\). That’s R default (R type 7)
- \((1/3,1/3)\) : \(p(k) = (k-1/3)/(n+1/3)\), then \(p(k) = \text{median}[F(x[k])]\). The resulting quantile estimates are approximately median-unbiased regardless of the distribution of x. (R type 8)
- \((3/8,3/8)\) : \(p(k) = (k-3/8)/(n+1/4)\), Blom. The resulting quantile estimates are approximately unbiased if x is normally distributed (R type 9)
- \((.4,.4)\) : approximately quantile unbiased (Cunnane)
- \((.35,.35)\): APL, used with PWM
- \((.3175, .3175)\): used in scipy.stats.probplot

**Parameters**

- **data** [array_like] Input data, as a sequence or array of dimension at most 2.
- **alpha** [float, optional] Plotting positions parameter. Default is 0.4.
- **beta** [float, optional] Plotting positions parameter. Default is 0.4.

**Returns**

- **positions** [MaskedArray] The calculated plotting positions.
scipy.stats.mstats.moment

scipy.stats.mstats.moment(a, moment=1, axis=0)
Calculates the nth moment about the mean for a sample.

Parameters
- a [array_like] data
- moment [int, optional] order of central moment that is returned
- axis [int or None, optional] Axis along which the central moment is computed. Default is 0. If None, compute over the whole array a.

Returns
- n-th central moment [ndarray or float] The appropriate moment along the given axis or over all values if axis is None. The denominator for the moment calculation is the number of observations, no degrees of freedom correction is done.

Notes
For more details about moment, see stats.moment.

scipy.stats.mstats.skew

scipy.stats.mstats.skew(a, axis=0, bias=True)
Computes the skewness of a data set.

Parameters
- a [ndarray] data
- axis [int or None, optional] Axis along which skewness is calculated. Default is 0. If None, compute over the whole array a.
- bias [bool, optional] If False, then the calculations are corrected for statistical bias.

Returns
- skewness [ndarray] The skewness of values along an axis, returning 0 where all values are equal.

Notes
For more details about skew, see stats.skew.

scipy.stats.mstats.tmean

scipy.stats.mstats.tmean(a, limits=None, inclusive=(True, True), axis=None)
Compute the trimmed mean.

Parameters
- a [array_like] Array of values.
- limits [None or (lower limit, upper limit), optional] Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None (default), then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval.
- inclusive [(bool, bool), optional] A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).
- axis [int or None, optional] Axis along which to operate. If None, compute over the whole array. Default is None.

Returns
tmean  [float]

Notes
For more details on tmean, see stats.tmean.

Examples

```python
>>> from scipy.stats import mstats
>>> a = np.array([[6, 8, 3, 0],
...                [3, 9, 1, 2],
...                [8, 7, 8, 2],
...                [5, 6, 0, 2],
...                [4, 5, 5, 2]])
>>> mstats.tmean(a, (2,5))
3.3
>>> mstats.tmean(a, (2,5), axis=0)
masked_array(data=[4.0, 5.0, 4.0, 2.0],
             mask=[False, False, False, False],
            fill_value=1e+20)
```

scipy.stats.mstats.tvar

```python
scipy.stats.mstats.tvar(a, limits=None, inclusive=(True, True), axis=0, ddof=1)
```
 Computes the trimmed variance

This function computes the sample variance of an array of values, while ignoring values which are outside of given limits.

**Parameters**

- `a` [array_like] Array of values.
- `limits` [None or (lower limit, upper limit), optional] Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None, then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval. The default value is None.
- `inclusive` [(bool, bool), optional] A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).
- `axis` [int or None, optional] Axis along which to operate. If None, compute over the whole array. Default is zero.

**Returns**

- `tvar` [float] Trimmed variance.

**Notes**

For more details on tvar, see stats.tvar.

scipy.stats.mstats.tmin

```python
scipy.stats.mstats.tmin(a, lowerlimit=None, axis=0, inclusive=True)
```
 Computes the trimmed minimum

**Parameters**

- `a` [array_like] array of values
lowerlimit
[None or float, optional] Values in the input array less than the given limit will be ignored. When lowerlimit is None, then all values are used. The default value is None.

axis
[int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array a.

inclusive
[(True, False), optional] This flag determines whether values exactly equal to the lower limit are included. The default value is True.

Returns
tmin [float, int or ndarray]

Notes
For more details on tmin, see stats.tmin.

Examples

```python
>>> from scipy.stats import mstats
>>> a = np.array([[6, 8, 3, 0],
...              [3, 2, 1, 2],
...              [8, 1, 8, 2],
...              [5, 3, 0, 2],
...              [4, 7, 5, 2]])
... >>> mstats.tmin(a, 5)
masked_array(data=[5, 7, 5, --],
             mask=[False, False, False, True],
             fill_value=999999)
```

scipy.stats.mstats.tmax

scipy.stats.mstats.tmax(a, upperlimit=None, axis=0, inclusive=True)
Compute the trimmed maximum

This function computes the maximum value of an array along a given axis, while ignoring values larger than a specified upper limit.

Parameters

- a [array_like] array of values
- upperlimit [None or float, optional] Values in the input array greater than the given limit will be ignored. When upperlimit is None, then all values are used. The default value is None.
- axis [int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array a.
- inclusive [(True, False), optional] This flag determines whether values exactly equal to the upper limit are included. The default value is True.

Returns
tmax [float, int or ndarray]

Notes
For more details on tmax, see stats.tmax.

Examples
>>> from scipy.stats import mstats
>>> a = np.array([[6, 8, 3, 0],
...                [3, 9, 1, 2],
...                [8, 7, 8, 2],
...                [5, 6, 0, 2],
...                [4, 5, 5, 2]])

>>> mstats.tmax(a, 4)
masked_array(data=[4, --, 3, 2],
            mask=[False, True, False, False],
           fill_value=999999)

scipy.stats.mstats.tsem

scipy.stats.mstats.tsem(a, limits=None, inclusive=(True, True), axis=0, ddof=1)
Compute the trimmed standard error of the mean.
This function finds the standard error of the mean for given values, ignoring values outside the given limits.

Parameters
a [array_like] array of values
limits [None, or (lower limit, upper limit), optional] Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None, then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval. The default value is None.
inclusive [(bool, bool), optional] A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).
axis [int or None, optional] Axis along which to operate. If None, compute over the whole array. Default is zero.
ddof [int, optional] Delta degrees of freedom. Default is 1.

Returns
tsem [float]

Notes
For more details on tsem, see stats.tsem.

scipy.stats.mstats.variation

scipy.stats.mstats.variation(a, axis=0)
Computes the coefficient of variation, the ratio of the biased standard deviation to the mean.

Parameters
a [array_like] Input array.
axis [int or None, optional] Axis along which to calculate the coefficient of variation. Default is 0. If None, compute over the whole array a.

Returns
variation [ndarray] The calculated variation along the requested axis.

Notes
For more details about variation, see stats.variation.
scipy.stats.mstats.find_repeats

scipy.stats.mstats.find_repeats(arr)
Find repeats in arr and return a tuple (repeats, repeat_count).
The input is cast to float64. Masked values are discarded.

Parameters

arr [sequence] Input array. The array is flattened if it is not 1D.

Returns

repeats [ndarray] Array of repeated values.
counts [ndarray] Array of counts.

scipy.stats.mstats.sem

scipy.stats.mstats.sem(a, axis=0, ddof=1)
Calculates the standard error of the mean of the input array.
Also sometimes called standard error of measurement.

Parameters

a [array_like] An array containing the values for which the standard error is returned.
axis [int or None, optional] If axis is None, ravel a first. If axis is an integer, this will
be the axis over which to operate. Defaults to 0.
ddof [int, optional] Delta degrees-of-freedom. How many degrees of freedom to adjust
for bias in limited samples relative to the population estimate of variance. Defaults
to 1.

Returns

s [ndarray or float] The standard error of the mean in the sample(s), along the input
axis.

Notes
The default value for ddof changed in scipy 0.15.0 to be consistent with stats.sem as well as with the
most common definition used (like in the R documentation).

Examples
Find standard error along the first axis:

```python
>>> from scipy import stats
>>> a = np.arange(20).reshape(5, 4)
>>> print(stats.mstats.sem(a))
[2.8284271247461903 2.8284271247461903 2.8284271247461903
 2.8284271247461903 2.8284271247461903]
```

Find standard error across the whole array, using n degrees of freedom:

```python
>>> print(stats.mstats.sem(a, axis=None, ddof=0))
1.2893796958227628
```

scipy.stats.mstats.trimmed_mean

scipy.stats.mstats.trimmed_mean(a, limits=(0.1, 0.1), inclusive=(1, 1), relative=True,
axis=None)
scipy.stats.mstats.trimmed_mean_ci

```python
scipy.stats.mstats.trimmed_mean_ci(data, limits=(0.2, 0.2), inclusive=(True, True), alpha=0.05, axis=None)
```

Selected confidence interval of the trimmed mean along the given axis.

**Parameters**

- **data** [array_like] Input data.
- **limits** [{None, tuple}, optional] None or a two item tuple. Tuple of the percentages to cut on each side of the array, with respect to the number of unmasked data, as floats between 0. and 1. If \( n \) is the number of unmasked data before trimming, then \((n * \text{limits}[0])\)th smallest data and \((n * \text{limits}[1])\)th largest data are masked. The total number of unmasked data after trimming is \( n * (1 - \text{sum(limits)}) \). The value of one limit can be set to None to indicate an open interval. Defaults to (0.2, 0.2).
- **inclusive** [(2,) tuple of boolean, optional] If relative==False, tuple indicating whether values exactly equal to the absolute limits are allowed. If relative==True, tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False). Defaults to (True, True).
- **alpha** [float, optional] Confidence level of the intervals. Defaults to 0.05.
- **axis** [int, optional] Axis along which to cut. If None, uses a flattened version of `data`. Defaults to None.

**Returns**

- **trimmed_mean_ci** [(2,) ndarray] The lower and upper confidence intervals of the trimmed data.

scipy.stats.mstats.trimmed_std

```python
scipy.stats.mstatstrimmed_std(a, limits=(0.1, 0.1), inclusive=(1, 1), relative=True, axis=None, ddof=0)
```

scipy.stats.mstats.trimmed_var

```python
scipy.stats.mstatstrimmed_var(a, limits=(0.1, 0.1), inclusive=(1, 1), relative=True, axis=None, ddof=0)
```

**Frequency statistics**

- **scoreatpercentile**(data, per[, limit, …]) Calculate the score at the given ‘per’ percentile of the sequence `a`

scipy.stats.mstats.scoreatpercentile

```python
scipy.stats.mstats.scoreatpercentile(data, per, limit=(), alphap=0.4, betap=0.4)
```

Calculate the score at the given ‘per’ percentile of the sequence `a`. For example, the score at per=50 is the median.

This function is a shortcut to `mquantile`

**Correlation functions**
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**scipy.stats.mstats.f_oneway**

`scipy.stats.mstats.f_oneway(*args)`

Performs a 1-way ANOVA, returning an F-value and probability given any number of groups. From Heiman, pp.394-7.

Usage: `f_oneway(*args)`, where *args is 2 or more arrays, one per treatment group.

**Returns**

- **statistic** [float] The computed F-value of the test.
- **pvalue** [float] The associated p-value from the F-distribution.

**scipy.stats.mstats.pearsonr**

`scipy.stats.mstats.pearsonr(x, y)`

Calculates a Pearson correlation coefficient and the p-value for testing non-correlation.

The Pearson correlation coefficient measures the linear relationship between two datasets. Strictly speaking, Pearson’s correlation requires that each dataset be normally distributed. Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply an exact linear relationship. Positive correlations imply that as x increases, so does y. Negative correlations imply that as x increases, y decreases.

The p-value roughly indicates the probability of an uncorrelated system producing datasets that have a Pearson correlation at least as extreme as the one computed from these datasets. The p-values are not entirely reliable but are probably reasonable for datasets larger than 500 or so.

**Parameters**

- **x** [1-D array_like] Input
- **y** [1-D array_like] Input

**Returns**

- **pearsonr** [float] Pearson’s correlation coefficient, 2-tailed p-value.
**scipy.stats.mstats.spearmanr**

```python
scipy.stats.mstats.spearmanr(x, y=None, use_ties=True, axis=None, nan_policy='propagate')
```

Calculates a Spearman rank-order correlation coefficient and the p-value to test for non-correlation.

The Spearman correlation is a nonparametric measure of the linear relationship between two datasets. Unlike the Pearson correlation, the Spearman correlation does not assume that both datasets are normally distributed. Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply a monotonic relationship. Positive correlations imply that as \( x \) increases, so does \( y \). Negative correlations imply that as \( x \) increases, \( y \) decreases.

Missing values are discarded pair-wise: if a value is missing in \( x \), the corresponding value in \( y \) is masked.

The p-value roughly indicates the probability of an uncorrelated system producing datasets that have a Spearman correlation at least as extreme as the one computed from these datasets. The p-values are not entirely reliable but are probably reasonable for datasets larger than 500 or so.

**Parameters**

- `x, y`: [1D or 2D array_like, y is optional] One or two 1-D or 2-D arrays containing multiple variables and observations. When these are 1-D, each represents a vector of observations of a single variable. For the behavior in the 2-D case, see under `axis`, below.
- `use_ties`: [bool, optional] DO NOT USE. Does not do anything, keyword is only left in place for backwards compatibility reasons.
- `axis`: [int or None, optional] If `axis=0` (default), then each column represents a variable, with observations in the rows. If `axis=1`, the relationship is transposed: each row represents a variable, while the columns contain observations. If `axis=None`, then both arrays will be raveled.

**Returns**

- `correlation`: [float] Spearman correlation coefficient
- `pvalue`: [float] 2-tailed p-value.

**References**


**scipy.stats.mstats.pointbiserialr**

```python
scipy.stats.mstats.pointbiserialr(x, y)
```

Calculates a point biserial correlation coefficient and its p-value.

**Parameters**

- `x`: [array_like of bools] Input array.
- `y`: [array_like] Input array.

**Returns**

- `correlation`: [float] R value
Notes
Missing values are considered pair-wise: if a value is missing in x, the corresponding value in y is masked.

For more details on `pointbiserialr`, see `stats.pointbiserialr`.

**scipy.stats.mstats.kendalltau**

```python
scipy.stats.mstats.kendalltau(x, y, use_ties=True, use_missing=False, method='auto')
```

Computes Kendall’s rank correlation tau on two variables x and y.

**Parameters**

- `x` [sequence] First data list (for example, time).
- `y` [sequence] Second data list.
- `use_ties` [{True, False}, optional] Whether ties correction should be performed.
- `use_missing` [{False, True}, optional] Whether missing data should be allocated a rank of 0 (False) or the average rank (True)
- `method`: {'auto', 'asymptotic', 'exact'}, optional Defines which method is used to calculate the p-value [1]. ‘asymptotic’ uses a normal approximation valid for large samples. ‘exact’ computes the exact p-value, but can only be used if no ties are present. ‘auto’ is the default and selects the appropriate method based on a trade-off between speed and accuracy.

**Returns**

- `correlation` [float] Kendall tau

**References**

[1]

**scipy.stats.mstats.kendalltau_seasonal**

```python
scipy.stats.mstats.kendalltau_seasonal(x)
```

Computes a multivariate Kendall’s rank correlation tau, for seasonal data.

**Parameters**

- `x` [2-D ndarray] Array of seasonal data, with seasons in columns.

**scipy.stats.mstats.linregress**

```python
scipy.stats.mstats.linregress(x, y=None)
```

Calculate a linear least-squares regression for two sets of measurements.

**Parameters**

- `x`, `y` [array_like] Two sets of measurements. Both arrays should have the same length. If only x is given (and y=None), then it must be a two-dimensional array where one dimension has length 2. The two sets of measurements are then found by splitting the array along the length-2 dimension.

**Returns**

- `slope` [float] slope of the regression line
- `intercept` [float] intercept of the regression line
SciPy Reference Guide, Release 1.2.0

rvalue  [float] correlation coefficient
pvalue  [float] two-sided p-value for a hypothesis test whose null hypothesis is that the slope is zero, using Wald Test with t-distribution of the test statistic.
stderr  [float] Standard error of the estimated gradient.

See also:

scipy.optimize.curve_fit

Use non-linear least squares to fit a function to data.

scipy.optimize.leastsq

Minimize the sum of squares of a set of equations.

Notes
Missing values are considered pair-wise: if a value is missing in x, the corresponding value in y is masked.

Examples

```python
>>> import matplotlib.pyplot as plt
>>> from scipy import stats

Generate some data:

```python
>>> np.random.seed(12345678)
>>> x = np.random.random(10)
>>> y = 1.6*x + np.random.random(10)
```

Perform the linear regression:

```python
>>> slope, intercept, r_value, p_value, std_err = stats.linregress(x, y)
>>> print("slope: %f intercept: %f" % (slope, intercept))
```

To get coefficient of determination (r_squared):

```python
>>> print("r-squared: %f" % r_value**2)
```

Plot the data along with the fitted line:

```python
>>> plt.plot(x, y, 'o', label='original data')
>>> plt.plot(x, intercept + slope*x, 'r', label='fitted line')
>>> plt.legend()
>>> plt.show()
```

scipy.stats.mstats.siegelslopes

scipy.stats.mstats.siegelslopes(y, x=None, method='hierarchical')

Computes the Siegel estimator for a set of points (x, y).

siegelslopes implements a method for robust linear regression using repeated medians to fit a line to the points (x, y). The method is robust to outliers with an asymptotic breakdown point of 50%.

Parameters

y [array_like] Dependent variable.
x: array_like or None, optional] Independent variable. If None, use `arange(len(y))` instead.

method: {'hierarchical', 'separate'} If 'hierarchical', estimate the intercept using the estimated slope `medslope` (default option). If 'separate', estimate the intercept independent of the estimated slope. See Notes for details.

Returns

- `medslope`: float] Estimate of the slope of the regression line.
- `medintercept`: float] Estimate of the intercept of the regression line.

See also:

-theilslopes

a similar technique without repeated medians

Notes

For more details on `siegelslopes`, see `scipy.stats.siegelslopes`.

`scipy.stats.mstats.theilslopes`

`scipy.stats.mstats.theilslopes(y, x=None, alpha=0.95)`
Computes the Theil-Sen estimator for a set of points (x, y).

theilslopes implements a method for robust linear regression. It computes the slope as the median of all slopes between paired values.

Parameters

- y: array_like] Dependent variable.
- x: [array_like or None, optional] Independent variable. If None, use `arange(len(y))` instead.
- alpha: [float, optional] Confidence degree between 0 and 1. Default is 95% confidence. Note that `alpha` is symmetric around 0.5, i.e. both 0.1 and 0.9 are interpreted as “find the 90% confidence interval”.
**Returns**

medslope  
[float] Theil slope.

medintercept  
[float] Intercept of the Theil line, as median(y) - medslope*median(x).

lo_slope  
[float] Lower bound of the confidence interval on medslope.

up_slope  
[float] Upper bound of the confidence interval on medslope.

See also:

siegelslopes  
A similar technique with repeated medians

Notes

For more details on theilslopes, see stats.theilslopes.

**scipy.stats.mstats.sen_seasonal_slopes**

**scipy.stats.mstats.sen_seasonal_slopes(x)**

**Statistical tests**

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<td>Calculates the T-test for the mean of ONE group of scores.</td>
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<td>Calculate a one-way chi square test.</td>
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<td>Tests whether a sample differs from a normal distribution.</td>
</tr>
</tbody>
</table>
scipy.stats.mstats.ttest_1samp

Calculates the T-test for the mean of ONE group of scores.

**Parameters**
- `a` [array_like] sample observation
- `popmean` [float or array_like] expected value in null hypothesis, if array_like than it must have the same shape as `a` excluding the axis dimension
- `axis` [int or None, optional] Axis along which to compute test. If None, compute over the whole array `a`.

**Returns**
- `statistic` [float or array] t-statistic
- `pvalue` [float or array] two-tailed p-value

**Notes**
For more details on `ttest_1samp`, see `stats.ttest_1samp`.

scipy.stats.mstats.ttest_onessamp

Calculates the T-test for the mean of ONE group of scores.

**Parameters**
- `a` [array_like] sample observation
- `popmean` [float or array_like] expected value in null hypothesis, if array_like than it must have the same shape as `a` excluding the axis dimension
- `axis` [int or None, optional] Axis along which to compute test. If None, compute over the whole array `a`.

**Returns**
- `statistic` [float or array] t-statistic
- `pvalue` [float or array] two-tailed p-value

**Notes**
For more details on `ttest_1samp`, see `stats.ttest_1samp`.

scipy.stats.mstats.ttest_ind

Calculates the T-test for the means of TWO INDEPENDENT samples of scores.

**Parameters**
- `a, b` [array_like] The arrays must have the same shape, except in the dimension corresponding to `axis` (the first, by default).
- `axis` [int or None, optional] Axis along which to compute test. If None, compute over the whole arrays, `a`, and `b`.
- `equal_var` [bool, optional] If True, perform a standard independent 2 sample test that assumes equal population variances. If False, perform Welch’s t-test, which does not assume equal population variance.

New in version 0.17.0.
Returns

- **statistic** [float or array] The calculated t-statistic.
- **pvalue** [float or array] The two-tailed p-value.

Notes

For more details on `ttest_ind`, see `stats.ttest_ind`.

### scipy.stats.mstats.ttest_rel

**scipy.stats.mstats.ttest_rel(a, b, axis=0)**

Calculates the T-test on TWO RELATED samples of scores, a and b.

Parameters

- **a, b** [array_like] The arrays must have the same shape.
- **axis** [int or None, optional] Axis along which to compute test. If None, compute over the whole arrays, a, and b.

Returns

- **statistic** [float or array] t-statistic
- **pvalue** [float or array] two-tailed p-value

Notes

For more details on `ttest_rel`, see `stats.ttest_rel`.

### scipy.stats.mstats.chisquare

**scipy.stats.mstats.chisquare(f_obs, f_exp=None, ddof=0, axis=0)**

Calculate a one-way chi square test.

The chi square test tests the null hypothesis that the categorical data has the given frequencies.

Parameters

- **f_obs** [array_like] Observed frequencies in each category.
- **f_exp** [array_like, optional] Expected frequencies in each category. By default the categories are assumed to be equally likely.
- **ddof** [int, optional] “Delta degrees of freedom”: adjustment to the degrees of freedom for the p-value. The p-value is computed using a chi-squared distribution with k - 1 - ddof degrees of freedom, where k is the number of observed frequencies. The default value of ddof is 0.
- **axis** [int or None, optional] The axis of the broadcast result of `f_obs` and `f_exp` along which to apply the test. If axis is None, all values in `f_obs` are treated as a single data set. Default is 0.

Returns

- **chisq** [float or ndarray] The chi-squared test statistic. The value is a float if `axis` is None or `f_obs` and `f_exp` are 1-D.
- **p** [float or ndarray] The p-value of the test. The value is a float if `ddof` and the return value `chisq` are scalars.

See also:

- `power_divergence`, `mstats.chisquare`
Notes
This test is invalid when the observed or expected frequencies in each category are too small. A typical rule is that all of the observed and expected frequencies should be at least 5.

The default degrees of freedom, k-1, are for the case when no parameters of the distribution are estimated. If p parameters are estimated by efficient maximum likelihood then the correct degrees of freedom are k-1-p. If the parameters are estimated in a different way, then the dof can be between k-1-p and k-1. However, it is also possible that the asymptotic distribution is not a chisquare, in which case this test is not appropriate.

References
[1], [2]

Examples
When just \( f_{\text{obs}} \) is given, it is assumed that the expected frequencies are uniform and given by the mean of the observed frequencies.

```python
>>> from scipy.stats import chisquare
>>> chisquare([16, 18, 16, 14, 12, 12])
(2.0, 0.84914503608460966)
```

With \( f_{\text{exp}} \) the expected frequencies can be given.

```python
>>> chisquare([16, 18, 16, 14, 12, 12], f_exp=[16, 16, 16, 16, 16, 8])
(3.5, 0.62338762774958223)
```

When \( f_{\text{obs}} \) is 2-D, by default the test is applied to each column.

```python
>>> obs = np.array([[[16, 18, 16, 14, 12, 12], [32, 24, 16, 28, 20, 24]]]).T
>>> obs.shape
(6, 2)
>>> chisquare(obs)
(array([ 2. , 6.66666667]), array([ 0.84914504, 0.24663415]))
```

By setting `axis=None`, the test is applied to all data in the array, which is equivalent to applying the test to the flattened array.

```python
>>> chisquare(obs, axis=None)
(23.31034482758621, 0.015975692534127565)
>>> chisquare(obs.ravel())
(23.31034482758621, 0.015975692534127565)
```

`ddof` is the change to make to the default degrees of freedom.

```python
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=1)
(2.0, 0.73575888234288467)
```

The calculation of the p-values is done by broadcasting the chi-squared statistic with `ddof`.

```python
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=[0,1,2])
(2.0, array([0.84914504, 0.73575888, 0.5724067 ]))
```

\( f_{\text{obs}} \) and \( f_{\text{exp}} \) are also broadcast. In the following, \( f_{\text{obs}} \) has shape (6,) and \( f_{\text{exp}} \) has shape (2, 6), so the result of broadcasting \( f_{\text{obs}} \) and \( f_{\text{exp}} \) has shape (2, 6). To compute the desired chi-squared statistics, we use `axis=1`:
```python
>>> chisquare([16, 18, 16, 14, 12, 12],
...          f_exp=[[16, 16, 16, 16, 16, 8], [8, 20, 20, 16, 12, 12]],
...          axis=1)
(array([ 3.5 , 9.25]), array([ 0.62338763, 0.09949846]))
```

**scipy.stats.mstats.ks_2samp**

**scipy.stats.mstats.ks_2samp(data1, data2, alternative='two-sided')**

Computes the Kolmogorov-Smirnov test on two samples. Missing values are discarded.

**Parameters**

- `data1` [array_like] First data set
- `data2` [array_like] Second data set
- `alternative` [{‘two-sided’, ‘less’, ‘greater’}, optional] Indicates the alternative hypothesis. Default is ‘two-sided’.

**Returns**

- `d` [float] Value of the Kolmogorov Smirnov test
- `p` [float] Corresponding p-value.

**scipy.stats.mstats.ks_twosamp**

**scipy.stats.mstats.ks_twosamp(data1, data2, alternative='two-sided')**

Computes the Kolmogorov-Smirnov test on two samples. Missing values are discarded.

**Parameters**

- `data1` [array_like] First data set
- `data2` [array_like] Second data set
- `alternative` [{‘two-sided’, ‘less’, ‘greater’}, optional] Indicates the alternative hypothesis. Default is ‘two-sided’.

**Returns**

- `d` [float] Value of the Kolmogorov Smirnov test
- `p` [float] Corresponding p-value.

**scipy.stats.mstats.mannwhitneyu**

**scipy.stats.mstats.mannwhitneyu(x, y, use_contiuity=True)**

Computes the Mann-Whitney statistic

Missing values in `x` and/or `y` are discarded.

**Parameters**

- `x` [sequence] Input
- `y` [sequence] Input
- `use_contiuity` [{True, False}, optional] Whether a continuity correction (1/2.) should be taken into account.
**Returns**

- **statistic** [float] The Mann-Whitney statistics
- **pvalue** [float] Approximate p-value assuming a normal distribution.

**scipy.stats.mstats.rankdata**

**scipy.stats.mstats.rankdata**(data, axis=None, use_missing=False)

Returns the rank (also known as order statistics) of each data point along the given axis.

If some values are tied, their rank is averaged. If some values are masked, their rank is set to 0 if use_missing is False, or set to the average rank of the unmasked values if use_missing is True.

**Parameters**

- **data** [sequence] Input data. The data is transformed to a masked array
- **axis** [(None, int), optional] Axis along which to perform the ranking. If None, the array is first flattened. An exception is raised if the axis is specified for arrays with a dimension larger than 2
- **use_missing** [bool, optional] Whether the masked values have a rank of 0 (False) or equal to the average rank of the unmasked values (True).

**scipy.stats.mstats.kruskal**

**scipy.stats.mstats.kruskal**(args)

Compute the Kruskal-Wallis H-test for independent samples

**Parameters**

- **sample1, sample2, ...** [array_like] Two or more arrays with the sample measurements can be given as arguments.

**Returns**

- **statistic** [float] The Kruskal-Wallis H statistic, corrected for ties
- **pvalue** [float] The p-value for the test using the assumption that H has a chi square distribution

**Notes**

For more details on kruskal, see stats.kruskal.

**Examples**

```python
>>> from scipy.stats.mstats import kruskal

Random samples from three different brands of batteries were tested to see how long the charge lasted. Results were as follows:
```

```python
>>> a = [6.3, 5.4, 5.7, 5.2, 5.0]
>>> b = [6.9, 7.0, 6.1, 7.9]
>>> c = [7.2, 6.9, 6.1, 6.5]
```

Test the hypothesis that the distribution functions for all of the brands’ durations are identical. Use 5% level of significance.

```python
>>> kruskal(a, b, c)
KruskalResult(statistic=7.113812154696133, pvalue=0.028526948491942164)
```
The null hypothesis is rejected at the 5% level of significance because the returned p-value is less than the critical value of 5%.

**scipy.stats.mstats.kruskalwallis**

**scipy.stats.mstats.kruskalwallis(*args)**  
Compute the Kruskal-Wallis H-test for independent samples

**Parameters**

sample1, sample2, ...
[array_like] Two or more arrays with the sample measurements can be given as arguments.

**Returns**

statistic [float] The Kruskal-Wallis H statistic, corrected for ties  
pvalue [float] The p-value for the test using the assumption that H has a chi square distribution

**Notes**

For more details on kruskal, see stats.kruskal.

**Examples**

```python
>>> from scipy.stats.mstats import kruskal
```

Random samples from three different brands of batteries were tested to see how long the charge lasted. Results were as follows:

```python
>>> a = [6.3, 5.4, 5.7, 5.2, 5.0]  
>>> b = [6.9, 7.0, 6.1, 7.9]  
>>> c = [7.2, 6.9, 6.1, 6.5]
```

Test the hypothesis that the distribution functions for all of the brands’ durations are identical. Use 5% level of significance.

```python
>>> kruskal(a, b, c)
KruskalResult(statistic=7.113812154696133, pvalue=0.028526948491942164)
```

The null hypothesis is rejected at the 5% level of significance because the returned p-value is less than the critical value of 5%.

**scipy.stats.mstats.friedmanchisquare**

**scipy.stats.mstats.friedmanchisquare(*args)**  
Friedman Chi-Square is a non-parametric, one-way within-subjects ANOVA. This function calculates the Friedman Chi-square test for repeated measures and returns the result, along with the associated probability value.

Each input is considered a given group. Ideally, the number of treatments among each group should be equal. If this is not the case, only the first n treatments are taken into account, where n is the number of treatments of the smallest group. If a group has some missing values, the corresponding treatments are masked in the other groups. The test statistic is corrected for ties.

Masked values in one group are propagated to the other groups.

**Returns**

statistic [float] the test statistic.
pvalue [float] the associated p-value.

scipy.stats.mstats.brunnermunzel

scipy.stats.mstats.brunnermunzel(x, y, alternative='two-sided', distribution='t')
 Computes the Brunner-Munzel test on samples x and y
 Missing values in x and/or y are discarded.

Parameters
x, y [array_like] Array of samples, should be one-dimensional.
alternative ['less', 'two-sided', or 'greater', optional] Whether to get the p-value for the one-sided hypothesis ('less' or 'greater') or for the two-sided hypothesis ('two-sided'). Defaults value is 'two-sided' .

distribution: 't' or 'normal', optional
 Whether to get the p-value by t-distribution or by standard normal distribution. Defaults value is 't' .

Returns
pvalue [float] p-value assuming an t distribution. One-sided or two-sided, depending on the choice of alternative and distribution.

See also:
mannwhitneyu
Mann-Whitney rank test on two samples.

Notes
For more details on brunnermunzel, see stats.brunnermunzel.

scipy.stats.mstats.skewtest

scipy.stats.mstats.skewtest(a, axis=0)
 Tests whether the skew is different from the normal distribution.

Parameters
a [array] The data to be tested
axis [int or None, optional] Axis along which statistics are calculated. Default is 0. If None, compute over the whole array a.

Returns
statistic [float] The computed z-score for this test.
pvalue [float] a 2-sided p-value for the hypothesis test

Notes
For more details about skewtest, see stats.skewtest.

scipy.stats.mstats.kurtosistest

scipy.stats.mstats.kurtosistest(a, axis=0)
 Tests whether a dataset has normal kurtosis

Parameters
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`array` array of the sample data

`axis` [int or None, optional] Axis along which to compute test. Default is 0. If None, compute over the whole array `a`.

**Returns**

- `statistic` [float] The computed z-score for this test.
- `pvalue` [float] The 2-sided p-value for the hypothesis test

**Notes**
For more details about `kurtosistest`, see `stats.kurtosistest`.

**scipy.stats.mstats.normaltest**

`scipy.stats.mstats.normaltest(a, axis=0)`
Tests whether a sample differs from a normal distribution.

**Parameters**

- `a` [array_like] The array containing the data to be tested.
- `axis` [int or None, optional] Axis along which to compute test. Default is 0. If None, compute over the whole array `a`.

**Returns**

- `statistic` [float or array] \( s^2 + k^2 \), where \( s \) is the z-score returned by `skewtest` and \( k \) is the z-score returned by `kurtosistest`.
- `pvalue` [float or array] A 2-sided chi squared probability for the hypothesis test.

**Notes**
For more details about `normaltest`, see `stats.normaltest`.

**Transformations**

- `obrientransform(*args)` Computes a transform on input data (any number of columns).
- `trim(a[, limits, inclusive, relative, axis])` Trims an array by masking the data outside some given limits.
- `trimmed_stde(a[, limits, inclusive, axis])` Returns the standard error of the trimmed mean along the given axis.
- `trimr(a[, limits, inclusive, axis])` Trims an array by masking some proportion of the data on each end.
- `trimtail(data[, proportiontocut, tail, ...])` Trims the data by masking values from one tail.
- `trimboth(data[, proportiontocut, inclusive, ...])` Trims the smallest and largest data values.
- `winsorize(a[, limits, inclusive, inplace, axis])` Returns a Winsorized version of the input array.
- `zmap(scores, compare[, axis, ddof])` Calculate the relative z-scores.
- `zscore(a[, axis, ddof])` Calculate the z score of each value in the sample, relative to the sample mean and standard deviation.

**scipy.stats.mstats.obrientransform**

`scipy.stats.mstats.obrientransform(*args)`
Computes a transform on input data (any number of columns). Used to test for homogeneity of variance prior to running one-way stats. Each array in *args is one level of a factor. If an `f_oneway()` run on the transformed data and found significant, variances are unequal. From Maxwell and Delaney, p.112.
Returns: transformed data for use in an ANOVA

```
scipy.stats.mstats.trim

scipy.stats.mstats.trim(a, limits=None, inclusive=(True, True), relative=False, axis=None)
```

Trims an array by masking the data outside some given limits.

Returns a masked version of the input array.

**Parameters**

- **a** [sequence] Input array
- **limits** [{None, tuple}, optional] If `relative` is False, tuple (lower limit, upper limit) in absolute values. Values of the input array lower (greater) than the lower (upper) limit are masked.
  
  If `relative` is True, tuple (lower percentage, upper percentage) to cut on each side of the array, with respect to the number of unmasked data.
  
  Noting n the number of unmasked data before trimming, the (n*limits[0])th smallest data and the (n*limits[1])th largest data are masked, and the total number of unmasked data after trimming is n*(1.-sum(limits)) In each case, the value of one limit can be set to None to indicate an open interval.
  
  If limits is None, no trimming is performed
- **inclusive** [{(bool, bool) tuple}, optional] If `relative` is False, tuple indicating whether values exactly equal to the absolute limits are allowed. If `relative` is True, tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).
- **relative** [bool, optional] Whether to consider the limits as absolute values (False) or proportions to cut (True).
- **axis** [int, optional] Axis along which to trim.

**Examples**

```python
>>> from scipy.stats.mstats import trim
>>> z = [1, 2, 3, 4, 5, 6, 7, 8, 9, 10]
>>> print(trim(z,(3,8)))
[-- -- 3 4 5 6 7 8 -- --]
>>> print(trim(z,(0.1,0.2),relative=True))
[-- 2 3 4 5 6 7 8 -- --]
```

```
scipy.stats.mstats.trima

scipy.stats.mstats.trima(a, limits=None, inclusive=(True, True))
```

Trims an array by masking the data outside some given limits.

Returns a masked version of the input array.

**Parameters**

- **a** [array_like] Input array.
- **limits** [{None, tuple}, optional] Tuple of (lower limit, upper limit) in absolute values.
  
  Values of the input array lower (greater) than the lower (upper) limit will be masked. A limit is None indicates an open interval.
- **inclusive** [{(bool, bool) tuple, optional} Tuple of (lower flag, upper flag), indicating whether values exactly equal to the lower (upper) limit are allowed.
scipy.stats.mstats.trimmed_stde

scipy.stats.mstats.trimmed_stde(a, limits=(0.1, 0.1), inclusive=(1, 1), axis=None)

Returns the standard error of the trimmed mean along the given axis.

**Parameters**

- **a** [sequence] Input array
- **limits** [(0.1, 0.1), tuple of float], optional] tuple (lower percentage, upper percentage) to cut on each side of the array, with respect to the number of unmasked data. If n is the number of unmasked data before trimming, the values smaller than n * limits[0] and the values larger than n * limits[1] are masked, and the total number of unmasked data after trimming is n * (1. - sum(limits)). In each case, the value of one limit can be set to None to indicate an open interval. If limits is None, no trimming is performed.
- **inclusive** [(bool, bool) tuple] optional Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).
- **axis** [int, optional] Axis along which to trim.

**Returns**

- **trimmed_stde** [scalar or ndarray]

scipy.stats.mstats.trimr

scipy.stats.mstats.trimr(a, limits=None, inclusive=(True, True), axis=None)

Trims an array by masking some proportion of the data on each end. Returns a masked version of the input array.

**Parameters**

- **a** [sequence] Input array.
- **limits** [None, tuple], optional] Tuple of the percentages to cut on each side of the array, with respect to the number of unmasked data, as floats between 0. and 1. Noting n the number of unmasked data before trimming, the (n*limits[0])th smallest data and the (n*limits[1])th largest data are masked, and the total number of unmasked data after trimming is n*(1.-sum(limits)). The value of one limit can be set to None to indicate an open interval.
- **inclusive** [(True, True) tuple], optional Tuple of flags indicating whether the number of data being masked on the left (right) end should be truncated (True) or rounded (False) to integers.
- **axis** [None, int], optional] Axis along which to trim. If None, the whole array is trimmed, but its shape is maintained.

scipy.stats.mstats.trimtail

scipy.stats.mstats.trimtail(data, proportiontocut=0.2, tail='left', inclusive=(True, True), axis=None)

Trims the data by masking values from one tail.

**Parameters**

- **data** [array_like] Data to trim.
- **proportiontocut** [float, optional] Percentage of trimming. If n is the number of unmasked values before trimming, the number of values after trimming is (1 - proportiontocut) * n. Default is 0.2.
tail  [{‘left’, ‘right’}, optional] If ‘left’ the proportiontocut lowest values will be masked. If ‘right’ the proportiontocut highest values will be masked. Default is ‘left’.

inclusive  [{(bool, bool) tuple}, optional] Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False). Default is (True, True).

axis  [int, optional] Axis along which to perform the trimming. If None, the input array is first flattened. Default is None.

Retruns
trimtail  [ndarray] Returned array of same shape as data with masked tail values.

scipy.stats.mstats.trimboth

scipy.stats.mstats.trimboth(data, proportiontocut=0.2, inclusive=(True, True), axis=None)
Trims the smallest and largest data values.

Trims the data by masking the int(proportiontocut * n) smallest and int(proportiontocut * n) largest values of data along the given axis, where n is the number of unmasked values before trimming.

Parameters

data  [ndarray] Data to trim.

proportiontocut  [float, optional] Percentage of trimming (as a float between 0 and 1). If n is the number of unmasked values before trimming, the number of values after trimming is (1 - 2 * proportiontocut) * n. Default is 0.2.

inclusive  [{(bool, bool) tuple}, optional] Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

axis  [int, optional] Axis along which to perform the trimming. If None, the input array is first flattened.

scipy.stats.mstats.winsorize

scipy.stats.mstats.winsorize(a, limits=None, inclusive=(True, True), inplace=False, axis=None)
Returns a Winsorized version of the input array.

The (limits[0])th lowest values are set to the (limits[0])th percentile, and the (limits[1])th highest values are set to the (1 - limits[1])th percentile. Masked values are skipped.

Parameters

a  [sequence] Input array.

limits  [{None, tuple of float}, optional] Tuple of the percentages to cut on each side of the array, with respect to the number of unmasked data, as floats between 0, and 1. Noting n the number of unmasked data before trimming, the (n * limits[0])th smallest data and the (n * limits[1])th largest data are masked, and the total number of unmasked data after trimming is n * (1 - sum(limits)) The value of one limit can be set to None to indicate an open interval.

inclusive  [{(True, True) tuple}, optional] Tuple indicating whether the number of data being masked on each side should be truncated (True) or rounded (False).

inplace  [{False, True}, optional] Whether to winsorize in place (True) or to use a copy (False).

axis  [{None, int}, optional] Axis along which to trim. If None, the whole array is trimmed, but its shape is maintained.

Notes
This function is applied to reduce the effect of possibly spurious outliers by limiting the extreme values.
scipy.stats.mstats.zmap

scipy.stats.mstats.zmap(scores, compare, axis=0, ddof=0)

Calculate the relative z-scores.

Return an array of z-scores, i.e., scores that are standardized to zero mean and unit variance, where mean and variance are calculated from the comparison array.

Parameters

- scores: array_like The input for which z-scores are calculated.
- compare: array_like The input from which the mean and standard deviation of the normalization are taken; assumed to have the same dimension as scores.
- axis: int or None, optional Axis over which mean and variance of compare are calculated. Default is 0. If None, compute over the whole array scores.
- ddof: int, optional Degrees of freedom correction in the calculation of the standard deviation. Default is 0.

Returns

zscore: array_like Z-scores, in the same shape as scores.

Notes

This function preserves ndarray subclasses, and works also with matrices and masked arrays (it uses asanyarray instead of asarray for parameters).

Examples

```python
>>> from scipy.stats import zmap
>>> a = [0.5, 2.0, 2.5, 3]
>>> b = [0, 1, 2, 3, 4]
>>> zmap(a, b)
array([-1.06066017, 0., 0.35355339, 0.70710678])
```

scipy.stats.mstats.zscore

scipy.stats.mstats.zscore(a, axis=0, ddof=0)

Calculate the z score of each value in the sample, relative to the sample mean and standard deviation.

Parameters

- a: array_like An array like object containing the sample data.
- axis: int or None, optional Axis along which to operate. Default is 0. If None, compute over the whole array a.
- ddof: int, optional Degrees of freedom correction in the calculation of the standard deviation. Default is 0.

Returns

zscore: array_like The z-scores, standardized by mean and standard deviation of input array a.

Notes

This function preserves ndarray subclasses, and works also with matrices and masked arrays (it uses asanyarray instead of asarray for parameters).

Examples

```python
>>> a = np.array([ 0.7972, 0.0767, 0.4383, 0.7866, 0.8091,
...  0.1954, 0.6307, 0.6599, 0.1065, 0.0508])
>>> from scipy import stats
(continues on next page)```
Computing along a specified axis, using n-1 degrees of freedom (ddof=1) to calculate the standard deviation:

```
>>> b = np.array([[ 0.3148, 0.0478, 0.6243, 0.4608],
...                [ 0.7149, 0.0775, 0.6072, 0.9656],
...                [ 0.6341, 0.1403, 0.9759, 0.4064],
...                [ 0.5918, 0.6948, 0.904, 0.3721],
...                [ 0.0921, 0.2481, 0.1188, 0.1366]])
```

```
>>> stats.zscore(b, axis=1, ddof=1)
array([[-0.19264823, -1.28415119, 1.07259584, 0.40420358],
       [ 0.33048416, -1.37380874, 0.04251374, 1.00081084],
       [ 0.26796377, -1.12598418, 1.23283094, -0.37481053],
       [-0.22095197, 0.24468594, 1.19042819, -1.21416216],
       [-0.82780366, 1.4457416 , -0.43867764, -0.1792603 ]])
```

Other

- `argstoarray(*args)` Constructs a 2D array from a group of sequences.
- `count_tied_groups(x[, use_missing])` Counts the number of tied values.
- `msign(x)` Returns the sign of x, or 0 if x is masked.
- `compare_medians_ms(group_1, group_2[, axis])` Compares the medians from two independent groups along the given axis.
- `median_cihs(data[, alpha, axis])` Computes the alpha-level confidence interval for the median of the data.
- `mjci(data[, prob, axis])` Returns the Maritz-Jarrett estimators of the standard error of selected experimental quantiles of the data.
- `mquantiles_cimj(data[, prob, alpha, axis])` Computes the alpha confidence interval for the selected quantiles of the data, with Maritz-Jarrett estimators.
- `rsh(data[, points])` Evaluates Rosenblatt’s shifted histogram estimators for each data point.

**scipy.stats.mstats.argstoarray**

- `scipy.stats.mstats.argstoarray(*args)` Constructs a 2D array from a group of sequences.

  Sequences are filled with missing values to match the length of the longest sequence.

  **Parameters**


  **Returns**

  - `argstoarray` [MaskedArray] A (m x n) masked array, where m is the number of arguments and n the length of the longest argument.

  **Notes**

  `numpy.ma.row_stack` has identical behavior, but is called with a sequence of sequences.
scipy.stats.mstats.count_tied_groups

scipy.stats.mstats.count_tied_groups(x, use_missing=False)
Counts the number of tied values.

Parameters

x [sequence] Sequence of data on which to counts the ties
use_missing [bool, optional] Whether to consider missing values as tied.

Returns

count_tied_groups [dict] Returns a dictionary (nb of ties: nb of groups).

Examples

```python
>>> from scipy.stats import mstats
>>> z = [0, 0, 2, 2, 2, 3, 3, 4, 5, 6]
>>> mstats.count_tied_groups(z)
{2: 1, 3: 2}
```

In the above example, the ties were 0 (3x), 2 (3x) and 3 (2x).

```python
>>> z = np.ma.array(([0, 0, 1, 2, 2, 2, 3, 3, 4, 5, 6])
>>> mstats.count_tied_groups(z)
{2: 2, 3: 1}
>>> z[[1,-1]] = np.ma.masked
>>> mstats.count_tied_groups(z, use_missing=True)
{2: 2, 3: 1}
```

scipy.stats.mstats.msign

scipy.stats.mstats.msign(x)
Returns the sign of x, or 0 if x is masked.

scipy.stats.mstats.compare_medians_ms

scipy.stats.mstats.compare_medians_ms(group_1, group_2, axis=None)
Compares the medians from two independent groups along the given axis.

The comparison is performed using the McKean-Schrader estimate of the standard error of the medians.

Parameters

- group_1 [array_like] First dataset. Has to be of size >=7.
- group_2 [array_like] Second dataset. Has to be of size >=7.
- axis [int, optional] Axis along which the medians are estimated. If None, the arrays are flattened. If axis is not None, then group_1 and group_2 should have the same shape.

Returns

cmpare_medians_ms [(float, ndarray)] If axis is None, then returns a float, otherwise returns a 1-D ndarray of floats with a length equal to the length of group_1 along axis.
scipy.stats.mstats.median_cihs

**scipy.stats.mstats.median_cihs(data, alpha=0.05, axis=None)**

Computes the alpha-level confidence interval for the median of the data.

Uses the Hettmasperger-Sheather method.

**Parameters**

- **data** [array_like] Input data. Masked values are discarded. The input should be 1D only, or `axis` should be set to None.
- **alpha** [float, optional] Confidence level of the intervals.
- **axis** [int or None, optional] Axis along which to compute the quantiles. If None, use a flattened array.

**Returns**

- `median_cihs` Alpha level confidence interval.

scipy.stats.mstats.mjci

**scipy.stats.mstats.mjci(data, prob=[0.25, 0.5, 0.75], axis=None)**

Returns the Maritz-Jarrett estimators of the standard error of selected experimental quantiles of the data.

**Parameters**

- **data** [ndarray] Data array.
- **prob** [sequence, optional] Sequence of quantiles to compute.
- **axis** [int or None, optional] Axis along which to compute the quantiles. If None, use a flattened array.

scipy.stats.mstats.mquantiles_cimj

**scipy.stats.mstats.mquantiles_cimj(data, prob=[0.25, 0.5, 0.75], alpha=0.05, axis=None)**

Computes the alpha confidence interval for the selected quantiles of the data, with Maritz-Jarrett estimators.

**Parameters**

- **data** [ndarray] Data array.
- **prob** [sequence, optional] Sequence of quantiles to compute.
- **alpha** [float, optional] Confidence level of the intervals.
- **axis** [int or None, optional] Axis along which to compute the quantiles. If None, use a flattened array.

**Returns**

- `ci_lower` [ndarray] The lower boundaries of the confidence interval. Of the same length as `prob`.
- `ci_upper` [ndarray] The upper boundaries of the confidence interval. Of the same length as `prob`. 
scipy.stats.mstats.rsh

scipy.stats.mstats.rsh(data, points=None)
Evaluates Rosenblatt’s shifted histogram estimators for each data point.

Rosenblatt’s estimator is a centered finite-difference approximation to the derivative of the empirical cumulative distribution function.

Parameters

data [sequence] Input data, should be 1-D. Masked values are ignored.
points [sequence or None, optional] Sequence of points where to evaluate Rosenblatt shifted histogram. If None, use the data.

6.27.18 Univariate and multivariate kernel density estimation (scipy.stats.kde)

gaussian_kde(dataset[, bw_method, weights]) Representation of a kernel-density estimate using Gaussian kernels.

scipy.stats.gaussian_kde
class scipy.stats.gaussian_kde(dataset, bw_method=None, weights=None)
Representation of a kernel-density estimate using Gaussian kernels.

Kernel density estimation is a way to estimate the probability density function (PDF) of a random variable in a non-parametric way. gaussian_kde works for both uni-variate and multi-variate data. It includes automatic bandwidth determination. The estimation works best for a unimodal distribution; bimodal or multi-modal distributions tend to be oversmoothed.

Parameters

dataset [array_like] Datapoints to estimate from. In case of univariate data this is a 1-D array, otherwise a 2-D array with shape (# of dims, # of data).
bw_method [str, scalar or callable, optional] The method used to calculate the estimator bandwidth. This can be ‘scott’, ‘silverman’, a scalar constant or a callable. If a scalar, this will be used directly as kde.factor. If a callable, it should take a gaussian_kde instance as only parameter and return a scalar. If None (default), ‘scott’ is used. See Notes for more details.
weights [array_like, optional] weights of datapoints. This must be the same shape as dataset. If None (default), the samples are assumed to be equally weighted.

Notes
Bandwidth selection strongly influences the estimate obtained from the KDE (much more so than the actual shape of the kernel). Bandwidth selection can be done by a “rule of thumb”, by cross-validation, by “plug-in methods” or by other means; see [3], [4] for reviews. gaussian_kde uses a rule of thumb, the default is Scott’s Rule.

Scott’s Rule [1], implemented as scotts_factor, is:

\[ n^{*\star}\left(-\frac{1}{d+4}\right), \]

with \( n \) the number of data points and \( d \) the number of dimensions. In the case of unequally weighted points, scotts_factor becomes:

\[ \text{neff}^{\star\star}\left(-\frac{1}{d+4}\right), \]
with \texttt{neff} the effective number of datapoints. Silverman’s Rule \cite{2}, implemented as \texttt{silverman_factor}, is:

\[
(n * (d + 2) / 4.)**(-1. / (d + 4)).
\]

or in the case of unequally weighted points:

\[
(neff * (d + 2) / 4.)**(-1. / (d + 4)).
\]

Good general descriptions of kernel density estimation can be found in \cite{1} and \cite{2}, the mathematics for this multi-dimensional implementation can be found in \cite{1}.

With a set of weighted samples, the effective number of datapoints \texttt{neff} is defined by:

\[
\text{neff} = \frac{\text{sum(weights)}^2}{\text{sum(weights}^2)}
\]

as detailed in \cite{5}.

References
\cite{1}, \cite{2}, \cite{3}, \cite{4}, \cite{5}

Examples
Generate some random two-dimensional data:

```python
>>> from scipy import stats
>>> def measure(n):
...     """Measurement model, return two coupled measurements."""
...     m1 = np.random.normal(size=n)
...     m2 = np.random.normal(scale=0.5, size=n)
...     return m1+m2, m1-m2

>>> m1, m2 = measure(2000)
>>> xmin = m1.min()
>>> xmax = m1.max()
>>> ymin = m2.min()
>>> ymax = m2.max()

Perform a kernel density estimate on the data:

```python
>>> X, Y = np.mgrid[xmin:xmax:100j, ymin:ymax:100j]
>>> positions = np.vstack([X.ravel(), Y.ravel()])
>>> values = np.vstack([m1, m2])
>>> kernel = stats.gaussian_kde(values)
>>> Z = np.reshape(kernel(positions).T, X.shape)
```  

Plot the results:

```python
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots()
>>> ax.imshow(np.rot90(Z), cmap=plt.cm.gist_earth_r,
...     extent=[xmin, xmax, ymin, ymax])
>>> ax.plot(m1, m2, 'k.', markersize=2)
```
Attributes

dataset [ndarray] The dataset with which `gaussian_kde` was initialized.
d [int] Number of dimensions.
n [int] Number of datapoints.
neff [int] Effective number of datapoints.

New in version 1.2.0.
factor [float] The bandwidth factor, obtained from `kde.covariance_factor`, with which the covariance matrix is multiplied.
covariance [ndarray] The covariance matrix of `dataset`, scaled by the calculated bandwidth (`kde.factor`).
inv_cov [ndarray] The inverse of `covariance`.

Methods

evaluate(points) Evaluate the estimated pdf on a set of points.
__call__(points) Evaluate the estimated pdf on a set of points.
integrate_gaussian(mean, cov) Multiply estimated density by a multivariate Gaussian and integrate over the whole space.
integrate_box_1d(low, high) Computes the integral of a 1D pdf between two bounds.
integrate_box(low_bounds, high_bounds[, maxpts]) Computes the integral of a pdf over a rectangular interval.
integrate_kde(other) Computes the integral of the product of this kernel density estimate with another.
pdf(x) Evaluate the estimated pdf on a provided set of points.
logpdf(x) Evaluate the log of the estimated pdf on a provided set of points.
resample([size]) Randomly sample a dataset from the estimated pdf.
set_bandwidth([bw_method]) Compute the estimator bandwidth with given method.
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<td>Computes the coefficient <code>(kde.factor)</code> that multiplies the data covariance matrix to obtain the kernel covariance matrix.</td>
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**scipy.stats.gaussian_kde.evaluate**

gaussian_kde.evaluate(points)

Evaluate the estimated pdf on a set of points.

**Parameters**

- **points**  
  - Type: $(\text{# of dimensions, } \text{# of points})$-array  
  - Alternatively, a $(\text{# of dimensions,})$-vector can be passed in and treated as a single point.

**Returns**

- **values**  
  - Type: $(\text{# of points,})$-array  
  - The values at each point.

**Raises**

- **ValueError**  
  - If the dimensionality of the input points is different than the dimensionality of the KDE.

**scipy.stats.gaussian_kde.__call__**

gaussian_kde.__call__(points)

Evaluate the estimated pdf on a set of points.

**Parameters**

- **points**  
  - Type: $(\text{# of dimensions, } \text{# of points})$-array  
  - Alternatively, a $(\text{# of dimensions,})$-vector can be passed in and treated as a single point.

**Returns**

- **values**  
  - Type: $(\text{# of points,})$-array  
  - The values at each point.

**Raises**

- **ValueError**  
  - If the dimensionality of the input points is different than the dimensionality of the KDE.

**scipy.stats.gaussian_kde.integrate_gaussian**

gaussian_kde.integrate_gaussian(mean, cov)

Multiply estimated density by a multivariate Gaussian and integrate over the whole space.

**Parameters**

- **mean**  
  - Type: array_like  
  - A 1-D array, specifying the mean of the Gaussian.

- **cov**  
  - Type: array_like  
  - A 2-D array, specifying the covariance matrix of the Gaussian.

**Returns**

- **result**  
  - Type: scalar  
  - The value of the integral.

**Raises**

- **ValueError**  
  - If the mean or covariance of the input Gaussian differs from the KDE’s dimensionality.
**scipy.stats.gaussian_kde.integrate_box_1d**

`gaussian_kde.integrate_box_1d(low, high)`
Computes the integral of a 1D pdf between two bounds.

**Parameters**
- **low** [scalar] Lower bound of integration.
- **high** [scalar] Upper bound of integration.

**Returns**
- **value** [scalar] The result of the integral.

**Raises**
- `ValueError` If the KDE is over more than one dimension.

**scipy.stats.gaussian_kde.integrate_box**

`gaussian_kde.integrate_box(low_bounds, high_bounds, maxpts=None)`
Computes the integral of a pdf over a rectangular interval.

**Parameters**
- **low_bounds** [array_like] A 1-D array containing the lower bounds of integration.
- **high_bounds** [array_like] A 1-D array containing the upper bounds of integration.
- **maxpts** [int, optional] The maximum number of points to use for integration.

**Returns**
- **value** [scalar] The result of the integral.

**scipy.stats.gaussian_kde.integrate_kde**

`gaussian_kde.integrate_kde(other)`
Computes the integral of the product of this kernel density estimate with another.

**Parameters**
- **other** [gaussian_kde instance] The other kde.

**Returns**
- **value** [scalar] The result of the integral.

**Raises**
- `ValueError` If the KDEs have different dimensionality.

**scipy.stats.gaussian_kde.pdf**

`gaussian_kde.pdf(x)`
Evaluate the estimated pdf on a provided set of points.

**Notes**
This is an alias for `gaussian_kde.evaluate`. See the `evaluate` docstring for more details.

**scipy.stats.gaussian_kde.logpdf**

`gaussian_kde.logpdf(x)`
Evaluate the log of the estimated pdf on a provided set of points.
scipy.stats.gaussian_kde.resample

*gaussian_kde.resample(size=None)*

Randomly sample a dataset from the estimated pdf.

**Parameters**

* size [int, optional] The number of samples to draw. If not provided, then the size is the same as the effective number of samples in the underlying dataset.

**Returns**

* resample [(self.d, size) ndarray] The sampled dataset.

scipy.stats.gaussian_kde.set_bandwidth

*gaussian_kde.set_bandwidth(bw_method=None)*

Compute the estimator bandwidth with given method. The new bandwidth calculated after a call to `set_bandwidth` is used for subsequent evaluations of the estimated density.

**Parameters**

* bw_method [str, scalar or callable, optional] The method used to calculate the estimator bandwidth. This can be 'scott', 'silverman', a scalar constant or a callable. If a scalar, this will be used directly as `kde.factor`. If a callable, it should take a `gaussian_kde` instance as only parameter and return a scalar. If None (default), nothing happens; the current `kde.covariance_factor` method is kept.

**Notes**

New in version 0.11.

**Examples**

```python
>>> import scipy.stats as stats
>>> x1 = np.array([-7, -5, 1, 4, 5.])
>>> kde = stats.gaussian_kde(x1)
>>> xs = np.linspace(-10, 10, num=50)
>>> y1 = kde(xs)
>>> kde.set_bandwidth(bw_method='silverman')
>>> y2 = kde(xs)
>>> kde.set_bandwidth(bw_method=kde.factor / 3.)
>>> y3 = kde(xs)
```

```python
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots()
>>> ax.plot(x1, np.ones(x1.shape) / (4. * x1.size), 'bo',
...         label='Data points (rescaled)')
>>> ax.plot(xs, y1, label='Scott (default)')
>>> ax.plot(xs, y2, label='Silverman')
>>> ax.plot(xs, y3, label='Const (1/3 * Silverman)')
>>> ax.legend()
>>> plt.show()
```

scipy.stats.gaussian_kde.covariance_factor

*gaussian_kde.covariance_factor()*

Computes the coefficient (`kde.factor`) that multiplies the data covariance matrix to obtain the kernel covariance matrix. The default is `scotts_factor`. A subclass can overwrite this method to provide a different method, or set it through a call to `kde.set_bandwidth`.

---

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For many more stat related functions install the software R and the interface package rpy.

### 6.28 Low-level callback functions

Some functions in SciPy take as arguments callback functions, which can either be python callables or low-level compiled functions. Using compiled callback functions can improve performance somewhat by avoiding wrapping data in Python objects.

Such low-level functions in Scipy are wrapped in `LowLevelCallable` objects, which can be constructed from function pointers obtained from ctypes, cffi, Cython, or contained in Python `PyCapsule` objects.

```python
LowLevelCallable
```

#### 6.28.1 scipy.LowLevelCallable

**class scipy.LowLevelCallable**

Low-level callback function.

**Parameters**

- **function**  
  [{'PyCapsule, ctypes function pointer, cffi function pointer}] Low-level callback function.

- **user_data**  
  [{'PyCapsule, ctypes void pointer, cffi void pointer}] User data to pass on to the callback function.

- **signature**  
  [str, optional] Signature of the function. If omitted, determined from `function`, if possible.

**Notes**

The argument `function` can be one of:

- PyCapsule, whose name contains the C function signature
- ctypes function pointer
- cffi function pointer

The signature of the low-level callback must match one of those expected by the routine it is passed
methods

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<tr>
<td><code>from_cython</code></td>
<td>Create a low-level callback function from an exported Cython function.</td>
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**signature**

Signature of the function.

**scipy.LowLevelCallable.from_cython**

```python
classmethod LowLevelCallable.from_cython(module, name, user_data=None, signature=None)
```

Create a low-level callback function from an exported Cython function.

**Parameters**

- `module` [module] Cython module where the exported function resides
- `name` [str] Name of the exported function
- `user_data` [{PyCapsule, ctypes void pointer, cffi void pointer}, optional] User data to pass on to the callback function.
- `signature` [str, optional] Signature of the function. If omitted, determined from `function`.

**See also:**

Functions accepting low-level callables:

- `scipy.integrate.quad`, `scipy.ndimage.generic_filter`, `scipy.ndimage.generic_filter1d`, `scipy.ndimage.geometric_transform`

**Usage examples:**

*Extending scipy.ndimage in C, Faster integration using low-level callback functions*
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