## 1 SciPy Tutorial

1.1 Introduction .................................................. 3
1.2 Basic functions .............................................. 5
1.3 Special functions (scipy.special) ......................... 9
1.4 Integration (scipy.integrate) ............................. 10
1.5 Optimization (scipy.optimize) ............................ 17
1.6 Interpolation (scipy.interpolate) ....................... 31
1.7 Fourier Transforms (scipy.fftpack) ...................... 42
1.8 Signal Processing (scipy.signal) ......................... 51
1.9 Linear Algebra (scipy.linalg) ............................ 69
1.10 Sparse Eigenvalue Problems with ARPACK ............. 82
1.11 Compressed Sparse Graph Routines (scipy.sparse.csgraph) .................. 85
1.12 Spatial data structures and algorithms (scipy.spatial) .................. 88
1.13 Statistics (scipy.stats) .................................. 94
1.14 Multidimensional image processing (scipy.ndimage) .............. 113
1.15 File IO (scipy.io) ..................................... 134
1.16 Weave (scipy.weave) .................................. 140

## 2 Contributing to SciPy

2.1 Contributing new code ..................................... 175
2.2 Contributing by helping maintain existing code ............. 176
2.3 Other ways to contribute .................................. 176
2.4 Recommended development setup .......................... 177
2.5 SciPy structure ............................................ 177
2.6 Useful links, FAQ, checklist .............................. 178

## 3 API - importing from Scipy

3.1 Guidelines for importing functions from Scipy ............. 181
3.2 API definition .............................................. 182

## 4 Release Notes

4.1 SciPy 0.16.0 Release Notes .............................. 185
4.2 SciPy 0.15.0 Release Notes .............................. 201
4.3 SciPy 0.14.0 Release Notes .............................. 216
4.4 SciPy 0.13.2 Release Notes .............................. 227
4.5 SciPy 0.13.1 Release Notes .............................. 227
4.6 SciPy 0.13.0 Release Notes .............................. 227
4.7 SciPy 0.12.1 Release Notes .............................. 234
4.8 SciPy 0.12.0 Release Notes .............................. 234
4.9 SciPy 0.11.0 Release Notes .............................. 240
4.10 SciPy 0.10.1 Release Notes ............................ 245
4.11 SciPy 0.10.0 Release Notes .......................................................... 246
4.12 SciPy 0.9.0 Release Notes .......................................................... 250
4.13 SciPy 0.8.0 Release Notes .......................................................... 253
4.14 SciPy 0.7.2 Release Notes .......................................................... 258
4.15 SciPy 0.7.1 Release Notes .......................................................... 258
4.16 SciPy 0.7.0 Release Notes .......................................................... 260

5 Reference .................................................................................. 267
5.1 Clustering package (scipy.cluster) .................................................... 267
5.2 K-means clustering and vector quantization (scipy.cluster.vq) ........... 267
5.3 Hierarchical clustering (scipy.cluster.hierarchy) ............................. 271
5.4 Constants (scipy.constants) .......................................................... 286
5.5 Discrete Fourier transforms (scipy.fftpack) ....................................... 302
5.6 Integration and ODEs (scipy.integrate) .......................................... 318
5.7 Interpolation (scipy.interpolate) ..................................................... 337
5.8 Input and output (scipy.io) ............................................................ 407
5.9 Linear algebra (scipy.linalg) ......................................................... 419
5.10 Low-level BLAS functions .......................................................... 478
5.11 Finding functions ................................................................ 478
5.12 BLAS Level 1 functions ............................................................... 479
5.13 BLAS Level 2 functions ............................................................... 494
5.14 BLAS Level 3 functions ............................................................... 506
5.15 Low-level LAPACK functions ...................................................... 513
5.16 Finding functions ................................................................ 513
5.17 All functions ........................................................................ 513
5.18 BLAS Functions for Cython .......................................................... 592
5.19 LAPACK functions for Cython ...................................................... 596
5.20 Interpolative matrix decomposition (scipy.linalg.interpolative) ....... 634
5.21 Miscellaneous routines (scipy.misc) ............................................. 643
5.22 Multi-dimensional image processing (scipy.ndimage) ...................... 654
5.23 Orthogonal distance regression (scipy.odr) ..................................... 709
5.24 Optimization and root finding (scipy.optimize) ............................... 718
5.25 Routines ............................................................................ 799
5.26 Examples ............................................................................ 800
5.27 Signal processing (scipy.signal) .................................................... 801
5.28 Sparse matrices (scipy.sparse) ...................................................... 949
5.29 Sparse linear algebra (scipy.sparse.linalg) .................................... 1051
5.30 Compressed Sparse Graph Routines (scipy.sparse.csgraph) .......... 1081
5.31 Spatial algorithms and data structures (scipy.spatial) ..................... 1093
5.32 Distance computations (scipy.spatial.distance) ............................. 1128
5.33 Special functions (scipy.special) ................................................. 1143
5.34 Statistical functions (scipy.stats) ................................................. 1200
5.35 Statistical functions for masked arrays (scipy.stats.mstats) ............ 1525
5.36 C/C++ integration (scipy.weave) ............................................... 1552

Bibliography ............................................................................. 1557

Python Module Index .................................................................. 1573

Index ...................................................................................... 1575
SciPy (pronounced “Sigh Pie”) is open-source software for mathematics, science, and engineering.
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 niche’s 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.

1.1.1 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>
<tr>
<td>weave</td>
<td>C/C++ integration</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 sub-packages individually, we will first look at some of these common functions.

### 1.1.2 Finding Documentation

SciPy and NumPy have documentation versions in both HTML and PDF format available at [http://docs.scipy.org/](http://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 than a list of the functions and classes defined in that module is printed. For example:

```python
>>> np.info(optimize.fmin)
    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)
```

Chapter 1. SciPy Tutorial
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
-----
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.

1.2 Basic functions
1.2.1 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
>>> concatenate(([3],[0]*5,arange(-1,1.002,2/9.0)))
```

with the `r_` command one can enter this as

```python
>>> 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
>>> mgrid[0:5,0:5]
array([[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]])

>>> mgrid[0:5:4j,0:5:4j]
array([[ 0. , 0. , 0. , 0. , 0.],
      [ 1.6667, 1.6667, 1.6667, 1.6667, 1.6667],
      [ 3.3333, 3.3333, 3.3333, 3.3333, 3.3333],
      [ 5. , 5., 5., 5., 5. ]],
      [[ 0., 1.6667, 3.3333, 5. ],
      [ 0., 1.6667, 3.3333, 5. ],
      [ 0., 1.6667, 3.3333, 5. ],
      [ 0., 1.6667, 3.3333, 5. ]])
```

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 stacking arrays) are also available.

### 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
>>> p = poly1d([3,4,5])
>>> print p
2
 3 x + 4 x + 5
>>> print p*p
4
 9 x + 24 x + 46 x + 40 x + 25
>>> print p.integ(k=6)
3
 3 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 = 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`. But, what if the function you have written is the result of some optimization or integration routine. Such functions 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:
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 = 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 \( n!/k!(n-k)! \) 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 approxima-
tion to the derivative of order \( \alpha \). 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 approxima-
tion to the \( \alpha \)-th derivative at a given point.

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(scipy.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.

1.3.1 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]
...     return np.cos(t) * np.cos(n*angle) * special.jn(n, distance*kth_zero)

>>> theta = np.r_[0:2*np.pi:50j]
>>> radius = np.r_[0:1:50j]
>>> 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])
```

```python
>>> import matplotlib.pyplot as plt
>>> from mpl_toolkits.mplot3d import Axes3D

>>> fig = plt.figure()
>>> ax = Axes3D(fig)
>>> ax.plot_surface(x, y, z, rstride=1, cstride=1, cmap=cm.jet)
>>> ax.set_xlabel('X')
>>> ax.set_ylabel('Y')
>>> ax.set_zlabel('Z')
>>> plt.show()
```

### 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.
```
Methods for Integrating Functions given fixed samples.

- **quad**: Integrate with given tolerance using Gaussian quadrature.
- **romberg**: Integrate func using Romberg integration.
- **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.

### 1.4.1 General integration (quad)

The function `quad` is provided to integrate a function of one variable between two points. The points can be \(\pm \infty\) to indicate infinite limits. For example, suppose you wish to integrate a Bessel function \(J_v(2.5, x)\) along the interval \([0, 4.5]\).

\[
I = \int_0^{4.5} J_{2.5}(x) \, dx.
\]

This could be computed using `quad`:

```python
>>> result = integrate.quad(lambda x: special.jv(2.5,x), 0, 4.5)
>>> print result
(1.1178179380783249, 7.8663172481899801e-09)

>>> I = sqrt(2/pi)*(18.0/27*sqrt(2)*cos(4.5)-4.0/27*sqrt(2)*sin(4.5)+
                 sqrt(2*pi)*special.fresnel(3/sqrt(pi))[0])
>>> print I
1.117817938088701

>>> print abs(result[0]-I)
1.03761443881e-11
```

The first argument to `quad` is a “callable” Python object (i.e, a function, method, or class instance). Notice the use of a lambda-function in this case as the argument. The next two arguments are the limits of integration. The return value is a tuple, with the first element holding the estimated value of the integral and the second element holding an upper bound on the error. Notice, that in this case, the true value of this integral is

\[
I = \sqrt{\frac{2}{\pi}} \left( \frac{18}{27} \sqrt{2} \cos(4.5) - \frac{4}{27} \sqrt{2} \sin(4.5) + \sqrt{2\pi} \text{Si} \left( \frac{3}{\sqrt{\pi}} \right) \right),
\]

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 + b

>>> a = 2
>>> b = 1
>>> I = quad(integrand, 0, 1, args=(a,b))
>>> I = (2.0, 2.220446049250313e-14)
```

Infinite inputs are also allowed in \texttt{quad} by using \texttt{\pm \infty} as one of the arguments. For example, suppose that a numerical value for the exponential integral:

\[ E_n(x) = \int_{\infty}^{1} e^{-xt} \, \frac{t^n}{t^n} \, dt. \]

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 \texttt{quad}:

```python
>>> from scipy.integrate import quad
>>> def integrand(t, n, x):
...     return exp(-x*t) / t**n

>>> def expint(n, x):
...     return quad(integrand, 1, Inf, args=(n, x))[0]

>>> vec_expint = vectorize(expint)

>>> vec_expint(3, arange(1.0, 4.0, 0.5))
array([ 0.1097, 0.0567, 0.0301, 0.0163, 0.0089, 0.0049])

>>> special.expn(3, 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 \texttt{quad} argument (though the error bound may underestimate the error due to possible numerical error in the integrand from the use of \texttt{quad}). The integral in this case is

\[ I_n = \int_{0}^{\infty} \int_{1}^{\infty} e^{-xt} \, \frac{t^n}{t^n} \, dt \, dx = \frac{1}{n}. \]

```python
>>> result = quad(lambda x: expint(3, x), 0, inf)
>>> print result
(0.3333333333333333, 2.8548934485373678e-09)

>>> I3 = 1.0/3.0
>>> print I3
0.333333333333

>>> print I3 - result[0]
8.77306560731e-11
```

This last example shows that multiple integration can be handled using repeated calls to \texttt{quad}.
1.4.2 General multiple integration (dblquad, tplquad, nquad)

The mechanics for double and triple integration have been wrapped up into the functions `dblquad` and `tplquad`. These functions take the function to integrate and four, or six arguments, respectively. The limits of all inner integrals need to be defined as functions.

An example of using double integration to compute several values of $I_n$ is shown below:

```python
>>> from scipy.integrate import quad, dblquad
>>> def I(n):
...   return dblquad(lambda t, x: exp(-x*t)/t**n, 0, Inf,
...   lambda x: 1, lambda x: Inf)

>>> print I(4)
(0.25000000000435768, 1.0518245707751597e-09)
>>> print I(3)
(0.33333333325010883, 2.8604069919261191e-09)
>>> print I(2)
(0.49999999999857514, 1.8855523253868967e-09)
```

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

$$I_n = \int_0^\infty \int_1^\infty \frac{e^{-xt}}{t^n} \, dt \, dx = \frac{1}{n}$$

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]]))
(0.20000000000002294, 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

$$I = \int_{y=0}^{1/2} \int_{x=0}^{1-2y} xy \, dx \, dy = \frac{1}{96}.$$
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])

which is the same result as before.

1.4.3 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).

1.4.4 Romberg Integration

Romberg’s method [WPR] is another method for numerically evaluating an integral. See the help function for romberg for further details.

1.4.5 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.

from scipy.integrate import simps
import numpy as np

def f(x):
    return x**2

def f2(x):
    return x**3

x = np.array([1,3,4])
y1 = f1(x)
I1 = integrate.simps(y1, x)
print(I1)
21.0
This corresponds exactly to
\[ \int_{1}^{4} x^2 \, dx = 21, \]
whereas integrating the second function

```python
>>> y2 = f2(x)
>>> I2 = integrate.simps(y2, x)
>>> print(I2)
61.5
```
does not correspond to
\[ \int_{1}^{4} x^3 \, dx = 63.75 \]
because the order of the polynomial in f2 is larger than two.

### 1.4.6 Faster integration using Ctypes

A user desiring reduced integration times may pass a C function pointer through `ctypes` 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. This can also be achieved using a library like Cython or F2Py that compiles Python. Additionally we have a speedup provided by the removal of function calls between C and Python in `quad` - this cannot be achieved through Cython or F2Py. This method will provide a speed increase of ~2x for trivial functions such as sine but can produce a much more noticeable increase (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.

`ctypes` integration can be done in a few simple steps:

1.) Write an integrand function in C with the function signature `double f(int n, double args[n])`, where `args` is an array containing the arguments of the function `f`.

```c
//testlib.c
double f(int n, double args[n]) {
    return args[0] - args[1] * args[2]; //corresponds to x0 - x1 * x2
}
```

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 -o testlib.so -fPIC 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 ctypes
>>> from scipy import integrate

>>> lib = ctypes.CDLL('/**/testlib.so') # Use absolute path to testlib
>>> func = lib.f # Assign specific function to name func (for simplicity)
>>> func.restype = ctypes.c_double
>>> func.argtypes = (ctypes.c_int, ctypes.c_double)
```
Note that the argtypes will always be (ctypes.c_int, ctypes.c_double) regardless of the number of parameters, and restype will always be ctypes.c_double.

4.) Now integrate the library function as normally, here using nquad:

```python
>>> integrate.nquad(func, [[0,10],[-10,0],[-1,1]])
(1000.0, 1.1102230246251565e-11)
```

And 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.

1.4.7 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 \( w(0) = \frac{1}{\sqrt{3} \Gamma\left(\frac{2}{3}\right)} \) and \( \frac{dw}{dz}|_{z=0} = -\frac{1}{\sqrt{3} \Gamma\left(\frac{1}{3}\right)} \). It is known that the solution to this differential equation with these boundary conditions is the Airy function

\[
w = Ai(z),
\]

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, \( y0 \), 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, \( f(y,t) \).
>>> from scipy.integrate import odeint
>>> from scipy.special import gamma, airy

>>> y1_0 = 1.0 / 3**(2.0/3.0) / gamma(2.0/3.0)
>>> y0_0 = -1.0 / 3**(1.0/3.0) / gamma(1.0/3.0)
>>> y0 = [y0_0, y1_0]

>>> def func(y, t):
...    return [t*y[1],y[0]]

>>> def gradient(y, t):
...    return [[0,t], [1,0]]

>>> x = arange(0, 4.0, 0.01)
>>> t = x

>>> ychk = airy(x)[0]
>>> y = odeint(func, y0, t)
>>> y2 = odeint(func, y0, t, Dfun=gradient)

>>> print ychk[:36:6]
[ 0.355028 0.339511 0.324068 0.308763 0.293658 0.278806]

>>> print y[:36:6,1]
[ 0.355028 0.339511 0.324067 0.308763 0.293658 0.278806]

References

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 (leastsq) and curve fitting (curve_fit) algorithms
4. Scalar univariate functions minimizers (minimize_scalar) and root finders (newton)
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.

1.5.1 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: \[ f(x) = \sum_{i=1}^{N-1} 100 (x_i - x_{i+1}^2)^2 + (1 - x_{i-1})^2. \] 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):
...     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:

\[
\frac{\partial f}{\partial x_j} = \sum_{i=1}^{N} 200 (x_i - x_{i-1}^2) (\delta_{i,j} - 2 x_{i-1} \delta_{i-1,j}) - 2 (1 - x_{i-1}) \delta_{i-1,j},
\]

\[
= 200 (x_j - x_{j-1}^2) - 400 x_j (x_{j+1} - x_j^2) - 2 (1 - x_j).
\]

This expression is valid for the interior derivatives. Special cases are

\[
\frac{\partial f}{\partial x_0} = -400 x_0 (x_1 - x_0^2) - 2 (1 - x_0),
\]

\[
\frac{\partial f}{\partial x_{N-1}} = 200 (x_{N-1} - x_{N-2}^2).
\]

A Python function which computes this gradient is constructed by the code-segment:
>>> 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-xm)
...     der[0] = -400*x[0]*(x[1]-x[0]**2) - 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
>>> print(res.x)
[ 1.  1.  1.  1.  1.]
```

**Newton-Conjugate-Gradient algorithm (method='Newton-CG')**

The method which requires the fewest function calls and is therefore often the fastest method to minimize functions of many variables uses the Newton-Conjugate Gradient algorithm. This method is a modified Newton's method and uses a conjugate gradient algorithm to (approximately) invert the local Hessian. Newton's method is based on fitting the function locally to a quadratic form: $f(x) \approx f(x_0) + \nabla f(x_0) \cdot (x - x_0) + \frac{1}{2} (x - x_0)^T H(x_0) (x - x_0)$. $whereH(x_0)$ 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 `CG` method, a function which computes the Hessian must be provided. The Hessian matrix itself does not need to be constructed, only

**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

\[
\frac{\partial^2 f}{\partial x_0^2} = 1200x_0^2 - 400x_1 + 2,
\]

\[
\frac{\partial^2 f}{\partial x_0 \partial x_1} = \frac{\partial^2 f}{\partial x_1 \partial x_0} = -400x_0,
\]

\[
\frac{\partial^2 f}{\partial x_{N-1} \partial x_{N-2}} = \frac{\partial^2 f}{\partial x_{N-2} \partial x_{N-1}} = -400x_{N-2},
\]

\[
\frac{\partial^2 f}{\partial x_{N-1}^2} = 200.
\]
For example, the Hessian when $N = 5$ is

\[
\begin{bmatrix}
1200x_0^2 - 400x_1 + 2 & -400x_0 & 0 & 0 & 0 \\
-400x_0 & 202 + 1200x_1^2 - 400x_2 & -400x_1 & 0 & 0 \\
0 & -400x_1 & 202 + 1200x_2^2 - 400x_3 & -400x_2 & 0 \\
0 & 0 & 202 + 1200x_3^2 - 400x_4 & 202 + 1200x_4^2 & -400x_3 \\
0 & 0 & 0 & 200 & -400x_4
\end{bmatrix}
\]

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 takes 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:

\[
H(x)p = \begin{pmatrix}
1200x_0^2 - 400x_1 + 2 & -400x_0 & 0 & 0 & 0 \\
-400x_0 & 202 + 1200x_1^2 - 400x_2 & -400x_1 & 0 & 0 \\
0 & -400x_1 & 202 + 1200x_2^2 - 400x_3 & -400x_2 & 0 \\
0 & 0 & 202 + 1200x_3^2 - 400x_4 & 202 + 1200x_4^2 & -400x_3 \\
0 & 0 & 0 & 200 & -400x_4
\end{pmatrix} \begin{pmatrix}
p_0 \\
p_1 \\
p_2 \\
p_3 \\
p_4
\end{pmatrix}
\]
SciPy Reference Guide, Release 0.16.0

...
options={'xtol': 1e-8, 'disp': True})
Optimization terminated successfully.
Current function value: 0.000000
Iterations: 20
Function evaluations: 23
Gradient evaluations: 20
Hessian evaluations: 44
>>> print(res.x)
[ 1. 1. 1. 1. 1.]

1.5.2 Constrained minimization of multivariate scalar functions (minimize)
The minimize function also provides an interface to several constrained minimization algorithm. As an example,
the Sequential Least SQuares Programming optimization algorithm (SLSQP) will be considered here. This algorithm
allows to deal with constrained minimization problems of the form:
min 𝐹 (𝑥)
subject to

𝐶𝑗 (𝑋) = 0,

𝑗 = 1, ..., MEQ

𝐶𝑗 (𝑥) ≥ 0,

𝑗 = MEQ + 1, ..., 𝑀

𝑋𝐿 ≤ 𝑥 ≤ 𝑋𝑈,

𝐼 = 1, ..., 𝑁.

As an example, let us consider the problem of maximizing the function: f(x, y) = 2 x y + 2 x - x2 −
2𝑦 2 𝑠𝑢𝑏𝑗𝑒𝑐𝑡𝑡𝑜𝑎𝑛𝑒𝑞𝑢𝑎𝑙𝑖𝑡𝑦𝑎𝑛𝑑𝑎𝑛𝑖𝑛𝑒𝑞𝑢𝑎𝑙𝑖𝑡𝑦𝑐𝑜𝑛𝑠𝑡𝑟𝑎𝑖𝑛𝑡𝑠𝑑𝑒𝑓 𝑖𝑛𝑒𝑑𝑎𝑠 :𝑡𝑜
𝑥3 − 𝑦 = 0
𝑦 − 1 ≥ 0The objective function and its derivative are defined as follows.
>>> def func(x, sign=1.0):
...
""" Objective function """
...
return sign*(2*x[0]*x[1] + 2*x[0] - x[0]**2 - 2*x[1]**2)
>>> def func_deriv(x, sign=1.0):
...
""" Derivative of objective function """
...
dfdx0 = sign*(-2*x[0] + 2*x[1] + 2)
...
dfdx1 = sign*(2*x[0] - 4*x[1])
...
return np.array([ dfdx0, dfdx1 ])

Note that since minimize only minimizes functions, the sign parameter is introduced to multiply the objective
function (and its derivative) by -1 in order to perform a maximization.
Then constraints are defined as a sequence of dictionaries, with keys type, fun and jac.
>>> cons = ({'type': 'eq',
...
'fun' : lambda x: np.array([x[0]**3 - x[1]]),
...
'jac' : lambda x: np.array([3.0*(x[0]**2.0), -1.0])},
...
{'type': 'ineq',
...
'fun' : lambda x: np.array([x[1] - 1]),
...
'jac' : lambda x: np.array([0.0, 1.0])})

Now an unconstrained optimization can be performed as:
>>> res = minimize(func, [-1.0,1.0], args=(-1.0,), jac=func_deriv,
...
method='SLSQP', options={'disp': True})
Optimization terminated successfully.
(Exit mode 0)
Current function value: -2.0
Iterations: 4
Function evaluations: 5
Gradient evaluations: 4

1.5. Optimization (scipy.optimize)

21


>>> print(res.x)
[ 2.  1.]

and a constrained optimization as:

```python
>>> res = minimize(func, [-1.0,1.0], args=(-1.0,), jac=func_deriv,
...                     constraints=cons, method='SLSQP', options={'disp': True})
Optimization terminated successfully.  (Exit mode 0)
Current function value: -1.00000018311
Iterations: 9
Function evaluations: 14
Gradient evaluations: 9
```

>>> print(res.x)
[ 1.00000009 1. ]

1.5.3 Least-square fitting (leastsq)

All of the previously-explained minimization procedures can be used to solve a least-squares problem provided the appropriate objective function is constructed. For example, suppose it is desired to fit a set of data \(\{x_i, y_i\}\) to a known model, \(y = f(x, p)\) where \(p\) is a vector of parameters for the model that need to be found. A common method for determining which parameter vector gives the best fit to the data is to minimize the sum of squares of the residuals. The residual is usually defined for each observed data-point as \(e_i(p, y_i, x_i) = \|y_i - f(x_i, p)\|\) An objective function to pass to any of the previous minimization algorithms to obtain a least squares fit is:

\[
J(p) = \sum_{i=0}^{N-1} e_i^2(p) 
\]

The leastsq algorithm performs this squaring and summing of the residuals automatically and returns the value of \(p\) which minimizes \(J(p) = e^T e\) directly. The user is also encouraged to provide the Jacobian matrix of the function (with derivatives down the columns or across the rows). If the Jacobian is not provided, it is estimated.

An example should clarify the usage. Suppose it is believed some measured data follow a sinusoidal pattern \(y_i = A \sin(2\pi k x_i + \theta)\) where the parameters \(A, k, \) and \(\theta\) are unknown. The residual vector is \(e_i = |y_i - A \sin(2\pi k x_i + \theta)|\). By defining a function to compute the residuals and (selecting an appropriate starting position), the least squares fit routine can be used to find the best fit parameters \(\hat{A}, \hat{k}, \hat{\theta}\). This is shown in the following example:

```python
>>> from numpy import arange, sin, pi, random, array
>>> x = arange(0, 6e-2, 6e-2 / 30)
>>> A, k, theta = 10, 1.0 / 3e-2, pi / 6
>>> y_true = A * sin(2 * pi * k * x + theta)
>>> y_meas = y_true + 2*random.randn(len(x))

>>> def residuals(p, y, x):
...     A, k, theta = p
...     err = y - A * sin(2 * pi * k * x + theta)
...     return err

>>> def peval(x, p):
...     return p[0] * sin(2 * pi * p[1] * x + p[2])

>>> p0 = [8, 1 / 2.3e-2, pi / 3]
>>> print(array(p0))
[ 8.  43.4783  1.0472]
```

```python
>>> from scipy.optimize import leastsq
>>> plsq = leastsq(residuals, p0, args=(y_meas, x))
```

```python
>>> print(plsq[0])
[ 10.9437  33.3605  0.5834]
```
1.5.4 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 **bs** 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 bs 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, bs=(4, 7), method='bounded')
>>> print(res.x)
5.33144184241
```

1.5.5 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 __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
>>> def custmin(fun, x0, args=(), maxfev=None, stepsize=0.1, ...
...     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))
```

```python
>>> x0 = [1.35, 0.9, 0.8, 1.1, 1.2]
>>> res = minimize(rosen, x0, method=custmin, options=dict(stepsize=0.05))
```
This will work just as well in case of univariate optimization:

```python
>>> 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:
...                 bestx = testy
...                 besty = 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))
```  

```python
res = minimize_scalar(f, bracket=(-3.5, 0), method=custmin,
... options=dict(stepsize = 0.05))
```  

```python
res.x
```

-2.0

### 1.5.6 Root finding

#### Scalar functions

If one has a single-variable equation, there are four different root finding algorithms that can be tried. Each of these algorithms requires 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.

#### 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 achieved 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, \( P_{n,m} \approx P(nh, mh) \), with a small grid spacing \( h \). The derivatives and integrals can then be approximated; for instance \( \partial_x^2 P(x, y) \approx (P(x + h, y) - 2P(x, y) + P(x - h, y))/h^2 \). The problem is then equivalent to finding the root of some function residual of \( P \), 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)
    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[:,-1] = (P_top - 2*P[:,-1] + P[:,-2])/hy/hy

    return d2x + d2y + 5*cosh(P).mean()**2

# 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()
```

1.5. Optimization (scipy.optimize)
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 \( J s = y \) one solves \( M J s = M y \): since matrix \( M J \) 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 \( \text{options[}'jac_options'[']inner_M'] \). 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, \( \left[ \frac{\partial^2}{\partial x^2} + \frac{\partial^2}{\partial y^2} \right] P \), 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

\[
\frac{\partial^2}{\partial x^2} \approx \frac{1}{h_x^2} \begin{pmatrix} -2 & 1 & 0 & 0 & \cdots \\ 1 & -2 & 1 & 0 & \cdots \\ 0 & 1 & -2 & 1 & \cdots \\ \cdots \end{pmatrix} = h_x^{-2} L
\]

so that the whole 2-D operator is represented by

\[
J_1 = \frac{\partial^2}{\partial x^2} + \frac{\partial^2}{\partial y^2} \approx h_x^{-2} L \otimes I + h_y^{-2} I \otimes L
\]

The matrix \( J_2 \) of the Jacobian corresponding to the integral is more difficult to calculate, and since all of it 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.spilu (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 \( M = J_1^{-1} \).
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
    # 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

    count = [0]
\[
d2y[:, -1] = (P_{\text{top}} - 2P[:, -1] + P[:, -2]) / hy/\text{hy}
\]

```python
return d2x + d2y + 5*cosh(P).mean()**2
```

```python
# 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
```

```python
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()
```

```python
if __name__ == '__main__':
    main()
```

Resulting run, first without preconditioning:

<table>
<thead>
<tr>
<th>Iteration</th>
<th>Residual</th>
<th>Step</th>
<th>Tol</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>803.614</td>
<td>1</td>
<td>0.000257947</td>
</tr>
<tr>
<td>1</td>
<td>345.912</td>
<td>1</td>
<td>0.166755</td>
</tr>
<tr>
<td>2</td>
<td>139.159</td>
<td>1</td>
<td>0.145657</td>
</tr>
<tr>
<td>3</td>
<td>27.3682</td>
<td>1</td>
<td>0.0348109</td>
</tr>
<tr>
<td>4</td>
<td>1.03303</td>
<td>1</td>
<td>0.00128227</td>
</tr>
<tr>
<td>5</td>
<td>0.0406634</td>
<td>1</td>
<td>0.00139451</td>
</tr>
<tr>
<td>6</td>
<td>0.0034434</td>
<td>1</td>
<td>0.000563597</td>
</tr>
<tr>
<td>7</td>
<td>0.00015367</td>
<td>1</td>
<td>0.00179246</td>
</tr>
<tr>
<td>8</td>
<td>6.7424e-06</td>
<td>1</td>
<td>0.00173256</td>
</tr>
</tbody>
</table>

Residual 3.57078908664e-07
Evaluations 317

and then with preconditioning:

<table>
<thead>
<tr>
<th>Iteration</th>
<th>Residual</th>
<th>Step</th>
<th>Tol</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>136.993</td>
<td>1</td>
<td>7.49599e-06</td>
</tr>
<tr>
<td>1</td>
<td>4.80983</td>
<td>1</td>
<td>0.00110945</td>
</tr>
<tr>
<td>2</td>
<td>0.195942</td>
<td>1</td>
<td>0.00149362</td>
</tr>
<tr>
<td>3</td>
<td>0.000563597</td>
<td>1</td>
<td>7.44604e-06</td>
</tr>
<tr>
<td>4</td>
<td>1.00698e-09</td>
<td>1</td>
<td>2.87308e-12</td>
</tr>
</tbody>
</table>

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:

1.6 Interpolation (scipy.interpolate)

There are several general interpolation facilities available in SciPy, for data in 1, 2, and higher dimensions:

- A class representing an interpolant (interp1d) in 1-D, offering several interpolation methods.
- Convenience function griddata offering a simple interface to interpolation in N dimensions (N = 1, 2, 3, 4, ...). 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.

1.6.1 1-D interpolation (interp1d)

The interp1d class in 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 be 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')
```
>>> 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()

1.6.2 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 $(x[i], y[i])$ 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]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')
```
```python
>>> 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()
```

![Image of interpolated plots](image-url)

1.6. Interpolation (`scipy.interpolate`)
1.6.3 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 `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 ($splev$) and its derivatives ($splev$, $splde$) at any point and the integral of the spline between any two points ($splint$). In addition, for cubic splines ($k = 3$) with 8 or more knots, the roots of the spline can be estimated ($sproot$). 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

>>> 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)

>>> plt.figure()
>>> plt.plot(x, y, 'x', xnew, ynew, xnew, 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

>>> 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

>>> def integ(x, tck, constant=-1):
...     x = np.atleast_1d(x)
...     out = np.zeros(x.shape, dtype=x.dtype)
...     for n in xrange(len(out)):
...         out[n] = interpolate.splint(0, x[n], tck)
...     out += constant
```python
>>> return out
>>> 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

```python
>>> print(interpolate.sproot(tck))
[ 0.  3.1416]
```

Roots of 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)
>>> plt.figure()
>>> plt.plot(x, y, 'x', out[0], out[1], np.sin(2*np.pi*unew), np.cos(2*np.pi*unew), x, y, 'b')
>>> plt.legend(['Linear', 'Cubic Spline', 'True'])
>>> plt.axis([-1.05, 1.05, -1.05, 1.05])
>>> plt.title('Spline of parametrically-defined curve')
>>> plt.show()
```
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.

>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> from scipy import interpolate

InterpolatedUnivariateSpline

>>> 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])

1.6. Interpolation (scipy.interpolate)
>>> plt.title('InterpolatedUnivariateSpline')
>>> plt.show()

InterpolatedUnivariateSpline

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 it’s 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))

```python
>>> plt.figure()
>>> plt.pcolor(x, y, z)
>>> plt.colorbar()
>>> plt.title("Sparsely sampled function.")
>>> plt.show()
```
Interpolate function over new 70x70 grid

```python
>>> xnew, ynew = np.mgrid[-1:1:70j, -1:1:70j]
>>> tck = interpolate.bisplrep(x, y, z, s=0)
>>> znew = interpolate.bisplev(xnew[:,0], ynew[0,:], tck)
>>> plt.figure()
>>> plt.pcolor(xnew, ynew, znew)
>>> plt.colorbar()
>>> plt.title("Interpolated 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.

1.6.4 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.

>>> 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)
>>> 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
>>> n = plt.normalize(-2., 2.)
>>> 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, 2)
>>> plt.ylim(-2, 2)
>>> plt.colorbar()

1.7 Fourier Transforms (scipy.fftpack)
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. [NR] provide an accessible introduction to Fourier analysis and its applications.

### 1.7.1 Fast Fourier transforms

#### One dimensional discrete Fourier transforms

The FFT $y[k]$ of length $N$ of the length-$N$ sequence $x[n]$ is defined as

$$ y[k] = \sum_{n=0}^{N-1} e^{-2\pi j \frac{k}{N}} x[n], $$

and the inverse transform is defined as follows

$$ x[n] = \frac{1}{N} \sum_{n=0}^{N-1} e^{2\pi j \frac{n}{N}} y[k]. $$

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
[ 4.50000000+0.0j  2.08155948-1.65109876j -1.83155948+1.60822041j
 -1.83155948-1.60822041j  2.08155948+1.65109876j]
>>> yinv = ifft(y)
>>> yinv
[ 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 samplepoints
>>> 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
>>> plt.plot(xf, 2.0/N * np.abs(yf[0:N/2]))
>>> plt.grid()
>>> plt.show()
```

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[1:N//2]), '-b')
>>> plt.semilogy(xf[1:N//2], 2.0/N * np.abs(ywf[1: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.

```python
>>> from scipy.fftpack import fftfreq
>>> freq = fftfreq(np.arange(8), 0.125)
[ 0.  1.  2.  3. -4. -3. -2. -1.]
```

In a similar spirit, the function `fftfshift` allows swapping the lower and upper halves of a vector, so that it becomes suitable for display.

```python
>>> from scipy.fftpack import fftfreq
>>> x = np.arange(8)
>>> sf.fftshift(x)
[4 5 6 7 0 1 2 3]
```

The example below plots the FFT of two complex exponentials; note the asymmetric spectrum.
```python
>>> from scipy.fftpack import fft, fftfreq, fftshift
>>> # number of signal points
>>> N = 400
>>> # sample spacing
>>> T = 1.0 / 800.0
>>> x = np.linspace(0.0, N*T, N)
>>> y = np.exp(50.0 * 1.j * 2.0*np.pi*x) + 0.5*np.exp(-80.0 * 1.j * 2.0*np.pi*x)
>>> yf = fft(y)
>>> xf = fftfreq(N, T)
>>> xf = fftshift(xf)
>>> yplot = fftshift(yf)
>>> import matplotlib.pyplot as plt

>>> plt.plot(xf, 1.0/N * np.abs(yplot))
>>> plt.grid()
>>> plt.show()
```

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: $[y[0], \text{Re}(y[1]), \text{Im}(y[1]), ..., \text{Re}(y[N/2])]$; in case $N$ being odd $[y[0], \text{Re}(y[1]), \text{Im}(y[1]), ..., \text{Re}(y[N/2]), \text{Im}(y[N/2])]$.

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)
[5.50+0.j  2.25-0.4330127j -2.75-1.29903811j  1.50+0.j
 -2.75+1.29903811j  2.25+0.4330127j]
>>> yr = rfft(x)
[5.5  2.25 -0.4330127 -2.75 -1.2990381 1.5 ]
>>> irfft(yr)
[1.  2.  1. -1.  1.5  1. ]
>>> x = np.array([1.0, 2.0, 1.0, -1.0, 1.5])
>>> fft(x)
[4.50000000+0.j  2.08155948-1.65109876j -1.83155948+1.60822041j
 -1.83155948-1.60822041j  2.08155948+1.65109876j]
>>> yr = rfft(x)
[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
>>> x, ((ax1, ax2, ax3), (ax4, ax5, ax6)) = plt.subplots(2, 3, sharex='col', sharey='row')
>>> 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.binary)
>>> 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.binary)
>>> 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.binary)
>>> plt.show()
```

**FFT convolution**

`scipy.fftpack.convolve` performs a convolution of two one-dimensional arrays in frequency domain.
1.7.2 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'`:

$$y[k] = \frac{x_0}{\sqrt{N}} + \frac{2}{\sqrt{N}} \sum_{n=1}^{N-1} x[n] \cos \left( \frac{\pi n(2k + 1)}{2N} \right), \quad 0 \leq k < N.$$
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')
[1.0, 2.0, 1.0, -1.0, 1.5]
>>> # scaling factor $2*N = 10$
>>> idct(dct(x, type=2), type=2)
[10.  20. -10.  15.]
>>> # no scaling factor
>>> idct(dct(x, type=2, norm='ortho'), type=2, norm='ortho')
[1.  2.  1. -1.  1.5]
>>> # scaling factor $2*N = 10$
>>> idct(dct(x, type=3), type=3)
[10.  20. -10.  15.]
>>> # no scaling factor
>>> idct(dct(x, type=3, norm='ortho'), type=3, norm='ortho')
[1.  2.  1. -1.  1.5]
>>> # scaling factor $2*(N-1) = 8$
>>> idct(dct(x, type=1), type=1)
[8.  16.  8. -8.  12.]
```

Example

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.

```python
>>> 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)
0.0010901402257
>>> 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)
0.0718818065008
>>> plt.plot(t, yr, 'g+')
```
1.7.3 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 off 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 (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 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 (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 (\( \text{norm}='\text{None}' \)):

\[
y[k] = (-1)^k x[N - 1] + 2 \sum_{n=0}^{N-2} x[n] \sin \left( \frac{\pi(n + 1)(k + 1/2)}{N} \right), \quad 0 \leq k < N.
\]

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)
[ 10. 20. 10. -10. 15.]

>>> # no scaling factor
>>> idst(dst(x, type=2, norm='ortho'), type=2, norm='ortho')
[ 1. 2. 1. -1. 1.5]

>>> # scaling factor \( 2*N = 10 \)
>>> idst(dst(x, type=3), type=3)
[ 10. 20. 10. -10. 15.]

>>> # no scaling factor
>>> idst(dst(x, type=3, norm='ortho'), type=3, norm='ortho')
[ 1. 2. 1. -1. 1.5]

>>> # scaling factor \( 2*(N+1) = 8 \)
>>> idst(dst(x, type=1), type=1)
[ 8. 16. 8. -8. 12.]
```

1.7.4 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*).

1.7.5 References

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.

1.8.1 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
The 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

\[ y''(x) = \frac{1}{\Delta x^2} \sum_j c_j \beta^{o''} \left( \frac{x}{\Delta x} - j \right). \]

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 subpackage 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 bspline basis function, \( \beta^o(x) \) for arbitrary order and \( x \). For large \( o \), the B-spline 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 (`gauss_spline`). The following code and figure uses spline-filtering to compute an edge-image (the second-derivative of a smoothed spline) of Lena's face which is an array returned by the command `misc.lena`. The command `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 `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.lena().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')
```
1.8.2 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 $512 \times 512$ image with this method would require multiplication of a $512^2 \times 512^2$ matrix with a $512^2$ vector. Just trying to store the $512^2 \times 512^2$ 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 $y[n] = 0$ for all $n > K + 1$ and $M + 1$ be that value for which $x[n] = 0$ for all $n > M + 1$, 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

\[
\begin{align*}
y[0] &= x[0] h[0] \\
&\quad \vdots \\
&\quad \vdots \\
&\quad \vdots \\
y[K+M] &= x[K] h[M].
\end{align*}
\]

Thus, the full discrete convolution of two finite sequences of lengths $K+1$ and $M+1$ respectively results in a finite sequence of length $K+M+1 = (K+1) + (M+1) - 1$.

One dimensional convolution is implemented in SciPy with the function `convolve`. This function takes as inputs the signals $x$, $h$, and an optional flag and returns the signal $y$. The optional flag 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 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)
[ 0.  1.  2.  3.  0.  0.  0.]
>>> signal.convolve(x, h, 'same')
[ 2.  3.  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., 1., 0., 0.], [0., 0., 1., 0.]])
>>> signal.convolve(x, h)
[[ 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.]
 [ 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.lena()
>>> 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()
```
Using `convolve` in the above example would take quite long to run. 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 frequency domain provided by the function `fftconvolve`.

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 `sepfir2d`. As an example we consider a Gaussian filter `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.lena()
>>> w = signal.gaussian(50, 5.0)
>>> image_new = signal.sepfir2d(image, w, w)

>>> plt.figure()
>>> plt.imshow(image)
>>> plt.gray()
>>> plt.title('Original image')
>>> plt.show()

Original image

>>> plt.figure()
>>> plt.imshow(image_new)
>>> plt.gray()
>>> plt.title('Filtered image')
>>> plt.show()
```

```python
>>> plt.figure()
>>> plt.imshow(image_new)
>>> plt.gray()
>>> plt.title('Filtered image')
>>> plt.show()
```
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 `lfilteric` 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 `lfilteric`.

```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)
[ 0.5 0.41666667 0.13888889 0.0462963 ]
>>> zi = signal.lfiltic(b, a, y=[2.])
>>> signal.lfilter(b, a, x, zi=zi)
[ 1.16666667, 0.63888889, 0.21296296, 0.07098765]
```

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 obtained with the scipy function `tf2zpk`; the inverse is provided by `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)
[-0.5] [ 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 `freqz` allows calculation of the frequency response of a system described by the coefficients $a_k$ and $b_k$. See the help of the `freqz` function of a comprehensive example.
Filter Design

Time-discrete filters can be classified into finite response (FIR) filters and infinite response (IIR) filters. FIR filters provide a linear phase response, whereas IIR filters do not exhibit this behaviour. Scipy provides functions for designing both types of filters.

**FIR Filter**

The function `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 `firwin` uses per default a normalized frequency defined such that the value 1 corresponds to the Nyquist frequency, whereas the function `freqz` is defined such that the value $\pi$ corresponds to the Nyquist frequency.

The function `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 `firwin2` and `freqz` (as explained above).

**IIR Filter**

Scipy provides two functions to directly design IIR `iirdesign` and `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. `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]')
```

---

Chapter 1. SciPy Tutorial
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 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 \( \sigma^2_x \) 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()
```
```python
>>> 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()
```

### 1.8.3 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

>>> 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, P_per_spec = signal.periodogram(x, fs, \'flattop\', scaling=\'spectrum\')
```
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 spectogram.

```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, 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

$$P_n(f) \left\{ \frac{\left( \sum_{j}^{N_t} X_j \cos \omega(t_j - \tau) \right)^2}{\sum_{j}^{N_t} \cos^2 \omega(t_j - \tau)} + \frac{\left( \sum_{j}^{N_t} X_j \sin \omega(t_j - \tau) \right)^2}{\sum_{j}^{N_t} \sin^2 \omega(t_j - \tau)} \right\}.$$ 

Here, $\omega \equiv 2\pi f$ is the angular frequency. The frequency dependent time offset $\tau$ is given by

$$\tan 2\omega \tau = \frac{\sum_{j}^{N_t} \sin 2\omega t_j}{\sum_{j}^{N_t} \cos 2\omega t_j}.$$ 

The `lombscargle` function calculates the periodogram using a slightly modified algorithm due to Townsend 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

$$\tan 2\omega \tau = \frac{2CS}{CC - SS}.$$ 

---


1.8. Signal Processing (scipy.signal)
Here,

\[ c_\tau = \cos \omega \tau, \quad s_\tau = \sin \omega \tau \]

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 \( N_f(2N_t + 3) \) trigonometric function evaluations giving a factor of \( \sim 2 \) speed increase over the straight-forward implementation.

### 1.8.4 Detrend

Scipy provides the function `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:

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 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.

1.9.1 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, 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]])
```
\[
\begin{bmatrix}
3 & 4
\end{bmatrix}
\]

```python
>>> A.I
matrix([[[-2., 1.],
          [ 1.5, -0.5]])
```

```python
>>> b = np.mat('[5 6]')
>>> b
matrix([[5, 6]])
```

```python
>>> b.T
matrix([[5],
         [6]])
```

```python
>>> 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]])
```

```python
>>> linalg.inv(A)
array([[[-2., 1.],
        [ 1.5, -0.5]])
```

```python
>>> b = np.array([[5,6]]) #2D array
>>> b
array([[5, 6]])
```

```python
>>> 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])
```

```python
>>> b.T #not matrix transpose!
array([5, 6])
```

```python
>>> A.dot(b) #does not matter for multiplication
array([17, 39])
```

`scipy.linalg` operations can be applied equally to `numpy.matrix` or to 2D `numpy.ndarray` objects.

### 1.9.2 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
>>> import numpy as np
>>> from scipy import linalg

>>> A = np.array([[1,2],[3,4]])
array([[1, 2],
       [3, 4]])

>>> linalg.inv(A)
array([[ 1.5, -0.5],
       [ 0.4, 1. ]])

>>> A.dot(linalg.inv(A)) #double check
array([[ 1.00000000e+00, 0.00000000e+00],
       [ 4.44089210e-16, 1.00000000e+00]])
```

### 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]])

>>> b = np.array([[5],[6]])

>>> linalg.inv(A).dot(b) #slow
array([[  6.66666667e-01,   0.00000000e+00],
       [  4.44089210e-16,   1.00000000e+00]])
```
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

$$ |A| = 1 \begin{vmatrix} 5 & 1 \\ 3 & 8 \end{vmatrix} - 3 \begin{vmatrix} 2 & 1 \\ 2 & 8 \end{vmatrix} + 5 \begin{vmatrix} 2 & 5 \\ 2 & 3 \end{vmatrix} = 1(5 \cdot 8 - 3 \cdot 1) - 3(2 \cdot 8 - 2 \cdot 1) + 5(2 \cdot 3 - 2 \cdot 5) = -25. $$

In SciPy this is computed as shown in this example:

```
>>> 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
```
For vector $x$, the order parameter can be any real number including $\infty$ or $-\infty$. The computed norm is

$$
\|x\| = \begin{cases}
\max |x_i| & \text{ord} = \infty \\
\min |x_i| & \text{ord} = -\infty \\
\left(\sum_i |x_i|^\text{ord}\right)^{1/\text{ord}} & |\text{ord}| < \infty.
\end{cases}
$$

For matrix $A$ the only valid values for norm are $\pm 2$, $\pm 1$, $\pm \infty$, and ‘fro’ (or ‘f’) Thus,

$$
\|A\| = \begin{cases}
\max_i \sum_j |a_{ij}| & \text{ord} = \infty \\
\min_i \sum_j |a_{ij}| & \text{ord} = -\infty \\
\max_j \sum_i |a_{ij}| & \text{ord} = 1 \\
\min_j \sum_i |a_{ij}| & \text{ord} = -1 \\
\max \sigma_i & \text{ord} = 2 \\
\min \sigma_i & \text{ord} = -2 \\
\sqrt{\text{trace}(A^H A)} & \text{ord} = \text{‘fro’}
\end{cases}
$$

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
>>> linalg.norm(A,-1)  # L1 norm (max row sum)
4
>>> linalg.norm(A,inf)  # L inf norm (max row sum)
7
```

### 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
\[
\sum_j \sum_i c_j f_j(x_i) f_n^*(x_i) = \sum_i y_i f_n^*(x_i)
\]

\[
A^H A c = A^H y
\]

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
\[
y = Ac + \epsilon.
\]

The command `linalg.lstsq` will solve the linear least squares problem for \( c \) given \( A \) and \( y \). In addition `linalg.pinv` or `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 `linalg.lstsq` and `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()
```
Data fitting with linalg.lstsq

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.

1.9.3 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

\[ v_H^T A = \lambda v_L^T \]

or

\[ A^H v_L = \lambda^* v_L. \]

With its default optional arguments, the command `linalg.eig` returns \( \lambda \) and \( v \). However, it can also return \( v_L \) and just \( \lambda \) by itself (`linalg.eigvals` returns just \( \lambda \) as well).

In addition, `linalg.eig` can also solve the more general eigenvalue problem

\[
A v = \lambda B v \\
A^H v_L = \lambda^* B^H v_L
\]

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

\[ A = BV\Lambda V^{-1} \]

where \( V \) is the collection of eigenvectors into columns and \( \Lambda \) 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
(-0.372281323269+0j) (5.37228132327+0j)
>>> print v[:,0]  #first eigenvector
[-0.82456484 0.56576746]
>>> print v[:,1]  #second eigenvector
[-0.14462181 0.89229942]
```
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 $A A^H$ are square hermitian matrices 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 $A A^H$.

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 in the unitary matrix $V$ while the eigenvectors of $A A^H$ 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]])
>>> A
array([[1, 2, 3],
       [4, 5, 6]])
>>> M,N = A.shape
>>> U,s,Vh = linalg.svd(A)
>>> Sig = linalg.diagsvd(s,M,N)
>>> U, Vh = U, Vh
>>> U
array([[-0.3863177 , -0.92236578],
       [-0.92236578, 0.3863177 ]])
>>> Sig
array([[ 9.5080320 , 0.         , 0.     ],
       [ 0.        , 0.77286964, 0.     ]])
>>> Vh
array([[ 0.80596391, 0.11238241, -0.58119908],
       [ 0.40824829, -0.81649658, 0.40824829]])
>>> U.dot(Sig.dot(Vh)) # check computation
array([[ 1.,  2.,  3.],
       [ 4.,  5.,  6.]]
```

LU decomposition

The LU decomposition finds a representation for the $M \times N$ matrix $A$ as

$$A = P L U$$

---

2. A hermitian matrix $D$ satisfies $D^H = D$.
3. A unitary matrix $D$ satisfies $D^H D = I = DD^H$ so that $D^{-1} = D^H$. 

1.9. Linear Algebra (scipy.linalg) 77
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 \( x^H Ax \geq 0 \) 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

\[
A = UΣV^H = QR
\]

implies that \( Q = U \) and \( R = ΣV^H \). 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 \( 2 \times 2 \) blocks
extrude from the main diagonal corresponding to any complex-valued eigenvalues. The command \texttt{linalg.schur} finds the Schur decomposition while the command \texttt{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 = 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)
>>> print T
[[ 9.90012467 1.78947961 -0.65498528]
 [ 0. 0.54993766 -1.57754789]
 [ 0. 0.51260928 0.54993766]]
>>> print T2
[[ 9.90012467 +0.00000000e+00j -0.32436598 +1.55463542e+00j
  -0.88619748 +5.69027615e-01j]
 [ 0.00000000 +0.00000000e+00j 0.54993766 +8.99258408e-01j
  1.06493862 +1.37016050e-17j]
 [ 0.00000000 +0.00000000e+00j 0.00000000 +0.00000000e+00j
  0.54993766 -8.99258408e-01j]]
>>> print abs(T1-T2) # different
[[ 1.24357637e-14 2.09205364e+00 6.56028192e-01]
 [ 0.00000000e+00 4.00296604e-16 1.83223097e+00]
 [ 0.00000000e+00 0.00000000e+00 4.57756680e-16]]
>>> print abs(Z1-Z2) # different
[[ 0.06833781 1.10591375 0.23662249]
 [ 0.11857169 0.5585604 0.29617525]
 [ 0.12624999 0.75656818 0.22975038]]
>>> T,Z,T1,Z1,T2,Z2 = map(mat,(T,Z,T1,Z1,T2,Z2))
>>> print abs(A-Z*T*Z.H) # same
[[ 1.11022302e-16 4.44089210e-16 4.44089210e-16]
 [ 4.44089210e-16 8.88178420e-16 2.66453526e-15]
 [ 8.88178420e-16 4.44089210e-16 2.66453526e-15]]
>>> print abs(A-Z1*T1*Z1.H) # same
[[ 1.00043248e-15 2.22301403e-15 5.55749485e-15]
 [ 3.11291538e-15 1.15463228e-14 1.15464861e-14]]
>>> print abs(A-Z2*T2*Z2.H) # same
[[ 3.34058710e-16 8.88178420e-16 4.18773089e-18]
 [ 1.48694940e-16 8.92966151e-16 8.92966151e-16]
 [ 1.3328956e-15 3.55373104e-15]]
```

### Interpolative Decomposition

\texttt{scipy.linalg.interpolative} contains routines for computing the interpolative decomposition (ID) of a matrix. For a matrix \( A \in \mathbb{C}^{m \times n} \) of rank \( k \leq \min\{m,n\} \) this is a factorization

\[
A \Pi = [A_{\Pi_1} \quad A_{\Pi_2}] = A_{\Pi_1} [I \quad T],
\]

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.

See also:

\texttt{scipy.linalg.interpolative} — for more information.
1.9.4 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. It can be defined for square matrices as

\[
e^A = \sum_{k=0}^{\infty} \frac{1}{k!} A^k.
\]

The command `linalg.expm3` uses this Taylor series definition to compute the matrix exponential. Due to poor convergence properties it is not often used.

Another method to compute the matrix exponential is to find an eigenvalue decomposition of \( A \):

\[
A = V \Lambda V^{-1}
\]

and note that

\[
e^A = Ve^\Lambda V^{-1}
\]

where the matrix exponential of the diagonal matrix \( \Lambda \) is just the exponential of its elements. This method is implemented in `linalg.expm2`.

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.

\[
A \equiv \exp(\log(A)).
\]

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 cosine can be defined using Euler’s identity as

\[
\sin(A) = \frac{e^{jA} - e^{-jA}}{2j},
\]

\[
\cos(A) = \frac{e^{jA} + e^{-jA}}{2}.
\]

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:

\[
\begin{align*}
\text{sinh}(A) &= \frac{e^A - e^{-A}}{2} \\
\text{cosh}(A) &= \frac{e^A + e^{-A}}{2} \\
\text{tanh}(A) &= \frac{\text{cosh}(A)}{\text{sinh}(A)}.
\end{align*}
\]

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 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
>>> A = random.rand(3,3)
>>> B = linalg.funm(A, lambda x: special.jv(0,x))
```

Note how, by virtue of how matrix analytic functions are defined, the Bessel function has acted on the matrix eigenvalues.

1.9.5 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><code>scipy.linalg.block_diag</code></td>
<td>Create a block diagonal matrix from the provided arrays.</td>
</tr>
<tr>
<td>circulant</td>
<td><code>scipy.linalg.circulant</code></td>
<td>Construct a circulant matrix.</td>
</tr>
<tr>
<td>companion</td>
<td><code>scipy.linalg.companion</code></td>
<td>Create a companion matrix.</td>
</tr>
<tr>
<td>Hadamard</td>
<td><code>scipy.linalg.hadamard</code></td>
<td>Construct a Hadamard matrix.</td>
</tr>
<tr>
<td>Hankel</td>
<td><code>scipy.linalg.hankel</code></td>
<td>Construct a Hankel matrix.</td>
</tr>
<tr>
<td>Hilbert</td>
<td><code>scipy.linalg.hilbert</code></td>
<td>Construct a Hilbert matrix.</td>
</tr>
<tr>
<td>Inverse Hilbert</td>
<td><code>scipy.linalg.invhilbert</code></td>
<td>Construct the inverse of a Hilbert matrix.</td>
</tr>
<tr>
<td>Leslie</td>
<td><code>scipy.linalg.leslie</code></td>
<td>Create a Leslie matrix.</td>
</tr>
<tr>
<td>Pascal</td>
<td><code>scipy.linalg.pascal</code></td>
<td>Create a Pascal matrix.</td>
</tr>
<tr>
<td>Toeplitz</td>
<td><code>scipy.linalg.toeplitz</code></td>
<td>Construct a Toeplitz matrix.</td>
</tr>
<tr>
<td>Van der Monde</td>
<td><code>numpy.vander</code></td>
<td>Generate a Van der Monde matrix.</td>
</tr>
</tbody>
</table>

For examples of the use of these functions, see their respective docstrings.

## 1.10 Sparse Eigenvalue Problems with ARPACK

### 1.10.1 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.

### 1.10.2 Basic Functionality

ARPACK can solve either standard eigenvalue problems of the form

\[
Ax = \lambda x
\]

or general eigenvalue problems of the form

\[
Ax = \lambda M x
\]

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`)
SciPy Reference Guide, Release 0.16.0

- `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.

### 1.10.3 Shift-Invert Mode

Shift invert mode relies on the following observation. For the generalized eigenvalue problem

\[ Ax = \lambda M x \]

it can be shown that

\[ (A - \sigma M)^{-1} M x = \nu x \]

where

\[ \nu = \frac{1}{\lambda - \sigma} \]

### 1.10.4 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
[ 29.1446102  30.05821805  31.19467646]
```
>>> import numpy as np
>>> np.dot(evecs_large.T, evecs_all[:, -3:])

```
[-1.  0.  0.]
[ 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')
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)
>>> print(evals_all[:3])
[ 0.0003783 0.00122714 0.00715878]
>>> print(evals_small)
[ 0.00037831 0.00122714 0.00715881]
>>> print(np.dot(evecs_small.T, evecs_all[:,:3]))
```

```
[[-0.99999989 0.00000024 -0.00000049]
 [-0.00000023 0.99999999 0.00000056]
 [ 0.00000031 -0.00000037 0.99999852]]
```

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', maxiter=5000)
>>> print(evals_all[:3])
[ 0.0003783 0.00122714 0.00715878]
>>> print(evals_small)
[ 0.0003783 0.00122714 0.00715878]
>>> print(np.dot(evecs_small.T, evecs_all[:,:3]))
```

```
[[ 1.0 0.0 0.0]
 [-0.0 -1.0 0.0]
 [ 0.0 -0.0 1.0]]
```

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 \( \nu = 1/(\sigma - \lambda) = 1/\lambda \), so our small eigenvalues \( \lambda \) become large eigenvalues \( \nu \).

```python
>>> evals_small, evecs_small = eigsh(X, 3, sigma=0, which='LM')
>>> print(evals_all[:3])
[ 0.0003783 0.00122714 0.00715878]
>>> print(evals_small)
[ 0.0003783 0.00122714 0.00715878]
>>> print(np.dot(evecs_small.T, evecs_all[:,:3]))
```

```
[[ 1. 0. 0.]
 [-0. -1. 0.]
 [ 0.  0. -1.]]
```

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:]
>>> print evals_all[i_sort]
[ 1.16577199 0.85081388 1.06642272]
>>> print evals_mid
[ 0.85081388 1.06642272 1.16577199]
>>> print np.dot(evecs_mid.T, evecs_all[:,i_sort])
[[-0. 1. 0.]
 [-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 `eigsh` and `eigs`, but the operation can also be specified by the user. See the docstring of `scipy.sparse.linalg.eigsh` and `scipy.sparse.linalg.eigs` for details.

### 1.10.5 References

### 1.11 Compressed Sparse Graph Routines (`scipy.sparse.csgraph`)

#### 1.11.1 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:

```
apet \rightarrow ait \rightarrow bit \rightarrow big \rightarrow bag \rightarrow mag \rightarrow 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 = map(str.lower, word_list)
>>> len(word_list)
586
```
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  # dtype('|S3')
>>> word_list.sort()  # sort for quick searching later
```

We have an array where each entry is three bytes. We’d like to find all pairs where exactly one byte 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='int8',
...                          buffer=word_list.data)
>>> word_bytes.shape
(586, 3)
```

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 / word_list.itemsize))
```

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'
>>> word_list[i2]  # 'man'
```

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)
>>> print distances[i2]
5.0
```

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']

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
```

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(15)]
[571, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1]
```

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.where(component_list == i)]) for i in range(1, 15)]
[['aha'], ['chi'], ['ebb'], ['ems', 'emu'], ['gnu'], ['ism'], ['khz'], ['nth'], ['ova'], ['qua'], ['ugh'], ['ups'], ['urn'], ['use']]
```

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)
>>> np.max(distances[~np.isinf(distances)])
13.0
```

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
>>> il, i2 = np.where(distances == 13)
>>> zip(word_list[il], word_list[i2])
[('imp', 'ohm'), ('imp', 'ohs'), ('ohm', 'imp'), ('ohm', 'ump'), ('ohs', 'imp'), ('ohs', 'ump'),
```
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[::-1]
['imp', 'amp', 'asp', 'ask', 'ark', 'are', 'aye', 'rye', 'roe', 'woe', 'woo', 'who', 'oho', 'ohm']
```

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.

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.

1.12.1 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.copy())
>>> 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
>>> 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
>>> 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
>>> 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
>>> 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
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
>>> tri = Delaunay(points, qhull_options="QJ Pp")
```

```python
points[tri.simplices]
array([[1, 1],
       [1, 0],
       [0, 0]],
      [[1, 1],
       [1, 1],
       [1, 0]],
      [[0, 1],
       [1, 1],
       [0, 0]],
      [[0, 1],
       [1, 1],
       [1, 1]])
```

Two new triangles appeared. However, we see that they are degenerate and have zero area.

### 1.12.2 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
```

```python
points = np.random.rand(30, 2)  # 30 random points in 2-D
```

```python
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
```

```python
plt.plot(points[:,0], points[:,1], 'o')
```

```python
for simplex in hull.simplices:
```

```python
plt.plot(points[simplex,0], points[simplex,1], 'k-')
```

```python
plt.show()
```
The same can be achieved with `scipy.spatial.convex_hull_plot_2d`.

### 1.12.3 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],
       [ 0.5,  1.5],
       [ 1.5,  1.5]])
```

The Voronoi vertices denote the set of points forming the polygonal edges of the Voronoi regions. In this case, there are 9 different regions:

```python
>>> vor.regions
[[-1, 0], [-1, 1], [1, -1, 0], [3, -1, 2], [-1, 3], [3, 1, 0, 2], [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:

```python
>>> vor.ridge_vertices
[[-1, 0], [0, 1], [-1, 3], [-1, 2], [2, 3], [-1, 3], [-1, 2], [0, 2], [1,]
```

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:

```python
>>> vor.ridge_points
array([[0, 3],
       [0, 1],
       [6, 3],
       [6, 7],
       [3, 4],
       [1, 2],
```
This information, taken together, is enough to construct the full diagram.

We can plot it as follows. First the points and the Voronoi vertices:

```python
gplt.plot(points[:,0], points[:,1], 'o')
gplt.plot(vor.vertices[:,0], vor.vertices[:,1], '*')
gplt.xlim(-1, 3); gplt.ylim(-1, 3)
```

Plotting the finite line segments goes as for the convex hull, but now we have to guard for the infinite edges:

```python
gfor simplex in vor.ridge_vertices:
g    simplex = np.asarray(simplex)
g    if np.all(simplex >= 0):
g        gplt.plot(vor.vertices[simplex,0], vor.vertices[simplex,1], 'k-')
```

The ridges extending to infinity require a bit more care:

```python
gcenter = points.mean(axis=0)
gfor pointidx, simplex in zip(vor.ridge_points, vor.ridge_vertices):
g    simplex = np.asarray(simplex)
g    if np.any(simplex < 0):
g        i = simplex[simplex >= 0][0] # finite end Voronoi vertex
g        t = points[pointidx[1]] - points[pointidx[0]] # tangent
g        t /= np.linalg.norm(t)
g        n = np.array([-t[1], t[0]]) # normal
g        midpoint = points[pointidx].mean(axis=0)
g        far_point = vor.vertices[i] + np.sign(np.dot(midpoint - center, n)) * n * 100
g        gplt.plot([vor.vertices[i,0], far_point[0]],
g                   [vor.vertices[i,1], far_point[1]], 'k--')
```

```python
gplt.show()
```

1.12. Spatial data structures and algorithms (scipy.spatial) 93
This plot can also be created using `scipy.spatial.voronoi_plot_2d`.

## 1.13 Statistics (scipy.stats)

### 1.13.1 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.

### 1.13.2 Random Variables

There are two general distribution classes that have been implemented for encapsulating *continuous random variables* and *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 added by the end user. (If you create one, please contribute it).

All of the statistics functions are located in the sub-package `scipy.stats` and a fairly complete listing of these functions can be obtained using `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: *Specific Points for Discrete Distributions*.

### Getting Help

First of all, all distributions are accompanied with help functions. To obtain just some basic information we can call

```python
>>> from scipy import stats
>>> from scipy.stats import norm
>>> print 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)
```

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__', '__doc__', '__getattribute__', '__hash__', '__init__', '__module__', '__new__', '__reduce__', '__reduce_ex__', '__repr__', '__setattr__', '__str__', '__weakref__', 'args', 'cdf', 'dist', 'entropy', 'isf', 'kwds', 'moment', 'pdf', 'pmf', 'ppf', 'rvs', 'sf', 'stats']
```

Finally, we can obtain the list of available distribution through introspection:
>>> import warnings
>>> warnings.simplefilter('ignore', DeprecationWarning)

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:', len(dist_continu)
number of continuous distributions: 84

>>> print 'number of discrete distributions: ', len(dist_discrete)
number of discrete distributions: 12

Common Methods

The main public methods for continuous RVs are:

- rvs: Random Variates
- pdf: Probability Density Function
- cdf: Cumulative Distribution Function
- 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])
```

```python
>>> 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 with np.vectorize.

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=5)
array([-0.35687759, 1.34347647, -0.11710531, -1.00725181, -0.51275702])
```
Don’t think that `norm.rvs(5)` generates 5 variates:

```python
>>> norm.rvs(5)
7.13624370075814
```

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 $\text{N}(0, \sigma^2)$ deviations in each component is `rice(R/\sigma, 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))
4.983550784784704
```

Thus, to explain the output of the example of the last section: `norm.rvs(5)` generates a single normally distributed random variate with mean `loc=5`, because of the default `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

\[ \gamma(x, a) = \frac{\lambda^a x^{a-1} e^{-\lambda x}}{\Gamma(a)} \]

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 probabilites 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:
Specific Points for Discrete Distributions

Discrete distributions have mostly the same basic methods as the continuous distributions. However, `pdf` is replaced by 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 distributions, the cumulative distribution function is in most standard cases strictly monotonic increasing in the bounds (a,b) and hence has 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:

\[
ppf(q) = \min\{x : \text{cdf}(x) \geq q, x \text{ integer}\}
\]

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([ 0.0001031991744066, 0.0521155830753351, 0.6083591331269301,
       0.9897832817337386])
>>> 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 calcula-
tion. To define a distribution, only one of pdf or cdf is necessary; all other methods can be derived using nu-
meric 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.

1.13.3 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.
```
```python
deterministic = deterministic_gen(name="deterministic")
deterministic.cdf(np.arange(-3, 3, 0.5))
array([ 0., 0., 0., 0., 1., 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, 5.83333333e+04, 4.16333634e-12, 4.16333634e-12, 4.16333634e-12, 4.16333634e-12])
```

Be aware of the performance issues mentions 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)
(4.163336342344337e-13, 0.0)
```

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
(1.000076872229173, 0.0010625571718182458)
```

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`, i.e.,
```python
from scipy.stats import rv_discrete
help(rv_discrete)
```

we learn that:

> “You can construct an arbitrary discrete rv where \( P(X=x_k) = p_k \) by passing to the `rv_discrete` initialization method (through the `values=` keyword) a tuple of sequences \((x_k, p_k)\) which describes only those values of \(X\) (\(x_k\)) that occur with nonzero probability (\(p_k\)).”

Next to this, there are some further requirements for this approach to work:

- The keyword `name` is required.
- The support points of the distribution \(x_k\) 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
npoints = 20  # number of integer support points of the distribution minus 1
npointsh = npoints / 2
npointsf = float(npoints)

nbound = 4  # bounds for the truncated normal
normbound = (1+1/npointsf) * 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))

And finally we can subclass rv_discrete:

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.

mean = -0.0000, variance = 6.3302, skew = 0.0000, kurtosis = -0.0076

nd_std = np.sqrt(normdiscrete.stats(moments='v'))

Testing the Implementation

Let’s generate a random sample and compare observed frequencies with the probabilities.

n_sample = 500
rvs = normdiscrete.rvs(size=n_sample)
rvsnd = rvs
f, l = np.histogram(rvs, bins=gridlimits)
sfreq = np.vstack([gridint, f, probs*n_sample]).T
print sfreq

1.13. Statistics (scipy.stats)
Next, we can test, whether our sample was generated by our normdiscrete distribution. This also verifies whether the random numbers are generated correctly.

The chisquare test requires that there are a minimum number of observations in each bin. We combine the tail bins into larger bins so that they contain enough observations.

```python
>>> f2 = np.hstack([f[:5].sum(), f[5:-5], f[-5:].sum()])
>>> p2 = np.hstack([probs[:5].sum(), probs[5:-5], probs[-5:].sum()])
>>> ch2, pval = stats.chisquare(f2, p2*n_sample)

>>> print 'chisquare for normdiscrete: chi2 = %6.3f pvalue = %6.4f' % (ch2, pval)
```

The pvalue in this case is high, so we can be quite confident that our random sample was actually generated by the distribution.
1.13.4 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.max(), x.min() # equivalent to np.max(x), np.min(x)
5.26327732981 -3.78975572422
```

```python
>>> print x.mean(), x.var() # equivalent to np.mean(x), np.var(x)
0.0140610663985 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 = 'mean = %6.4f, variance = %6.4f, skew = %6.4f, kurtosis = %6.4f'
>>> print sstr %(m, v, s, k)
mean = 0.0000, variance = 1.2500, skew = 0.0000, kurtosis = 1.0000
>>> print 'distribution: ',
    distribution:
>>> print sstr %(sm, sv, ss, sk)
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 = %6.3f pvalue = %6.4f' % stats.ttest_1samp(x, m)
t-statistic = 0.391 pvalue = 0.6955
```

The pvalue 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 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)
```
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 took on the normal distribution.

```python
d, pval = stats.kstest((x-x.mean())/x.std(), 'norm')
```

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)
```

```python
>>> print 'critical values from ppf at 1 %, 5 % and 10 % %8.4f %8.4f %8.4f
      % (crit01, crit05, crit10)
```

```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
```

```python
>>> print 'sample %-frequency at 1 %, 5 % and 10 % tail %8.4f %8.4f %8.4f
      % (freq01, freq05, freq10)
```

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
```
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.

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.

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:

These two tests are combined in the normality test
>>> print 'normaltest teststat = %6.3f pvalue = %6.4f' % 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 = %6.3f pvalue = %6.4f' %
   ... 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 = %6.3f pvalue = %6.4f' % stats.normaltest(stats.t.rvs(10, size=100))
  normaltest teststat = 4.698 pvalue = 0.0955
>>> print 'normaltest teststat = %6.3f pvalue = %6.4f' % 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.

### 1.13.5 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)
(-0.54890361750888583, 0.5831943748663857)
```

Test with sample with different means:

```python
>>> rvs3 = stats.norm.rvs(loc=8, scale=10, size=500)
>>> stats.ttest_ind(rvs1, rvs3)
(-4.5334142901750321, 6.507128186505895e-006)
```

#### 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)
(0.025999999999999995, 0.99541195173064878)
```

In the second example, with different location, i.e. means, we can reject the null hypothesis since the pvalue is below 1%
>>> stats.ks_2samp(rvs1, rvs3)
(0.11399999999999999, 0.0027132103661283141)

1.13.6 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)  # rug plot
>>> ax.plot(x_eval, kde1(x_eval), 'k-', label="Scott's Rule")
>>> ax.plot(x_eval, kde1(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.

```python
>>> def my_kde_bandwidth(obj, fac=1./5):
...     """We use Scott's Rule, multiplied by a constant factor."""
...     return np.power(obj.n, -1./(obj.d+4)) * fac
```

```python
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)

>>> ax.plot(x1, np.zeros(x1.shape), 'b+', ms=20)  # rug plot
```

```python
>>> kde3 = stats.gaussian_kde(x1, bw_method=my_kde_bandwidth)
>>> ax.plot(x_eval, kde3(x_eval), 'g-', label="With smaller BW")
```

```python
>>> plt.show()
```

We see that if we set bandwidth to be very narrow, the obtained estimate for the probability density function (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
	sxs = np.linspace(x1.min()-1, x1.max()+1, 200)

t1 = stats.gaussian_kde(x1)
t2 = 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

>>> 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)
```

![Plot of Normal (top) and Student's T (bottom) distributions](image)
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 \texttt{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:

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.

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()
1.14 Multidimensional image processing (scipy.ndimage)

1.14.1 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.

1.14.2 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
>>> 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])
```

### 1.14.3 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 = array([[0,1,0],[1,1,1],[0,1,0]])

>>> footprint
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
>>> 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, 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, 0, 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
The boundary conditions can be selected using the `mode` parameter which must be a string with the name of the boundary condition. Following boundary conditions are currently supported:

<table>
<thead>
<tr>
<th>Mode</th>
<th>Description</th>
<th>Example</th>
</tr>
</thead>
<tbody>
<tr>
<td>nearest</td>
<td>Use the value at the boundary</td>
<td>([1 \ 2 \ 3] \rightarrow [1 \ 1 \ 2 \ 3 \ 3])</td>
</tr>
<tr>
<td>wrap</td>
<td>Periodically replicate the array</td>
<td>([1 \ 2 \ 3] \rightarrow [3 \ 1 \ 2 \ 3 \ 1])</td>
</tr>
<tr>
<td>reflect</td>
<td>Reflect the array at the boundary</td>
<td>([1 \ 2 \ 3] \rightarrow [1 \ 1 \ 2 \ 3 \ 3])</td>
</tr>
<tr>
<td>constant</td>
<td>Use a constant value, default is 0.0</td>
<td>([1 \ 2 \ 3] \rightarrow [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 results 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 and to construct the Laplace filter:
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:

`derivative2(input, axis, output, mode, cval, *extra_arguments, **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:

```python
>>> def d2(input, axis, output, mode, cval):
...     return correlate1d(input, [1, -2, 1], axis, output, mode, cval, 0)
...
>>> a = zeros((5, 5))
>>> a[2, 2] = 1
>>> generic_laplace(a, d2)
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.]]
```

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 = zeros((5, 5))
>>> a[2, 2] = 1
>>> 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 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 calculated 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:

```python
derivative(input, axis, output, mode, cval, *extra_arguments, **extra_keywords)
```

It should calculate the derivative along the dimension \( \text{axis} \). If \( \text{output} \) is not None it should use that for the output and return None, otherwise it should return the result. \( \text{mode}, \text{cval} \) have the usual meaning.

The \textit{extra_arguments} and \textit{extra_keywords} arguments can be used to pass a tuple of extra arguments and a dictionary of named arguments that are passed to \textit{derivative} at each call.

For example, the \texttt{sobel} function fits the required signature:

```python
>>> a = zeros((5, 5))
>>> a[2, 2] = 1
>>> 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 \texttt{generic_laplace} for examples of using the \textit{extra_arguments} and \textit{extra_keywords} arguments.

The \texttt{sobel} and \texttt{prewitt} functions fit the required signature and can therefore directly be used with \texttt{generic_gradient_magnitude}. The following function implements the gradient magnitude using Gaussian derivatives:

The function \texttt{gaussian_gradient_magnitude} calculates the gradient magnitude using \texttt{gaussian_filter} to calculate the first derivatives. The standard-deviations of the Gaussian filter along each axis are passed through the parameter \textit{sigma} as a sequence or numbers. If \textit{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 \texttt{PyCObject} (see \textit{Extending ndimage in C} for more information).

The \texttt{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 \texttt{generic_filter1d} function iterates over the lines of an array and calls \textit{function} at each line. The arguments that are passed to \textit{function} are one-dimensional arrays of the tFloat64 type. The first contains the values of the current line. It is extended at the beginning end the end, according to the \textit{filter_size} and \textit{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 = 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 \texttt{generic_filter1d} as follows:

```python
>>> def fnc(iline, oline):
...     oline[...] = iline[:-2] + 2 * iline[1:-1] + 3 * iline[2:]
... >>> generic_filter1d(a, fnc, 3)
array([[ 3, 8, 14, 17],
```
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 tFloat64 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 = 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 * array([1, 3])).sum()
... >>> 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 `generic_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.

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(buffer, weights):
...     weights = asarray(weights)
...     return (buffer * weights).sum()
... ```
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:

```python
>>> a = 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 * array([1, 3])).sum()
...         print self.coordinates
...         # calculate the next coordinates:
...         axes = range(len(self.shape))
...         axes.reverse()
...         for jj in axes:
...             if self.coordinates[jj] < self.shape[jj] - 1:
...                 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]])
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:

```python
class fncl_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 = 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

fnc = fncl_class(shape = (3,4))
generic_filter1d(a, fnc.filter, 3)
```

The example for `generic_filter1d` then becomes this:

```python
class fnc1d_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 = 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

fnc = fnc1d_class(shape = (3,4))
generic_filter1d(a, fnc.filter, 3)
```

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:

```python
class fnc1d_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 = 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

fnc = fnc1d_class(shape = (3,4))
generic_filter1d(a, fnc.filter, 3)
```

The example for `generic_filter1d` then becomes this:

```python
class fnc1d_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 = 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

fnc = fnc1d_class(shape = (3,4))
generic_filter1d(a, fnc.filter, 3)
```

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.

### 1.14.4 Interpolation functions

This section describes various interpolation functions that are based on B-spline theory. A good introduction to B-splines can be found in: M. Unser, “Splines: A Perfect Fit for Signal and Image Processing.” IEEE Signal Processing Magazine, vol. 16, no. 6, pp. 22-38, November 1999.

#### 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 `spline_filter` function calculates a multidimensional spline filter.

**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.

#### 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 `Filter functions` for the multidimensional filter functions. Therefore these functions all support a `mode` parameter that determines how the boundaries are handled, and a `cval` parameter that gives a constant value in case that the ‘constant’ mode is used.

The `geometric_transform` function applies an arbitrary geometric transform to the input. The given `mapping` function is called at each point in the output to find the corresponding coordinates in the input. `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 = arange(12).reshape(4,3).astype(np.float64)
>>> def shift_func(output_coordinates):
...     return (output_coordinates[0] - 0.5, output_coordinates[1] - 0.5)
...     
>>> geometric_transform(a, shift_func)
array([[ 0.    ,  0.    ,  0.    ],
       [ 0.    ,  1.3625,  2.7375],
       [ 0.75  ,  0.    ,  0.    ],
       [ 1.3625,  1.3625,  1.3625]])
```
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 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],
       [ 0. , 4.8125, 6.1875],
       [ 0. , 8.2625, 9.6375]])
```

**Note:** The mapping function can also be written in C and passed using a PyCObject. See *Extending 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 = arange(12).reshape(4,3).astype(np.float64)
>>> a
array([[ 0., 1., 2.],
       [ 3., 4., 5.],
       [ 6., 7., 8.],
       [ 9., 10., 11.]])
>>> map_coordinates(a, [[0.5, 2], [0.5, 1]])
array([ 1.3625 , 7. ])
```

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.
1.14.5 Morphology

Binary morphology

Binary morphology (need something to put here).

The `generate_binary_structure` function 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:

```python
>>> generate_binary_structure(2, 1)
array([[False, True, False],
       [ True, True, True],
       [False, True, False]], dtype=bool)
>>> generate_binary_structure(2, 2)
array([[ True, True, True],
       [ True, True, True],
       [ True, True, True]], dtype=bool)
```

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 = array([[0, 1, 0], [1, 1, 1], [0, 1, 0]])
>>> a = 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]])
>>> binary_dilation(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
>>> struct = generate_binary_structure(2, 1)
>>> struct
array([[False,  True, False],
       [ True,  True,  True],
       [False,  True, False]], dtype=bool)
>>> 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 `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. 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`.

1.14. Multidimensional image processing (`scipy.ndimage`) 125
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.

Similar to binary erosion 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 the a grey-scale closing and the input.

1.14.6 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 distancemetrics 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 Int32).

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 (Float64 and Int32).


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 (Float64 and 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.

### 1.14.7 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
>>> a = 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]])
array([[1, 1, 1, 0, 0, 0],
       [0, 1, 1, 0, 1, 0],
       [0, 0, 0, 1, 1, 1],
       [0, 0, 0, 0, 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:

```python
>>> where(a > 1, 1, 0)
array([[1, 1, 1, 0, 0, 0],
       [1, 1, 0, 1, 0],
       [0, 0, 1, 1, 1],
       [0, 0, 0, 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:

```python
>>> a = 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]])
array([[1, 1, 1, 0, 0, 0],
       [0, 1, 1, 0, 1, 0],
       [0, 0, 0, 1, 1, 1],
       [0, 0, 0, 0, 1, 0]])
```

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:
>>> a = 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(a, s)
(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]]), 2)

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:

>>> a = 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(a, s)[0]
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]])

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:

>>> l, n = label([1, 0, 1, 0, 1])
>>> l
array([1 0 2 0 3])
>>> l = where(l != 2, l, 0)
>>> l
array([1 0 0 0 3])
>>> label(l)[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 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:

>>> input = array([[0, 0, 0, 0, 0, 0],
            [0, 1, 1, 1, 1, 1],
            [0, 1, 0, 0, 0, 1],
            [0, 1, 0, 0, 0, 1],
            [0, 1, 0, 0, 0, 1],
            [0, 1, 1, 1, 1, 1]], np.uint8)
>>> markers = 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],
            [0, 0, 0, 2, 0, 0],
            [0, 0, 0, 0, 0, 0]], np.uint8)
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 = 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, 2, 0, 0, 0],
...                   [0, 0, 0, 0, 0, 0, 0],
...                   [0, 0, 0, 0, 0, 0, 0],
...                   [0, 0, 0, 0, 0, 0, -1]], np.int8)
```

```python
>>> watershed_ift(input, markers)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [-1, -1, 2, 2, 2, -1, -1],
       [-1, -1, 2, 2, 2, 2, -1],
       [-1, -1, 2, 2, 2, 2, -1],
       [-1, -1, 2, 2, 2, -1, -1],
       [-1, -1, -1, -1, -1, -1, -1]], dtype=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 = 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, 2, 0, 0, 0],
...                   [0, 0, 0, 0, 0, 0, 0],
...                   [0, 0, 0, 0, 0, 0, 0],
...                   [0, 0, 0, 0, 0, 0, -1]], np.int8)
```

```python
>>> watershed_ift(input, markers)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [-1, -1, 2, 2, 2, 2, -1],
       [-1, -1, 2, 2, 2, 2, -1],
       [-1, -1, 2, 2, 2, -1, -1],
       [-1, -1, 2, 2, 2, -1, -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
>>> watershed_ift(input, markers,
...     structure = [[1,1,1], [1,1,1], [1,1,1]])
array([[[-1, -1, -1, -1, -1, -1, -1],
        [-1, 2, 2, 2, 2, 2, -1],
        [-1, 2, 2, 2, 2, 2, -1],
        [-1, 2, 2, 2, 2, 2, -1],
        [-1, 2, 2, 2, 2, 2, -1],
        [-1, 2, 2, 2, 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 `UInt8` and `UInt16`.

### 1.14.8 Object measurements

Given an array of labeled objects, the properties of the individual objects can be measured. The `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 `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 = array([[0,1,0,0,0],[0,1,1,0,1],[0,0,0,1,1],[0,0,0,0,1]])
>>> l, n = label(a)
>>> 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]])
```

`find_objects` returns slices for all objects, unless the `max_label` parameter is larger than zero, in which case only the first `max_label` objects are returned. If an index is missing in the `label` array, None is return instead of a slice. For example:

```python
>>> find_objects([1, 0, 3, 4], max_label = 3)
[(slice(0, 1, None),), None, (slice(2, 3, None),)]
```

The list of slices generated by `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 = arange(4 * 6).reshape(4, 6)
>>> mask = 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]])
>>> labels = label(mask)[0]
>>> slices = find_objects(labels)
```

Then we can calculate the sum of the elements in the second object:

```python
>>> 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:
For large arrays and small objects it is more efficient to call the measurement functions after slicing the array:

```python
>>> 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
>>> 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 `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 `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 `minimum`, `maximum`, `minimum_position`, and `maximum_position` that are described above.

The `center_of_mass` function calculates the center of mass of the 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 `histogram` function calculates a histogram of the 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. Histograms are defined by their minimum (`min`), maximum (`max`) and the number of bins (`bins`). They are returned as one-dimensional arrays of type `Int32`.

### 1.14.9 Extending `ndimage` in C

A few functions in the `scipy.ndimage` take a call-back argument. This can be a python function, but also a `PyCObject` containing a pointer to a C function. To use this feature, you must write your own C extension that defines the function, and define a Python function that returns a `PyCObject` containing a pointer to this function.

An example of a function that supports this is `geometric_transform` (see [Interpolation functions](#)). You can pass it a python callable object that defines a mapping from all output coordinates to corresponding coordinates in the input array. This mapping function can also be a C function, which generally will be much more efficient, since the overhead of calling a python function at each element is avoided.

For example to implement a simple shift function we define the following function:

```c
static int _shift_function(int *output_coordinates, double* input_coordinates,
                            int output_rank, int input_rank, void *callback_data)
{
    int ii;
    /* get the shift from the callback data pointer: */
    double shift = *(double*)callback_data;
    /* calculate the coordinates: */
    for(ii = 0; ii < irank; ii++)
        icoor[ii] = ocoor[ii] - shift;
    /* return OK status: */
    return 1;
}
```

This function is called at every element of the output array, passing the current coordinates in the `output_coordinates` array. On return, the `input_coordinates` array must contain the coordinates at which the input is interpolated. The ranks of the input and output array are passed through `output_rank` and `input_rank`. The value of the shift is passed through the `callback_data` argument, which is a pointer to void. The function returns an error status, in this case always 1, since no error can occur.

A pointer to this function and a pointer to the shift value must be passed to `geometric_transform`. Both are passed by a single `PyCObject` which is created by the following python extension function:

```python
static PyObject *
py_shift_function(PyObject *obj, PyObject *args)
{
    double shift = 0.0;
    if (!PyArg_ParseTuple(args, "d", &shift)) {
        PyErr_SetString(PyExc_RuntimeError, "invalid parameters");
        return NULL;
    } else {
        /* assign the shift to a dynamically allocated location: */
        double *cdata = (double*)malloc(sizeof(double));
        *cdata = shift;
        /* wrap function and callback_data in a CObject: */
        return PyCObject_FromVoidPtrAndDesc(_shift_function, cdata,
                                            _destructor);
    }
}
```
The value of the shift is obtained and then assigned to a dynamically allocated memory location. Both this data pointer and the function pointer are then wrapped in a PyCObject, which is returned. Additionally, a pointer to a destructor function is given, that will free the memory we allocated for the shift value when the PyCObject is destroyed. This destructor is very simple:

```c
static void
_destructor(void* cobject, void* cdata)
{
    if (cdata)
        free(cdata);
}
```

To use these functions, an extension module is built:

```c
static PyMethodDef methods[] = {
    {"shift_function", (PyCFunction)py_shift_function, METH_VARARGS, "}},
    {NULL, NULL, 0, NULL}
};

void
initexample(void)
{
    Py_InitModule("example", methods);
}
```

This extension can then be used in Python, for example:

```python
>>> import example
>>> array = arange(12).reshape((4, 3)).astype(np.float64)
>>> fnc = example.shift_function(0.5)
>>> geometric_transform(array, fnc)
array([[ 0.  0.  0. ],
       [ 0.  1.3625  2.7375],
       [ 0.  4.8125  6.1875],
       [ 0.  8.2625  9.6375]])
```

C callback functions for use with ndimage functions must all be written according to this scheme. The next section lists the ndimage functions that accept a C callback function and gives the prototype of the callback function.

### 1.14.10 Functions that support C callback functions

The ndimage functions that support C callback functions are described here. Obviously, the prototype of the function that is provided to these functions must match exactly that what they expect. Therefore we give here the prototypes of the callback functions. All these callback functions accept a void callback_data pointer that must be wrapped in a PyCObject using the Python PyCObject_FromVoidPtrAndDesc function, which can also accept a pointer to a destructor function to free any memory allocated for callback_data. If callback_data is not needed, PyCObject_FromVoidPtr may be used instead. The callback functions must return an integer error status that is equal to zero if something went wrong, or 1 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.

The function generic_filter (see Generic filter functions) accepts a callback function with the following prototype:

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 valued should be returned in the return_value argument.
The function `generic_filter1d` (see *Generic filter functions*) accepts a callback function with the following prototype:

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 the `input_line` array. The length of the input line (after extension) is passed through `input_length`. The callback function should apply the 1D filter and store the result in the array passed through `output_line`. The length of the output line is passed through `output_length`.

The function `geometric_transform` (see *Interpolation functions*) expects a function with the following prototype:

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.

### 1.15 File IO (scipy.io)

See also:

`numpy-reference.routines.io` (in numpy)

#### 1.15.1 MATLAB files

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<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>
</tr>
<tr>
<td><code>whosmat(file_name[, appendmat])</code></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:

```python
>>> import scipy.io as sio
```

If you are using IPython, try tab completing on `sio`. Among the many options, you will find:

- `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:

- `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
e = 1:12
a =
  1 2 3 4 5 6 7 8 9 10 11 12

e = 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

e = save -6 octave_a.mat a
ls octave_a.mat
```

Now, to Python:

```python
c = sio.loadmat('octave_a.mat')
c
```

```python
octave_a = c['a'][0,:][0,:,:]
octave_a
```

Now let’s try the other way round:

```python
import numpy as np
c = np.arange(10)
c.shape
```

```python
sio.savemat('np_vector.mat', {'c':c})
```

Then back to Octave:

```
```
```plaintext
octave:8> load np_vector.mat
octave:9> vect =
    0 1 2 3 4 5 6 7 8 9
octave:10> size(vect) =
    1 10
```

If you want to inspect the contents of a MATLAB file without reading the data into memory, use the `whosmat` command:

```plaintext
>>> 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).

```plaintext
octave:11> my_struct = struct('field1', 1, 'field2', 2)
my_struct =
    field1 = 1
    field2 = 2
```

```plaintext
octave:12> save -6 octave_struct.mat my_struct
```

We can load this in Python:

```plaintext
>>> 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
(array([1.0], [2.0])
```

```plaintext
>>> 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:
>>> val = oct_struct[0,0]

and:

octave:13> size(my_struct)
an =

    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']
>>> oct_struct.shape
()
```

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`.

```python
>>> 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`:

```python
>>> 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'
```}

```python
>>> 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:

```python
>>> a_dict = {'field1': 0.5, 'field2': 'a string'}
>>> sio.savemat('saved_struct.mat', {'a_dict': a_dict})
```

loaded as:

```octave
octave:21> load saved_struct
octave:22> a_dict
```

```octave
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([(0.0, ''), (0.0, '')],
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:

```
>>> 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.dtype)
float64
```

Saving to a MATLAB cell array just involves making a numpy object array:

```
>>> obj_arr = np.zeros((2,), dtype=np.object)
>>> obj_arr[0] = 1
>>> obj_arr[1] = 'a string'
>>> obj_arr
array([1.0, 'a string'], dtype=object)
>>> 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
}  
```
1.15.2 IDL files

readsav(file_name[, idict, python_dict, ...])  Read an IDL .sav file

1.15.3 Matrix Market files

mminfo(source)  Queries the contents of the Matrix Market file ‘filename’ to extract size and storage information.
mread(source)  Reads the contents of a Matrix Market file ‘filename’ into a matrix.
mmwrite(target, a[, comment, field, precision])  Writes the sparse or dense array a to a Matrix Market formatted file.

1.15.4 Wav sound files (scipy.io.wavfile)

read(filename[, mmap])  Return the sample rate (in samples/sec) and data from a WAV file
write(filename, rate, data)  Write a numpy array as a WAV file

1.15.5 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.

See the WEKA website for more details about arff format and available datasets.

Examples

```python
>>> from scipy.io import arff
>>> from cStringIO 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)

>>> 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')
```

loadarff(f)  Read an arff file.
1.15.6 **Netcdf** *(scipy.io.netcdf)*

```python
cold_file(filename[, mode, mmap, version]) A file object for NetCDF data.
```

Allows reading of NetCDF files (version of pupynere package)

### 1.16 Weave *(scipy.weave)*

#### 1.16.1 Outline
1.16. **Weave** (*scipy.weave*)

- **Outline**
- **Introduction**
- **Requirements**
- **Installation**
- **Testing**
  - Testing Notes:
- **Benchmarks**
- **Inline**
  - More with printf
  - More examples
    - Binary search
    - Dictionary Sort
    - NumPy – cast/copy/transpose
    - wxPython
  - Keyword Option
  - Inline Arguments
  - Distutils keywords
    - Keyword Option Examples
    - Returning Values
    - The issue with `locals()`
    - A quick look at the code
- **Technical Details**
- **Passing Variables in/out of the C/C++ code**
- **Type Conversions**
  - NumPy Argument Conversion
  - String, List, Tuple, and Dictionary Conversion
  - File Conversion
  - Callable, Instance, and Module Conversion
  - Customizing Conversions
- **The Catalog**
  - Function Storage
  - Catalog search paths and the PYTHONCOMPILER variable
- **Blitz**
  - Requirements
  - Limitations
  - NumPy efficiency issues: What compilation buys you
  - The Tools
    - Parser
    - Blitz and NumPy
  - Type definitions and coercion
  - Cataloging Compiled Functions
  - Checking Array Sizes
  - Creating the Extension Module
- **Extension Modules**
  - A Simple Example
  - Fibonacci Example
  - Customizing Type Conversions – Type Factories
  - Things I wish `weave` did
1.16.2 Introduction

The `scipy.weave` (below just `weave`) package provides tools for including C/C++ code within Python code. This offers both another level of optimization to those who need it, and an easy way to modify and extend any supported extension libraries such as wxPython and hopefully VTK soon. Inlining C/C++ code within Python generally results in speed ups of 1.5x to 30x speed-up over algorithms written in pure Python (However, it is also possible to slow things down...). Generally algorithms that require a large number of calls to the Python API don’t benefit as much from the conversion to C/C++ as algorithms that have inner loops completely convertible to C.

There are three basic ways to use `weave`. The `weave.inline()` function executes C code directly within Python, and `weave.blitz()` translates Python NumPy expressions to C++ for fast execution. `blitz()` was the original reason `weave` was built. For those interested in building extension libraries, the `ext_tools` module provides classes for building extension modules within Python.

Most of `weave`’s functionality should work on Windows and Unix, although some of its functionality requires gcc or a similarly modern C++ compiler that handles templates well. Up to now, most testing has been done on Windows 2000 with Microsoft’s C++ compiler (MSVC) and with gcc (mingw32 2.95.2 and 2.95.3-6). All tests also pass on Linux (RH 7.1 with gcc 2.96), and I’ve had reports that it works on Debian also (thanks Pearu).

The `inline` and `blitz` provide new functionality to Python (although I’ve recently learned about the PyInline project which may offer similar functionality to `inline`). On the other hand, tools for building Python extension modules already exists (SWIG, SIP, pycpp, CXX, and others). As of yet, I’m not sure where `weave` fits in this spectrum. It is closest in flavor to CXX in that it makes creating new C/C++ extension modules pretty easy. However, if you’re wrapping a gaggle of legacy functions or classes, SWIG and friends are definitely the better choice. `weave` is set up so that you can customize how Python types are converted to C types in `weave`. This is great for `inline()`, but, for wrapping legacy code, it is more flexible to specify things the other way around – that is how C types map to Python types. This `weave` does not do. I guess it would be possible to build such a tool on top of `weave`, but with good tools like SWIG around, I’m not sure the effort produces any new capabilities. Things like function overloading are probably easily implemented in `weave` and it might be easier to mix Python/C code in function calls, but nothing beyond this comes to mind. So, if you’re developing new extension modules or optimizing Python functions in C, `weave.ext_tools()` might be the tool for you. If you’re wrapping legacy code, stick with SWIG.

The next several sections give the basics of how to use `weave`. We’ll discuss what’s happening under the covers in more detail later on. Serious users will need to at least look at the type conversion section to understand how Python variables map to C/C++ types and how to customize this behavior. One other note. If you don’t know C or C++ then these docs are probably of very little help to you. Further, it’d be helpful if you know something about writing Python extensions. `weave` does quite a bit for you, but for anything complex, you’ll need to do some conversions, reference counting, etc.

Note: `weave` is actually part of the SciPy package. However, it also works fine as a standalone package (you can install from scipy/weave with `python setup.py install`). The examples here are given as if it is used as a stand alone package. If you are using from within scipy, you can use `from scipy import weave` and the examples will work identically.

1.16.3 Requirements

- Python
  
  I use 2.1.1. Probably 2.0 or higher should work.

- C++ compiler

  `weave` uses `distutils` to actually build extension modules, so it uses whatever compiler was originally used to build Python. `weave` itself requires a C++ compiler. If you used a C++ compiler to build Python, your probably fine.
On Unix gcc is the preferred choice because I’ve done a little testing with it. All testing has been done with gcc, but I expect the majority of compilers should work for inline and ext_tools. The one issue I’m not sure about is that I’ve hard coded things so that compilations are linked with the stdc++ library. Is this standard across Unix compilers, or is this a gcc-ism?

For blitz(), you’ll need a reasonably recent version of gcc. 2.95.2 works on windows and 2.96 looks fine on Linux. Other versions are likely to work. Its likely that KAI’s C++ compiler and maybe some others will work, but I haven’t tried. My advice is to use gcc for now unless your willing to tinker with the code some.

On Windows, either MSVC or gcc (mingw32) should work. Again, you’ll need gcc for blitz() as the MSVC compiler doesn’t handle templates well.

I have not tried Cygwin, so please report success if it works for you.

• NumPy

The python NumPy module is required for blitz() to work and for numpy.distutils which is used by weave.

### 1.16.4 Installation

There are currently two ways to get weave. First, weave is part of SciPy and installed automatically (as a sub-package) whenever SciPy is installed. Second, since weave is useful outside of the scientific community, it has been setup so that it can be used as a stand-alone module.

The stand-alone version can be downloaded from here. Instructions for installing should be found there as well.

### 1.16.5 Testing

Once weave is installed, fire up python and run its unit tests.

```
>>> import weave
>>> weave.test()
runs long time... spews tons of output and a few warnings
...

Ran 184 tests in 158.418s
OK

This takes a while, usually several minutes. On Unix with remote file systems, I’ve had it take 15 or so minutes. In the end, it should run about 180 tests and spew some speed results along the way. If you get errors, they’ll be reported at the end of the output. Please report errors that you find. Some tests are known to fail at this point.

If you only want to test a single module of the package, you can do this by running test() for that specific module.
```
```
>>> import weave.scalar_spec
>>> weave.scalar_spec.test()

Ran 7 tests in 23.284s
```

1.16. Weave (scipy.weave)
Testing Notes:

- Windows 1

I’ve had some test fail on windows machines where I have msvc, gcc-2.95.2 (in c:\gcc-2.95.2), and gcc-2.95.3-6 (in c:\gcc) all installed. My environment has c:\gcc in the path and does not have c:\gcc-2.95.2 in the path. The test process runs very smoothly until the end where several test using gcc fail with cpp0 not found by g++. If I check os.system(‘gcc -v’) before running tests, I get gcc-2.95.3-6. If I check after running tests (and after failure), I get gcc-2.95.2. ??huh?? The os.environ[‘PATH’] still has c:\gcc first in it and is not corrupted (msvc/distutils messes with the environment variables, so we have to undo its work in some places). If anyone else sees this, let me know - - it may just be an quirk on my machine (unlikely). Testing with the gcc- 2.95.2 installation always works.

- Windows 2

If you run the tests from PythonWin or some other GUI tool, you’ll get a ton of DOS windows popping up periodically as weave spawns the compiler multiple times. Very annoying. Anyone know how to fix this?

- wxPython

wxPython tests are not enabled by default because importing wxPython on a Unix machine without access to a X-term will cause the program to exit. Anyone know of a safe way to detect whether wxPython can be imported and whether a display exists on a machine?

1.16.6 Benchmarks

This section has not been updated from old scipy weave and Numeric....

This section has a few benchmarks – thats all people want to see anyway right? These are mostly taken from running files in the weave/example directory and also from the test scripts. Without more information about what the test actually do, their value is limited. Still, their here for the curious. Look at the example scripts for more specifics about what problem was actually solved by each run. These examples are run under windows 2000 using Microsoft Visual C++ and python2.1 on a 850 MHz PIII laptop with 320 MB of RAM. Speed up is the improvement (degredation) factor of weave compared to conventional Python functions. The blitz() comparisons are shown compared to NumPy.

Table 1.7: inline and ext_tools

<table>
<thead>
<tr>
<th>Algorithm</th>
<th>Speed up</th>
</tr>
</thead>
<tbody>
<tr>
<td>binary search</td>
<td>1.50</td>
</tr>
<tr>
<td>fibonacci (recursive)</td>
<td>82.10</td>
</tr>
<tr>
<td>fibonacci (loop)</td>
<td>9.17</td>
</tr>
<tr>
<td>return None</td>
<td>0.14</td>
</tr>
<tr>
<td>map</td>
<td>1.20</td>
</tr>
<tr>
<td>dictionary sort</td>
<td>2.54</td>
</tr>
<tr>
<td>vector quantization</td>
<td>37.40</td>
</tr>
</tbody>
</table>

Table 1.8: blitz – double precision

<table>
<thead>
<tr>
<th>Algorithm</th>
<th>Speed up</th>
</tr>
</thead>
<tbody>
<tr>
<td>a = b + c 512x512</td>
<td>3.05</td>
</tr>
<tr>
<td>a = b + c + d 512x512</td>
<td>4.59</td>
</tr>
<tr>
<td>5 pt avg. filter, 2D Image 512x512</td>
<td>9.01</td>
</tr>
<tr>
<td>Electromagnetics (FDTD) 100x100x100</td>
<td>8.61</td>
</tr>
</tbody>
</table>

The benchmarks shown blitz in the best possible light. NumPy (at least on my machine) is significantly worse for double precision than it is for single precision calculations. If your interested in single precision results, you can pretty much divide the double precision speed up by 3 and you’ll be close.
## 1.16.7 Inline

`inline()` compiles and executes C/C++ code on the fly. Variables in the local and global Python scope are also available in the C/C++ code. Values are passed to the C/C++ code by assignment much like variables are passed into a standard Python function. Values are returned from the C/C++ code through a special argument called `return_val`. Also, the contents of mutable objects can be changed within the C/C++ code and the changes remain after the C code exits and returns to Python. (more on this later)

Here's a trivial `printf` example using `inline()`:

```python
>>> import weave
>>> a = 1
>>> weave.inline('printf("%d\n",a);',['a'])
1
```

In this, its most basic form, `inline(c_code, var_list)` requires two arguments. `c_code` is a string of valid C/C++ code. `var_list` is a list of variable names that are passed from Python into C/C++. Here we have a simple `printf` statement that writes the Python variable `a` to the screen. The first time you run this, there will be a pause while the code is written to a .cpp file, compiled into an extension module, loaded into Python, cataloged for future use, and executed. On windows (850 MHz PIII), this takes about 1.5 seconds when using Microsoft's C++ compiler (MSVC) and 6-12 seconds using gcc (mingw32 2.95.2). All subsequent executions of the code will happen very quickly because the code only needs to be compiled once. If you kill and restart the interpreter and then execute the same code fragment again, there will be a much shorter delay in the fractions of seconds range. This is because `weave` stores a catalog of all previously compiled functions in an on disk cache. When it sees a string that has been compiled, it loads the already compiled module and executes the appropriate function.

**Note:** If you try the `printf` example in a GUI shell such as IDLE, PythonWin, PyShell, etc., you’re unlikely to see the output. This is because the C code is writing to stdout, instead of to the GUI window. This doesn’t mean that `inline` doesn’t work in these environments – it only means that standard out in C is not the same as the standard out for Python in these cases. Non input/output functions will work as expected.

Although effort has been made to reduce the overhead associated with calling `inline`, it is still less efficient for simple code snippets than using equivalent Python code. The simple `printf` example is actually slower by 30% or so than using Python `print` statement. And, it is not difficult to create code fragments that are 8-10 times slower using `inline` than equivalent Python. However, for more complicated algorithms, the speedup can be worthwhile – anywhere from 1.5-30 times faster. Algorithms that have to manipulate Python objects (sorting a list) usually only see a factor of 2 or so improvement. Algorithms that are highly computational or manipulate NumPy arrays can see much larger improvements. The examples/vq.py file shows a factor of 30 or more improvement on the vector quantization algorithm that is used heavily in information theory and classification problems.

### More with printf

MSVC users will actually see a bit of compiler output that distutils does not suppress the first time the code executes:

```python
>>> weave.inline(r'printf("%d\n",a);',['a'])
sc_e013937dcb8c647ac62438874e5795131.cpp
Creating library C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp
\Release\sc_e013937dcb8c647ac62438874e5795131.lib and
object C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\sc_e013937dcb8c647ac62438874e5795131.obj
1
```

Nothing bad is happening, its just a bit annoying. * Anyone know how to turn this off?*

This example also demonstrates using ‘raw strings’. The `r` preceding the code string in the last example denotes that this is a ‘raw string’. In raw strings, the backslash character is not interpreted as an escape character, and so it isn’t necessary to use a double backslash to indicate that the ‘n’ is meant to be interpreted in the C `printf` statement.
instead of by Python. If your C code contains a lot of strings and control characters, raw strings might make things easier. Most of the time, however, standard strings work just as well.

The `printf` statement in these examples is formatted to print out integers. What happens if `a` is a string? `inline` will happily, compile a new version of the code to accept strings as input, and execute the code. The result?

```python
>>> a = 'string'
>>> weave.inline(r'printf("%d\n",a);',['a'])
32956972
```

In this case, the result is non-sensical, but also non-fatal. In other situations, it might produce a compile time error because `a` is required to be an integer at some point in the code, or it could produce a segmentation fault. Its possible to protect against passing `inline` arguments of the wrong data type by using asserts in Python.

```python
>>> a = 'string'
>>> def protected_printf(a):
...     assert(type(a) == type(1))
...     weave.inline(r'printf("%d\n",a);',['a'])
>>> protected_printf(1)
1
>>> protected_printf('string')
AssertionError...
```

For printing strings, the format statement needs to be changed. Also, weave doesn’t convert strings to char*. Instead it uses CXX Py::String type, so you have to do a little more work. Here we convert it to a C++ std::string and then ask for the char* version.

```python
>>> a = 'string'
>>> weave.inline(r'printf("%s\n",std::string(a).c_str());',['a'])
string
```

XXX

This is a little convoluted. Perhaps strings should convert to std::string objects instead of CXX objects. Or maybe to char*.

As in this case, C/C++ code fragments often have to change to accept different types. For the given printing task, however, C++ streams provide a way of a single statement that works for integers and strings. By default, the stream objects live in the std (standard) namespace and thus require the use of std::.

```python
>>> weave.inline('std::cout << a << std::endl;',['a'])
1
>>> a = 'string'
>>> weave.inline('std::cout << a << std::endl;',['a'])
string
```

Examples using `printf` and `cout` are included in examples/print_example.py.

**More examples**

This section shows several more advanced uses of `inline`. It includes a few algorithms from the Python Cookbook that have been re-written in inline C to improve speed as well as a couple examples using NumPy and wxPython.

**Binary search**

Lets look at the example of searching a sorted list of integers for a value. For inspiration, we’ll use Kalle Svensson’s `binary_search()` algorithm from the Python Cookbook. His recipe follows:
def binary_search(seq, t):
    min = 0; max = len(seq) - 1
    while 1:
        if max < min:
            return -1
        m = (min + max) / 2
        if seq[m] < t:
            min = m + 1
        elif seq[m] > t:
            max = m - 1
        else:
            return m

This Python version works for arbitrary Python data types. The C version below is specialized to handle integer values. There is a little type checking done in Python to assure that we’re working with the correct data types before heading into C. The variables seq and t don’t need to be declared because weave handles converting and declaring them in the C code. All other temporary variables such as min, max, etc. must be declared – it is C after all. Here’s the new mixed Python/C function:

def c_int_binary_search(seq,t):
    # do a little type checking in Python
    assert(type(t) == type(1))
    assert(type(seq) == type([]))

    # now the C code
    code = ""
    #line 29 "binary_search.py"
    int val, m, min = 0;
    int max = seq.length() - 1;
    PyObject *py_val;
    for(;;)
    {
        if (max < min )
        {
            return_val = Py::new_reference_to(Py::Int(-1));
            break;
        }
        m = (min + max) /2;
        val = py_to_int(PyList_GetItem(seq.ptr(),m),"val");
        if (val < t)
            min = m + 1;
        else if (val > t)
            max = m - 1;
        else
        {
            return_val = Py::new_reference_to(Py::Int(m));
            break;
        }
    }
    ""
    return inline(code,['seq','t'])

We have two variables seq and t passed in. t is guaranteed (by the assert) to be an integer. Python integers are converted to C int types in the transition from Python to C. seq is a Python list. By default, it is translated to a CXX list object. Full documentation for the CXX library can be found at its website. The basics are that the CXX provides C++ class equivalents for Python objects that simplify, or at least object orientify, working with Python objects in C/C++. For example, seq.length() returns the length of the list. A little more about CXX and its class methods, etc. is in the Type Conversions section.
Note: CXX uses templates and therefore may be a little less portable than another alternative by Gordan McMillan called SCXX which was inspired by CXX. It doesn’t use templates so it should compile faster and be more portable. SCXX has a few less features, but it appears to me that it would mesh with the needs of weave quite well. Hopefully xxx_spec files will be written for SCXX in the future, and we’ll be able to compare on a more empirical basis. Both sets of spec files will probably stick around, it just a question of which becomes the default.

Most of the algorithm above looks similar in C to the original Python code. There are two main differences. The first is the setting of return_val instead of directly returning from the C code with a return statement. return_val is an automatically defined variable of type PyObject* that is returned from the C code back to Python. You’ll have to handle reference counting issues when setting this variable. In this example, CXX classes and functions handle the dirty work. All CXX functions and classes live in the namespace Py::. The following code converts the integer \( m \) to a CXX Int() object and then to a PyObject* with an incremented reference count using Py::new_reference_to().

```cpp
return_val = Py::new_reference_to(Py::Int(m));
```

The second big differences shows up in the retrieval of integer values from the Python list. The simple Python `seq[i]` call balloons into a C Python API call to grab the value out of the list and then a separate call to `py_to_int()` that converts the PyObject* to an integer. `py_to_int()` includes both a NULL check and a `PyInt_Check()` call as well as the conversion call. If either of the checks fail, an exception is raised. The entire C++ code block is executed with a try/catch block that handles exceptions much like Python does. This removes the need for most error checking code.

It is worth note that CXX lists do have indexing operators that result in code that looks much like Python. However, the overhead in using them appears to be relatively high, so the standard Python API was used on the `seq.ptr()` which is the underlying PyObject* of the List object.

The #line directive that is the first line of the C code block isn’t necessary, but it’s nice for debugging. If the compilation fails because of the syntax error in the code, the error will be reported as an error in the Python file “binary_search.py” with an offset from the given line number (29 here).

So what was all our effort worth in terms of efficiency? Well not a lot in this case. The examples/binary_search.py file runs both Python and C versions of the functions As well as using the standard `bisect` module. If we run it on a 1 million element list and run the search 3000 times (for 0-2999), here are the results we get:

```none
C:\home\ejw\weave\examples> python binary_search.py
Binary search for 3000 items in 1000000 length list of integers:
speed in python: 0.159999966621
speed of bisect: 0.121000051498
speed up: 1.32
speed in c: 0.110000014305
speed up: 1.45
speed in c(no asserts): 0.0900000333786
speed up: 1.78
```

So, we get roughly a 50-75% improvement depending on whether we use the Python asserts in our C version. If we move down to searching a 10000 element list, the advantage evaporates. Even smaller lists might result in the Python version being faster. I’d like to say that moving to NumPy lists (and getting rid of the GetItem() call) offers a substantial speed up, but my preliminary efforts didn’t produce one. I think the log(N) algorithm is to blame. Because the algorithm is nice, there just isn’t much time spent computing things, so moving to C isn’t that big of a win. If there are ways to reduce conversion overhead of values, this may improve the C/Python speed up. Anyone have other explanations or faster code, please let me know.

**Dictionary Sort**

The demo in examples/dict_sort.py is another example from the Python CookBook. This submission, by Alex Martelli, demonstrates how to return the values from a dictionary sorted by their keys:
def sortedDictValues3(adict):
    keys = adict.keys()
    keys.sort()
    return map(adict.get, keys)

Alex provides 3 algorithms and this is the 3rd and fastest of the set. The C version of this same algorithm follows:

def c_sort(adict):
    assert type(adict) == type({})
    code = ""
    #line 21 "dict_sort.py"
    Py::List keys = adict.keys();
    Py::List items(keys.length()); keys.sort();
    PyObject* item = NULL;
    for(int i = 0; i < keys.length();i++)
    {
        item = PyList_GET_ITEM(keys.ptr(),i);
        item = PyDict_GetItem(adict.ptr(),item);
        Py_XINCREF(item);
        PyList_SetItem(items.ptr(),i,item);
    }
    return_val = Py::new_reference_to(items);
    ""
    return inline_tools.inline(code, ['adict'], verbose=1)

Like the original Python function, the C++ version can handle any Python dictionary regardless of the key/value pair types. It uses CXX objects for the most part to declare python types in C++, but uses Python API calls to manipulate their contents. Again, this choice is made for speed. The C++ version, while more complicated, is about a factor of 2 faster than Python.

C:\home\ej\wrk\scipy\weave\examples> python dict_sort.py
Dict sort of 1000 items for 300 iterations:
speed in python: 0.319999933243
[0, 1, 2, 3, 4]
speed in c: 0.151000022888
speed up: 2.12
[0, 1, 2, 3, 4]

NumPy – cast/copy/transpose

CastCopyTranspose is a function called quite heavily by Linear Algebra routines in the NumPy library. Its needed in part because of the row-major memory layout of multi-demensional Python (and C) arrays vs. the col-major order of the underlying Fortran algorithms. For small matrices (say 100x100 or less), a significant portion of the common routines such as LU decompostision or singular value decompostion are spent in this setup routine. This shouldn't happen. Here is the Python version of the function using standard NumPy operations.

def _castCopyAndTranspose(type, array):
    if a.typecode() == type:
        cast_array = copy.copy(NumPy.transpose(a))
    else:
        cast_array = copy.copy(NumPy.transpose(a).astype(type))
    return cast_array

And the following is a inline C version of the same function:

from weave.blitz_tools import blitz_type_factories
from weave import scalar_spec
from weave import inline

def _cast_copy_transpose(type,a_2d):

1.16. Weave (scipy.weave)
```
assert(len(shape(a_2d)) == 2)
new_array = zeros(shape(a_2d),type)
NumPy_type = scalar_spec.NumPy_to_blitz_type_mapping[type]
code = \
""
for(int i = 0;i < _Na_2d[0]; i++)
    for(int j = 0; j < _Na_2d[1]; j++)
        new_array(i,j) = (%s) a_2d(j,i);
""
inline(code,
        ['new_array','a_2d'],
        type_factories = blitz_type_factories,compiler='gcc')
return new_array
```

This example uses blitz++ arrays instead of the standard representation of NumPy arrays so that indexing is simpler to write. This is accomplished by passing in the blitz++ “type factories” to override the standard Python to C++ type conversions. Blitz++ arrays allow you to write clean, fast code, but they also are sloooow to compile (20 seconds or more for this snippet). This is why they aren’t the default type used for Numeric arrays (and also because most compilers can’t compile blitz arrays...). `inline()` is also forced to use ‘gcc’ as the compiler because the default compiler on Windows (MSVC) will not compile blitz code. (‘gcc’ I think will use the standard compiler on Unix machine instead of explicitly forcing gcc (check this)) Comparisons of the Python vs inline C++ code show a factor of 3 speed up. Also shown are the results of an “inplace” transpose routine that can be used if the output of the linear algebra routine can overwrite the original matrix (this is often appropriate). This provides another factor of 2 improvement.

```
wxPython
inline knows how to handle wxPython objects. That’s nice in and of itself, but it also demonstrates that the type conversion mechanism is reasonably flexible. Chances are, it won’t take a ton of effort to support special types you might have. The examples/wx_example.py borrows the scrolled window example from the wxPython demo, accept that it mixes inline C code in the middle of the drawing function.

def DoDrawing(self, dc):
    red = wxNamedColour("RED");
    blue = wxNamedColour("BLUE");
    grey_brush = wxLIGHT_GREY_BRUSH;
    code = \
    """#
    line 108 "wx_example.py"
    dc->BeginDrawing();
    dc->SetPen(wxPen(*red,4,wxSOLID));
    dc->DrawRectangle(5,5,50,50);
    dc->SetBrush(*grey_brush);
    dc->SetPen(wxPen(*blue,4,wxSOLID));
    dc->DrawRectangle(15, 15, 50, 50);
    """
    inline(code,["dc","red","blue","grey_brush"])  
    dc.SetFont(wxFont(14, wxSWISS, wxNORMAL, wxNORMAL))
    dc.SetTextForeground(wxColour(0xFF, 0x20, 0xFF))
```
Here, some of the Python calls to wx objects were just converted to C++ calls. There isn’t any benefit, it just demonstrates the capabilities. You might want to use this if you have a computationally intensive loop in your drawing code that you want to speed up. On windows, you’ll have to use the MSVC compiler if you use the standard wxPython DLLs distributed by Robin Dunn. That’s because MSVC and gcc, while binary compatible in C, are not binary compatible for C++. In fact, its probably best, no matter what platform you’re on, to specify that `inline` use the same compiler that was used to build wxPython to be on the safe side. There isn’t currently a way to learn this info from the library – you just have to know. Also, at least on the windows platform, you’ll need to install the wxWindows libraries and link to them. I think there is a way around this, but I haven’t found it yet – I get some linking errors dealing with `wxString`. One final note. You’ll probably have to tweak `weave/wx_spec.py` or `weave/wx_info.py` for your machine’s configuration to point at the correct directories etc. There. That should sufficiently scare people into not even looking at this... :)

**Keyword Option**

The basic definition of the `inline()` function has a slew of optional variables. It also takes keyword arguments that are passed to `distutils` as compiler options. The following is a formatted cut/paste of the argument section of `inline`’s doc-string. It explains all of the variables. Some examples using various options will follow.

```python
def inline(code, arg_names, local_dict = None, global_dict = None,
          force = 0,
          compiler='',
          verbose = 0,
          support_code = None,
          customize=None,
          type_factories = None,
          auto_downcast=1,
          **kw):
```

`inline` has quite a few options as listed below. Also, the keyword arguments for `distutils` extension modules are accepted to specify extra information needed for compiling.

**Inline Arguments**

code string. A string of valid C++ code. It should not specify a return statement. Instead it should assign results that need to be returned to Python in the return_val. `arg_names` list of strings. A list of Python variable names that should be transferred from Python into the C/C++ code. `local_dict` optional. dictionary. If specified, it is a dictionary of values that should be used as the local scope for the C/C++ code. `global_dict` optional. dictionary. If specified, it is a dictionary of values that should be used as the global scope for the C/C++ code. `force` optional. 0 or 1. default 0. If 1, the C++ code is compiled every time `inline` is called. This is really only useful for debugging, and probably only useful if you’re editing `support_code` a lot. `compiler` optional. string. The name of compiler to use when compiling. On windows, it understands ‘msvc’ and ‘gcc’ as well as all the compiler names understood by `distutils`. On Unix, it’ll only understand the values understood by `distutils`. (I should add ‘gcc’ though to this).

On windows, the compiler defaults to the Microsoft C++ compiler. If this isn’t available, it looks for mingw32 (the gcc compiler).
On Unix, it’ll probably use the same compiler that was used when compiling Python. Cygwin’s behavior should be similar.

verbose optional. 0, 1, or 2. default 0. Specifies how much much information is printed during the compile phase of inlining code. 0 is silent (except on windows with msvc where it still prints some garbage). 1 informs you when compiling starts, finishes, and how long it took. 2 prints out the command lines for the compilation process and can be useful if you’re having problems getting code to work. Its handy for finding the name of the .cpp file if you need to examine it. verbose has no affect if the compilation isn’t necessary. support_code optional. string. A string of valid C++ code declaring extra code that might be needed by your compiled function. This could be declarations of functions, classes, or structures. customize optional. base_info.custom_info object. An alternative way to specify support_code, headers, etc. needed by the function see the weave.base_info module for more details. (not sure this’ll be used much). type_factories optional. list of type specification factories. These guys are what convert Python data types to C/C++ data types. If you’d like to use a different set of type conversions than the default, specify them here. Look in the type conversions section of the main documentation for examples. auto_downcast optional. 0 or 1. default 1. This only affects functions that have Numeric arrays as input variables. Setting this to 1 will cause all floating point values to be cast as float instead of double if all the NumPy arrays are of type float. If even one of the arrays has type double or double complex, all variables maintain there standard types.

Distutils keywords

**inline()** also accepts a number of distutils keywords for controlling how the code is compiled. The following descriptions have been copied from Greg Ward’s distutils.extension.Extension class doc- strings for convenience: sources [string] list of source filenames, relative to the distribution root (where the setup script lives), in Unix form (slash- separated) for portability. Source files may be C, C++, SWIG (.i), platform- specific resource files, or whatever else is recognized by the “build_ext” command as source for a Python extension. Note: The module_path file is always appended to the front of this list include_dirs [string] list of directories to search for C/C++ header files (in Unix form for portability) define_macros [(name : string, value : string|None)] list of macros to define; each macro is defined using a 2-tuple, where ‘value’ is either the string to define it to or None to define it without a particular value (equivalent of “#define FOO” in source or -DFOO on Unix C compiler command line) undef_macros [string] list of macros to undefine explicitly library_dirs [string] list of directories to search for C/C++ libraries at link time libraries [string] list of library names (not filenames or paths) to link against runtime_library_dirs [string] list of directories to search for C/C++ libraries at run time (for shared extensions, this is when the extension is loaded) extra_objects [string] list of extra files to link with (eg. object files not implied by ‘sources’, static library that must be explicitly specified, binary resource files, etc.) extra_compile_args [string] any extra platform- and compiler-specific information to use when compiling the source files in ‘sources’. For platforms and compilers where “command line” makes sense, this is typically a list of command-line arguments, but for other platforms it could be anything. extra_link_args [string] any extra platform- and compiler-specific information to use when linking object files together to create the extension (or to create a new static Python interpreter). Similar interpretation as for ‘extra_compile_args’. export_symbols [string] list of symbols to be exported from a shared extension. Not used on all platforms, and not generally necessary for Python extensions, which typically export exactly one symbol: “init” + extension_name.

Keyword Option Examples

We’ll walk through several examples here to demonstrate the behavior of inline and also how the various arguments are used. In the simplest (most) cases, code and arg_names are the only arguments that need to be specified. Here’s a simple example run on Windows machine that has Microsoft VC++ installed.

```python
>>> from weave import inline
>>> a = 'string'
>>> code = ""
...   int l = a.length();
...   return_val = Py::new_reference_to(Py::Int(l));
... ""
>>> inline(code, ['a'])
sc_86e98826b65b047fffd2cd5f479c627f12.cpp
```
Creating library C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\sc_86e98826b65b047fffd2cd5f479c627f12.lib
and object C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\sc_86e98826b65b047fffd2cd5f479c627f12.exp

>>> inline(code, ['a'])

When `inline` is first run, you’ll notice that pause and some trash printed to the screen. The “trash” is actually part of
the compiler’s output that distutils does not supress. The name of the extension file, `sc_bighonkingnumber.cpp`, is
generated from the SHA-256 check sum of the C/C++ code fragment. On Unix or windows machines with only gcc
installed, the trash will not appear. On the second call, the code fragment is not compiled since it already exists, and
only the answer is returned. Now kill the interpreter and restart, and run the same code with a different string.

```python
>>> from weave import inline
>>> a = 'a longer string'
>>> code = ""
...     int l = a.length();
...     return_val = Py::new_reference_to(Py::Int(l));
... ""
>>> inline(code, ['a'])
15
```

Notice this time, `inline()` did not recompile the code because it found the compiled function in the persistent
catalog of functions. There is a short pause as it looks up and loads the function, but it is much shorter than compiling
would require.

You can specify the local and global dictionaries if you’d like (much like `exec` or `eval()` in Python), but if they
aren’t specified, the “expected” ones are used – i.e. the ones from the function that called `inline()`. This is
accomplished through a little call frame trickery. Here is an example where the local_dict is specified using the same
code example from above:

```python
>>> a = 'a longer string'
>>> b = 'an even longer string'
>>> my_dict = {'a':b}
>>> inline(code, ['a'])
15
>>> inline(code, ['a'], my_dict)
21
```

Every time the `code` is changed, `inline` does a recompile. However, changing any of the other options in `inline`
does not force a recompile. The `force` option was added so that one could force a recompile when tinkering with
other variables. In practice, it is just as easy to change the `code` by a single character (like adding a space some place)
to force the recompile.

**Note:** It also might be nice to add some methods for purging the cache and on disk catalogs.

I use `verbose` sometimes for debugging. When set to 2, it’ll output all the information (including the name of
the `.cpp` file) that you’d expect from running a make file. This is nice if you need to examine the generated code to
see where things are going haywire. Note that error messages from failed compiles are printed to the screen even if
`verbose` is set to 0.

The following example demonstrates using gcc instead of the standard msvc compiler on windows using same code
fragment as above. Because the example has already been compiled, the `force=1` flag is needed to make `inline()`
ignore the previously compiled version and recompile using gcc. The `verbose` flag is added to show what is printed out:
```python
>>> inline(code, ['a'], compiler='gcc', verbose=2, force=1)
running build_ext
c:\gcc-2.95.2\bin\g++.exe -mno-cygwin -mdll -O2 -w -Wstrict-prototypes -IC:
\home\ej\wrk\scipy\weave -IC:\Python21\Include -c C:\DOCUME~1\eric\LOCAL
S-1\Temp\python21_compiled\sc_86e98826b65b047fffd2cd5f479c627f13.cpp
skipping C:\home\ej\wrk\scipy\weave\CXX\cxxextensions.c
(C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\sc_86e98826b65b047fffd2cd5f479c627f13.o up-to-date)
skipping C:\home\ej\wrk\scipy\weave\CXX\cxxsupport.cxx
(C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\cxxsupport.o up-to-date)
skipping C:\home\ej\wrk\scipy\weave\CXX\IndirectPythonInterface.cxx
(C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\indirectpythoninterface.o up-to-date)
skipping C:\home\ej\wrk\scipy\weave\CXX\cxx_extensions.cxx
(C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\cxx_extensions.o up-to-date)
writing C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\sc_86e98826b65b047fffd2cd5f479c627f13.def
c:\gcc-2.95.2\bin\dllwrap.exe --driver-name g++ -mno-cygwin
-mdll -static --output-lib C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\libsc_86e98826b65b047fffd2cd5f479c627f13.a
-C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\indirectpythoninterface.o
-C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\cxxsupport.o
-C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\cxx_extensions.o
-LC:\Python21\libs
-o C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\sc_86e98826b65b047fffd2cd5f479c627f13.pyd
15
That's quite a bit of output. verbose=1 just prints the compile time.
```
customize is a left over from a previous way of specifying compiler options. It is a custom_info object that can specify quite a bit of information about how a file is compiled. These info objects are the standard way of defining compile information for type conversion classes. However, I don’t think they are as handy here, especially since we’ve exposed all the keyword arguments that distutils can handle. Between these keywords, and the support_code option, I think customize may be obsolete. We’ll see if anyone cares to use it. If not, it’ll get axed in the next version.

The type_factories variable is important to people who want to customize the way arguments are converted from Python to C. We’ll talk about this in the next chapter xx of this document when we discuss type conversions.

auto_downcast handles one of the big type conversion issues that is common when using NumPy arrays in conjunction with Python scalar values. If you have an array of single precision values and multiply that array by a Python scalar, the result is upcast to a double precision array because the scalar value is double precision. This is not usually the desired behavior because it can double your memory usage. auto_downcast goes some distance towards changing the casting precedence of arrays and scalars. If your only using single precision arrays, it will automatically downcast all scalar values from double to single precision when they are passed into the C++ code. This is the default behavior. If you want all values to keep their default type, set auto_downcast to 0.

Returning Values

Python variables in the local and global scope transfer seamlessly from Python into the C++ snippets. And, if inline were to completely live up to its name, any modifications to variables in the C++ code would be reflected in the Python variables when control was passed back to Python. For example, the desired behavior would be something like:

```python
# THIS DOES NOT WORK
>>> a = 1
>>> weave.inline("a++;",['a'])
>>> a
2
```

Instead you get:

```python
>>> a = 1
>>> weave.inline("a++;",['a'])
>>> a
1
```

Variables are passed into C++ as if you are calling a Python function. Python’s calling convention is sometimes called “pass by assignment”. This means its as if a c_a = a assignment is made right before inline call is made and the c_a variable is used within the C++ code. Thus, any changes made to c_a are not reflected in Python’s a variable. Things do get a little more confusing, however, when looking at variables with mutable types. Changes made in C++ to the contents of mutable types are reflected in the Python variables.

```python
>>> a= [1,2]
>>> weave.inline("PyList_SetItem(a.ptr(),0,PyInt_FromLong(3));","a'")
>>> print a
[3, 2]
```

So modifications to the contents of mutable types in C++ are seen when control is returned to Python. Modifications to immutable types such as tuples, strings, and numbers do not alter the Python variables. If you need to make changes to an immutable variable, you’ll need to assign the new value to the “magic” variable return_val in C++. This value is returned by the inline() function:

```python
>>> a = 1
>>> a = weave.inline("return_val = Py::new_reference_to(Py::Int(a+1));","a'")
>>> a
2
```
The return_val variable can also be used to return newly created values. This is possible by returning a tuple. The following trivial example illustrates how this can be done:

```python
# python version
def multi_return():
    return 1, '2nd'

# C version.
def c_multi_return():
    code = ""
    results = py::tuple(2);
    results[0] = 1;
    results[1] = "2nd";
    return_val = results;
    ""
    return inline_tools.inline(code)
```

The example is available in examples/tuple_return.py. It also has the dubious honor of demonstrating how much inline() can slow things down. The C version here is about 7-10 times slower than the Python version. Of course, something so trivial has no reason to be written in C anyway.

The issue with locals() inline passes the locals() and globals() dictionaries from Python into the C++ function from the calling function. It extracts the variables that are used in the C++ code from these dictionaries, converts them to C++ variables, and then calculates using them. It seems like it would be trivial, then, after the calculations were finished to then insert the new values back into the locals() and globals() dictionaries so that the modified values were reflected in Python. Unfortunately, as pointed out by the Python manual, the locals() dictionary is not writable.

I suspect locals() is not writable because there are some optimizations done to speed lookups of the local namespace. I’m guessing local lookups don’t always look at a dictionary to find values. Can someone “in the know” confirm or correct this? Another thing I’d like to know is whether there is a way to write to the local namespace of another stack frame from C++. If so, it would be possible to have some clean up code in compiled functions that wrote final values of variables in C++ back to the correct Python stack frame. I think this goes a long way toward making inline truly live up to its name. I don’t think we’ll get to the point of creating variables in Python for variables created in C – although I suppose with a C/C++ parser you could do that also.

A quick look at the code

weave generates a C++ file holding an extension function for each inline code snippet. These file names are generated using from the SHA-256 signature of the code snippet and saved to a location specified by the PYTHON-COMPILED environment variable (discussed later). The cpp files are generally about 200-400 lines long and include quite a few functions to support type conversions, etc. However, the actual compiled function is pretty simple. Below is the familiar printf example:

```python
>>> import weave
>>> a = 1
>>> weave.inline('printf("%d\n",a);', ['a'])
1
```

And here is the extension function generated by inline:

```c
static PyObject* compiled_func(PyObject* self, PyObject* args)
{
    py::object return_val;
    int exception_occurred = 0;
    PyObject *py__locals = NULL;
    PyObject *py__globals = NULL;
    PyObject *py_a;
```
py_a = NULL;

if(!PyArg_ParseTuple(args,"OO:compiled_func",&py__locals,&py__globals))
    return NULL;

try
{
    PyObject* raw_locals = py_to_raw_dict(py__locals,"_locals");
    PyObject* raw_globals = py_to_raw_dict(py__globals,"_globals");
    /* argument conversion code */
    py_a = get_variable("a",raw_locals,raw_globals);
    int a = convert_to_int(py_a,"a");
    /* inline code */
    /* NDARRAY API VERSION 90907 */
    printf("%d\n",a);  /* I would like to fill in changed locals and globals here...*/
}

  catch(...)
  {
    return_val = py::object();
    exception_occured = 1;
  }

  /* cleanup code */
  if(!(!PyObject*)return_val && !exception_occured)
  {
    return_val = Py_None;
  }
  return return_val.disown();
}

Every inline function takes exactly two arguments – the local and global dictionaries for the current scope. All variable
values are looked up out of these dictionaries. The lookups, along with all inline code execution, are done within a C++ try block. If the variables aren’t found, or there is an error converting a Python variable to the appropriate type in C++, an exception is raised. The C++ exception is automatically converted to a Python exception by SCXX and returned to Python. The py_to_int() function illustrates how the conversions and exception handling works.

py_to_int first checks that the given PyObject* pointer is not NULL and is a Python integer. If all is well, it calls the Python API to convert the value to an int. Otherwise, it calls handle_bad_type() which gathers information about what went wrong and then raises a SCXX TypeError which returns to Python as a TypeError.

```c
int py_to_int(PyObject* py_obj,char* name)
{
    if (!py_obj || !PyInt_Check(py_obj))
        handle_bad_type(py_obj,"int", name);
    return (int) PyInt_AsLong(py_obj);
}
```

```c
void handle_bad_type(PyObject* py_obj, char* good_type, char* var_name)
{
    char msg[500];
    sprintf(msg,"received '%s' type instead of '%s' for variable '%s'",
            find_type(py_obj),good_type,var_name);
    throw Py::TypeError(msg);
}
```

```c
char* find_type(PyObject* py_obj)
{
    if(py_obj == NULL) return "C NULL value";
    if(PyCallable_Check(py_obj)) return "callable";
    if(PyString_Check(py_obj)) return "string";
    if(PyInt_Check(py_obj)) return "int";
    return NULL;
}
```
if (PyFloat_Check(py_obj)) return "float";
if (PyDict_Check(py_obj)) return "dict";
if (PyList_Check(py_obj)) return "list";
if (PyTuple_Check(py_obj)) return "tuple";
if (PyFile_Check(py_obj)) return "file";
if (PyModule_Check(py_obj)) return "module";

// should probably do more interaction (and thinking) on these.
if (PyCallable_Check(py_obj) && PyInstance_Check(py_obj)) return "callable";
if (PyInstance_Check(py_obj)) return "instance";
if (PyCallable_Check(py_obj)) return "callable";
return "unknown type";
}

Since the inline is also executed within the try/catch block, you can use CXX exceptions within your code. It is usually a bad idea to directly return from your code, even if an error occurs. This skips the clean up section of the extension function. In this simple example, there isn’t any clean up code, but in more complicated examples, there may be some reference counting that needs to be taken care of here on converted variables. To avoid this, either uses exceptions or set return_val to NULL and use if/then’s to skip code after errors.

Technical Details

There are several main steps to using C/C++ code within Python:

1. Type conversion
2. Generating C/C++ code
3. Compile the code to an extension module
4. Catalog (and cache) the function for future use

Items 1 and 2 above are related, but most easily discussed separately. Type conversions are customizable by the user if needed. Understanding them is pretty important for anything beyond trivial uses of inline. Generating the C/C++ code is handled by ext_function and ext_module classes and . For the most part, compiling the code is handled by distutils. Some customizations were needed, but they were relatively minor and do not require changes to distutils itself. Cataloging is pretty simple in concept, but surprisingly required the most code to implement (and still likely needs some work). So, this section covers items 1 and 4 from the list. Item 2 is covered later in the chapter covering the ext_tools module, and distutils is covered by a completely separate document xxx.

Passing Variables in/out of the C/C++ code

Note: Passing variables into the C code is pretty straightforward, but there are subtleties to how variable modifications in C are returned to Python. see Returning Values for a more thorough discussion of this issue.

Type Conversions

Note: Maybe xxx_converter instead of xxx_specification is a more descriptive name. Might change in future version?

By default, inline() makes the following type conversions between Python and C++ types.
Table 1.9: Default Data Type Conversions

<table>
<thead>
<tr>
<th>Python</th>
<th>C++</th>
</tr>
</thead>
<tbody>
<tr>
<td>int</td>
<td>int</td>
</tr>
<tr>
<td>float</td>
<td>double</td>
</tr>
<tr>
<td>complex</td>
<td>std::complex</td>
</tr>
<tr>
<td>string</td>
<td>py::string</td>
</tr>
<tr>
<td>list</td>
<td>py::list</td>
</tr>
<tr>
<td>dict</td>
<td>py::dict</td>
</tr>
<tr>
<td>tuple</td>
<td>py::tuple</td>
</tr>
<tr>
<td>file</td>
<td>FILE*</td>
</tr>
<tr>
<td>callable</td>
<td>py::object</td>
</tr>
<tr>
<td>instance</td>
<td>py::object</td>
</tr>
<tr>
<td>numpy.ndarray</td>
<td>PyArrayObject*</td>
</tr>
<tr>
<td>wxXXX</td>
<td>wxXXX*</td>
</tr>
</tbody>
</table>

The Py:: namespace is defined by the SCXX library which has C++ class equivalents for many Python types. std:: is the namespace of the standard library in C++.

Note:
- I haven’t figured out how to handle long int yet (I think they are currently converted to int - - check this).
- Hopefully VTK will be added to the list soon

Python to C++ conversions fill in code in several locations in the generated inline extension function. Below is the basic template for the function. This is actually the exact code that is generated by calling weave.inline(" ").

The /* inline code */ section is filled with the code passed to the inline() function call. The /*argument conversion code*/ and /* cleanup code */ sections are filled with code that handles conversion from Python to C++ types and code that deallocates memory or manipulates reference counts before the function returns. The following sections demonstrate how these two areas are filled in by the default conversion methods. * Note: I’m not sure I have reference counting correct on a few of these. The only thing I increase/decrease the ref count on is NumPy arrays. If you see an issue, please let me know.

**NumPy Argument Conversion**

Integer, floating point, and complex arguments are handled in a very similar fashion. Consider the following inline function that has a single integer variable passed in:

```python
>>> a = 1
>>> inline("",['a'])
```

The argument conversion code inserted for a is:

```python
/* argument conversion code */
int a = py_to_int (get_variable("a",raw_locals,raw_globals),"a");
```

get_variable() reads the variable a from the local and global namespaces. py_to_int() has the following form:

```c
static int py_to_int(PyObject* py_obj,char* name)
{
    if (!py_obj || !PyInt_Check(py_obj))
        handle_bad_type(py_obj,"int", name);
    return (int) PyInt_AsLong(py_obj);
}
```
Similarly, the float and complex conversion routines look like:

```c
static double py_to_float(PyObject* py_obj, char* name)
{
    if (!py_obj || !PyFloat_Check(py_obj))
        handle_bad_type(py_obj, "float", name);
    return PyFloat_AsDouble(py_obj);
}
```

```c
static std::complex py_to_complex(PyObject* py_obj, char* name)
{
    if (!py_obj || !PyComplex_Check(py_obj))
        handle_bad_type(py_obj, "complex", name);
    return std::complex(PyComplex_RealAsDouble(py_obj),
                         PyComplex_ImagAsDouble(py_obj));
}
```

NumPy conversions do not require any clean up code.

**String, List, Tuple, and Dictionary Conversion**

Strings, Lists, Tuples and Dictionary conversions are all converted to SCXX types by default. For the following code,

```python
>>> a = [1]
>>> inline("", ["a"])```

The argument conversion code inserted for `a` is:

```c
/* argument conversion code */
Py::List a = py_to_list(get_variable("a", raw_locals, raw_globals), "a");
```

`get_variable()` reads the variable `a` from the local and global namespaces. `py_to_list()` and its friends have the following form:

```c
static Py::List py_to_list(PyObject* py_obj, char* name)
{
    if (!py_obj || !PyList_Check(py_obj))
        handle_bad_type(py_obj, "list", name);
    return Py::List(py_obj);
}
```

```c
static Py::String py_to_string(PyObject* py_obj, char* name)
{
    if (!PyString_Check(py_obj))
        handle_bad_type(py_obj, "string", name);
    return Py::String(py_obj);
}
```

```c
static Py::Dict py_to_dict(PyObject* py_obj, char* name)
{
    if (!py_obj || !PyDict_Check(py_obj))
        handle_bad_type(py_obj, "dict", name);
    return Py::Dict(py_obj);
}
```

```c
static Py::Tuple py_to_tuple(PyObject* py_obj, char* name)
{
    if (!py_obj || !PyTuple_Check(py_obj))
        handle_bad_type(py_obj, "tuple", name);
    ```
return Py::Tuple(py_obj);
}

SCXX handles reference counts on for strings, lists, tuples, and dictionaries, so clean up code isn’t necessary.

**File Conversion**

For the following code,

```python
>>> a = open("bob",'w')
```

```python
>>> inline("",['a'])
```

The argument conversion code is:

```c
/* argument conversion code */
PyObject* py_a = get_variable("a",raw_locals,raw_globals);
FILE* a = py_to_file(py_a,"a");
```

`get_variable()` reads the variable `a` from the local and global namespaces. `py_to_file()` converts `PyObject*` to a `FILE*` and increments the reference count of the `PyObject*`:

```c
FILE* py_to_file(PyObject* py_obj, char* name)
{
    if (!py_obj || !PyFile_Check(py_obj))
        handle_bad_type(py_obj,"file", name);

    Py_INCREF(py_obj);
    return PyFile_AsFile(py_obj);
}
```

Because the `PyObject*` was incremented, the clean up code needs to decrement the counter

```c
/* cleanup code */
Py_XDECREF(py_a);
```

It's important to understand that file conversion only works on actual files – i.e. ones created using the `open()` command in Python. It does not support converting arbitrary objects that support the file interface into C `FILE*` pointers. This can affect many things. For example, in initial `printf()` examples, one might be tempted to solve the problem of C and Python IDE's (PythonWin, PyCrust, etc.) writing to different stdout and stderr by using `fprintf()` and passing in `sys.stdout` and `sys.stderr`. For example, instead of

```python
>>> weave.inline('printf("hello\n");')
```

You might try:

```python
>>> buf = sys.stdout
>>> weave.inline('fprintf(buf,"hello\n");',['buf'])
```

This will work as expected from a standard python interpreter, but in PythonWin, the following occurs:

```python
>>> buf = sys.stdout
>>> weave.inline('fprintf(buf,"hello\n");',['buf'])
```

Traceback (most recent call last):
  File "", line 1, in ?
  File "C:\Python21\weave\inline_tools.py", line 315, in inline
      auto_downcast = auto_downcast,
  File "C:\Python21\weave\inline_tools.py", line 386, in compile_function
    type_factories = type_factories)
  File "C:\Python21\weave\ext_tools.py", line 197, in __init__
    auto_downcast, type_factories)
```

1.16. Weave (scipy.weave)
File "C:\Python21\weave\ext_tools.py", line 390, in assign_variable_types
raise TypeError, format_error_msg(errors)
TypeError: {'buf': "Unable to convert variable 'buf' to a C++ type."}

The traceback tells us that inline() was unable to convert ‘buf’ to a C++ type (If instance conversion was implemented, the error would have occurred at runtime instead). Why is this? Let’s look at what the buf object really is:

```python
>>> buf
pywin.framework.interact.InteractiveView instance at 00EAD014
```

PythonWin has reassigned `sys.stdout` to a special object that implements the Python file interface. This works great in Python, but since the special object doesn’t have a FILE* pointer underlying it, `fprintf` doesn’t know what to do with it (well this will be the problem when instance conversion is implemented...).

Callable, Instance, and Module Conversion

**Note:** Need to look into how ref counts should be handled. Also, Instance and Module conversion are not currently implemented.

```python
>>> def a():
    pass
>>> inline('"", ['a'])
```

Callable and instance variables are converted to PyObject*. Nothing is done to their reference counts.

```c
/* argument conversion code */
PyObject* a = py_to_callable(get_variable("a", raw_locals, raw_globals), "a");
```

get_variable() reads the variable a from the local and global namespaces. The `py_to_callable()` and `py_to_instance()` don’t currently increment the ref count.

```c
PyObject* py_to_callable(PyObject* py_obj, char* name)
{
    if (!py_obj || !PyCallable_Check(py_obj))
        handle_bad_type(py_obj, "callable", name);
    return py_obj;
}
```

```c
PyObject* py_to_instance(PyObject* py_obj, char* name)
{
    if (!py_obj || !PyFile_Check(py_obj))
        handle_bad_type(py_obj, "instance", name);
    return py_obj;
}
```

There is no cleanup code for callables, modules, or instances.

Customizing Conversions

Converting from Python to C++ types is handled by `xxx_specification` classes. A type specification class actually serve in two related but different roles. The first is in determining whether a Python variable that needs to be converted should be represented by the given class. The second is as a code generator that generates C++ code needed to convert from Python to C++ types for a specific variable.

When

```python
>>> a = 1
>>> weave.inline('printf("%d",a);',['a'])
```
is called for the first time, the code snippet has to be compiled. In this process, the variable ‘a’ is tested against a list of type specifications (the default list is stored in weave/ext_tools.py). The first specification in the list is used to represent the variable.

Examples of xxx_specification are scattered throughout numerous “xxx_spec.py” files in the weave package. Closely related to the xxx_specification classes are yyy_info classes. These classes contain compiler, header, and support code information necessary for including a certain set of capabilities (such as blitz++ or CXX support) in a compiled module. xxx_specification classes have one or more yyy_info classes associated with them. If you’d like to define your own set of type specifications, the current best route is to examine some of the existing spec and info files. Maybe looking over sequence_spec.py and cxx_info.py are a good place to start. After defining specification classes, you’ll need to pass them into inline using the type_factories argument. A lot of times you may just want to change how a specific variable type is represented. Say you’d rather have Python strings converted to std::string or maybe char* instead of using the CXX string object, but would like all other type conversions to have default behavior. This requires that a new specification class that handles strings is written and then prepended to a list of the default type specifications. Since it is closer to the front of the list, it effectively overrides the default string specification. The following code demonstrates how this is done: ...

**The Catalog**

catalog.py has a class called catalog that helps keep track of previously compiled functions. This prevents inline() and related functions from having to compile functions every time they are called. Instead, catalog will check an in memory cache to see if the function has already been loaded into python. If it hasn’t, then it starts searching through persistent catalogs on disk to see if it finds an entry for the given function. By saving information about compiled functions to disk, it isn’t necessary to re-compile functions every time you stop and restart the interpreter. Functions are compiled once and stored for future use.

When inline(cpp_code) is called the following things happen:

1. A fast local cache of functions is checked for the last function called for cpp_code. If an entry for cpp_code doesn’t exist in the cache or the cached function call fails (perhaps because the function doesn’t have compatible types) then the next step is to check the catalog.

2. The catalog class also keeps an in-memory cache with a list of all the functions compiled for cpp_code. If cpp_code has ever been called, then this cache will be present (loaded from disk). If the cache isn’t present, then it is loaded from disk.

   If the cache is present, each function in the cache is called until one is found that was compiled for the correct argument types. If none of the functions work, a new function is compiled with the given argument types. This function is written to the on-disk catalog as well as into the in-memory cache.

3. When a lookup for cpp_code fails, the catalog looks through the on-disk function catalogs for the entries. The PYTHONCOMPILED variable determines where to search for these catalogs and in what order. If PYTHONCOMPILED is not present several platform dependent locations are searched. All functions found for cpp_code in the path are loaded into the in-memory cache with functions found earlier in the search path closer to the front of the call list.

   If the function isn’t found in the on-disk catalog, then the function is compiled, written to the first writable directory in the PYTHONCOMPILED path, and also loaded into the in-memory cache.

**Function Storage**

Function caches are stored as dictionaries where the key is the entire C++ code string and the value is either a single function (as in the ‘level 1’ cache) or a list of functions (as in the main catalog cache). On disk catalogs are stored in the same manner using standard Python shelves.

Early on, there was a question as to whether md5 checksums of the C++ code strings should be used instead of the actual code strings. I think this is the route inline Perl took. Some (admittedly quick) tests of the md5 vs. the entire string showed that using the entire string was at least a factor of 3 or 4 faster for Python. I think this is because it is
more time consuming to compute the md5 value than it is to do look-ups of long strings in the dictionary. Look at the examples/md5_speed.py file for the test run.

**Catalog search paths and the PYTHONCOMPILED variable**

The default location for catalog files on Unix is ~/.pythonXX_compiled where XX is version of Python being used. If this directory doesn't exist, it is created the first time a catalog is used. The directory must be writable. If, for any reason it isn’t, then the catalog attempts to create a directory based on your user id in the /tmp directory. The directory permissions are set so that only you have access to the directory. If this fails, I think you’re out of luck. I don’t think either of these should ever fail though. On Windows, a directory called pythonXX_compiled is created in the user’s temporary directory.

The actual catalog file that lives in this directory is a Python shelf with a platform specific name such as “nt21compiled_catalog” so that multiple OSes can share the same file systems without trampling on each other. Along with the catalog file, the .cpp and .so or .pyd files created by inline will live in this directory. The catalog file simply contains keys which are the C++ code strings with values that are lists of functions. The function lists point at functions within these compiled modules. Each function in the lists executes the same C++ code string, but compiled for different input variables.

You can use the PYTHONCOMPILED environment variable to specify alternative locations for compiled functions. On Unix this is a colon (‘:’) separated list of directories. On windows, it is a (‘;’) separated list of directories. These directories will be searched prior to the default directory for a compiled function catalog. Also, the first writable directory in the list is where all new compiled function catalogs, .cpp and .so or .pyd files are written. Relative directory paths (‘.’ and ‘..’) should work fine in the PYTHONCOMPILED variable as should environment variables. There is a “special” path variable called MODULE that can be placed in the PYTHONCOMPILED variable. It specifies that the compiled catalog should reside in the same directory as the module that called it. This is useful if an admin wants to build a lot of compiled functions during the build of a package and then install them in site-packages along with the package. User’s who specify MODULE in their PYTHONCOMPILED variable will have access to these compiled functions. Note, however, that if they call the function with a set of argument types that it hasn’t previously been built for, the new function will be stored in their default directory (or some other writable directory in the PYTHONCOMPILED path) because the user will not have write access to the site-packages directory.

An example of using the PYTHONCOMPILED path on bash follows:

```bash
PYTHONCOMPILED=MODULE:/some/path;export PYTHONCOMPILED;
```

If you are using python21 on linux, and the module bob.py in site-packages has a compiled function in it, then the catalog search order when calling that function for the first time in a python session would be:

```
/usr/lib/python21/site-packages/linuxpython_compiled
/some/path/linuxpython_compiled
~/.python21_compiled/linuxpython_compiled
```

The default location is always included in the search path.

**Note:** hmmm. see a possible problem here. I should probably make a sub- directory such as /usr/lib/python21/site-packages/python21_compiled/linuxpython_compiled so that library files compiled with python21 are tried to link with python22 files in some strange scenarios. Need to check this.

The in-module cache (in `weave.inline_tools` reduces the overhead of calling inline functions by about a factor of 2. It can be reduced a little more for type loop calls where the same function is called over and over again if the cache was a single value instead of a dictionary, but the benefit is very small (less than 5%) and the utility is quite a bit less. So, we’ll stick with a dictionary as the cache.

### 1.16.8 Blitz
Note: most of this section is lifted from old documentation. It should be pretty accurate, but there may be a few discrepancies.

**weave.blitz()** compiles NumPy Python expressions for fast execution. For most applications, compiled expressions should provide a factor of 2-10 speed-up over NumPy arrays. Using compiled expressions is meant to be as unobtrusive as possible and works much like pythons exec statement. As an example, the following code fragment takes a 5 point average of the 512x512 2d image, b, and stores it in array, a:

```python
from scipy import * # or from NumPy import *
a = ones((512,512), Float64)
b = ones((512,512), Float64)
# ...do some stuff to fill in b...
# now average
a[1:-1,1:-1] = (b[1:-1,1:-1] + b[2:,1:-1] + b[:-2,1:-1] \\
              + b[1:-1,2:] + b[1:-1,:-2]) / 5.
```

To compile the expression, convert the expression to a string by putting quotes around it and then use **weave.blitz**:

```python
import weave
expr = "a[1:-1,1:-1] = (b[1:-1,1:-1] + b[2:,1:-1] + b[:-2,1:-1] \\
              + b[1:-1,2:] + b[1:-1,:-2]) / 5."
weave.blitz(expr)
```

The first time **weave.blitz** is run for a given expression and set of arguments, C++ code that accomplishes the exact same task as the Python expression is generated and compiled to an extension module. This can take up to a couple of minutes depending on the complexity of the function. Subsequent calls to the function are very fast. Furthermore, the generated module is saved between program executions so that the compilation is only done once for a given expression and associated set of array types. If the given expression is executed with a new set of array types, the code must be compiled again. This does not overwrite the previously compiled function – both of them are saved and available for execution.

The following table compares the run times for standard NumPy code and compiled code for the 5 point averaging.

<table>
<thead>
<tr>
<th>Method</th>
<th>Run Time (seconds)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Standard NumPy</td>
<td>0.46349</td>
</tr>
<tr>
<td>blitz (1st time compiling)</td>
<td>78.95526</td>
</tr>
<tr>
<td>blitz (subsequent calls)</td>
<td>0.05843 (factor of 8 speedup)</td>
</tr>
</tbody>
</table>

These numbers are for a 512x512 double precision image run on a 400 MHz Celeron processor under RedHat Linux 6.2.

Because of the slow compile times, its probably most effective to develop algorithms as you usually do using the capabilities of scipy or the NumPy module. Once the algorithm is perfected, put quotes around it and execute it using **weave.blitz**. This provides the standard rapid prototyping strengths of Python and results in algorithms that run close to that of hand coded C or Fortran.

**Requirements**

Currently, the **weave.blitz** has only been tested under Linux with gcc-2.95-3 and on Windows with Mingw32 (2.95.2). Its compiler requirements are pretty heavy duty (see the [blitz++ home page](#)), so it won’t work with just any compiler. Particularly MSVC++ isn’t up to sniff. A number of other compilers such as KAI++ will also work, but my suspicions are that gcc will get the most use.

**Limitations**

1. Currently, **weave.blitz** handles all standard mathematical operators except for the ** power operator. The built-in trigonometric, log, floor/ceil, and fabs functions might work (but haven’t been tested). It also handles all
types of array indexing supported by the NumPy module. numarray’s NumPy compatible array indexing modes are likewise supported, but numarray’s enhanced (array based) indexing modes are not supported.

weave.blitz does not currently support operations that use array broadcasting, nor have any of the special purpose functions in NumPy such as take, compress, etc. been implemented. Note that there are no obvious reasons why most of this functionality cannot be added to scipy.weave, so it will likely trickle into future versions. Using `slice()` objects directly instead of `start:stop:step` is also not supported.

2. Currently Python only works on expressions that include assignment such as

```
>>> result = b + c + d
```

This means that the result array must exist before calling `weave.blitz`. Future versions will allow the following:

```
>>> result = weave.blitz_eval("b + c + d")
```

3. `weave.blitz` works best when algorithms can be expressed in a “vectorized” form. Algorithms that have a large number of if/thens and other conditions are better hand-written in C or Fortran. Further, the restrictions imposed by requiring vectorized expressions sometimes preclude the use of more efficient data structures or algorithms. For maximum speed in these cases, hand-coded C or Fortran code is the only way to go.

4. `weave.blitz` can produce different results than NumPy in certain situations. It can happen when the array receiving the results of a calculation is also used during the calculation. The NumPy behavior is to carry out the entire calculation on the right hand side of an equation and store it in a temporary array. This temporary array is assigned to the array on the left hand side of the equation. blitz, on the other hand, does a “running” calculation of the array elements assigning values from the right hand side to the elements on the left hand side immediately after they are calculated. Here is an example, provided by Prabhu Ramachandran, where this happens:

```
# 4 point average.
>>> expr = "u[1:-1, 1:-1] = (u[0:-2, 1:-1] + u[2:, 1:-1] + \\
... "u[1:-1,0:-2] + u[1:-1, 2:])*0.25"
>>> u = zeros((5, 5), 'd'); u[0, :] = 100
>>> exec (expr)
>>> u
array([[ 100. , 100. , 100. , 100. , 100. ],
[ 0. , 25. , 25. , 25. , 0. ],
[ 0. , 0. , 0. , 0. , 0. ],
[ 0. , 0. , 0. , 0. , 0. ],
[ 0. , 0. , 0. , 0. , 0. ]])
```

```
>>> u = zeros((5, 5), 'd'); u[0, :] = 100
>>> weave.blitz (expr)
>>> u
array([[ 100. , 100. , 100. , 100. , 100. ],
[ 0. , 6.25 , 9.375 , 10.546875 , 0. ],
[ 0. , 1.5625 , 2.734375 , 3.3203125 , 0. ],
[ 0. , 0. , 0. , 0. , 0. ]])
```

You can prevent this behavior by using a temporary array.

```
>>> u = zeros((5, 5), 'd'); u[0, :] = 100
>>> temp = zeros((4, 4), 'd');
>>> expr = "temp = (u[0:-2, 1:-1] + u[2:, 1:-1] + \\
... "u[1:-1,0:-2] + u[1:-1, 2:])*0.25;"  \\
... "u[1:-1,1:-1] = temp"
>>> weave.blitz (expr)
>>> u
array([[ 100. , 100. , 100. , 100. , 100. ],
[ 0. , 6.25 , 9.375 , 10.546875 , 0. ],
[ 0. , 1.5625 , 2.734375 , 3.3203125 , 0. ],
[ 0. , 0. , 0. , 0. , 0. ]])
```
5. One other point deserves mention lest people be confused. `weave.blitz` is not a general purpose Python->C compiler. It only works for expressions that contain NumPy arrays and/or Python scalar values. This focused scope concentrates effort on the computationally intensive regions of the program and sidesteps the difficult issues associated with a general purpose Python->C compiler.

**NumPy efficiency issues: What compilation buys you**

Some might wonder why compiling NumPy expressions to C++ is beneficial since operations on NumPy array operations are already executed within C loops. The problem is that anything other than the simplest expression are executed in less than optimal fashion. Consider the following NumPy expression:

\[
a = 1.2 \times b + c \times d
\]

When NumPy calculates the value for the 2d array, \(a\), it does the following steps:

\[
\begin{align*}
temp1 &= 1.2 \times b \\
temp2 &= c \times d \\
a &= temp1 + temp2
\end{align*}
\]

Two things to note. Since \(c\) is an (perhaps large) array, a large temporary array must be created to store the results of \(1.2 \times b\). The same is true for \(temp2\). Allocation is slow. The second thing is that we have 3 loops executing, one to calculate \(temp1\), one for \(temp2\) and one for adding them up. A C loop for the same problem might look like:

```c
for(int i = 0; i < M; i++)
    for(int j = 0; j < N; j++)
        a[i,j] = 1.2 * b[i,j] + c[i,j] * d[i,j]
```

Here, the 3 loops have been fused into a single loop and there is no longer a need for a temporary array. This provides a significant speed improvement over the above example (write me and tell me what you get).

So, converting NumPy expressions into C/C++ loops that fuse the loops and eliminate temporary arrays can provide big gains. The goal, then, is to convert NumPy expression to C/C++ loops, compile them in an extension module, and then call the compiled extension function. The good news is that there is an obvious correspondence between the NumPy expression above and the C loop. The bad news is that NumPy is generally much more powerful than this simple example illustrates and handling all possible indexing possibilities results in loops that are less than straightforward to write. (Take a peek at NumPy for confirmation). Luckily, there are several available tools that simplify the process.

**The Tools**

`weave.blitz` relies heavily on several remarkable tools. On the Python side, the main facilitators are Jerme Hylton’s parser module and Travis Oliphant’s NumPy module. On the compiled language side, Todd Veldhuizen’s blitz++ array library, written in C++ (shhh. don’t tell David Beazley), does the heavy lifting. Don’t assume that, because it’s C++, it’s much slower than C or Fortran. Blitz++ uses a jaw dropping array of template techniques (metaprogramming, template expression, etc) to convert innocent-looking and readable C++ expressions into to code that usually executes within a few percentage points of Fortran code for the same problem. This is good. Unfortunately all the template raz-ma-taz is very expensive to compile, so the 200 line extension modules often take 2 or more minutes to compile. This isn’t so good. `weave.blitz` works to minimize this issue by remembering where compiled modules live and reusing them instead of re-compiling every time a program is re-run.
**Parser**

Tearing NumPy expressions apart, examining the pieces, and then rebuilding them as C++ (blitz) expressions requires a parser of some sort. I can imagine someone attacking this problem with regular expressions, but it’d likely be ugly and fragile. Amazingly, Python solves this problem for us. It actually exposes its parsing engine to the world through the `parser` module. The following fragment creates an Abstract Syntax Tree (AST) object for the expression and then converts to a (rather unpleasant looking) deeply nested list representation of the tree.

```python
>>> import parser
>>> import scipy.weave.misc
>>> ast = parser.suite("a = b * c + d")
>>> ast_list = ast.tolist()
>>> sym_list = scipy.weave.misc.translate_symbols(ast_list)
>>> pprint.pprint(sym_list)
['file_input',
 ['stmt',
  ['simple_stmt',
   ['small_stmt',
    ['testlist',
     ['test',
      ['and_test',
       ['not_test',
        ['comparison',
         ['expr',
          ['xor_expr',
           ['and_expr',
            ['shift_expr',
             ['arith_expr',
              ['term',
               ['factor', ['power', ['atom', ['NAME', 'a']]]],
              ['EQUAL', '='],
              ['testlist',
               ['test',
                ['and_test',
                 ['not_test',
                  ['comparison',
                   ['expr',
                    ['xor_expr',
                     ['and_expr',
                      ['shift_expr',
                       ['arith_expr',
                        ['term',
                         ['factor', ['power', ['atom', ['NAME', 'b']]]],
                         ['STAR', '*'],
                         ['factor', ['power', ['atom', ['NAME', 'c']]]],
                         ['PLUS', '+']
                        ],
                        ['term',
                         ['factor', ['power', ['atom', ['NAME', 'd']]]]
                      ],
                      ['NEWLINE', '']
                     ],
                     ['ENDMARKER', '']
                    ],
                    ['ENDMARKER', '']
                   ],
                   ['ENDMARKER', '']
                  ],
                  ['ENDMARKER', '']
                 ],
                 ['ENDMARKER', '']
                ],
                ['ENDMARKER', '']
               ],
               ['ENDMARKER', '']
              ],
              ['ENDMARKER', '']
             ],
             ['ENDMARKER', '']
            ],
            ['ENDMARKER', '']
           ],
           ['ENDMARKER', '']
          ],
          ['ENDMARKER', '']
         ],
         ['ENDMARKER', '']
        ],
        ['ENDMARKER', '']
       ],
       ['ENDMARKER', '']
      ],
      ['ENDMARKER', '']
     ],
     ['ENDMARKER', '']
    ],
    ['ENDMARKER', '']
   ],
   ['ENDMARKER', '']
  ],
  ['ENDMARKER', '']
]
```

Despite its looks, with some tools developed by Jermey H., it’s possible to search these trees for specific patterns (sub-trees), extract the sub-tree, manipulate them converting python specific code fragments to blitz code fragments, and then re-insert it in the parse tree. The parser module documentation has some details on how to do this. Traversing the new blitzified tree, writing out the terminal symbols as you go, creates our new blitz++ expression string.
Blitz and NumPy

The other nice discovery in the project is that the data structure used for NumPy arrays and blitz arrays is nearly identical. NumPy stores “strides” as byte offsets and blitz stores them as element offsets, but other than that, they are the same. Further, most of the concept and capabilities of the two libraries are remarkably similar. It is satisfying that two completely different implementations solved the problem with similar basic architectures. It is also fortuitous. The work involved in converting NumPy expressions to blitz expressions was greatly diminished. As an example, consider the code for slicing an array in Python with a stride:

```python
>>> a = b[0:4:2] + c
>>> a
[0,2,4]
```

In Blitz it is as follows:

```cpp
Array<2,int> b(10);
Array<2,int> c(3);
// ...
Array<2,int> a = b(Range(0,3,2)) + c;
```

Here the range object works exactly like Python slice objects with the exception that the top index (3) is inclusive where as Python’s (4) is exclusive. Other differences include the type declarations in C++ and parentheses instead of brackets for indexing arrays. Currently, weave.blitz handles the inclusive/exclusive issue by subtracting one from upper indices during the translation. An alternative that is likely more robust/maintainable in the long run is to write a PyRange class that behaves like Python’s range. This is likely very easy.

The stock blitz also doesn’t handle negative indices in ranges. The current implementation of the `blitz()` has a partial solution to this problem. It calculates and index that starts with a ‘-’ sign by subtracting it from the maximum index in the array so that:

```
upper index limit
/-----
```

```
b[:i-j] -> b(Range(0,i+j))
```

A solution is to calculate all indices up front using if/then to handle the +/- cases. This is a little work and results in more code, so it hasn’t been done. I’m holding out to see if blitz++ can be modified to handle negative indexing, but haven’t looked into how much effort is involved yet. While it needs fixin’, I don’t think there is a ton of code where this is an issue.

The actual translation of the Python expressions to blitz expressions is currently a two part process. First, all x:y:z slicing expression are removed from the AST, converted to `slice(x,y,z)` and re-inserted into the tree. Any math needed on these expressions (subtracting from the maximum index, etc.) are also preformed here. `_beg` and `_end` are used as special variables that are defined as `blitz::fromBegin` and `blitz::toEnd`.

```
a[i+j:i+j+1,:] = b[2:3,:]
```

becomes a more verbose:

```
a[slice(i+j,i+j+1),slice(_beg,_end)] = b[slice(2,3),slice(_beg,_end)]
```

The second part does a simple string search/replace to convert to a blitz expression with the following translations:

```
slice(_beg,_end) -> _all  # not strictly needed, but cuts down on code.
slice -> blitz::Range
```
_all is defined in the compiled function as blitz::Range.all(). These translations could of course happen directly in the syntax tree. But the string replacement is slightly easier. Note that namespaces are maintained in the C++ code to lessen the likelihood of name clashes. Currently no effort is made to detect name clashes. A good rule of thumb is don’t use values that start with ‘_’ or ‘py_’ in compiled expressions and you’ll be fine.

**Type definitions and coercion**

So far we’ve glossed over the dynamic vs. static typing issue between Python and C++. In Python, the type of value that a variable holds can change through the course of program execution. C/C++, on the other hand, forces you to declare the type of value a variables will hold prior at compile time. *weave.blitz* handles this issue by examining the types of the variables in the expression being executed, and compiling a function for those explicit types. For example:

```python
a = ones((5,5),Float32)
b = ones((5,5),Float32)
weave.blitz("a = a + b")
```

When compiling this expression to C++, *weave.blitz* sees that the values for `a` and `b` in the local scope have type `Float32`, or ‘float’ on a 32 bit architecture. As a result, it compiles the function using the float type (no attempt has been made to deal with 64 bit issues).

What happens if you call a compiled function with array types that are different than the ones for which it was originally compiled? No biggie, you’ll just have to wait on it to compile a new version for your new types. This doesn’t overwrite the old functions, as they are still accessible. See the catalog section in the inline() documentation to see how this is handled. Suffice to say, the mechanism is transparent to the user and behaves like dynamic typing with the occasional wait for compiling newly typed functions.

When working with combined scalar/array operations, the type of the array is *always* used. This is similar to the saves-space flag that was recently added to NumPy. This prevents issues with the following expression perhaps unexpectedly being calculated at a higher (more expensive) precision that can occur in Python:

```python
>>> a = array((1,2,3),typecode = Float32)
>>> b = a * 2.1 # results in b being a Float64 array.
```

In this example,

```python
>>> a = ones((5,5),Float32)
>>> b = ones((5,5),Float32)
>>> weave.blitz("b = a * 2.1")
```

the 2.1 is cast down to a float before carrying out the operation. If you really want to force the calculation to be a double, define `a` and `b` as double arrays.

One other point of note. Currently, you must include both the right hand side and left hand side (assignment side) of your equation in the compiled expression. Also, the array being assigned to must be created prior to calling *weave.blitz*. I’m pretty sure this is easily changed so that a compiled_eval expression can be defined, but no effort has been made to allocate new arrays (and discern their type) on the fly.

**Cataloging Compiled Functions**

See The Catalog section in the *weave.inline()* documentation.
Checking Array Sizes

Surprisingly, one of the big initial problems with compiled code was making sure all the arrays in an operation were of compatible type. The following case is trivially easy:

\[ a = b + c \]

It only requires that arrays \( a, b, \) and \( c \) have the same shape. However, expressions like:

\[ a[i+j:i+j+1,:) = b[2:3,:) + c \]

are not so trivial. Since slicing is involved, the size of the slices, not the input arrays, must be checked. Broadcasting complicates things further because arrays and slices with different dimensions and shapes may be compatible for math operations (broadcasting isn’t yet supported by weave.blitz). Reductions have a similar effect as their results are different shapes than their input operand. The binary operators in NumPy compare the shapes of their two operands just before they operate on them. This is possible because NumPy treats each operation independently. The intermediate (temporary) arrays created during sub-operations in an expression are tested for the correct shape before they are combined by another operation. Because weave.blitz fuses all operations into a single loop, this isn’t possible. The shape comparisons must be done and guaranteed compatible before evaluating the expression.

The solution chosen converts input arrays to “dummy arrays” that only represent the dimensions of the arrays, not the data. Binary operations on dummy arrays check that input array sizes are compatible and return a dummy array with the size correct size. Evaluating an expression of dummy arrays traces the changing array sizes through all operations and fails if incompatible array sizes are ever found.

The machinery for this is housed in weave.size_check. It basically involves writing a new class (dummy array) and overloading its math operators to calculate the new sizes correctly. All the code is in Python and there is a fair amount of logic (mainly to handle indexing and slicing) so the operation does impose some overhead. For large arrays (i.e. 50x50x50), the overhead is negligible compared to evaluating the actual expression. For small arrays (i.e. 16x16), the overhead imposed for checking the shapes with this method can cause the weave.blitz to be slower than evaluating the expression in Python.

What can be done to reduce the overhead? (1) The size checking code could be moved into C. This would likely remove most of the overhead penalty compared to NumPy (although there is also some calling overhead), but no effort has been made to do this. (2) You can also call weave.blitz with check_size=0 and the size checking isn’t done. However, if the sizes aren’t compatible, it can cause a core-dump. So, foregoing size checking isn’t advisable until your code is well debugged.

Creating the Extension Module

weave.blitz uses the same machinery as weave.inline to build the extension module. The only difference is the code included in the function is automatically generated from the NumPy array expression instead of supplied by the user.

1.16.9 Extension Modules

weave.inline and weave.blitz are high level tools that generate extension modules automatically. Under the covers, they use several classes from weave.ext_tools to help generate the extension module. The main two classes are ext_module and ext_function (I’d like to add ext_class and ext_method also). These classes simplify the process of generating extension modules by handling most of the “boiler plate” code automatically.

Note: inline actually sub-classes weave.ext_tools.ext_function to generate slightly different code than the standard ext_function. The main difference is that the standard class converts function arguments to C types, while inline always has two arguments, the local and global dicts, and the grabs the variables that need to be converted to C from these.
A Simple Example

The following simple example demonstrates how to build an extension module within a Python function:

```python
# examples/increment_example.py
from weave import ext_tools
def build_increment_ext():
    """ Build a simple extension with functions that increment numbers.
    The extension will be built in the local directory.
    """
    mod = ext_tools.ext_module('increment_ext')
    a = 1 # effectively a type declaration for 'a' in the
    # following functions.
    ext_code = "return_val = Py::new_reference_to(Py::Int(a+1));"
    func = ext_tools.ext_function('increment',ext_code,['a'])
    mod.add_function(func)
    ext_code = "return_val = Py::new_reference_to(Py::Int(a+2));"
    func = ext_tools.ext_function('increment_by_2',ext_code,['a'])
    mod.add_function(func)
    mod.compile()
```

The function `build_increment_ext()` creates an extension module named `increment_ext` and compiles it to a shared library (.so or .pyd) that can be loaded into Python. `increment_ext` contains two functions, `increment` and `increment_by_2`. The first line of `build_increment_ext()`:

```python
mod = ext_tools.ext_module('increment_ext')
```

creates an `ext_module` instance that is ready to have `ext_function` instances added to it. `ext_function` instances are created much with a calling convention similar to `weave.inline()`. The most common call includes a C/C++ code snippet and a list of the arguments for the function. The following:

```python
ext_code = "return_val = Py::new_reference_to(Py::Int(a+1));"
func = ext_tools.ext_function('increment',ext_code,['a'])
```

creates a C/C++ extension function that is equivalent to the following Python function:

```python
def increment(a):
    return a + 1
```

A second method is also added to the module and then,

```python
mod.compile()
```

is called to build the extension module. By default, the module is created in the current working directory. This example is available in the `examples/increment_example.py` file found in the `weave` directory. At the bottom of the file in the module’s “main” program, an attempt to import `increment_ext` without building it is made. If this fails (the module doesn’t exist in the PYTHONPATH), the module is built by calling `build_increment_ext()`. This approach only takes the time-consuming (a few seconds for this example) process of building the module if it hasn’t been built before.

```python
if __name__ == "__main__":
    try:
        import increment_ext
    except ImportError:
        build_increment_ext()
```
import increment_ext
a = 1
print 'a, a+1:', a, increment_ext.increment(a)
print 'a, a+2:', a, increment_ext.increment_by_2(a)

Note: If we were willing to always pay the penalty of building the C++ code for a module, we could store the SHA-256 checksum of the C++ code along with some information about the compiler, platform, etc. Then, ext_module.compile() could try importing the module before it actually compiles it, check the SHA-256 checksum and other meta-data in the imported module with the meta-data of the code it just produced and only compile the code if the module didn’t exist or the meta-data didn’t match. This would reduce the above code to:

if __name__ == "__main__":
    build_increment_ext()

    a = 1
    print 'a, a+1:', a, increment_ext.increment(a)
    print 'a, a+2:', a, increment_ext.increment_by_2(a)

Note: There would always be the overhead of building the C++ code, but it would only actually compile the code once. You pay a little in overhead and get cleaner “import” code. Needs some thought.

If you run increment_example.py from the command line, you get the following:

[eric@n0]$ python increment_example.py
a, a+1: 1 2
a, a+2: 1 3

If the module didn’t exist before it was run, the module is created. If it did exist, it is just imported and used.

Fibonacci Example

text examples/fibonacci.py provides a little more complex example of how to use ext_tools. Fibonacci numbers are a series of numbers where each number in the series is the sum of the previous two: 1, 1, 2, 3, 5, 8, etc. Here, the first two numbers in the series are taken to be 1. One approach to calculating Fibonacci numbers uses recursive function calls. In Python, it might be written as:

def fib(a):
    if a <= 2:
        return 1
    else:
        return fib(a-2) + fib(a-1)

In C, the same function would look something like this:

int fib(int a)
{
    if(a <= 2)
        return 1;
    else
        return fib(a-2) + fib(a-1);
}

Recursion is much faster in C than in Python, so it would be beneficial to use the C version for fibonacci number calculations instead of the Python version. We need an extension function that calls this C function to do this. This is possible by including the above code snippet as “support code” and then calling it from the extension function.
Support code snippets (usually structure definitions, helper functions and the like) are inserted into the extension module C/C++ file before the extension function code. Here is how to build the C version of the fibonacci number generator:

```python
def build_fibonacci():
    """ Builds an extension module with fibonacci calculators. """
    mod = ext_tools.ext_module('fibonacci_ext')
a = 1  # this is effectively a type declaration

    # recursive fibonacci in C
    fib_code = ""
        int fib1(int a)
        {
            if(a <= 2)
                return 1;
            else
                return fib1(a-2) + fib1(a-1);
        }
    ""

    ext_code = ""
        int val = fib1(a);
        return_val = Py::new_reference_to(Py::Int(val));
    ""

    fib = ext_tools.ext_function('fib',ext_code,['a'])
    fib.customize.add_support_code(fib_code)
    mod.add_function(fib)
    mod.compile()
```

XXX More about custom_info, and what xxx_info instances are good for.

**Note:** recursion is not the fastest way to calculate fibonacci numbers, but this approach serves nicely for this example.

### 1.16.10 Customizing Type Conversions – Type Factories

not written

### 1.16.11 Things I wish weave did

It is possible to get name clashes if you uses a variable name that is already defined in a header automatically included (such as stdio.h) For instance, if you try to pass in a variable named stdout, you’ll get a cryptic error report due to the fact that stdio.h also defines the name. weave should probably try and handle this in some way. Other things...
CHAPTER TWO

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.

Note: You may want to check the latest version of this guide, which is available at: https://github.com/scipy/scipy/blob/master/HACKING.rst.txt

2.1 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](https://www.python.org/dev/peps/pep-0008/). In order to check that your code conforms to PEP8, you can use the [pep8 package](https://pypi.org/project/pep8/) 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](https://pypi.org/project/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](https://docs.scipy.org/doc/scipy/reference/api.html).

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](https://git-scm.com/) section of the NumPy documentation and on the [Github help pages](https://help.github.com/). 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.

### 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 or style, 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.

### 2.3 Other ways to contribute

There are many ways to contribute other than contributing code. Participating in discussions on the scipy-user and scipy-dev mailing lists is a contribution in itself. The [scipy.org website](https://www.scipy.org/) contains a lot of information on the SciPy
community and can always use a new pair of hands.

## 2.4 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:

```bash
$ 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:

```bash
$ python runtests.py -v
$ python runtests.py -v -s optimize
$ python runtests.py -v -t scipy/special/tests/test_basic.py: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.

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.

## 2.5 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

2.6 Useful links, FAQ, checklist

2.6.1 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 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 (and preferably also Bento configuration files - bento.info and bscript)?
• 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?

2.6.2 Useful SciPy documents

• The how to document guidelines
• NumPy/SciPy testing guidelines
• SciPy API
• SciPy maintainers
• NumPy/SciPy git workflow

2.6.3 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 (MIT, Apache, ...) then it’s OK. Code which is GPL-licensed, has no clear license,
SciPy Reference Guide, Release 0.16.0

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. See also license compatibility.

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:

$ 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:

$ pip install Numpy Nose Cython

After that, you can install a development version of Scipy, for example via:

$ 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:

$ 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:

$ export PYTHONPATH=$PWD

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.

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:
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:

$ 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.

How do I write tests with test generators?

The Nose test framework supports so-called test generators, which can come useful if you need to have multiple tests where just a parameter changes. Using test generators so that they are more useful than harmful is tricky, and we recommend the following pattern:

```python
def test_something():
    some_array = (...)

    def check(some_param):
        c = compute_result(some_array, some_param)
        known_result = (...)
        assert_allclose(c, known_result)

    for some_param in ['a', 'b', 'c']:
        yield check, some_param
```

We require the following:

- All asserts and all computation that is tested must only be reached after a yield. (Rationale: the generator body is part of no test, and a failure in it will show neither the test name nor for what parameters the test failed.)
- Arrays must not be passed as yield parameters. Either use variables from outer scope (eg. with some index passed to yield), or capulate test data to a class with a sensible __repr__. (Rationale: Nose truncates the printed form of arrays in test output, and this makes it impossible to know for what parameters a test failed. Arrays are big, and clutter test output unnecessarily.)
- Test generators cannot be used in test classes inheriting from unittest.TestCase; either use object as base class, or use standalone test functions. (Rationale: Nose does not run test generators in TestCase-inheriting classes.)

If in doubt, do not use test generators. You can track for what parameter things failed also by passing err_msg=repr((param1, param2, ...)) to the various assert functions.
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.

3.1 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.

### 3.2 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
  - vq
  - hierarchy
- scipy.constants
- scipy.fftpack
- scipy.integrate
- scipy.interpolate
- scipy.io
  - arff
  - harwell_boeing
  - idl
  - matlab
  - netcdf
  - wavfile
- scipy.linalg
  - scipy.linalg.blas
  - scipy.linalg.lapack
  - scipy.linalg.interpolative
- scipy.misc
• scipy.ndimage
• scipy.odr
• scipy.optimize
• scipy.signal
• scipy.sparse
  – linalg
  – csgraph
• scipy.spatial
  – distance
• scipy.special
• scipy.stats
  – distributions
  – mstats
• scipy.weave
4.1 SciPy 0.16.0 Release Notes

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`.
4.1.1 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 scipy.linalg.qr_delete, scipy.linalg.qr_insert and scipy.linalg.qr_update for updating QR decompositions were added.

The function scipy.linalg.solve_circulant solves a linear system with a circulant coefficient matrix.

The function scipy.linalg.inv_pascal computes the inverse of a Pascal matrix.

The function scipy.linalg.solve_toeplitz, a Levinson-Durbin Toeplitz solver, was added.

Added wrapper for potentially useful LAPACK function *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 *gelsd and *gelsy.

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

Wrappers for *gtsv and *ptsv, which solve A*X = B for tri-diagonal matrix A, were added.

**scipy.signal** improvements

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

- scipy.signal.sosfilt
- scipy.signal.sosfilt_zi
- scipy.signal.sos2tf
- scipy.signal.sos2zpk
- scipy.signal.tf2sos
- scipy.signal.zpk2sos.

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

The function 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 scipy.signal.filtfilt.

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

An exponential (Poisson) window was added as scipy.signal.exponential, and a Tukey window was added as scipy.signal.tukey.
The function for computing digital filter group delay was added as `scipy.signal.group_delay`.

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

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

**scipy.sparse improvements**

The function `scipy.sparse.norm`, which computes sparse matrix norms, was added.

The function `scipy.sparse.random`, which allows to draw random variates from an arbitrary distribution, was added.

**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`.

### 4.1.2 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.
4.1.3 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`.

4.1.4 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.

4.1.5 Authors

- @axiru +
- @endolith
- Elliott Sales de Andrade +
- Anne Archibald
- Yoshiki Vázquez Baeza +
- Sylvain Bellemare
- Felix Berkenkamp +
- Raoul Bourquin +
- Matthew Brett
- Per Brodtkorb
- Christian Brueffer
- Lars Buitinck
- Evgeni Burovski
- 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 Grigorievskiy +
• Hans Moritz Gunther +
• Jonas Hahnfeld +
• Charles Harris
• Ian Henriksen
• Andreas Hilboll
• Åsmund Hjulstad +
• Jan Schlüter +
• Janko Slavič +
• Daniel Jensen +
• Johannes Ballé +
• Terry Jones +
• 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 +
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: Typos 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 provided
• #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 isolve 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)
• #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 transfrom
• #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

4.1. SciPy 0.16.0 Release Notes 193
• #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 toeplitz 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 numpy 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...
4.1. SciPy 0.16.0 Release Notes

- #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_ltitisys.py
• #4716: DEP: deprecate mstats.signaltonoise ...
• #4717: MAINT: basinhopping: fix error in tests, silence /0 warning....
• #4718: ENH: stats: can specify f-shapes to fix in fitting by name

4.1. SciPy 0.16.0 Release Notes 199
SciPy Reference Guide, Release 0.16.0

- #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
- #4765: 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 funm_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 PPpoly 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.py.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

4.2 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
    * scipy.integrate
  - Authors
    * Issues closed
    * Pull requests

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.
4.2.1 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.csgraph` 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.

### 4.2.2 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](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.

### 4.2.3 Backwards incompatible changes

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

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

### 4.2.4 Authors

- Abject +
- Ankit Agrawal +
- Sylvain Bellemare +
- Matthew Brett
- Christian Brodbeck
- Christian Brueffer
- Lars Buitinck
- Evgeni Burovski
- Pierre de Buyl +
- Greg Caporaso +
- CJ Carey
- Jacob Carey +
- Thomas A Caswell
- Helder Cesar +
• Jacob Vanderplas
• Joris Vankerschaver
• Bastian Venthur +
• Pauli Virtanen
• Stefan van der Walt
• Yuxiang Wang +
• James T. Webber
• Warren Weckesser
• Axl West +
• Nathan Woods
• Benda Xu +
• Víctor Zabalza +
• 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.ltisys.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?)
• #3663: 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

4.2. SciPy 0.15.0 Release Notes
• #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...
• #3898: skimage test broken by minmax filter change
• #3901: scipy sparse errors with numpy master
• #3905: DOC: optimize: linprog docstring has two “Returns” sections
• #3915: DOC: sphinx warnings because of **kwds in the stats distributions...
• #3935: Split stats.distributions files in tutorial
• #3969: gh-3607 breaks backward compatibility in ode solver banded jacobians
• #4025: DOC: signal: The return value of find_peaks_cwt is not documented.
• #4029: scipy.stats.nbinom.logpmf(0,1,1) returns nan. Correct value is...
• #4032: ERROR: test_imresize (test_pilutil.TestPILUtil)
• #4038: errors do not propagate through scipy.integrate.odeint properly
• #4171: orthogonal_procrustes always returns scale.
• #4176: Solving the Discrete Lyapunov Equation does not work with matrix...

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: linprog function for linear programming
• #3348: BUG: add proper error handling when using interp2d on regular...
• #3351: ENH: Add MLS method
• #3382: 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...
• #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 fromidl.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 mstats docstrings to user-visible functions
• #3574: Fixes multiple bugs in mstats.theilslopes

4.2. Scipy 0.15.0 Release Notes
• #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.basin hopping 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 thread safe
• #3650: BUG: sparse: smarter random index selection
• #3652: fix wrong option name in power_divergence docstring 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 lfitic
• #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 numyys 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: spheroidal -> 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/quadpack 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...
#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 romb’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 NL_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: fix 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 spl ev 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/streams.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 procrastus 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

4.3 SciPy 0.14.0 Release Notes

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.

4.3.1 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.

4.3.2 Deprecated features

anneal

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.

4.3.3 Backwards incompatible changes

`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.

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.

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

The method \texttt{p.derivatives} has been removed.

### 4.3.4 Other changes

### 4.3.5 Authors

- Marc Abramowitz +
- Anders Bech 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
- David Menendez Hurtado +
- Matthieu Dartiailh +
- Christoph Deil +
- Jörg Dietrich +
- endolith
- Francisco de la Peña +
- Ben FrantzDale +
- Jim Garrison +
- André Gaul
- Christoph Gohlke
- Ralf Gommers
- Robert David Grant
- Alex Griffing
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: lpnm 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
• #3030: relative entropy using scipy.stats.distribution.entropy when...
• #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
• #3067: cumtrapz not working as expected
• #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 ‘squeueclidean’ 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
• #3066: 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...
• #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 maintenance 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 sparsertools manually instead via SWIG
• #3460: TST: open image file in binary mode
• #3467: BUG: fix validation in csgraph.shortest_path

4.4 SciPy 0.13.2 Release Notes

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

4.4.1 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

4.5 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.

4.5.1 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

4.6 SciPy 0.13.0 Release Notes
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
4.6.1 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 >= B`, `A != 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:
>>> A[A > 0.5] = 1  # since Boolean sparse matrices work
>>> A[:,2,:3] = 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 \( x \times \log(y) \) and give 0 when \( x == 0 \).

**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” (http://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.

### 4.6.2 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.

### 4.6.3 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 `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.

4.6.4 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.

4.6.5 Authors

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

- Jorge Cañardo Alastuey +
- Tom Aldcroft +
- Max Bolingbroke +
- Joseph Jon Booker +
- François Boulogne
- Matthew Brett
- Christian Brodbeck +
- Per Brodtkorb +
• Christian Brueffer +
• Lars Buitinck
• Evgeni Burovski +
• Tim Cera
• Lawrence Chan +
• David Cournapeau
• Drazen Lucanin +
• Alexander J. Dunlap +
• endolith
• André Gaul +
• Christoph Gohlke
• Ralf Gommers
• Alex Griffing +
• Blake Griffith +
• Charles Harris
• Bob Helmbold +
• Andreas Hilboll
• Kat Huang +
• Oleksandr (Sasha) Huziy +
• Gert-Ludwig Ingold +
• Thouis (Ray) Jones
• Juan Luis Cano Rodríguez +
• Robert Kern
• Andreas Kloeckner +
• Sytse Knypstra +
• Gustav Larsson +
• Denis Laxalde
• Christopher Lee
• Tim Leslie
• Wendy Liu +
• Clemens Novak +
• Takuya Oshima +
• Josef Perktold
• Illia Polosukhin +
• Przemek Porebski +
• Steve Richardson +
4.7 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.

4.8 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.

### 4.8.1 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**

dcipy.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. Basinhopping 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) is 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.

4.8.2 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.

4.8.3 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.)

4.8.4 Authors

- Anton Akhmerov +
- Alexander Eberspächer +
- Anne Archibald
- Jisk Attema +
- K.-Michael Aye +
- bemasc +
- Sebastian Berg +
• MinRK
• Sturla Molden +
• Eric Moore +
• mszep +
• Matt Newville +
• Vlad Niculae
• Travis Oliphant
• David Parker +
• Fabian Pedregosa
• Josef Perktold
• Zach Ploskey +
• Alex Reinhart +
• Gilles Rochefort +
• Ciro Duran Santilli +
• Jan Schlueter +
• Jonathan Scholz +
• Anthony Scopatz
• Skipper Seabold
• Fabrice Silva +
• Scott Sinclair
• Jacob Stevenson +
• Sturla Molden +
• Julian Taylor +
• thorstenkranz +
• John Travers +
• True Price +
• Nicky van Foreest
• Jacob Vanderplas
• Patrick Varilly
• Daniel Velkov +
• Pauli Virtanen
• Stefan van der Walt
• Warren Weckesser

A total of 75 people contributed to this release. People with a “+” by their names contributed a patch for the first time.
4.9 SciPy 0.11.0 Release Notes

Contents

- SciPy 0.11.0 Release Notes
  - New features
    - Sparse Graph Submodule
    - scipy.optimize improvements
      - Unified interfaces to minimizers
      - Unified interface to root finding algorithms
    - scipy.linalg improvements
      - New matrix equation solvers
      - QZ and QR Decomposition
      - Pascal matrices
    - Sparse matrix construction and operations
    - LSMR iterative solver
    - Discrete Sine Transform
    - scipy.interpolate improvements
      - Binned statistics (scipy.stats)
  - Deprecated features
  - Backwards incompatible changes
    - Removal of scipy.maxentropy
    - Minor change in behavior of splev
    - Behavior of scipy.integrate.complex_ode
    - Minor change in behavior of T-tests
  - Other changes
  - Authors

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.

4.9.1 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`, `sign`, `expm1`, `log1p`, `deg2rad`, `rad2deg`, `floor`, `ceil` and `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`.

**4.9.2 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.

**4.9.3 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.])
>>> 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.

### 4.9.4 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.

### 4.9.5 Authors

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

- Jeff Armstrong
4.10 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.

4.10.1 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.
4.10.2 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

4.11 SciPy 0.10.0 Release Notes

Contents

- SciPy 0.10.0 Release Notes
  - New features
    - Bento: new optional build system
    - Generalized and shift-invert eigenvalue problems in scipy.sparse.linalg
    - Discrete-Time Linear Systems (scipy.signal)
    - Enhancements to scipy.signal
    - Additional decomposition options (scipy.linalg)
    - Additional special matrices (scipy.linalg)
    - Enhancements to scipy.stats
    - Enhancements to scipy.special
    - Basic support for Harwell-Boeing file format for sparse matrices
  - Deprecated features
    - scipy.maxentropy
    - scipy.lib.blas
    - Numscors build system
  - Backwards-incompatible changes
  - Other changes
  - Authors

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.
4.11.1 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 $\logit(p) = \log\left(\frac{p}{1-p}\right)$ and $\expit(x) = \frac{1}{1+\exp(-x)}$ 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)

4.11.2 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 scikits.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.

4.11.3 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'`)

4.11.4 Other changes

`sctypy.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.

4.11.5 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
- FISH 2000 +
- Michael McNeil Forbes +
- Matty G +
- Christoph Gohlke
- Ralf Gommers
- Yaroslav Halchenko
- Charles Harris
- Thouis (Ray) Jones +
- Chris Jordan-Squire +
- Robert Kern
- Chris Lasher +
- Wes McKinney +
- Travis Oliphant
- Fabian Pedregosa
- Josef Perktold
- Thomas Robitaille +
- Pim Schellart +
- Anthony Scopatz +
- Skipper Seabold +
- Fazlul Shahriar +
- David Simcha +
- Scott Sinclair +
4.12 SciPy 0.9.0 Release Notes

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.

4.12.1 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.

4.12.2 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

http://github.com/scipy/scipy

4.12.3 New features

Delaunay tesselations (scipy.spatial)

Scipy now includes routines for computing Delaunay tesselations 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)).

4.12.4 Deprecated features

Obsolete nonlinear solvers (in **scipy.optimize**)

The following nonlinear solvers from **scipy.optimize** are deprecated:

- **broyden_modifed** (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**)

4.12.5 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, corrcov, 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.

4.12.6 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:

```python
import numpy as nprom 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

4.13 SciPy 0.8.0 Release Notes
SciPy 0.8.0 is the culmination of 17 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 0.8.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.

### 4.13.1 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.
4.13.2 Major documentation improvements

SciPy documentation is greatly improved.

4.13.3 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.

4.13.4 New features

DCT support (scipy.fftpack)

New realtransforms 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 http://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 naïve 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.
4.13.5 Removed features

scipy.stsci: the package was removed

The module scipy.misc.limits was removed.

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: 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.

4.14 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.

4.15 SciPy 0.7.1 Release Notes

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

Bugs fixed:
- Several fixes in Matlab file IO

Bugs fixed:
- Work around a failure with Python 2.6

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

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

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

4.15.1 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.

4.15.2 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.
4.16 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.

4.16.1 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.

### 4.16.2 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 http://docs.scipy.org/ and correct the issues.

### 4.16.3 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 all ready paid off, given the rapid increase in tests. To run the full test suite:

```bash
>>> 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.

### 4.16.4 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.

### 4.16.5 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.
4.16.6 Sparse Matrices

Sparse matrices have seen extensive improvements. There is now support for integer dtypes such as `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 constructs 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.

4.16.7 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.

### 4.16.8 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

### 4.16.9 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 `fclustdata` 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.

### 4.16.10 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,

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.

### 4.16.11 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.

### 4.16.12 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.

### 4.16.13 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.

### 4.16.14 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).

### 4.16.15 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.

### 4.16.16 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.

### 4.16.17 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.
4.16.18 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/funs.h (line 27). You can make the change in the installed scipy (in site-packages).
5.1 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.

5.2 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.

scipy.cluster.vq.whiten(obs[, check_finite]) Normalize a group of observations on a per feature basis.  

**Parameters**
- obs : ndarray  
  Each row of the array is an observation. The columns are the features seen during each observation.

```python
>>> #
>>> obs = [[ 1., 1., 1.],  #o0
          [ 2., 2., 2.],  #o1
          [ 3., 3., 3.],  #o2
          [ 4., 4., 4.]]  #o3
```

- check_finite : bool, optional

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.
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]])
```

#### 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.

- `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]))

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 centroids until sufficient progress cannot be made, i.e. the change in distortion since the last iteration is less than some threshold. This yields a code book mapping centroids to codes and vice versa.
Distortion is defined as the sum of the squared differences between the observations and the corresponding centroid.

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 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

- **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 distortion between the observations passed and the centroids generated.

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
>>> features = array([[ 1.9, 2.3],
...                     [ 1.5, 2.5],
...                     [ 0.8, 0.6],
...                     [ 0.4, 1.8],
...                     [ 0.1, 0.1]],
```

5.2. K-means clustering and vector quantization (scipy.cluster.vq)
... [[ 0.2,1.8],
... [ 2.0,0.5],
... [ 0.3,1.5],
... [ 1.0,1.0]])
>>> whitened = whiten(features)
>>> book = array((whitened[0],whitened[2]))
>>> kmeans(whitened,book)
(array([[ 2.3110306 , 2.86287398],
       [ 0.93218041, 1.24398691]]), 0.85684700941625547)

>>> from numpy import
>>> random.seed((1000,2000))
>>> codes = 3
>>> kmeans(whitened,codes)
(array([[ 2.3110306 , 2.86287398],
       [ 1.32544402, 0.65607529],
       [ 0.40782893, 2.02786907]]), 0.5196582527686241)

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
center 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)

minit : str, optional
Method for initialization. Available methods are ‘random’, ‘points’, ‘uniform’, and
’matrix’:
‘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.
‘uniform’: generate k observations from the data from a uniform distribution defined
by the data set (unsupported).
‘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 inifinities 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.

### 5.2.1 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. Each step of the k-means algorithm refines the choices of centroids to reduce distortion. The change in distortion is used as a stopping criterion: when the change is lower than a threshold, the k-means algorithm is not making sufficient progress and terminates. 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.

### 5.3 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.

```python
fcluster(Z, t[, criterion, depth, R, monocrit])  Forms flat clusters from the hierarchical clustering defined by the linkage matrix Z.

fclusterdata(X, t[, criterion, metric, ...])   Cluster observation data using a given metric.

leaders(Z, T)                                 Returns the root nodes in a hierarchical clustering.
```

**scipy.cluster.hierarchy.fcluster**

Forms flat clusters from the hierarchical clustering defined by the linkage matrix Z.

```
Parameters

Z : ndarray
    The hierarchical clustering encoded with the matrix returned by the linkage function.

t : float
```

# 5.3. Hierarchical clustering (scipy.cluster.hierarchy)

271
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
[Find 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. \( \text{monocrit} \) 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:

\[
\text{MI} = \text{maxinconsts}(Z, R)
\]

\[
\text{cluster}(Z, t=3, \text{criterion}='\text{maxclust_monocrit}', \text{monocrit}=\text{MI})
\]

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 \( n-1 \). \( \text{monocrit}[i] \) 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 \( c \), \( \text{monocrit}[i] \geq \text{monocrit}[j] \).

Returns

fccluster : ndarray
An array of length \( n \). \( T[i] \) is the flat cluster number to which original observation \( i \) belongs.

scipy.cluster.hierarchy.fclusterdata(X, t, criterion='inconsistent', metric='euclidean', depth=2, method='single', R=None)

Cluster observation data using a given metric.

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.
t : float
    The threshold to apply when forming flat clusters.

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.

Notes

This function is similar to the MATLAB function clusterdata.

scipy.cluster.hierarchy.leaders(Z, T)
    Returns the root nodes in a hierarchical clustering.

    Returns the root nodes in a hierarchical clustering corresponding to a cut defined by a flat cluster assignment vector T. See the fcluster function for more information on the format of T.

    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 descendents 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 leaf nodes descendents with cluster node i)

    • there does not exist a leaf that is not descendent 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.

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.
For example: if L[3]=2 and M[3]=8, the flat cluster with id 8’s leader is linkage node 2.

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.
These are routines for agglomerative clustering.

- **linkage(y[, method, metric])** Performs hierarchical/agglomerative clustering on the condensed distance matrix y.
  - **single**(y) Performs single/min/nearest linkage on the condensed distance matrix y
  - **complete**(y) Performs complete/max/farthest point linkage on a condensed distance matrix
  - **average**(y) Performs average/UPGMA linkage on a condensed distance matrix
  - **weighted**(y) Performs weighted/WPGMA linkage on the condensed distance matrix.
  - **centroid**(y) Performs centroid/UPGMC linkage.
  - **median**(y) Performs median/WPGMC linkage.
  - **ward**(y) Performs Ward’s linkage on a condensed or redundant distance matrix.

```python
scipy.cluster.hierarchy.\texttt{linkage}(y, \texttt{method}='single', \texttt{metric}='euclidean')
```

Performs hierarchical/agglomerative clustering on the condensed distance matrix y.

- y must be a \((n^2)\) 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 4 by \((n-1)\) 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
    
    \[ d(u, v) = \frac{\sum_{ij} d(u[i], v[j])}{(|u| \times |v|)} \]

    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
\[ d(u, v) = \frac{(dist(s, v) + dist(t, v))}{2} \]
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 chose a different minimum than the MATLAB version.

Parameters

**y** : ndarray
A condensed or redundant 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.

**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. See the distance.pdist function for a list of valid distance metrics. The customized distance can also be used. See the distance.pdist function for details.

Returns

**Z** : ndarray
The hierarchical clustering encoded as a linkage matrix.

scipy.cluster.hierarchy.single(y)
Performs single/min/nearest linkage on the condensed distance matrix y

Parameters

**y** : ndarray
The upper triangular of the distance matrix. The result of pdist is returned in this form.

Returns

**Z** : ndarray
The linkage matrix.

See also:

**linkage** for advanced creation of hierarchical clusterings.

5.3. Hierarchical clustering (scipy.cluster.hierarchy) 275
scipy.cluster.hierarchy.complete(y)
Performs 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

scipy.cluster.hierarchy.average(y)
Performs 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 the linkage function documentation for more information on its structure.

See also:

linkage  for advanced creation of hierarchical clusterings.

scipy.cluster.hierarchy.weighted(y)
Performs 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 the linkage function documentation for more information on its structure.

See also:

linkage  for advanced creation of hierarchical clusterings.

scipy.cluster.hierarchy.centroid(y)
Performs centroid/UPGMC linkage.

See linkage for more information on the return structure and algorithm.

The following are common calling conventions:

1. Z = centroid(y)
   Performs centroid/UPGMC linkage on the condensed distance matrix y. See linkage for more information on the return structure and algorithm.

2. Z = centroid(X)
   Performs centroid/UPGMC 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

\( y : \text{ndarray} \)

A condensed or redundant distance matrix. A condensed distance matrix is a flat array containing the upper triangular of the distance matrix. This is the form that \texttt{pdist} returns. Alternatively, a collection of \( m \) observation vectors in \( n \) dimensions may be passed as a \( m \) by \( n \) array.

Returns

\( Z : \text{ndarray} \)

A linkage matrix containing the hierarchical clustering. See the \texttt{linkage} function documentation for more information on its structure.

See also:

\texttt{linkage} for advanced creation of hierarchical clusterings.

\texttt{scipy.cluster.hierarchy.median}(y)

Performs median/WPGMC linkage.

See \texttt{linkage} for more information on the return structure and algorithm.

The following are common calling conventions:

1. \( Z = \text{median}(y) \)
   
   Performs median/WPGMC linkage on the condensed distance matrix \( y \). See \texttt{linkage} for more information on the return structure and algorithm.

2. \( Z = \text{median}(X) \)
   
   Performs median/WPGMC linkage on the observation matrix \( X \) using Euclidean distance as the distance metric. See \texttt{linkage} for more information on the return structure and algorithm.

Parameters

\( y : \text{ndarray} \)

A condensed or redundant distance matrix. A condensed distance matrix is a flat array containing the upper triangular of the distance matrix. This is the form that \texttt{pdist} returns. Alternatively, a collection of \( m \) observation vectors in \( n \) dimensions may be passed as a \( m \) by \( n \) array.

Returns

\( Z : \text{ndarray} \)

The hierarchical clustering encoded as a linkage matrix.

See also:

\texttt{linkage} for advanced creation of hierarchical clusterings.

\texttt{scipy.cluster.hierarchy.ward}(y)

Performs Ward's linkage on a condensed or redundant distance matrix.

See \texttt{linkage} for more information on the return structure and algorithm.

The following are common calling conventions:

1. \( Z = \text{ward}(y) \)
   
   Performs Ward’s linkage on the condensed distance matrix \( Z \). See \texttt{linkage} for more information on the return structure and algorithm.

2. \( Z = \text{ward}(X) \)
   
   Performs Ward’s linkage on the observation matrix \( X \) using Euclidean distance as the distance metric. See \texttt{linkage} for more information on the return structure and algorithm.

Parameters

\( y : \text{ndarray} \)

A condensed or redundant distance matrix. A condensed distance matrix is a flat array containing the upper triangular of the distance matrix. This is the form that \texttt{pdist} returns. Alternatively, a collection of \( m \) observation vectors in \( n \) dimensions may be passed as a \( m \) by \( n \) array.

Returns

\( Z : \text{ndarray} \)
The hierarchical clustering encoded as a linkage matrix.

See also:

*linkage* for advanced creation of hierarchical clusterings.

These routines compute statistics on hierarchies.

- `scipy.cluster.hierarchy.cophenet(Z[, Y])`: Calculates the cophenetic distances between each observation in the hierarchical clustering defined by the linkage matrix `Z`. The cophenetic distances are calculated by finding the distance between clusters `s` and `t`, where `s` and `t` are joined by a direct parent cluster `u`, 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**
  - `Z`: ndarray
    The hierarchical clustering encoded as an array (see `linkage` function).
  - `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 cophentric 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`.

- `scipy.cluster.hierarchy.from_mlab_linkage(Z)`: Converts 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`: ndarray
    A linkage matrix generated by MATLAB(TM).

  **Returns**
  - `ZS`: ndarray
    A linkage matrix compatible with this library.

- `scipy.cluster.hierarchy.inconsistent(Z, d=2)`: Calculates inconsistency statistics on a linkage.

  **Note:** This function behaves similarly to the MATLAB(TM) inconsistent function.
**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 5 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:

\[
\frac{Z[i, 2] - R[i, 0]}{R[i, 1]}
\]

**scipy.cluster.hierarchy.maxinconsts(Z, R)**

Returns the maximum inconsistency coefficient for each non-singleton cluster and its descendents.

**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.

**scipy.cluster.hierarchy.maxdists(Z)**

Returns 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, \(MD[i] = Z[Q(i)-n, 2].\max()\) where \(Q(i)\) is the set of all node indices below and including node \(i\).

**scipy.cluster.hierarchy.maxRstat(Z, R, i)**

Returns the maximum statistic for each non-singleton cluster and its descendents.

**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 \(j\).

**scipy.cluster.hierarchy.to_mlab_linkage(Z)**

Converts 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 this library.
Routines for visualizing flat clusters.

```
dendrogram(Z[, p, truncate_mode, ...])  Plots the hierarchical clustering as a dendrogram.
```

Plots 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 height of the top of the U-link is the distance between its children clusters. It is also the cophenetic distance between original observations in the two children clusters. It is expected that the distances in Z[:,2] be monotonic, otherwise crossings appear in the dendrogram.

### 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**/’none’
    No truncation is performed (Default).
  - **lastp**
    The last p non-singleton 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.
  - **mlab**
    This corresponds to MATLAB(TM) behavior. (not implemented yet)
  - **level**/’mtica’
    No more than p levels of the dendrogram tree are displayed. This corresponds to Mathematica(TM) behavior.
- **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'` \n  Plots the root at the top, and plot descendent links going downwards. (default).

- `'bottom'` \n  Plots the root at the bottom, and plot descendent links going upwards.

- `'left'` \n  Plots the root at the left, and plot descendent links going right.

- `'right'` \n  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 $\text{labels}[i]$ 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` \n  Nothing is done.

- `'ascending'` or `True`
  The child with the minimum number of original objects in its cluster is plotted first.

- `'descendent'`
  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` \n  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 $k < 2n - 1$. 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:

5.3. Hierarchical clustering (`scipy.cluster.hierarchy`) 281
# First define the leaf label function.

```python
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.

```python
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
across the long connecting line 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 fol-
lowing 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* < 2*n*−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.

These are data structures and routines for representing hierarchies as tree objects.

### `ClusterNode(id[, left, right, dist, count])`
A tree node class for representing a cluster.

### `leaves_list(Z)`
Returns a list of leaf node ids

### `to_tree(Z[, rd])`
Converts a hierarchical clustering encoded in the matrix *Z* (by linkage) into an easy-to-

**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.

See also:

`to_tree` for converting a linkage matrix \( Z \) into a tree object.

### Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>get_count()</code></td>
<td>The number of leaf nodes (original observations) belonging to the cluster node ( nd ). If the target node is a leaf, 1 is returned.</td>
</tr>
<tr>
<td><code>get_id()</code></td>
<td>The identifier of the target node.</td>
</tr>
<tr>
<td><code>get_left()</code></td>
<td>Return a reference to the left child tree object.</td>
</tr>
<tr>
<td><code>get_right()</code></td>
<td>Returns a reference to the right child tree object.</td>
</tr>
<tr>
<td><code>is_leaf()</code></td>
<td>Returns True if the target node is a leaf.</td>
</tr>
<tr>
<td><code>pre_order()</code></td>
<td>Performs pre-order traversal without recursive function calls.</td>
</tr>
</tbody>
</table>

**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.

**ClusterNode.get_id()**  
The identifier of the target node.

**Returns**

- `id`: int
  - The identifier of the target node.

**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.

**ClusterNode.get_right()**  
Returns a reference to the right child tree object.

**Returns**

- `right`: ClusterNode
  - The left child of the target node. If the node is a leaf, None is returned.

**ClusterNode.is_leaf()**  
Returns True if the target node is a leaf.

**Returns**

- `leafness`: bool
  - True if the target node is a leaf node.

**ClusterNode.pre_order**

- `(func=<function <lambda> at 0x7fa4127d22a8>)`

  Performs 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:
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.

**scipy.cluster.hierarchy.leaves_list(Z)**

Returns 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 linkage for more information.

**Returns**

- leaves_list : ndarray
  The list of leaf node ids.

**scipy.cluster.hierarchy.to_tree(Z, rd=False)**

Converts a hierarchical clustering encoded in the matrix Z (by linkage) into an easy-to-use tree object.

The reference r to the root ClusterNode object is returned.

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, 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 dictionary mapping cluster ids to ClusterNode references. If a cluster id is less than n, then it corresponds to a singleton cluster (leaf node). See linkage for more information on the assignment of cluster ids to clusters.

**Returns**

- L : list
  The pre-order traversal.

These are predicates for checking the validity of linkage and inconsistency matrices as well as for checking isomorphism of two flat cluster assignments.

**is_valid_im(R[, warning, throw, name])**

Returns True if the inconsistency matrix passed is valid.

**is_valid_linkage(Z[, warning, throw, name])**

Checks the validity of a linkage matrix.

**is_isomorphic(T1, T2)**

Determines if two different cluster assignments are equivalent.

**is_monotonic(Z)**

Returns True if the linkage passed is monotonic.

**correspond(Z, Y)**

Checks for correspondence between linkage and condensed distance matrices

**num_obs_linkage(Z)**

Returns the number of original observations of the linkage matrix passed.

**scipy.cluster.hierarchy.is_valid_im(R, warning=False, throw=False, name=None)**
Returns True if the inconsistency matrix passed is valid.

It must be a \( n \) by 4 numpy 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.

**scipy.cluster.hierarchy.is_valid_linkage**

Checks the validity of a linkage matrix.

A linkage matrix is valid if it is a two dimensional ndarray (type double) with \( n \) rows and 4 columns. The first two columns must contain indices between 0 and \( 2n - 1 \). For a given row \( i \), \( 0 \leq Z[i,0] \leq i + n - 1 \) and \( 0 \leq Z[i,1] \leq i + n - 1 \) (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 iff the inconsistency matrix is valid.

**scipy.cluster.hierarchy.is_isomorphic**

Determines 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.

**scipy.cluster.hierarchy.is_monotonic**

Returns 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.

**scipy.cluster.hierarchy.correspond**

Checks 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.

```python
scipy.cluster.hierarchy.num_obs_linkage(Z)
```

Returns the number of original observations of the linkage matrix passed.

**Parameters**

- **Z**: ndarray
  The linkage matrix on which to perform the operation.

**Returns**

- **n**: int
  The number of original observations in the linkage.

Utility routines for plotting:

```python
set_link_color_palette(palette)
```

Set list of matplotlib color codes for dendrogram color_threshold.

```python
scipy.cluster.hierarchy.set_link_color_palette(palette)
```

Set list of matplotlib color codes for dendrogram color_threshold.

**Parameters**

- **palette**: list
  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.

### 5.3.1 References

- MATLAB and MathWorks are registered trademarks of The MathWorks, Inc.
- Mathematica is a registered trademark of The Wolfram Research, Inc.

### 5.4 Constants (scipy.constants)

Physical and mathematical constants and units.

#### 5.4.1 Mathematical constants

<table>
<thead>
<tr>
<th>pi</th>
<th>Pi</th>
</tr>
</thead>
<tbody>
<tr>
<td>golden</td>
<td>Golden ratio</td>
</tr>
</tbody>
</table>
5.4.2 Physical constants

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>c</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), $\varepsilon_0$</td>
</tr>
<tr>
<td>h</td>
<td>the Planck constant $h$</td>
</tr>
<tr>
<td>hbar</td>
<td>$\hbar = h/(2\pi)$</td>
</tr>
<tr>
<td>G</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>R</td>
<td>molar gas constant</td>
</tr>
<tr>
<td>alpha</td>
<td>fine-structure constant</td>
</tr>
<tr>
<td>N_A</td>
<td>Avogadro constant</td>
</tr>
<tr>
<td>k</td>
<td>Boltzmann constant</td>
</tr>
<tr>
<td>sigma</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>m_p</td>
<td>proton mass</td>
</tr>
<tr>
<td>m_n</td>
<td>neutron mass</td>
</tr>
</tbody>
</table>

Constants database

In addition to the above variables, scipy.constants also contains the 2010 CODATA recommended values [CODATA2010] database containing more physical constants.

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>value(key)</td>
<td>Value in physical_constants indexed by key</td>
</tr>
<tr>
<td>unit(key)</td>
<td>Unit in physical_constants indexed by key</td>
</tr>
<tr>
<td>precision(key)</td>
<td>Relative precision in physical_constants indexed by key</td>
</tr>
<tr>
<td>find([sub, disp])</td>
<td>Return list of codata.physical_constant keys containing a given string.</td>
</tr>
</tbody>
</table>

**ConstantWarning** Accessing a constant no longer in current CODATA data set

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.constants import codata
>>> codata.value('elementary charge')
1.6021766487e-19
```

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.constants import codata
>>> codata.unit(u'proton mass')
'kg'
```

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.constants import codata
>>> codata.precision(u'proton mass')
4.96226989798e-08
```

scipy.constants.find(sub=None, disp=False)
Return list of codata.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.

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>Property</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>alpha particle mass</td>
<td>6.6465675e-27 kg</td>
</tr>
<tr>
<td>alpha particle mass energy equivalent</td>
<td>5.97191967e-10 J</td>
</tr>
<tr>
<td>alpha particle mass energy equivalent in MeV</td>
<td>3727.37924 MeV</td>
</tr>
<tr>
<td>alpha particle mass in u</td>
<td>4.00150617913 u</td>
</tr>
<tr>
<td>alpha particle molar mass</td>
<td>0.00400150617912 kg mol^-1</td>
</tr>
<tr>
<td>alpha particle-electron mass ratio</td>
<td>7294.2995361</td>
</tr>
<tr>
<td>alpha particle-proton mass ratio</td>
<td>3.97259968933</td>
</tr>
<tr>
<td>Angstrom star</td>
<td>1.00001495e-10 m</td>
</tr>
<tr>
<td>atomic mass constant</td>
<td>1.660538921e-27 kg</td>
</tr>
<tr>
<td>atomic mass constant energy equivalent</td>
<td>1.492417954e-10 J</td>
</tr>
<tr>
<td>atomic mass constant energy equivalent in MeV</td>
<td>931.494061 MeV</td>
</tr>
<tr>
<td>atomic mass unit-electron volt relationship</td>
<td>931494061.0 eV</td>
</tr>
<tr>
<td>atomic mass unit-hartree relationship</td>
<td>34231776.845 E_h</td>
</tr>
<tr>
<td>atomic mass unit-hertz relationship</td>
<td>2.2523427168e+23 Hz</td>
</tr>
<tr>
<td>atomic mass unit-inverse meter relationship</td>
<td>7.5130066042e+14 m^-1</td>
</tr>
<tr>
<td>atomic mass unit-joule relationship</td>
<td>1.492417954e-10 J</td>
</tr>
<tr>
<td>atomic mass unit-kilogram relationship</td>
<td>1.08095408e+13 K</td>
</tr>
<tr>
<td>atomic mass unit-kilogram relationship</td>
<td>1.660538921e-27 kg</td>
</tr>
<tr>
<td>atomic unit of 1st hyperpolarizability</td>
<td>3.206361449e-53 C^3 m^3 J^-2</td>
</tr>
<tr>
<td>atomic unit of 2nd hyperpolarizability</td>
<td>6.23358054e-65 C^4 m^4 J^-3</td>
</tr>
<tr>
<td>atomic unit of action</td>
<td>1.054571726e-34 J s</td>
</tr>
<tr>
<td>atomic unit of charge</td>
<td>1.602176565e-19 C</td>
</tr>
<tr>
<td>atomic unit of charge density</td>
<td>1.081202338e+12 C m^-3</td>
</tr>
<tr>
<td>atomic unit of current</td>
<td>0.00662361795 A</td>
</tr>
<tr>
<td>atomic unit of electric dipole mom.</td>
<td>8.47835326e-30 C m</td>
</tr>
<tr>
<td>atomic unit of electric field</td>
<td>5.14220652e+11 V m^-1</td>
</tr>
<tr>
<td>atomic unit of electric field gradient</td>
<td>9.717362e+21 V m^-2</td>
</tr>
<tr>
<td>atomic unit of electric polarizability</td>
<td>1.6487772754e-41 C^2 m^2 J^-1</td>
</tr>
<tr>
<td>atomic unit of electric potential</td>
<td>27.21138505 V</td>
</tr>
<tr>
<td>atomic unit of electric quadrupole mom.</td>
<td>4.486551331e-40 C m^2</td>
</tr>
<tr>
<td>atomic unit of energy</td>
<td>4.35974434e-18 J</td>
</tr>
<tr>
<td>atomic unit of force</td>
<td>8.23872278e-08 N</td>
</tr>
<tr>
<td>atomic unit of length</td>
<td>5.2917721092e-11 m</td>
</tr>
<tr>
<td>atomic unit of mag. dipole mom.</td>
<td>1.854801936e-23 J T^-1</td>
</tr>
<tr>
<td>atomic unit of mag. flux density</td>
<td>235051.7464 T</td>
</tr>
<tr>
<td>atomic unit of magnetizability</td>
<td>7.891036607e-29 J T^-2</td>
</tr>
<tr>
<td>atomic unit of mass</td>
<td>9.10938291e-31 kg</td>
</tr>
<tr>
<td>atomic unit of mom.um</td>
<td>1.99285174e-24 kg m s^-1</td>
</tr>
<tr>
<td>atomic unit of permittivity</td>
<td>1.11265005605e-10 F m^-1</td>
</tr>
<tr>
<td>atomic unit of time</td>
<td>2.4188843265e-17 s</td>
</tr>
<tr>
<td>atomic unit of velocity</td>
<td>2187691.26379 m s^-1</td>
</tr>
<tr>
<td>Avogadro constant</td>
<td>6.02214129e+23 mol^-1</td>
</tr>
<tr>
<td>Bohr magneton</td>
<td>9.27400968e-24 J T^-1</td>
</tr>
<tr>
<td>Bohr magneton in eV/T</td>
<td>5.788318066e-05 eV T^-1</td>
</tr>
<tr>
<td>Bohr magneton in Hz/T</td>
<td>13996245550.0 Hz T^-1</td>
</tr>
<tr>
<td>Bohr magneton in inverse meters per tesla</td>
<td>46.6864989 m^-1 T^-1</td>
</tr>
<tr>
<td>Bohr magneton in K/T</td>
<td>0.67171388 K T^-1</td>
</tr>
<tr>
<td>Bohr radius</td>
<td>5.2917721092e-11 m</td>
</tr>
<tr>
<td>Boltzmann constant</td>
<td>1.3806488e-23 J K^-1</td>
</tr>
<tr>
<td>Boltzmann constant in eV/K</td>
<td>8.6173324e-05 eV K^-1</td>
</tr>
</tbody>
</table>
Table 5.11 – continued from previous page

<table>
<thead>
<tr>
<th>Description</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Boltzmann constant in Hz/K</td>
<td>20836618000.0 Hz K^-1</td>
</tr>
<tr>
<td>Boltzmann constant in inverse meters per kelvin</td>
<td>69.503476 m^-1 K^-1</td>
</tr>
<tr>
<td>characteristic impedance of vacuum</td>
<td>376.730313462 ohm</td>
</tr>
<tr>
<td>classical electron radius</td>
<td>2.8179403267e-15 m</td>
</tr>
<tr>
<td>Compton wavelength</td>
<td>2.4263102389e-12 m</td>
</tr>
<tr>
<td>Compton wavelength over 2 pi</td>
<td>3.86159268e-13 m</td>
</tr>
<tr>
<td>conductance quantum</td>
<td>7.7480917346e-05 S</td>
</tr>
<tr>
<td>conventional value of Josephson constant</td>
<td>4.835979e+14 Hz V^-1</td>
</tr>
<tr>
<td>conventional value of von Klitzing constant</td>
<td>25812.807 ohm</td>
</tr>
<tr>
<td>Cu x unit</td>
<td>1.00207697e-13 m</td>
</tr>
<tr>
<td>deuteron g factor</td>
<td>0.8574382308</td>
</tr>
<tr>
<td>deuteron mag. mom.</td>
<td>4.33073489e-27 J T^-1</td>
</tr>
<tr>
<td>deuteron mag. mom. to Bohr magneton ratio</td>
<td>0.000469754556</td>
</tr>
<tr>
<td>deuteron mag. mom. to nuclear magneton ratio</td>
<td>0.8574382308</td>
</tr>
<tr>
<td>deuteron mass</td>
<td>3.34358348e-27 kg</td>
</tr>
<tr>
<td>deuteron mass energy equivalent</td>
<td>3.00506297e-10 J</td>
</tr>
<tr>
<td>deuteron mass energy equivalent in MeV</td>
<td>1875.612859 MeV</td>
</tr>
<tr>
<td>deuteron mass in u</td>
<td>2.01355321271 u</td>
</tr>
<tr>
<td>deuteron molar mass</td>
<td>0.00201355321271 kg mol^-1</td>
</tr>
<tr>
<td>deuteron rms charge radius</td>
<td>2.142e-15 m</td>
</tr>
<tr>
<td>deuteron-electron mag. mom. ratio</td>
<td>-0.000464345537</td>
</tr>
<tr>
<td>deuteron-electron mass ratio</td>
<td>367.4829652</td>
</tr>
<tr>
<td>deuteron-neutron mag. mom. ratio</td>
<td>-0.44820652</td>
</tr>
<tr>
<td>deuteron-proton mag. mom. ratio</td>
<td>0.307012207</td>
</tr>
<tr>
<td>deuteron-proton mass ratio</td>
<td>1.99900750097</td>
</tr>
<tr>
<td>electric constant</td>
<td>8.85418781762e-12 F m^-1</td>
</tr>
<tr>
<td>electron charge to mass quotient</td>
<td>-1.758820088e+11 C kg^-1</td>
</tr>
<tr>
<td>electron g factor</td>
<td>-2.00231930436</td>
</tr>
<tr>
<td>electron gyromag. ratio</td>
<td>1.760859708e+11 s^-1 T^-1</td>
</tr>
<tr>
<td>electron gyromag. ratio over 2 pi</td>
<td>28024.95266 MHz T^-1</td>
</tr>
<tr>
<td>electron mag. mom.</td>
<td>-9.2847643e-24 J T^-1</td>
</tr>
<tr>
<td>electron mag. mom. anomaly</td>
<td>0.00119365218076</td>
</tr>
<tr>
<td>electron mag. mom. to Bohr magneton ratio</td>
<td>-1.0011965218</td>
</tr>
<tr>
<td>electron mag. mom. to nuclear magneton ratio</td>
<td>-1838.2819709</td>
</tr>
<tr>
<td>electron mass</td>
<td>9.10938291e-31 kg</td>
</tr>
<tr>
<td>electron mass energy equivalent</td>
<td>8.18710506e-14 J</td>
</tr>
<tr>
<td>electron mass energy equivalent in MeV</td>
<td>0.510998928 MeV</td>
</tr>
<tr>
<td>electron mass in u</td>
<td>0.00054857990946 u</td>
</tr>
<tr>
<td>electron molar mass</td>
<td>5.4857990946e-07 kg mol^-1</td>
</tr>
<tr>
<td>electron to alpha particle mass ratio</td>
<td>0.00013709355578</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>1.602176565e-19 J</td>
</tr>
<tr>
<td>electron volt-atomic mass unit relationship</td>
<td>1.07354415e-09 u</td>
</tr>
<tr>
<td>electron volt-hartree relationship</td>
<td>0.03674932379 E_h</td>
</tr>
<tr>
<td>electron volt-hertz relationship</td>
<td>2.417989348e+14 Hz</td>
</tr>
<tr>
<td>electron volt-inverse meter relationship</td>
<td>806554.429 m^-1</td>
</tr>
<tr>
<td>electron volt-joule relationship</td>
<td>1.602176565e-19 J</td>
</tr>
<tr>
<td>electron volt_kelvin relationship</td>
<td>11604.519 K</td>
</tr>
<tr>
<td>electron volt-kilogram relationship</td>
<td>1.782661845e-36 kg</td>
</tr>
</tbody>
</table>

Continued on next page

5.4. Constants (scipy.constants) 291
| electron-deuteron mag. mom. ratio | -2143.923498 |
| electron-deuteron mass ratio | 0.00027244371095 |
| electron-helion mass ratio | 0.00018195430761 |
| electron-muon mag. mom. ratio | 206.7669896 |
| electron-muon mass ratio | 0.00483633166 |
| electron-neutron mag. mom. ratio | 960.9205 |
| electron-neutron mass ratio | 0.00054386734461 |
| electron-proton mag. mom. ratio | -658.2106848 |
| electron-proton mass ratio | 0.00054461702178 |
| electron-tau mass ratio | 0.000287592 |
| electron-triton mass ratio | 0.00018192000653 |
| elementary charge | 1.602176565e-19 C |
| elementary charge over h | 2.417989348e+14 A J^-1 |
| Faraday constant | 96485.3365 C mol^-1 |
| Faraday constant for conventional electric current | 96485.321 C mol^-1 |
| Fermi coupling constant | 1.166364e-05 GeV^-2 |
| fine-structure constant | 0.0072973525698 |
| first radiation constant | 3.74177153e-16 W m^2 |
| first radiation constant for spectral radiance | 1.19104269e-16 W m^2 sr^-1 |
| Hartree energy | 4.35974434e-18 J |
| Hartree energy in eV | 27.21138505 eV |
| hartree-atomic mass unit relationship | 2.921262346e-08 u |
| hartree-electron volt relationship | 27.21138505 eV |
| hartree-hertz relationship | 6.57968392073e+15 Hz |
| hartree-inverse meter relationship | 21947463.1371 m^-1 |
| hartree-joule relationship | 4.35974434e-18 J |
| hartree-kilocalorie relationship | 315775.04 K |
| hartree-kilogram relationship | 4.8506979e-35 kg |
| helion g factor | -4.255250613 |
| helion mag. mom. | -1.074617486e-26 J T^-1 |
| helion mag. mom. to Bohr magneton ratio | -0.001158740958 |
| helion mag. mom. to nuclear magneton ratio | -2.12762306 |
| helion mass | 5.00641234e-27 kg |
| helion mass energy equivalent | 4.49953902e-10 J |
| helion mass energy equivalent in MeV | 2808.391482 MeV |
| helion mass in u | 3.0149322468 u |
| helion molar mass | 0.0030149322468 kg mol^-1 |
| helion-electron mass ratio | 5495.8852754 |
| helion-proton mass ratio | 2.9931526707 |
| hertz-atomic mass unit relationship | 4.4398216689e-24 u |
| hertz-electron volt relationship | 4.135667516e-15 eV |
| hertz-hartree relationship | 1.519829846e-16 E_h |
| hertz-inverse meter relationship | 3.3356409198e-09 m^-1 |
| hertz-joule relationship | 6.62606957e-34 J |
| hertz-kilocalorie relationship | 4.7992434e-11 K |
| hertz-kilogram relationship | 7.37249668e-51 kg |
| inverse fine-structure constant | 137.035999074 |
| inverse meter-atomic mass unit relationship | 1.33102506e-15 |
| inverse meter-electron volt relationship | 1.23984193e-06 eV |
| inverse meter-hartree relationship | 4.55633525276e-08 E_h |

Continued on next page
<table>
<thead>
<tr>
<th>Relationship</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Inverse meter-hertz relationship</td>
<td>299792458.0 Hz</td>
</tr>
<tr>
<td>Inverse meter-joule relationship</td>
<td>1.98645684e-25 J</td>
</tr>
<tr>
<td>Inverse meter-kelvin relationship</td>
<td>0.01438777 K</td>
</tr>
<tr>
<td>Inverse meter-kilogram relationship</td>
<td>2.210218902e-42 kg</td>
</tr>
<tr>
<td>Inverse of conductance quantum</td>
<td>12906.4037217 ohm</td>
</tr>
<tr>
<td>Josephson constant</td>
<td>4.8359787e+14 Hz V^-1</td>
</tr>
<tr>
<td>Joule-atomic mass unit relationship</td>
<td>6700535850.0 u</td>
</tr>
<tr>
<td>Joule-electron volt relationship</td>
<td>6.24150934e+18 eV</td>
</tr>
<tr>
<td>Joule-hartree relationship</td>
<td>2.29371248e+17 E_h</td>
</tr>
<tr>
<td>Joule-hertz relationship</td>
<td>1.509190311e+33 Hz</td>
</tr>
<tr>
<td>Joule-inverse meter relationship</td>
<td>5.03411701e+24 m^-1</td>
</tr>
<tr>
<td>Joule-kelvin relationship</td>
<td>7.2429716ee+22 K</td>
</tr>
<tr>
<td>Joule-kilogram relationship</td>
<td>1.11265005605e-17 kg</td>
</tr>
<tr>
<td>Kelvin-atomic mass unit relationship</td>
<td>9.2510868e-14 u</td>
</tr>
<tr>
<td>Kelvin-electron volt relationship</td>
<td>8.6173324e-05 eV</td>
</tr>
<tr>
<td>Kelvin-hartree relationship</td>
<td>3.1668114e-06 E_h</td>
</tr>
<tr>
<td>Kelvin-hertz relationship</td>
<td>20836618000.0 Hz</td>
</tr>
<tr>
<td>Kelvin-inverse meter relationship</td>
<td>69.503476 m^-1</td>
</tr>
<tr>
<td>Kelvin-joule relationship</td>
<td>1.3806488e-23 J</td>
</tr>
<tr>
<td>Kilogram-atomic mass unit relationship</td>
<td>1.536179e-40 kg</td>
</tr>
<tr>
<td>Kilogram-electron volt relationship</td>
<td>6.0221429e+26 u</td>
</tr>
<tr>
<td>Kilogram-hartree relationship</td>
<td>5.609588585e+35 eV</td>
</tr>
<tr>
<td>Kilogram-hertz relationship</td>
<td>2.061485968e+34 E_h</td>
</tr>
<tr>
<td>Kilogram-inverse meter relationship</td>
<td>1.356392608e+50 Hz</td>
</tr>
<tr>
<td>Kilogram-joule relationship</td>
<td>4.5244373e+41 m^-1</td>
</tr>
<tr>
<td>Kilogram-kelvin relationship</td>
<td>8.975517873e+16 J</td>
</tr>
<tr>
<td>Kilogram-kilogram relationship</td>
<td>6.5096582e+39 K</td>
</tr>
<tr>
<td>Lattice parameter of silicon</td>
<td>5.431020504e-10 m</td>
</tr>
<tr>
<td>Loschmidt constant (273.15 K, 100 kPa)</td>
<td>2.6516462e+25 m^-3</td>
</tr>
<tr>
<td>Loschmidt constant (273.15 K, 101.325 kPa)</td>
<td>2.6867805e+25 m^-3</td>
</tr>
<tr>
<td>Mag. constant</td>
<td>1.25663706144e-06 N A^-2</td>
</tr>
<tr>
<td>Mag. flux quantum</td>
<td>2.067833758e-15 Wb</td>
</tr>
<tr>
<td>Mo x unit</td>
<td>1.00209952e-13 m</td>
</tr>
<tr>
<td>Molar gas constant</td>
<td>8.3144621 J mol^-1 K^-1</td>
</tr>
<tr>
<td>Molar mass constant</td>
<td>0.001 kg mol^-1</td>
</tr>
<tr>
<td>Molar mass of carbon-12</td>
<td>0.012 kg mol^-1</td>
</tr>
<tr>
<td>Molar Planck constant</td>
<td>3.9903127176e-10 J s mol^-1</td>
</tr>
<tr>
<td>Molar Planck constant times c</td>
<td>0.119626565779 J m mol^-1</td>
</tr>
<tr>
<td>Molar volume of ideal gas (273.15 K, 100 kPa)</td>
<td>0.022710953 m^3 mol^-1</td>
</tr>
<tr>
<td>Molar volume of ideal gas (273.15 K, 101.325 kPa)</td>
<td>0.022413968 m^3 mol^-1</td>
</tr>
<tr>
<td>Molar volume of silicon</td>
<td>1.205883303e-05 m^3 mol^-1</td>
</tr>
<tr>
<td>Muon Compton wavelength</td>
<td>1.173444103e-14 m</td>
</tr>
<tr>
<td>Muon Compton wavelength over 2 pi</td>
<td>1.867594294e-15 m</td>
</tr>
<tr>
<td>Muon g factor</td>
<td>-2.00235318418</td>
</tr>
<tr>
<td>Muon mag. mom.</td>
<td>-4.49044807e-26 J T^-1</td>
</tr>
<tr>
<td>Muon mag. mom. anomaly</td>
<td>0.00116592091</td>
</tr>
<tr>
<td>Muon mag. mom. to Bohr magneton ratio</td>
<td>-0.00484197044</td>
</tr>
<tr>
<td>Muon mag. mom. to nuclear magneton ratio</td>
<td>-8.89059697</td>
</tr>
<tr>
<td>Muon mass</td>
<td>1.883531475e-28 kg</td>
</tr>
<tr>
<td>Muon mass energy equivalent</td>
<td>1.692833667e-11 J</td>
</tr>
</tbody>
</table>

Continued on next page

5.4. Constants (scipy.constants)
<table>
<thead>
<tr>
<th>Description</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>muon mass energy equivalent in MeV</td>
<td>105.6583715 MeV</td>
</tr>
<tr>
<td>muon mass in u</td>
<td>0.1134289267 u</td>
</tr>
<tr>
<td>muon molar mass</td>
<td>0.0001134289267 kg mol⁻¹</td>
</tr>
<tr>
<td>muon-electron mass ratio</td>
<td>206.7682843</td>
</tr>
<tr>
<td>muon-neutron mass ratio</td>
<td>0.1124545177</td>
</tr>
<tr>
<td>muon-proton mag. mom. ratio</td>
<td>-3.18334107</td>
</tr>
<tr>
<td>muon-proton mass ratio</td>
<td>0.1126095272</td>
</tr>
<tr>
<td>muon-tau mass ratio</td>
<td>0.0594649</td>
</tr>
<tr>
<td>natural unit of action</td>
<td>1.054571726e-34 J s</td>
</tr>
<tr>
<td>natural unit of action in eV s</td>
<td>6.58211928e-16 eV s</td>
</tr>
<tr>
<td>natural unit of energy</td>
<td>8.18710506e-14 J</td>
</tr>
<tr>
<td>natural unit of energy in MeV</td>
<td>0.510998928 MeV</td>
</tr>
<tr>
<td>natural unit of length</td>
<td>3.86159268e-13 m</td>
</tr>
<tr>
<td>natural unit of mass</td>
<td>9.10938291e-31 kg</td>
</tr>
<tr>
<td>natural unit of mom.um</td>
<td>2.73092429e-22 kg m s⁻¹</td>
</tr>
<tr>
<td>natural unit of mom.um in MeV/c</td>
<td>0.510998928 MeV/c</td>
</tr>
<tr>
<td>natural unit of time</td>
<td>1.28808866833e-21 s</td>
</tr>
<tr>
<td>natural unit of velocity</td>
<td>299792458.0 m s⁻¹</td>
</tr>
<tr>
<td>neutron Compton wavelength</td>
<td>1.3195090968e-15 m</td>
</tr>
<tr>
<td>neutron Compton wavelength over 2 pi</td>
<td>2.1001941568e+16 m</td>
</tr>
<tr>
<td>neutron g factor</td>
<td>-3.82608545</td>
</tr>
<tr>
<td>neutron gyromag. ratio</td>
<td>183247179.0 s⁻¹ T⁻¹</td>
</tr>
<tr>
<td>neutron gyromag. ratio over 2 pi</td>
<td>29.1646943 MHz T⁻¹</td>
</tr>
<tr>
<td>neutron mag. mom.</td>
<td>-9.6623647e-27 J T⁻¹</td>
</tr>
<tr>
<td>neutron mag. mom. to Bohr magneton ratio</td>
<td>-0.00104187563</td>
</tr>
<tr>
<td>neutron mag. mom. to nuclear magneton ratio</td>
<td>-1.91304272</td>
</tr>
<tr>
<td>neutron mass</td>
<td>1.674927351e-27 kg</td>
</tr>
<tr>
<td>neutron mass energy equivalent</td>
<td>1.505349631e-10 J</td>
</tr>
<tr>
<td>neutron mass energy equivalent in MeV</td>
<td>939.565379 MeV</td>
</tr>
<tr>
<td>neutron mass in u</td>
<td>1.008664916 kg</td>
</tr>
<tr>
<td>neutron molar mass</td>
<td>0.001008664916 kg mol⁻¹</td>
</tr>
<tr>
<td>neutron to shielded proton mag. mom. ratio</td>
<td>-0.68499694</td>
</tr>
<tr>
<td>neutron-electron mag. mom. ratio</td>
<td>0.00104066882</td>
</tr>
<tr>
<td>neutron-electron mass ratio</td>
<td>1838.6836605</td>
</tr>
<tr>
<td>neutron-muon mass ratio</td>
<td>8.892484</td>
</tr>
<tr>
<td>neutron-proton mag. mom. ratio</td>
<td>-0.68497934</td>
</tr>
<tr>
<td>neutron-proton mass difference</td>
<td>2.30557392e-30</td>
</tr>
<tr>
<td>neutron-proton mass difference energy equivalent</td>
<td>2.0721465e-13</td>
</tr>
<tr>
<td>neutron-proton mass difference energy equivalent in MeV</td>
<td>1.29333217</td>
</tr>
<tr>
<td>neutron-proton mass difference in u</td>
<td>0.00138844919</td>
</tr>
<tr>
<td>neutron-proton mass ratio</td>
<td>1.00137841917</td>
</tr>
<tr>
<td>neutron-tau mass ratio</td>
<td>0.52879</td>
</tr>
<tr>
<td>Newtonian constant of gravitation</td>
<td>6.67384e-11 m³ s⁻¹ kg⁻¹</td>
</tr>
<tr>
<td>Newtonian constant of gravitation over h-bar c</td>
<td>6.70837e-39 (GeV/c²) s⁻²</td>
</tr>
<tr>
<td>nuclear magneton</td>
<td>5.05078353e-27 J T⁻¹</td>
</tr>
<tr>
<td>nuclear magneton in eV/T</td>
<td>3.1524512605e-08 eV T⁻¹</td>
</tr>
<tr>
<td>nuclear magneton in inverse meters per tesla</td>
<td>0.02542623527 m⁻¹ T⁻¹</td>
</tr>
<tr>
<td>nuclear magneton in K/T</td>
<td>0.00036582682 K T⁻¹</td>
</tr>
<tr>
<td>nuclear magneton in MHz/T</td>
<td>7.6259357 MHz T⁻¹</td>
</tr>
<tr>
<td>Planck constant</td>
<td>6.62606957e-34 J s</td>
</tr>
</tbody>
</table>

Continued on next page
<table>
<thead>
<tr>
<th>Description</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Planck constant in eV s</td>
<td>4.135667516e-15 eV s</td>
</tr>
<tr>
<td>Planck constant over 2 π</td>
<td>1.054571726e-34 J s</td>
</tr>
<tr>
<td>Planck constant over 2 π in eV s</td>
<td>6.58211928e-16 eV s</td>
</tr>
<tr>
<td>Planck constant over 2 π times c in MeV fm</td>
<td>197.3269718 MeV fm</td>
</tr>
<tr>
<td>Planck length</td>
<td>1.616199e-35 m</td>
</tr>
<tr>
<td>Planck mass</td>
<td>2.17651e-08 kg</td>
</tr>
<tr>
<td>Planck mass energy equivalent in GeV</td>
<td>1.220932e+19 GeV</td>
</tr>
<tr>
<td>Planck temperature</td>
<td>1.416833e+32 K</td>
</tr>
<tr>
<td>Planck time</td>
<td>5.39106e-44 s</td>
</tr>
<tr>
<td>proton charge to mass quotient</td>
<td>95788335.8 C kg^-1</td>
</tr>
<tr>
<td>proton Compton wavelength</td>
<td>1.32140985623e-15 m</td>
</tr>
<tr>
<td>proton Compton wavelength over 2 π</td>
<td>2.1030891047e-16 m</td>
</tr>
<tr>
<td>proton g factor</td>
<td>5.585694713</td>
</tr>
<tr>
<td>proton gyromag. ratio</td>
<td>267522200.5 s^-1 T^-1</td>
</tr>
<tr>
<td>proton gyromag. ratio over 2 π</td>
<td>42.5774806 MHz T^-1</td>
</tr>
<tr>
<td>proton mag. mom.</td>
<td>1.410606743e-26 J T^-1</td>
</tr>
<tr>
<td>proton mag. mom. to Bohr magneton ratio</td>
<td>0.00152103221</td>
</tr>
<tr>
<td>proton mag. mom. to nuclear magneton ratio</td>
<td>2.792847356</td>
</tr>
<tr>
<td>proton mag. shielding correction</td>
<td>2.5694e-05</td>
</tr>
<tr>
<td>proton mass</td>
<td>1.672621777e-27 kg</td>
</tr>
<tr>
<td>proton mass energy equivalent</td>
<td>1.503277484e-10 J</td>
</tr>
<tr>
<td>proton mass energy equivalent in MeV</td>
<td>938.272046 MeV</td>
</tr>
<tr>
<td>proton mass in u</td>
<td>1.0072760681 u</td>
</tr>
<tr>
<td>proton molar mass</td>
<td>0.00100727646681 kg mol^-1</td>
</tr>
<tr>
<td>proton rms charge radius</td>
<td>8.775e-16 m</td>
</tr>
<tr>
<td>proton-electron mass ratio</td>
<td>1836.13267245</td>
</tr>
<tr>
<td>proton-muon mass ratio</td>
<td>8.88024331</td>
</tr>
<tr>
<td>proton-neutron mag. mom. ratio</td>
<td>-1.45989806</td>
</tr>
<tr>
<td>proton-neutron mass ratio</td>
<td>0.99862347826</td>
</tr>
<tr>
<td>proton-tau mass ratio</td>
<td>0.528063</td>
</tr>
<tr>
<td>quantum of circulation</td>
<td>0.0003636947552 m^2 s^-1</td>
</tr>
<tr>
<td>quantum of circulation times 2</td>
<td>0.0007273895104 m^2 s^-1</td>
</tr>
<tr>
<td>Rydberg constant</td>
<td>10973731.5685 m^-1</td>
</tr>
<tr>
<td>Rydberg constant times c in Hz</td>
<td>3.28984196036e+15 Hz</td>
</tr>
<tr>
<td>Rydberg constant times hc in eV</td>
<td>13.60569253 eV</td>
</tr>
<tr>
<td>Rydberg constant times hc in J</td>
<td>2.17987217e-18 J</td>
</tr>
<tr>
<td>Sackur-Tetrode constant (1 K, 100 kPa)</td>
<td>-1.1517078</td>
</tr>
<tr>
<td>Sackur-Tetrode constant (1 K, 101.325 kPa)</td>
<td>-1.1648708</td>
</tr>
<tr>
<td>second radiation constant</td>
<td>0.01438777 m K</td>
</tr>
<tr>
<td>shielded hellion gyromag. ratio</td>
<td>203789465.9 s^-1 T^-1</td>
</tr>
<tr>
<td>shielded hellion gyromag. ratio over 2 pi</td>
<td>32.43410084 MHz T^-1</td>
</tr>
<tr>
<td>shielded hellion mag. mom.</td>
<td>-1.07455304e-16 J</td>
</tr>
<tr>
<td>shielded hellion mag. mom. to Bohr magneton ratio</td>
<td>-0.01158671471</td>
</tr>
<tr>
<td>shielded hellion mag. mom. to nuclear magneton ratio</td>
<td>-2.127497718</td>
</tr>
<tr>
<td>shielded hellion to proton mag. mom. ratio</td>
<td>-0.7671766558</td>
</tr>
<tr>
<td>shielded hellion to shielded proton mag. mom. ratio</td>
<td>-0.76717681313</td>
</tr>
<tr>
<td>shielded proton gyromag. ratio</td>
<td>267515326.8 s^-1 T^-1</td>
</tr>
<tr>
<td>shielded proton gyromag. ratio over 2 pi</td>
<td>42.5763866 MHz T^-1</td>
</tr>
<tr>
<td>shielded proton mag. mom.</td>
<td>1.410570499e-26 J T^-1</td>
</tr>
<tr>
<td>shielded proton mag. mom. to Bohr magneton ratio</td>
<td>0.0015209993128</td>
</tr>
</tbody>
</table>

Continued on next page
<table>
<thead>
<tr>
<th>Property</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>shielded proton mag. mom. to nuclear magneton ratio</td>
<td>2.792775598</td>
</tr>
<tr>
<td>speed of light in vacuum</td>
<td>299792458.0 m s^{-1}</td>
</tr>
<tr>
<td>standard acceleration of gravity</td>
<td>9.80665 m s^{-2}</td>
</tr>
<tr>
<td>standard atmosphere</td>
<td>101325.0 Pa</td>
</tr>
<tr>
<td>standard-state pressure</td>
<td>100000.0 Pa</td>
</tr>
<tr>
<td>Stefan-Boltzmann constant</td>
<td>5.670373e-08 W m^{-2} K^{-4}</td>
</tr>
<tr>
<td>tau Compton wavelength</td>
<td>6.97787e-16 m</td>
</tr>
<tr>
<td>tau Compton wavelength over 2 pi</td>
<td>1.11056e-16 m</td>
</tr>
<tr>
<td>tau mass</td>
<td>3.16747e-27 kg</td>
</tr>
<tr>
<td>tau mass energy equivalent</td>
<td>2.84678e-10 J</td>
</tr>
<tr>
<td>tau mass energy equivalent in MeV</td>
<td>1776.82 MeV</td>
</tr>
<tr>
<td>tau mass in u</td>
<td>1.90749 u</td>
</tr>
<tr>
<td>tau molar mass</td>
<td>0.00190749 kg mol^{-1}</td>
</tr>
<tr>
<td>tau-electron mass ratio</td>
<td>3477.15</td>
</tr>
<tr>
<td>tau-muon mass ratio</td>
<td>16.8167</td>
</tr>
<tr>
<td>tau-neutron mass ratio</td>
<td>1.89111</td>
</tr>
<tr>
<td>tau-proton mass ratio</td>
<td>1.89372</td>
</tr>
<tr>
<td>Thomson cross section</td>
<td>6.652458734e-29 m^2</td>
</tr>
<tr>
<td>triton g factor</td>
<td>5.957924896</td>
</tr>
<tr>
<td>triton mag. mom.</td>
<td>1.504609447e-26 J T^{-1}</td>
</tr>
<tr>
<td>triton mag. mom. to Bohr magneton ratio</td>
<td>0.001622393657</td>
</tr>
<tr>
<td>triton mag. mom. to nuclear magneton ratio</td>
<td>2.978962448</td>
</tr>
<tr>
<td>triton mass</td>
<td>5.0073563e-27 kg</td>
</tr>
<tr>
<td>triton mass energy equivalent</td>
<td>4.50038741e-10 J</td>
</tr>
<tr>
<td>triton mass energy equivalent in MeV</td>
<td>2808.921005 MeV</td>
</tr>
<tr>
<td>triton mass in u</td>
<td>3.0155007134 u</td>
</tr>
<tr>
<td>triton molar mass</td>
<td>0.0030155007134 kg mol^{-1}</td>
</tr>
<tr>
<td>triton-electron mass ratio</td>
<td>5496.9215267</td>
</tr>
<tr>
<td>triton-proton mass ratio</td>
<td>2.9937170308</td>
</tr>
<tr>
<td>unified atomic mass unit</td>
<td>1.660538921e-27 kg</td>
</tr>
<tr>
<td>von Klitzing constant</td>
<td>25812.8074434 ohm</td>
</tr>
<tr>
<td>weak mixing angle</td>
<td>0.2223</td>
</tr>
<tr>
<td>Wien frequency displacement law constant</td>
<td>58789254000.0 Hz K^{-1}</td>
</tr>
<tr>
<td>Wien wavelength displacement law constant</td>
<td>0.0028977721 m K</td>
</tr>
<tr>
<td>(220) lattice spacing of silicon</td>
<td>1.920155714e-10 m</td>
</tr>
</tbody>
</table>
5.4.3 Units

SI prefixes

<table>
<thead>
<tr>
<th>Prefix</th>
<th>Exponent</th>
</tr>
</thead>
<tbody>
<tr>
<td>yotta</td>
<td>$10^{24}$</td>
</tr>
<tr>
<td>zetta</td>
<td>$10^{21}$</td>
</tr>
<tr>
<td>exa</td>
<td>$10^{18}$</td>
</tr>
<tr>
<td>peta</td>
<td>$10^{15}$</td>
</tr>
<tr>
<td>tera</td>
<td>$10^{12}$</td>
</tr>
<tr>
<td>giga</td>
<td>$10^9$</td>
</tr>
<tr>
<td>mega</td>
<td>$10^6$</td>
</tr>
<tr>
<td>kilo</td>
<td>$10^3$</td>
</tr>
<tr>
<td>hecto</td>
<td>$10^2$</td>
</tr>
<tr>
<td>deka</td>
<td>$10^1$</td>
</tr>
<tr>
<td>deci</td>
<td>$10^{-1}$</td>
</tr>
<tr>
<td>centi</td>
<td>$10^{-2}$</td>
</tr>
<tr>
<td>milli</td>
<td>$10^{-3}$</td>
</tr>
<tr>
<td>micro</td>
<td>$10^{-6}$</td>
</tr>
<tr>
<td>nano</td>
<td>$10^{-9}$</td>
</tr>
<tr>
<td>pico</td>
<td>$10^{-12}$</td>
</tr>
<tr>
<td>femto</td>
<td>$10^{-15}$</td>
</tr>
<tr>
<td>atto</td>
<td>$10^{-18}$</td>
</tr>
<tr>
<td>zepto</td>
<td>$10^{-21}$</td>
</tr>
</tbody>
</table>

Binary prefixes

<table>
<thead>
<tr>
<th>Prefix</th>
<th>Exponent</th>
</tr>
</thead>
<tbody>
<tr>
<td>kibi</td>
<td>$2^{10}$</td>
</tr>
<tr>
<td>mebi</td>
<td>$2^{20}$</td>
</tr>
<tr>
<td>gibi</td>
<td>$2^{30}$</td>
</tr>
<tr>
<td>tebi</td>
<td>$2^{40}$</td>
</tr>
<tr>
<td>pebi</td>
<td>$2^{50}$</td>
</tr>
<tr>
<td>exbi</td>
<td>$2^{60}$</td>
</tr>
<tr>
<td>zebi</td>
<td>$2^{70}$</td>
</tr>
<tr>
<td>yobi</td>
<td>$2^{80}$</td>
</tr>
</tbody>
</table>

Weight

<table>
<thead>
<tr>
<th>Unit</th>
<th>Description</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 (avoirdupous) in kg</td>
</tr>
<tr>
<td>oz</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>
</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>arcsec</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>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>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>bar</td>
<td>one bar in pascals</td>
</tr>
<tr>
<td>torr</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>Conversion</th>
</tr>
</thead>
<tbody>
<tr>
<td>liter</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_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_imp</td>
<td>one fluid ounce (UK) in cubic meters</td>
</tr>
<tr>
<td>bbl</td>
<td>one barrel in cubic meters</td>
</tr>
</tbody>
</table>

### Speed

<table>
<thead>
<tr>
<th>Unit</th>
<th>Conversion</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>knot</td>
<td>one knot in meters per second</td>
</tr>
</tbody>
</table>

### Temperature

<table>
<thead>
<tr>
<th>Unit</th>
<th>Conversion</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>

### scipy.constants

- **C2K(C)**: Convert Celsius to Kelvin
  - **Parameters**: `C` : array_like
    - Celsius temperature(s) to be converted.
  - **Returns**: `K` : float or array of floats
    - Equivalent Kelvin temperature(s).

  **Notes**
  
  Computes \( K = C + \) `zero_Celsius` where `zero_Celsius` = 273.15, i.e., (the absolute value of) temperature “absolute zero” as measured in Celsius.

  **Examples**

  ```python
  >>> from scipy.constants.constants import C2K
  >>> C2K(_np.array([-40, 40.0]))
  array([ 233.15,  313.15])
  ```

- **K2C(K)**: Convert Kelvin to Celsius
  - **Parameters**: `K` : array_like
    - Kelvin temperature(s) to be converted.
  - **Returns**: `C` : float or array of floats
Equivalent Celsius temperature(s).

**Notes**

Computes $C = K - \text{zero\_Celsius}$ where $\text{zero\_Celsius} = 273.15$, i.e., (the absolute value of) temperature “absolute zero” as measured in Celsius.

**Examples**

```python
>>> from scipy.constants.constants import K2C
>>> K2C(_np.array([233.15, 313.15]))
array([-40., 40.])
```

**scipy.constants.F2C(F)**

Convert Fahrenheit to Celsius

**Parameters**

- **F**: array_like
  Fahrenheit temperature(s) to be converted.

**Returns**

- **C**: float or array of floats
  Equivalent Celsius temperature(s).

**Notes**

Computes $C = (F - 32) / 1.8$.

**Examples**

```python
>>> from scipy.constants.constants import F2C
>>> F2C(_np.array([-40, 40.0]))
array([-40. , 4.44444444])
```

**scipy.constants.C2F(C)**

Convert Celsius to Fahrenheit

**Parameters**

- **C**: array_like
  Celsius temperature(s) to be converted.

**Returns**

- **F**: float or array of floats
  Equivalent Fahrenheit temperature(s).

**Notes**

Computes $F = 1.8 \times C + 32$.

**Examples**

```python
>>> from scipy.constants.constants import C2F
>>> C2F(_np.array([-40, 40.0]))
array([-40., 104.])
```

**scipy.constants.F2K(F)**

Convert Fahrenheit to Kelvin

**Parameters**

- **F**: array_like
  Fahrenheit temperature(s) to be converted.

**Returns**

- **K**: float or array of floats
  Equivalent Kelvin temperature(s).

**Notes**

Computes $K = (F - 32)/1.8 + \text{zero\_Celsius}$ where $\text{zero\_Celsius} = 273.15$, i.e., (the absolute value of) temperature “absolute zero” as measured in Celsius.
Examples

```python
>>> from scipy.constants.constants import F2K
>>> F2K(_np.array([-40, 104]))
array([ 233.15, 313.15])
```

`scipy.constants.K2F(K)`
Convert Kelvin to Fahrenheit

**Parameters**
- `K`: array_like
  Kelvin temperature(s) to be converted.

**Returns**
- `F`: float or array of floats
  Equivalent Fahrenheit temperature(s).

**Notes**
Computes $F = 1.8 \times (K - \text{zero}_\text{Celsius}) + 32$ where $\text{zero}_\text{Celsius} = 273.15$, i.e., (the absolute value of) temperature “absolute zero” as measured in Celsius.

Examples

```python
>>> from scipy.constants.constants import K2F
>>> K2F(_np.array([233.15, 313.15]))
array([-40., 104.])
```

Energy

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>eV</td>
<td>one electron volt in Joules</td>
</tr>
<tr>
<td>calorie</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_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>Symbol</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>hp</td>
<td>one horsepower in watts</td>
</tr>
</tbody>
</table>

Force

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dyn</td>
<td>one dyne in newtons</td>
</tr>
<tr>
<td>lbf</td>
<td>one pound force in newtons</td>
</tr>
<tr>
<td>kgf</td>
<td>one kilogram force in newtons</td>
</tr>
</tbody>
</table>

Optics

- `lambda2nu(lambda_)` Convert wavelength to optical frequency
- `nu2lambda(nu)` Convert optical frequency to wavelength.
scipy.constants.lambda2nu \(\lambda\)  
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.constants import lambda2nu  
>>> lambda2nu(_np.array((1, speed_of_light)))  
array([2.99792458e+08, 1.00000000e+00])  
```

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.constants import nu2lambda  
>>> nu2lambda(_np.array((1, speed_of_light)))  
array([2.99792458e+08, 1.00000000e+00])  
```

5.4.4 References

5.5 Discrete Fourier transforms (scipy.fftpack)

5.5.1 Fast Fourier Transforms (FFTs)

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>fft(x, n, axis, overwrite_x)</td>
<td>Return discrete Fourier transform of real or complex sequence.</td>
</tr>
<tr>
<td>ifft(x, n, axis, overwrite_x)</td>
<td>Return discrete inverse Fourier transform of real or complex sequence.</td>
</tr>
<tr>
<td>fft2(x, shape, axes, overwrite_x)</td>
<td>2-D discrete Fourier transform.</td>
</tr>
<tr>
<td>ifft2(x, shape, axes, overwrite_x)</td>
<td>2-D discrete inverse Fourier transform of real or complex sequence.</td>
</tr>
<tr>
<td>fftn(x, shape, axes, overwrite_x)</td>
<td>Return multidimensional discrete Fourier transform.</td>
</tr>
<tr>
<td>ifftn(x, shape, axes, overwrite_x)</td>
<td>Return inverse multi-dimensional discrete Fourier transform of arbitrary type sequence.</td>
</tr>
<tr>
<td>rfft(x, n, axis, overwrite_x)</td>
<td>Discrete Fourier transform of a real sequence.</td>
</tr>
<tr>
<td>irfft(x, n, axis, overwrite_x)</td>
<td>Return inverse discrete Fourier transform of real sequence x.</td>
</tr>
<tr>
<td>dct(x, type, n, axis, norm, overwrite_x)</td>
<td>Return the Discrete Cosine Transform of arbitrary type sequence x.</td>
</tr>
<tr>
<td>idct(x, type, n, axis, norm, overwrite_x)</td>
<td>Return the Inverse Discrete Cosine Transform of an arbitrary type sequence.</td>
</tr>
<tr>
<td>dst(x, type, n, axis, norm, overwrite_x)</td>
<td>Return the Discrete Sine Transform of arbitrary type sequence x.</td>
</tr>
</tbody>
</table>
**idst** (x[, type, n, axis, norm, overwrite_x])  
Return the Inverse Discrete Sine Transform of an arbitrary type sequence.

```python
c scipy.fftpack.idst (x, type, n, axis, norm, overwrite_x)  
```

Parameters:
- **x**: array_like  
  Array to Fourier transform.
- **type**: int, optional  
  Type of discrete sine transform (see Notes). 
  - 1: sine (sin(kt)/k)
  - 2: cosine (cos(kt)/k)
  - 3: sinh (sinh(kt)/k)
  - 4: cosh (cosh(kt)/k)
- **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).
- **norm**: str or None, optional  
  Normalization mode (see Notes). The default value is None.
- **overwrite_x**: bool, optional  
  If True, the contents of x can be destroyed; the default is False.

Returns:
- **z**: complex ndarray  
  with the elements:
  - \[y(0), y(1), \ldots, y(n/2), y(1-n/2), \ldots, y(-1)\] if n is even
  - \[y(0), y(1), \ldots, y((n-1)/2), y(-(n-1)/2), \ldots, y(-1)\] if n is odd
  where:
  \[y(j) = \sum_{k=0}^{n-1} x[k] \exp(-\sqrt{-1} \times j \times k \times \frac{2 \times \pi}{n}), j = 0..r-1\]
  Note that \[y(-j) = y(n-j).conjugate()\].

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 \([-4, -3, -2, -1, 0, 1, 2, 3]\). To rearrange the fft output so that the zero-frequency component is centered, like \([-4, -3, -2, -1, 0, 1, 2, 3]\), use \texttt{fftshift}.

For \( n \) even, \( A[n/2] \) contains the sum of the positive and negative-frequency terms. For \( n \) even and \( x \) real, \( A[n/2] \) will always be real.

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 FFT” algorithm is automatically used, which roughly halves the computation time. To increase efficiency a little further, use \texttt{rfft}, which does the same calculation, but only outputs half of the symmetrical spectrum. If the data is both real and symmetrical, the \texttt{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
```

```python
scipy.fftpack.ifft(x, n=None, axis=-1, overwrite_x=False)
```

Return discrete inverse Fourier transform of real or complex sequence.

The returned complex array contains $y(0), y(1), \ldots, y(n-1)$ where

$$y(j) = (x * \exp(2\pi\sqrt{-1}j\cdot\text{np.arange}(n)/n)).\text{mean}().$$

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**: ndarray of floats
  The inverse discrete Fourier transform.

See also:

- **fft**
  Forward FFT

Notes

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.

```python
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.

```python
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(x, shape=None, axes=None, overwrite_x=False)
Return multidimensional discrete Fourier transform.

The returned array contains:

\[ Y[\ldots, j\_d, \ldots] = \frac{1}{p} \sum [k\_l=0\ldots n\_l-1, \ldots, k\_d=0\ldots n\_d-1] X[k\_l, \ldots, k\_d] \times \prod [i=1\ldots d] \exp(-\sqrt{-1} \times 2 \times \pi / n\_i \times j\_i \times k\_i) \]

where \( d = \text{len}(x.\text{shape}) \) and \( n = x.\text{shape} \). Note that \( Y[\ldots, -j\_i, \ldots] = Y[\ldots, n\_i-j\_i, \ldots].\text{conjugate()} \).

Parameters
- **x**: array_like
  The (n-dimensional) array to transform.
- **shape**: tuple of ints, optional
  The shape of the result. If both \( \text{shape} \) and \( \text{axes} \) (see below) are None, \( \text{shape} \) is \( x.\text{shape} \); if \( \text{shape} \) is None but \( \text{axes} \) is not None, then \( \text{shape} \) is \( \text{scipy.\text{take}(x.\text{shape}, \text{axes}, \text{axis}=0)} \). If \( \text{shape}[i] > x.\text{shape}[i] \), the i-th dimension is padded with zeros. If \( \text{shape}[i] < x.\text{shape}[i] \), the i-th dimension is truncated to length \( \text{shape}[i] \).
- **axes**: array_like of ints, optional
  The axes of \( x \) (\( y \) if \( \text{shape} \) is not None) along which the transform is applied.
- **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:
- ifftn

Examples

```python
>>> from scipy.fftpack import fftn, ifftn
>>> y = (-np.arange(16), 8 - np.arange(16), np.arange(16))
>>> np.allclose(y, ifftn(fftn(y)))
True
```

scipy.fftpack.ifftn(x, shape=None, axes=None, overwrite_x=False)
Return inverse multi-dimensional discrete Fourier transform of arbitrary type sequence \( x \).

The returned array contains:

\[ y[\ldots, j\_d, \ldots] = \frac{1}{p} \times \sum [k\_l=0\ldots n\_l-1, \ldots, k\_d=0\ldots n\_d-1] x[k\_l, \ldots, k\_d] \times \prod [i=1\ldots d] \exp(\sqrt{-1} \times 2 \times \pi / n\_i \times j\_i \times k\_i) \]

where \( d = \text{len}(x.\text{shape}), n = x.\text{shape}, \) and \( p = \text{prod}[i=1\ldots d] n\_i \).

For description of parameters see fftn.

See also:
- fftn

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

5.5. Discrete Fourier transforms (scipy.fftpack) 305
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:

- \([y(0), \Re(y(1)), \Im(y(1)), \ldots, \Re(y(n/2))]\) if \( n \) is even
- \([y(0), \Re(y(1)), \Im(y(1)), \ldots, \Re(y(n/2)), \Im(y(n/2))]\) if \( n \) is odd

where:

\[
y(j) = \sum_{k=0}^{n-1} x[k] \cdot \exp(-\sqrt{-1} \cdot j \cdot k \cdot 2 \cdot \pi / n)
\]
\( j = 0 \ldots n-1 \)

Note that \( y(-j) == y(n-j).\text{conjugate()} \).

See also:

- `fft`, `irfft`, `scipy.fftpack.basic`

Notes

Within numerical accuracy, \( y == \text{rfft}(\text{irfft}(y)) \).

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(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 \( n < x.shape[axis] \), \( x \) 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**

- \( \text{irfft} \) : ndarray of floats
  The inverse discrete Fourier transform.

See also:

- `rfft`, `ifft`

Notes

The returned real array contains:
[y(0), y(1), ..., y(n-1)]

where for n is even:
\[
y(j) = \frac{1}{n} \left( \sum_{k=1}^{n/2-1} (x[2k-1] + \sqrt{-1} \times x[2k]) \times \exp(\sqrt{-1} \times j \times k \times 2 \pi / n) \right) + \text{c.c.} + x[0] + (-1)^{j} \times x[n-1]
\]

and for n is odd:
\[
y(j) = \frac{1}{n} \left( \sum_{k=1}^{(n-1)/2} (x[2k-1] + \sqrt{-1} \times x[2k]) \times \exp(\sqrt{-1} \times j \times k \times 2 \pi / n) \right) + \text{c.c.} + x[0]
\]

c.c. denotes complex conjugate of preceding expression.

For details on input parameters, see \texttt{rfft}.

\texttt{scipy.fftpack.dct} (x, type=2, n=None, axis=-1, norm=None, overwrite_x=False)

Return the Discrete Cosine Transform of arbitrary type sequence x.

**Parameters**

\begin{itemize}
  \item \texttt{x} : array_like
    The input array.
  \item \texttt{type} : \{1, 2, 3\}, optional
    Type of the DCT (see Notes). Default type is 2.
  \item \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]}.
  \item \texttt{axis} : int, optional
    Axis along which the dct is computed; the default is over the last axis (i.e., \texttt{axis=-1}).
  \item \texttt{norm} : \{None, ‘ortho’\}, optional
    Normalization mode (see Notes). Default is None.
  \item \texttt{overwrite_x} : bool, optional
    If True, the contents of \texttt{x} can be destroyed; the default is False.
\end{itemize}

**Returns**

\begin{itemize}
  \item \texttt{y} : ndarray of real
    The transformed input array.
\end{itemize}

See also:

\texttt{idct}  
Inverse DCT

**Notes**

For a single dimension array \texttt{x}, \texttt{dct(x, norm=’ortho’)} is equal to MATLAB \texttt{dct(x)}.

There are theoretically 8 types of the DCT, 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.

**Type I**

There are several definitions of the DCT-I; we use the following (for \texttt{norm=None}):
\[
y[k] = x[0] + (-1)^{k} \times x[N-1] + 2 \times \sum_{n=1}^{N-2} x[n] \times \cos(\pi \times k \times n / (N-1))
\]

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**
There are several definitions of the DCT-II; we use the following (for norm=None):

\[ y[k] = 2 \sum_{n=0}^{N-1} x[n] \cos\left(\frac{\pi k (2n+1)}{2N}\right), \quad 0 \leq k < N. \]

If norm='ortho', \( y[k] \) is multiplied by a scaling factor \( f \):

\[ f = \sqrt{\frac{1}{4N}} \text{ if } k = 0, \]
\[ f = \sqrt{\frac{1}{2N}} \text{ otherwise}. \]

Which makes the corresponding matrix of coefficients orthonormal \( \mathbf{O} \mathbf{O}' = \mathbf{I} \).

Type III

There are several definitions, we use the following (for norm=None):

\[ y[k] = x[0] + 2 \sum_{n=1}^{N-1} x[n] \cos\left(\frac{\pi (k+0.5)n}{N}\right), \quad 0 \leq k < N. \]

or, for norm='ortho' and \( 0 \leq k < N \):

\[ y[k] = x[0] \sqrt{\frac{1}{N}} + \sqrt{\frac{2}{N}} \sum_{n=1}^{N-1} x[n] \cos\left(\frac{\pi (k+0.5)n}{N}\right) \]

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.

References

[R36], [R37]

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 (x, type=2, n=None, axis=-1, norm=None, 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}, optional
  Type of the DCT (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 idct 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
    idct : ndarray of real
        The transformed input array.

See also:

dct
    Forward DCT

Notes
For a single dimension array x, idct(x, norm='ortho') is equal to MATLAB 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. For the definition of these types, see dct.

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.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}, 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 off sets [R38], 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.

\[ y[k] = 2 \sum_{n=0}^{N-1} x[n] \sin\left(\pi (k+1) (n+1) / (N+1)\right) \]

Only None is supported as normalization mode for DCT-I. Note also that the DCT-I is only supported for input size > 1 The (unnormalized) DCT-I is its own inverse, up to a factor 2(N+1).

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.

\[ y[k] = 2 \sum_{n=0}^{N-1} x[n] \sin\left(\pi (k+1) (n+0.5) / N\right), \quad 0 \leq k < N. \]

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.

\[ y[k] = x[N-1]*(-1)**k + 2 \sum_{n=0}^{N-2} x[n] \sin\left(\pi (k+0.5) (n+1) / N\right), \quad 0 \leq k < N. \]

The (unnormalized) DCT-III is the inverse of the (unnormalized) DCT-II, up to a factor 2N. The orthonormalized DST-III is exactly the inverse of the orthonormalized DCT-II.

New in version 0.11.0.

References

[R38] 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}, 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.

### 5.5.2 Differential and pseudo-differential operators

```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:

\[
y_j = \text{pow}(\sqrt{-1} \times j \times 2 \times \pi / \text{period}, \text{order}) \times x_j
\]
\[y_0 = 0 \text{ if order is not 0.} \]

**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 \( 2 \times \pi \).

**Notes**
If \( \text{sum}(x, \text{axis}=0) = 0 \) then \( \text{diff}(\text{diff}(x, k), -k) = x \) (within numerical accuracy).

For odd order and even \( \text{len}(x) \), the Nyquist mode is taken zero.

```python
c 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) * coth(j * h * 2 * pi / period) * 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 \( \sum(x, \text{axis}=0) == 0 \) and \( n = \text{len}(x) \) is odd then \( \text{tilbert}(\text{itilbert}(x)) == x \).

If \( 2 * \pi * h / \text{period} \) 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.

```python
scipy.fftpack.itilbert(x, h, period=None, _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:

\[
y_j = -\sqrt{-1} \cdot \tanh(j \cdot h \cdot 2 \cdot \pi / \text{period}) \cdot x_j
y_0 = 0
\]

For more details, see \( \text{tilbert} \).

```python
scipy.fftpack.hilbert(x, _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:

\[
y_j = \sqrt{-1} \cdot \text{sign}(j) \cdot x_j
y_0 = 0
\]

**Parameters**

- **x**: array_like
  - The input array, should be periodic.
- **_cache**: dict, optional
  - Dictionary that contains the kernel used to do a convolution with.

**Returns**

- **y**: ndarray
  - The transformed input.

**Notes**

If \( \sum(x, \text{axis}=0) == 0 \) 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 \( \text{scipy.signal.hilbert} \) does have an extra -1 factor compared to this function.

```python
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:
```python
y_j = -sqrt(-1)*sign(j) * x_j
y_0 = 0

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:
y_j = -sqrt(-1)*cosh(j*a*2*pi/period)/sinh(j*b*2*pi/period) * x_j
y_0 = 0

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.
period : float, optional
    The period of the sequence. Default period is 2*pi.

Returns
cs_diff : ndarray
    Pseudo-derivative of periodic sequence x.

Notes
For even len(x), the Nyquist mode of x is taken as zero.
```

```python
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:
y_j = sqrt(-1)*sinh(j*a*2*pi/period)/cosh(j*b*2*pi/period) * x_j
y_0 = 0

Parameters
x : array_like
    Input array.
a,b : float
    Defines the parameters of the sinh/cosh pseudo-differential operator.
period : float, optional
    The period of the sequence x. Default is 2*pi.

Notes
sc_diff(cs_diff(x,a,b),b,a) == x For even len(x), the Nyquist mode of x is taken as zero.
```

```python
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:
y_j = sinh(j*a*2*pi/period)/sinh(j*b*2*pi/period) * x_j
y_0 = a/b * 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.
```

5.5. Discrete Fourier transforms (scipy.fftpack)
SciPy Reference Guide, Release 0.16.0

Notes

\[
ss\_diff(ss\_diff(x,a,b),b,a) == x
\]

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:

\[
y\_j = \frac{\cosh(j*a*2*pi/period)}{\cosh(j*b*2*pi/period)} * x\_j
\]

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(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:

\[
y\_j = e^{j*a*2*pi/period*sqrt(-1)} * x\_f
\]

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.

Returns

- **shift**: ndarray
  Shifted periodic sequence x.

5.5.3 Helper functions

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>fftshift(x[, axes])</td>
<td>Shift the zero-frequency component to the center of the spectrum.</td>
</tr>
<tr>
<td>ifftshift(x[, axes])</td>
<td>The inverse of fftshift.</td>
</tr>
<tr>
<td>fftfreq(n[, d])</td>
<td>Return the Discrete Fourier Transform sample frequencies.</td>
</tr>
<tr>
<td>rfftfreq(n[, d])</td>
<td>DFT sample frequencies (for usage with rfft, irfft).</td>
</tr>
</tbody>
</table>

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
  Shifted array.
The shifted array.

See also:

\texttt{ifftshift} The inverse of \texttt{fftshift}.

\textbf{Examples}

\begin{verbatim}
>>> freqs = np.fft.fftfreq(10, 0.1)
>>> freqs
array([ 0., 1., 2., 3., 4., -5., -4., -3., -2., -1.])
>>> np.fft.fftshift(freqs)
array([-5., -4., -3., -2., -1., 0., 1., 2., 3., 4.])
\end{verbatim}

Shift the zero-frequency component only along the second axis:

\begin{verbatim}
>>> freqs = np.fft.fftfreq(9, d=1./9).reshape(3, 3)
>>> freqs
array([[ 0., 1., 2.],
       [ 3., 4., -4.],
       [-3., -2., -1.]])
>>> np.fft.fftshift(freqs, axes=(1,))
array([[ 2., 0., 1.],
       [-4., 3., 4.],
       [-1., -3., -2.]])
\end{verbatim}

\texttt{scipy.fftpack.ifftshift} (\texttt{x, axes=None})

The inverse of \texttt{fftshift}.

\textbf{Parameters}

\begin{itemize}
  \item \texttt{x}: array_like
    
    Input array.
    \item \texttt{axes} : int or shape tuple, optional
    
    Axes over which to calculate. Defaults to None, which shifts all axes.
\end{itemize}

\textbf{Returns}

\begin{itemize}
  \item \texttt{y}: ndarray
    
    The shifted array.
\end{itemize}

See also:

\texttt{fftshift} Shift zero-frequency component to the center of the spectrum.

\textbf{Examples}

\begin{verbatim}
>>> 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.]])
\end{verbatim}

\texttt{scipy.fftpack.fftfreq} (\texttt{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 \( d \):
SciPy Reference Guide, Release 0.16.0

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
gap = np.array([-2, 8, 6, 4, 1, 0, 3, 5], dtype=float)
gap_fft = np.fft.fft(gap)
n = gap.size
timestep = 0.1
freq = np.fft.fftfreq(n, d=timestep)
array([ 0. , 1.25, 2.5 , 3.75, 5. , 3.75, 2.5 , 1.25])```

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 = [0,1,1,2,2,...,n/2-1,n/2-1,n/2] / (d*n) if n is even
f = [0,1,1,2,2,...,n/2-1,n/2-1,n/2,n/2] / (d*n) if n 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)
array([ 0. , 1.25, 1.25, 2.5 , 2.5 , 3.75, 3.75, 5. ])
```

Note that fftshift, ifftshift and fftfreq are numpy functions exposed by fftpack; importing them from numpy should be preferred.

### 5.5.4 Convolutions (scipy.fftpack.convolve)

**convolve**(x,omega,[swap_real_imag,overwrite_x])

Wrapper for convolve.

**convolve_z**(x,omega_real,omega_imag,[overwrite_x])

Wrapper for convolve_z.

Continued on next page
Table 5.17 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>init_convolution_kernel(...)</td>
<td>Wrapper for init_convolution_kernel.</td>
</tr>
<tr>
<td>destroy_convolve_cache()</td>
<td>Wrapper for destroy_convolve_cache.</td>
</tr>
</tbody>
</table>

```python
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(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

*Other Parameters*

- **overwrite_x**: input int, optional
  - Default: 0

```python
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:

```python
def kernel_func(k): return kernel_func
```

Required arguments:

- **k**: input int

Return objects:

```python
kernel_func : float
```
5.6 Integration and ODEs (scipy.integrate)

5.6.1 Integrating functions, given function object

```python
cscipy.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, limitst=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
  A Python function or method to integrate. If `func` takes many arguments, it is integrated along the axis corresponding to the first argument. If the user desires improved integration performance, then `f` may instead be a ctypes function of the form:
  ```python
  def f(n, args):
    return scipy.integrate.quad(f, 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, limitst=50)
  ```
- `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.

**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 $K\leq M/2+2$ or $L=M+1-K$ otherwise. Let $I$ be the sequence \texttt{infodict[‘iord’]} and let $E$ be the sequence \texttt{infodict[‘elist’]}. Then $E[I[1]], \ldots, E[I[L]]$ 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 \texttt{infodict[‘pts’]}, then $(aa, bb)$ has level $l$ if $|bb-aa| = |pts[2]-pts[1]| \times 2^l$.

‘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, \texttt{weight} and \texttt{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 \texttt{weight} and the corresponding weighting functions are.

<table>
<thead>
<tr>
<th>weight</th>
<th>Weight function used</th>
<th>wvar</th>
</tr>
</thead>
<tbody>
<tr>
<td>‘cos’</td>
<td>\texttt{cos(w*x)}</td>
<td>\texttt{wvar = w}</td>
</tr>
<tr>
<td>‘sin’</td>
<td>\texttt{sin(w*x)}</td>
<td>\texttt{wvar = w}</td>
</tr>
<tr>
<td>‘alg’</td>
<td>\texttt{g(x) = ((x-a)**alpha)*((b-x)**beta)}</td>
<td>\texttt{wvar = (alpha, beta)}</td>
</tr>
<tr>
<td>‘alg-loga’</td>
<td>\texttt{g(x)*log(x-a)}</td>
<td>\texttt{wvar = (alpha, beta)}</td>
</tr>
<tr>
<td>‘alg-logb’</td>
<td>\texttt{g(x)*log(b-x)}</td>
<td>\texttt{wvar = (alpha, beta)}</td>
</tr>
<tr>
<td>‘alg-log’</td>
<td>\texttt{g(x)*log(x-a)*log(b-x)}</td>
<td>\texttt{wvar = (alpha, beta)}</td>
</tr>
<tr>
<td>‘cauchy’</td>
<td>\texttt{1/(x-c)}</td>
<td>\texttt{wvar = c}</td>
</tr>
</tbody>
</table>

\texttt{wvar} holds the parameter \texttt{w}, \texttt{(alpha, beta)}, or \texttt{c} depending on the weight selected. In these expressions, \texttt{a} and \texttt{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 \texttt{infodict[‘momcom’]} then the moments have been computed for intervals of length $|b-a| \times 2^l$, $l=0,1,\ldots,M_c$.

‘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 $|b-a| \times 2^l$.

‘chebmo’  A rank-2 array of shape (25, $\text{maxp1}$) 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 \texttt{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 \texttt{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 \texttt{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 \(M_f=\text{limlst}\), whose first \(K_f\) elements contain the integral contribution over the interval \((a+(k-1)c, a+kc)\) where \(c = (2\cdot\text{floor}(|w|) + 1) * \pi / |w|\) and \(k=1,2,\ldots,K_f\).

‘erlst’ A rank-1 array of length \(M_f\) containing the error estimate corresponding to the interval in the same position in \text{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 \text{infodict}[‘rslist’]. See the explanation dictionary (last entry in the output tuple) for the meaning of the codes.

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.)  # analytical result
21.3333333333
```

Calculate \(\int_0^\infty e^{-x} \, dx\)

```python
>>> invexp = lambda x: np.exp(-x)
>>> integrate.quad(invexp, 0, np.inf)
(1.0, 5.842605999138044e-11)
```

Calculate \(\int_0^1 x^2 + y^2 \, dx\) 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.*

>>> 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)
lib.integrate.quad(lib.func,0,1,(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
```

\[ \text{scipy.integrate.dblquad} \text{ (func, a, b, gfun, hfun, args=(), epsabs=1.49e-08, epsrel=1.49e-08)} \]

Compute a double integral.

5.6. Integration and ODEs (scipy.integrate) 321
Return the double (definite) integral of $\text{func}(y, x)$ from $x = a..b$ and $y = gfun(x)..hfun(x)$.

**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
  The lower boundary curve in y which is a function taking a single floating point argument (x) and returning a floating point result: a lambda function can be useful here.
- **hfun**: callable
  The upper boundary curve in y (same requirements as gfun).
- **args**: sequence, optional
  Extra arguments to pass to func.
- **epsabs**: float, optional
  Absolute tolerance passed directly to the inner 1-D quadrature integration. Default is 1.49e-8.
- **epsrel**: float, optional
  Relative tolerance of the inner 1-D integrals. Default is 1.49e-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
- **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

**scipy.integrate.tplquad**

Compute a triple (definite) integral.

Return the triple integral of $\text{func}(z, y, x)$ from $x = a..b$, $y = gfun(x)..hfun(x)$, and $z = qfun(x,y)..rfun(x,y)$.

**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
  The lower boundary curve in y which is a function taking a single floating point argument (x) and returning a floating point result: a lambda function can be useful here.
**hfun**: function
The upper boundary curve in y (same requirements as `gfun`).

**qfun**: function
The lower boundary surface in z. It must be a function that takes two floats in the order (x, y) and returns a float.

**rfun**: function
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

**scipy.integrate.nquad** *(func, ranges, args=None, opts=None)*
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
  The function to be integrated. Has arguments of `x0`, `x1`, ..., `xn`, `t0`, `tm`, where integration is carried out over `x0`, `x1`, ..., `xn`, which must be floats. Function signature should be `func(x0, x1, ..., xn, t0, t1, ..., tm)`. Integration is carried out in order. That is, integration over `x0` is the innermost integral, and `xn` is the outermost. If performance is a concern, this function may be a ctypes function of the form:

  \[ f(int n, double args[n]) \]
where \( n \) is the number of extra parameters and \( \text{args} \) is an array of doubles of the additional parameters. This function may then be compiled to a dynamic/shared library then imported through \textit{ctypes}, setting the function's argtypes to (\texttt{c_int, c_double}), and the function's restype to (\texttt{c_double}). Its pointer may then be passed into \texttt{nquad} normally. This allows the underlying Fortran library to evaluate the function in the innermost integration calls without callbacks to Python, and also speeds up the evaluation of the function itself.

**ranges**: iterable object

Each element of ranges may be either a sequence of 2 numbers, or else a callable that returns such a sequence. \( \text{ranges}[0] \) 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. e.g. if \( \text{func} = f(x_0, x_1, x_2) \), then \( \text{ranges}[0] \) may be defined as either \( (a, b) \) or else as \( (a, b) = \text{range}(x_1, x_2) \).

**args**: iterable object, optional

Additional arguments \( t_0, \ldots, t_n \), required by \( \text{func} \).

**opts**: iterable object or dict, optional

Options to be passed to \textit{quad}. May be empty, a dict, or a sequence of dicts or functions that return a dict. If empty, the default options from \texttt{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. \( \text{opts}[0] \) corresponds to integration over \( x_0 \), and so on. The available options together with their default values are:

- \( \text{epsabs} = 1.49e-08 \)
- \( \text{epsrel} = 1.49e-08 \)
- \( \text{limit} = 50 \)
- \( \text{points} = \) None
- \( \text{weight} = \) None
- \( \text{wvar} = \) None
- \( \text{wopts} = \) None

The \textit{full_output} option from \textit{quad} is unavailable, due to the complexity of handling the large amount of data such an option would return for this kind of nested integration. For more information on these options, see \textit{quad} and \textit{quad_explain}.

**Returns**

- **result**: float
  The result of the integration.
- **abserr**: float
  The maximum of the estimates of the absolute error in the various integration results.

See also:

- \textit{quad} - 1-dimensional numerical integration
- \texttt{dblquad, tplquad}
- \textit{fixed_quad} - fixed-order Gaussian quadrature
- \textit{quadrature} - adaptive Gaussian quadrature

**Examples**

```python
>>> 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]],
```

324 Chapter 5. Reference
```python
>>> 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 * (t0*x2 + t1*x3) - 1,
...             scale * (t0*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)
```

The `scipy.integrate.fixed_quad` function is used to compute a definite integral using fixed-order Gaussian quadrature. It integrates the function `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).
- `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

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

5.6. Integration and ODEs (scipy.integrate) 325
SciPy Reference Guide, Release 0.16.0

**simps**  integrators for sampled data
**cumtrapz**  cumulative integration for sampled data
**ode**  ODE integrator
**odeint**  ODE integrator

**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.

- **miniter**: int, optional
  
  Minimum order of Gaussian quadrature.

**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
`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 \textit{function} (a function of one variable) over the interval \((a, b)\).

If \textit{show} is 1, the triangular array of the intermediate results will be printed. If \textit{vec_func} is True (default is False), then \textit{function} is assumed to support vector arguments.

\textbf{Parameters}  
\begin{itemize}
  \item function : callable  
  Function to be integrated.
  \item a : float  
  Lower limit of integration.
  \item b : float  
  Upper limit of integration.
\end{itemize}

\textbf{Returns}  
\begin{itemize}
  \item results : float  
  Result of the integration.
\end{itemize}

\textbf{Other Parameters}  
\begin{itemize}
  \item args : tuple, optional  
  Extra arguments to pass to function. Each element of \textit{args} will be passed as a single argument to \textit{func}. Default is to pass no extra arguments.
  \item tol, rtol : float, optional  
  The desired absolute and relative tolerances. Defaults are 1.48e-8.
  \item show : bool, optional  
  Whether to print the results. Default is False.
  \item divmax : int, optional  
  Maximum order of extrapolation. Default is 10.
  \item vec_func : bool, optional  
  Whether \textit{func} handles arrays as arguments (i.e whether it is a “vector” function). Default is False.
\end{itemize}

\textbf{See also:}

\textit{fixed_quad} Fixed-order Gaussian quadrature.
\textit{quad}    Adaptive quadrature using QUADPACK.
\textit{dblquad} Double integrals.
\textit{tplquad} Triple integrals.
\textit{romb}    Integrators for sampled data.
\textit{simps}   Integrators for sampled data.
\textit{cumtrapz} Cumulative integration for sampled data.
\textit{ode} ODE integrator.
\textit{odeint} ODE integrator.

\textbf{References}

[R39]

\textbf{Examples}

Integrate a gaussian from 0 to 1 and compare to the error function.
```python
>>> from scipy import integrate
>>> from scipy.special import erf

```gments 
```python
>>> 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]
Steps  StepSize  Results
1  1.000000  0.385872
2  0.500000  0.412631  0.421551
4  0.250000  0.419184  0.421368  0.421356
8  0.125000  0.420810  0.421352  0.421350
16  0.062500  0.421215  0.421350  0.421350
32  0.031250  0.421317  0.421350  0.421350
32  0.031250  0.421317  0.421350  0.421350

The final result is 0.421350396475 after 33 function evaluations.
>>> print ("%.8f %.8f" % (2*result, erf(1)))
0.842701 0.842701
```

5.6.2 Integrating functions, given fixed samples

<table>
<thead>
<tr>
<th>cumtrapz(y[, x, dx, axis, initial])</th>
<th>Cumulatively integrate y(x) using the composite trapezoidal rule.</th>
</tr>
</thead>
<tbody>
<tr>
<td>simps(y[, x, dx, axis, even])</td>
<td>Integrate y(x) using samples along the given axis and the composite Simpson’s rule.</td>
</tr>
<tr>
<td>romb(y[, dx, axis, show])</td>
<td>Romberg integration using samples of a function.</td>
</tr>
</tbody>
</table>

```python
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
    Values to integrate.
x : array_like, optional
    The coordinate to integrate along. If None (default), use spacing dx between consecutive elements in y.
dx : int, optional
    Spacing between elements of y. Only used if x is None.
axis : int, optional
    Specifies the axis to cumulate. Default is -1 (last axis).
initial : scalar, optional
    If given, uses this value as the first value in 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** *(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`: {'avg', 'first', 'str'}, optional

---

5.6. Integration and ODEs (scipy.integrate) 329
SciPy Reference Guide, Release 0.16.0

`'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.

```python
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 \(2^n \times 1\) 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
### 5.6.3 Integrators of ODE systems

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>odeint</code></td>
<td>Integrate a system of ordinary differential equations.</td>
</tr>
<tr>
<td><code>ode</code></td>
<td>A generic interface class to numeric integrators.</td>
</tr>
<tr>
<td><code>complex_ode</code></td>
<td>A wrapper of <code>ode</code> for complex systems.</td>
</tr>
</tbody>
</table>

```python
defodeint(func, y0, t[, args, Dfun, col_deriv, ...])
    Integrate a system of ordinary differential equations.

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:

\[
dy/dt = \text{func}(y, t0, \ldots)
\]

where \( y \) can be a vector.

**Parameters**

- `func` : callable(y, t0, ...)
  
  Computes the derivative of \( y \) at \( t0 \).
- `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.
- `args` : tuple, optional
  
  Extra arguments to pass to function.
- `Dfun` : callable(y, t0, ...)
  
  Gradient (Jacobian) of \( \text{func} \).
- `col_deriv` : bool, optional
  
  True if \( D\text{fun} \) defines derivatives down columns (faster), otherwise \( D\text{fun} \) 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

**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.
```

---

See also:

- `scipy.special` for orthogonal polynomials (special) for Gaussian quadrature roots and weights for other weighting factors and regions.
**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 t 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 t 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 (e / ewt) 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.

**h0** : float, (0: solver-determined), optional

The step size to be attempted on the first step.

**hmax** : 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:

ode  a more object-oriented integrator based on VODE.
quadr for finding the area under a curve.

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) \( jac = df/dy \).

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). f should return a scalar, array or list (not a tuple).
jac : callable jac(t, y, *jac_args), optional  
Jacobian of the rhs. jac[i, j] = d f[i] / d y[j]. jac_args is set by calling 
set_f_params(*args).

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 im-
plementation. It provides implicit Adams method (for non-stiff problems) and a method based on back-
ward 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

**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
- `max_step` is `None` if solver is supposed to handle step size control itself, otherwise the maximum allowed step size.
- `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 Geneve, Dept. de Mathematiques CH-1211 Geneve 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, r.integrate(r.t+dt))
```

Attributes

| t | (float) Current time. |
| y | (ndarray) Current variable values. |

Methods

| 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. |

ode.integrate(t, step=0, relax=0)

Find y=y(t), set y as an initial condition, and return y.

ode.set_f_params(*args)

Set extra parameters for user-supplied function f.
ode.set_initial_value(y, t=0.0)
Set initial conditions y(t) = y.

ode.set_integrator(name, **integrator_params)
Set integrator by name.

Parameters

name : str
Name of the integrator.

integrator_params :
Additional parameters for the integrator.

ode.set_jac_params(*args)
Set extra parameters for user-supplied function jac.

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

ode.successful()
Check if integration was successful.

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] = d f[i] / d y[j]. jac_args is set by calling
set_f_params(*args).

Examples

For usage examples, see ode.

Attributes

<table>
<thead>
<tr>
<th>t</th>
<th>(float) Current time.</th>
</tr>
</thead>
<tbody>
<tr>
<td>y</td>
<td>(ndarray) Current variable values.</td>
</tr>
</tbody>
</table>

Methods

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.

complex_ode.integrate(t, step=0, relax=0)
Find y=y(t), set y as an initial condition, and return y.
complex_ode.set_f_params(*args)
    Set extra parameters for user-supplied function f.

complex_ode.set_initial_value(y, t=0.0)
    Set initial conditions y(t) = y.

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.

complex_ode.set_jac_params(*args)
    Set extra parameters for user-supplied function jac.

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 soloution y.shape == (n,)
        solout should return -1 to stop integration otherwise it should return None or 0

complex_ode.successful()
    Check if integration was successful.

5.7 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 (uni-variate and multivariate) interpolation classes, Lagrange and Taylor polynomial interpolators, and wrappers for FITPACK and DFITPACK functions.

5.7.1 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.
PiecewisePolynomial(xi, yi[, orders, ...])  Piecewise polynomial curve specified by points and derivatives
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.
piecewise_polynomial_interpolate(xi, yi, x)  Convenience function for piecewise polynomial interpolation.
pchip_interpolate(xi, yi, x[, der, axis])  Convenience function for pchip interpolation.
Akima1DInterpolator(x, y[, axis])  Akima 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

class scipy.interpolate.interp1d(x, y, kind='linear', axis=-1, copy=True, bounds_error=True, 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.

**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’ where ‘slinear’, ‘quadratic’ and ‘cubic’ refer to a spline interpolation of first, second or third order) 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.
- **fill_value**: float, optional
  If provided, then this value will be used to fill in for requested points outside of the data range. If not provided, then the default is NaN.
- **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:**

- splrep, splev
- UnivariateSpline
  An object-oriented wrapper of the FITPACK routines.

**interp2d** 2-D interpolation

**Examples**

```python
>>> 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()
```
Methods

__call__(x) Evaluate the interpolant

Interpld.__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.

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(i*pi/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”.

**Methods**

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>_call_</td>
<td>Evaluate the interpolating polynomial at the points x</td>
</tr>
<tr>
<td>add_xi(xi[, yi])</td>
<td>Add more x values to the set to be interpolated</td>
</tr>
<tr>
<td>set_yi(yi[, axis])</td>
<td>Update the y values to be interpolated</td>
</tr>
</tbody>
</table>

**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 \(\text{len}(x)\), where \(N\) is the degree of the polynomial.

**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.

**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.

**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 correspond-
ing 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. More-
ever, 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 [R44].

References
[R44]

Examples
To produce a polynomial that is zero at 0 and 1 and has derivative 2 at 0, call

```python
>>> 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_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.

Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong><strong>call</strong>(x)</strong></td>
<td>Evaluate the interpolant</td>
</tr>
<tr>
<td><strong>derivative(x[, der])</strong></td>
<td>Evaluate one derivative of the polynomial at the point x</td>
</tr>
<tr>
<td><strong>derivatives(x[, der])</strong></td>
<td>Evaluate many derivatives of the polynomial at the point x</td>
</tr>
</tbody>
</table>

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.

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.

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 func-
tion value as 0th derivative.

Returns

d : ndarray
Array with derivatives; d[j] contains the j-th derivative. Shape of d[j] is deter-
mined by replacing the interpolation axis in the original array with the shape of
x.

Examples

>>> KroghInterpolator([0,0,0],[1,2,3]).derivatives(0)
array([1.0,2.0,3.0])
>>> KroghInterpolator([0,0,0],[1,2,3]).derivatives([0,0])
array([[1.0,1.0],
       [2.0,2.0],
       [3.0,3.0]])

class scipy.interpolate.PiecewisePolynomial(xi, yi=None, orders=None, direction=None, axis=0)
Piecewise polynomial curve specified by points and derivatives

This class represents a curve that is a piecewise polynomial. It passes through a list of points and has specified
derivatives at each point. The degree of the polynomial may vary from segment to segment, as may the number
of derivatives available. The degree should not exceed about thirty.

Appending points to the end of the curve is efficient.

Parameters

xi : array_like
A sorted 1-d array of x-coordinates.
yi : array_like or list of array_likes
yi[i][j] is the j-th derivative known at xi[i] (for axis=0).
orders : list of int, or int, optional
A list of polynomial orders, or a single universal order.
direction : {None, 1, -1}, optional
Indicates whether the xi are increasing or decreasing:
   +1 : increasing values
   -1 : decreasing values
None : direction will be deduced from the first two elements of xi
axis : int, optional
Axis in the yi array corresponding to the x-coordinate values.

Notes

If orders is None, or orders[i] is None, then the degree of the polynomial segment is exactly the degree required to match all i available derivatives at both endpoints. If orders[i] is not None, then some derivatives will be ignored. The code will try to use an equal number of derivatives from each end; if the total number of derivatives needed is odd, it will prefer the rightmost endpoint. If not enough derivatives are available, an exception is raised.

Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>call</strong>(x)</td>
<td>Evaluate the interpolant</td>
</tr>
<tr>
<td>append(xi, yi[, order])</td>
<td>Append a single point with derivatives to the PiecewisePolynomial</td>
</tr>
<tr>
<td>derivative(x[, der])</td>
<td>Evaluate one derivative of the polynomial at the point x</td>
</tr>
<tr>
<td>derivatives(x[, der])</td>
<td>Evaluate many derivatives of the polynomial at the point x</td>
</tr>
<tr>
<td>extend(xi, yi[, orders])</td>
<td>Extend the PiecewisePolynomial by a list of points</td>
</tr>
</tbody>
</table>

**PiecewisePolynomial.__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.

**PiecewisePolynomial.append(xi, yi, order=None)**

Append a single point with derivatives to the PiecewisePolynomial

**Parameters**

- xi : float
  Point to add.
- yi : array_like
  yi is the list of derivatives known at xi.
- order : int or None, optional
  A polynomial order, or instructions to use the highest possible order.

**PiecewisePolynomial.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.

**PiecewisePolynomial.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

```python
g Kush interpolator([0,0,0],[1,2,3]).derivatives(0)  # array([1.0,2.0,3.0])
>>> KroghInterpolator([0,0,0],[1,2,3]).derivatives([0,0])  # array([[1.0,1.0], [2.0,2.0], [3.0,3.0]])
```

PiecewisePolynomial.extend(xi, yi, orders=None)

Extend the PiecewisePolynomial by a list of points

- **xi**: array_like
  - A sorted list of x-coordinates.
- **yi**: list of lists of length N1
  - yi[i] (if axis == 0) is the list of derivatives known at xi[i].
- **orders**: int or list of ints, optional
  - A list of polynomial orders, or a single universal order.

class scipy.interpolate.PchipInterpolator(x, y, axis=0, extrapolate=None)

PCHIP 1-d monotonic cubic interpolation

- **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

Notes

The first derivatives are guaranteed to be continuous, but the second derivatives may jump at x_k.

Preserves monotonicity in the interpolation data and does not overshoot if the data is not smooth.

Determines the derivatives at the points x_k, d_k, by using PCHIP algorithm:
Let $m_k$ be the slope of the $k$th segment (between $k$ and $k+1$). If $m_k=0$ or $m_{k-1}=0$ or $\text{sgn}(m_k) \neq \text{sgn}(m_{k-1})$ then $d_k = 0$ else use weighted harmonic mean:

$$w_1 = 2h_k + h_{k-1}, \quad w_2 = h_k + 2h_{k-1}$$

$$1/d_k = 1/(w_1 + w_2)*(w_1/m_k + w_2/m_{k-1})$$

where $h_k$ is the spacing between $x_k$ and $x_{k+1}$.

Methods

```python
PchipInterpolator.__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.
```

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, 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 $[a, b]$.

PchipInterpolator.derivative(nu=1)
Construct a new piecewise polynomial representing the derivative.

Parameters

- **nu**: int, optional
  Order of derivative to evaluate. (Default: 1) If negative, the antiderivative is returned.

Returns

- **bp**: BPoly
  Piecewise polynomial of order $k' = k - nu$ representing the derivative of this polynomial.

PchipInterpolator.antiderivative(nu=1)
Construct a new piecewise polynomial representing the antiderivative.

Parameters

- **nu**: int, optional
  Order of derivative to evaluate. (Default: 1) If negative, the derivative is returned.

Returns

- **bp**: BPoly
  Piecewise polynomial of order $k' = k + nu$ representing the antiderivative of this polynomial.

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**
- $\mathbf{x}_i$ : array_like
  - 1-d array of $x$ coordinates of the points the polynomial should pass through.
- $\mathbf{y}_i$ : array_like
  - The $y$ coordinates of the points the polynomial should pass through.
- $\mathbf{x}$ : scalar or array_like
  - Points to evaluate the interpolator at.
- $\mathbf{axis}$ : int, optional
  - Axis in the $\mathbf{y}_i$ array corresponding to the $x$-coordinate values.

**Returns**
- $\mathbf{y}$ : scalar or array_like
  - Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of $\mathbf{x}$.

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 $\mathbf{x}_i$ (but possibly varying $\mathbf{y}_i$ or $\mathbf{x}$) you should use the class BarycentricInterpolator. This is what this function uses internally.

**scipy.interpolate.krogh_interpolate** ($\mathbf{x}_i$, $\mathbf{y}_i$, $\mathbf{x}$, der=0, $\mathbf{axis}$=0)

Convenience function for polynomial interpolation.

See KroghInterpolator for more details.

**Parameters**
- $\mathbf{x}_i$ : array_like
  - Known $x$-coordinates.
- $\mathbf{y}_i$ : array_like
  - Known $y$-coordinates, of shape ($\mathbf{x}_i$.size, $R$). Interpreted as vectors of length $R$, or scalars if $R=1$.
- $\mathbf{x}$ : array_like
  - Point or points at which to evaluate the derivatives.
- $\text{der}$ : 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.
- $\mathbf{axis}$ : int, optional
  - Axis in the $\mathbf{y}_i$ array corresponding to the $x$-coordinate values.

**Returns**
- $\mathbf{d}$ : 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 $\mathbf{y}_i$ 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.piecewise_polynomial_interpolate(xi, yi, x, orders=None, der=0, axis=0)

Convenience function for piecewise polynomial interpolation.

**Parameters**
- **xi**: array_like
  A sorted list of x-coordinates.
- **yi**: list of lists
  yi[i] is the list of derivatives known at xi[i].
- **x**: scalar or array_like
  Coordinates at which to evaluate the polynomial.
- **orders**: int or list of ints, optional
  A list of polynomial orders, or a single universal order.
- **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**
- **y**: ndarray
  Interpolated values or derivatives. If multiple derivatives were requested, these are given along the first axis.

See also:
- PiecewisePolynomial

**Notes**
If orders is None, or orders[i] is None, then the degree of the polynomial segment is exactly the degree required to match all i available derivatives at both endpoints. If orders[i] is not None, then some derivatives will be ignored. The code will try to use an equal number of derivatives from each end; if the total number of derivatives needed is odd, it will prefer the rightmost endpoint. If not enough derivatives are available, an exception is raised.

Construction of these piecewise polynomials can be an expensive process; if you repeatedly evaluate the same polynomial, consider using the class PiecewisePolynomial (which is what this function does).

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
  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**
- **y**: scalar or array_like
The result, of length R or length M or M by R,

**See also:**

PchipInterpolator

```python
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

**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**


**Methods**

```python
Akima1DInterpolator.__call__(x[, nu, extrapolate])
Evaluate the piecewise polynomial or its derivative

Akima1DInterpolator.derivative([nu])
Construct a new piecewise polynomial representing the derivative.

Akima1DInterpolator.antiderivative([nu])
Construct a new piecewise polynomial representing the antiderivative.

Akima1DInterpolator.roots([discontinuity, extrapolate])
Find real roots of the piecewise polynomial.
```

**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, 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 \([a, b]\).

Akima1DInterpolator.derivative \((nu=1)\)

Construct a new piecewise polynomial representing the derivative.

Parameters

- **nu**: int, optional
  - Order of derivative to evaluate. (Default: 1) 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 \([a, b]\).

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: 1) 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.

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, optional
  - Whether to return roots from the polynomial extrapolated based on first and last intervals.

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, 0, -1], [1, 0, 0]]).T, [-2, 1, 2])
>>> pp.roots()
array([-1., 1.])
```

class `scipy.interpolate.PPoly`

Piecewise polynomial in terms of coefficients and breakpoints

The polynomial in the \(i\)th interval is \(x[i] \leq xp < x[i+1]\):

\[
S = \sum \text{c[m, i]} \times (xp - x[i])^{(k-m)} \text{ for m in range(k+1)}
\]

where \(k\) is the degree of the polynomial. This representation is the local power basis.

**Parameters**

- **c**: ndarray, shape \((k, m, ...)\)
  - Polynomial coefficients, order \(k\) and \(m\) intervals
- **x**: ndarray, shape \((m+1,)\)
  - Polynomial breakpoints. These must be sorted in increasing order.
- **extrapolate**: bool, optional
  - Whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. Default: 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[, 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.
- `integrate(a, b[, extrapolate])`: Compute a definite integral over a piecewise polynomial.
- `roots([discontinuity, extrapolate])`: Find real roots of the piecewise polynomial.
- `extend(c, x[, right])`: Add additional breakpoints and coefficients to the polynomial.
- `from_spline(tck[, extrapolate])`: Construct a piecewise polynomial from a spline
- `from_bernstein_basis(bp[, extrapolate])`: Construct a piecewise polynomial in the power basis from a polynomial in Bernstein basis.
- `construct_fast(c, x[, extrapolate, axis])`: Construct the piecewise polynomial without making checks.
PPoly.__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, 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 \([a, b]\).

PPoly.derivative(nu=1)
Construct a new piecewise polynomial representing the derivative.

**Parameters**
- nu : int, optional
  Order of derivative to evaluate. (Default: 1) 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 \([a, b]\).

PPoly.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: 1) 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.

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, optional
Whether to extrapolate to out-of-bounds points based on first and last intervals,
or to return NaNs.

Returns ig : array_like
Definite integral of the piecewise polynomial over \([a, b]\)

PPoly.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, optional
Whether to return roots from the polynomial extrapolated based on first and last intervals.

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 discontinuity 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, 0, -1], [1, 0, 0]]).T, [-2, 1, 2])
>>> pp.roots()
array([-1., 1.])
```

PPoly.extend (c, x, right=True)
Add additional breakpoints and coefficients to the polynomial.

Parameters c : ndarray, size (k, m, ...)
Additional coefficients for polynomials in intervals self.x[-1]
<= x < x_right[0], x_right[0] <= x < x_right[1], ...
x_right[m-2] <= x < x_right[m-1]
x : ndarray, size (m,)
Additional breakpoints. Must be sorted and either to the right or to the left of the
current breakpoints.
right : bool, optional
Whether the new intervals are to the right or to the left of the current intervals.

classmethod PPoly.from_spline (tck, extrapolate=None)
Construct a piecewise polynomial from a spline

Parameters tck : A spline, as returned by splrep
extrapolate : bool, optional
Whether to extrapolate to out-of-bounds points based on first and last intervals,
or to return NaNs. Default: True.
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, optional
  Whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. Default: True.

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.

class scipy.interpolate.BPoly(c, x, extrapolate=None, axis=0)

Piecewise polynomial in terms of coefficients and breakpoints

The polynomial in the i-th interval $x[i] \leq x < x[i+1]$ is written in the Bernstein polynomial basis:

$$S = \sum c[a, i] \times b(a, k; x) \text{ for } a \text{ in range}(k+1)$$

where $k$ is the degree of the polynomial, and:

$$b(a, k; x) = \binom{k}{a} \times t^k \times (1 - t)^{k - a}$$

with $t = (x - x[i]) / (x[i+1] - x[i])$.

**Parameters**

- **c**: ndarray, shape (k, m, ...)
  Polynomial coefficients, order $k$ and $m$ intervals
- **x**: ndarray, shape (m+1,)
  Polynomial breakpoints. These must be sorted in increasing order.
- **extrapolate**: bool, optional
  Whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. Default: True.
- **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
>>> 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

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>x</td>
<td>(ndarray) Breakpoints.</td>
</tr>
<tr>
<td>c</td>
<td>(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.</td>
</tr>
<tr>
<td>axis</td>
<td>(int) Interpolation axis.</td>
</tr>
</tbody>
</table>

Methods

- **__call__**(x[, nu, extrapolate])
  Evaluate the piecewise polynomial or its derivative
- **extend**(c, x[, right])
  Add additional breakpoints and coefficients to the polynomial.
- **derivative**(nu)
  Construct a new piecewise polynomial representing the derivative.
- **antiderivative**(nu)
  Construct a new piecewise polynomial representing the antiderivative.
- **integrate**(a, b[, extrapolate])
  Compute a definite integral over a piecewise polynomial.
- **construct_fast**(c, x[, extrapolate, axis])
  Construct the piecewise polynomial without making checks.
- **from_power_basis**(pp[, extrapolate])
  Construct a piecewise polynomial in Bernstein basis from a power basis polynomial.
- **from_derivatives**(xi, yi[, orders, extrapolate])
  Construct a piecewise polynomial in the Bernstein basis, compatible with the specified values and derivatives at breakpoints.

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, 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 \([a, b]\).

BPoly.extend(c, x, right=True)
Add additional breakpoints and coefficients to the polynomial.

**Parameters**

- **c** : ndarray, size (k, m, ...)
  Additional coefficients for polynomials in intervals \(self.x[-1] \leq x < x\_right[0], \ x\_right[0] \leq x < x\_right[1], \ ..., \ x\_right[m-2] \leq x < x\_right[m-1]\)
- **x** : ndarray, size (m,)
  Additional breakpoints. Must be sorted and either to the right or to the left of the current breakpoints.
- **right** : bool, optional
  Whether the new intervals are to the right or to the left of the current intervals.

BPoly.derivative(nu=1)
Construct a new piecewise polynomial representing the derivative.

**Parameters**

- **nu** : int, optional
Order of derivative to evaluate. (Default: 1) If negative, the antiderivative is returned.

Returns

bp : BPoly

Piecewise polynomial of order \( k2 = k - \text{nu} \) representing the derivative of this polynomial.

BPoly.antiderivative(nu=1)

Construct a new piecewise polynomial representing the antiderivative.

Parameters

nu : int, optional

Order of derivative to evaluate. (Default: 1) If negative, the derivative is returned.

Returns

bp : BPoly

Piecewise polynomial of order \( k2 = k + \text{nu} \) representing the antiderivative of this polynomial.

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, optional

Whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. Defaults to self.extrapolate.

Returns

array_like

Definite integral of the piecewise polynomial over \([a, b]\)

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.

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, optional

Whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. Default: True.

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, optional

Whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. Default: 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
>>> BPoly.from_derivatives([0, 1], [[1, 2], [3, 4]])

Creates a polynomial \( f(x) \) of degree 3, defined on \([0, 1]\) such that \( f(0) = 1, df/dx(0) = 2, f(1) = 3, df/dx(1) = 4 \)

```n

```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:

\[
f(x) = \begin{cases} 
  x \times (1 - x), & 0 \leq x < 1 \\
  2 \times (x - 1), & 1 \leq x \leq 2 
\end{cases}
\]

So that \( f'(1-0) = -1 \) and \( f'(1+0) = 2 \)

5.7.2 Multivariate interpolation

Unstructured data:

- `griddata(points, values, xi[, method, ...])`: Interpolate unstructured D-dimensional data.
- `LinearNDInterpolator(points, values[, ...])`: Piecewise linear interpolant in N dimensions.
- `NearestNDInterpolator(points, values)`: Nearest-neighbour interpolation in N dimensions.
- `CloughTocher2DInterpolator(points, values[, tol])`: Piecewise cubic, C1 smooth, curvature-minimizing interpolant in 2D.
- `Rbf(*args)`: A class for radial basis function approximation/interpolation of n-dimensional data.
- `interp2d(x, y, z[, kind, copy, ...])`: Interpolate over a 2-D grid.

SciPy's `griddata` function:

```python
scipy.interpolate.griddata(points, values, xi, method='linear', fill_value=nan, rescale=False)

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`: ndarray of float, shape (M, D)
  Points at which to interpolate data.
  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  tesselate 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.

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.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')
```

5.7. Interpolation (scipy.interpolate)
```python
>>> plt.title('Linear')
>>> plt.subplot(221)
>>> plt.imshow(grid_z2.T, extent=(0, 1, 0, 1), origin='lower')
>>> plt.title('Cubic')
>>> plt.gcf().set_size_inches(6, 6)
```
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 [R45], and on each triangle performing linear barycentric interpolation.

References
[R45]

Methods

__call__ (xi)  Evaluate interpolator at given points.

LinearNDInterpolator. __call__ (xi)
Evaluate interpolator at given points.

Parameters
xi : ndarray of float, shape (..., ndim)
Points where to interpolate data at.

class scipy.interpolate.NearestNDInterpolator (points, values)
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.

Notes
Uses scipy.spatial.cKDTree

Methods

__call__ (*args)  Evaluate interpolator at given points.

NearestNDInterpolator. __call__ (*args)
Evaluate interpolator at given points.

Parameters
xi : ndarray of float, shape (... ndim)
Points where to interpolate data at.

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 `nan`.
- **tol** : float, optional
  Absolute/relative tolerance for gradient estimation.
- **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 [R43], and constructing a piecewise cubic interpolating Bezier polynomial on each triangle, using a Clough-Tocher scheme [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 [Nielson83, Renka84].

**References**

[R43], [CT], [Nielson83], [Renka84]

**Methods**

- **__call__(xi)** Evaluate interpolator at given points.

```
CloughTocher2DInterpolator.__call__(xi)
```
Evaluate interpolator at given points.

**class** 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':
  '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)

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 : 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. E.g. the default:

```python
def euclidean_norm(x1, x2):
    return sqrt( ((x1 - x2)**2).sum(axis=0) )
```

which is called with x1=x1[ndims,newaxis,:] and x2=x2[ndims,:,newaxis] such that the result is a matrix of the distances from each point in x1 to each point in x2.

Examples

```python
>>> rbfi = Rbf(x, y, z, d)  # radial basis function interpolator instance
>>> di = rbfi(xi, yi, zi)  # interpolated values
```

Methods

```python
Rbf.__call__(*args)
```

class scipy.interpolate.interp2d(x, y, z, kind='linear', copy=True, bounds_error=False, fill_value=nan)

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.

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]]
  ```
  Otherwise, x and y must specify the full coordinates for each point, for example:
  ```python
  >>> x = [0,1,2,0,1,2]; y = [0,0,0,3,3,3]; z = [1,2,3,4,5,6]
  ```
  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.

5.7. Interpolation (scipy.interpolate)
kind : {'linear', 'cubic', 'quintic'}, optional
The kind of spline interpolation to use. Default is 'linear'.

抄 : 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
(0), values outside the domain are extrapolated.

Returns
values_x : ndarray, shape xi.shape[:-1] + values.shape[ndim:]
Interpolated values at input coordinates.

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

interpld 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

```python
interp2d.__call__(x, y[, dx, dy, assume_sorted]) Interpolate the function.
```

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:

```python
scipy.interpolate.interpn(points, values, xi[, method, ...]) Multidimensional interpolation on regular grids.
```

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.

**Returns**
- `z` : 2D array with shape (len(y), len(x))
  - The interpolated values.
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 “nearest”, and “splinef2d”. “splinef2d” is only supported for 2-dimensional data.
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. Extrapolation is not supported by method “splinef2d”.

Returns values_x : ndarray, shape xi.shape[:-1] + values.shape[ndim:]
Interpolated values at input coordinates.

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.
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.

New in version 0.14.

**References**
[R46], [R47], [R48]

**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**

**__call__(xi[, method])** Interpolation at coordinates

```python
RegularGridInterpolator.__call__(xi, method=None)
```

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”.

**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)]`.
- `kx, ky`: ints, optional  
  Degrees of the bivariate spline. Default is 3.
- `s`: float, optional  
  Positive smoothing factor defined for estimation condition:  
  \[ \sum(w[i]*(z[i]-s(x[i], y[i])))**2, \text{axis}=0 \leq s \]  
  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**

- `__call__(x, y, [mth, dx, dy, grid])`  
  Evaluate the spline or its derivatives at given positions.
- `eval(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.
- `get_residual()`  
  Return weighted sum of squared residuals of the spline
- `integral(xa, xb, ya, yb)`  
  Evaluate the integral of the spline over area `[xa,xb] x [ya,yb]`.

**RectBivariateSpline**

- `__call__(x, y, mth=None, 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.
- `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.
mth : str
    Deprecated argument. Has no effect.

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.

RectBivariateSpline.get_coeffs()
    Return spline coefficients.

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.

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)

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.interpolation.map_coordinates

5.7.3 1-D Splines

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.

class scipy.interpolate.UnivariateSpline(x, y, w=None, bbox=[None, None], k=3, s=None,
    ext=0, check_finite=False)
    One-dimensional smoothing spline fit to a given set of data points.
    Fits a spline y = spl(x) of degree k to the provided x, y data. s specifies the number of knots by specifying a
    smoothing condition.

    Parameters
    x : (N,) array_like
        1-D array of independent input data. Must be increasing.
y : (N,) array_like
   1-D array of dependent input data, of the same length as x.

w : (N,) array_like, optional
   Weights for spline fitting. Must be positive. If None (default), weights are all equal.

bbox : (2,) array_like, optional
   2-sequence specifying the boundary of the approximation interval. If None (default),
   bbox=[x[0], x[-1]].

k : int, optional
   Degree of the smoothing spline. Must be <= 5. Default is k=3, a cubic spline.

s : float or None, optional
   Positive smoothing factor used to choose the number of knots. Number of knots will
   be increased until the smoothing condition is satisfied:

   \[ \sum_{i} (w[i] \times (y[i]-spl(x[i])))^2, \text{axis}=0 \] \leq s

   If None (default), s = len(w) which should be a good value if 1/w[i] is an
   estimate of the standard deviation of y[i]. If 0, spline will interpolate through all
   data points.

ext : int or str, optional
   Controls the extrapolation mode for elements not in the interval defined by the knot
   sequence.
   • if ext=0 or ‘extrapolate’, return the extrapolated value.
   • if ext=1 or ‘zeros’, return 0
   • if ext=2 or ‘raise’, raise a ValueError
   • if ext=3 or ‘const’, return the boundary value.
   The default value 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 or
non-sensical results) if the inputs do contain infinities or NaNs. Default is False.

See also:

InterpolatedUnivariateSpline
   Subclass with smoothing forced to 0

LSQUnivariateSpline
   Subclass in which knots are user-selected instead of being set by smoothing condition

splrep
   An older, non object-oriented wrapping of FITPACK

splev, sproot, splint, spalde

BivariateSpline
   A similar class for two-dimensional spline interpolation

Notes

The number of data points must be larger than the spline degree k.

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:

>>> w = np.isnan(y)
>>> y[w] = 0.
>>> spl = UnivariateSpline(x, y, 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.)
Examples

```python
>>> import matplotlib.pyplot as plt
>>> from scipy.interpolate import UnivariateSpline

>>> x = np.linspace(-3, 3, 50)
>>> y = np.exp(-x**2) + 0.1 * np.random.randn(50)

>>> plt.plot(x, y, 'ro', ms=5)

Use the default value for the smoothing parameter:

```python
>>> spl = UnivariateSpline(x, y)
>>> xs = np.linspace(-3, 3, 1000)
>>> plt.plot(xs, spl(xs), 'g', lw=3)
```

Manually change the amount of smoothing:

```python
>>> spl.set_smoothing_factor(0.5)
>>> plt.plot(xs, spl(xs), 'b', lw=3)
```

```python
plt.show()
```

Methods

```python
__call__(x[, nu, ext])
Evaluate spline (or its nu-th derivative) at positions x.

antiderivative([n])
Construct a new spline representing the antiderivative of this spline.

derivative([n])
Construct a new spline representing the derivative of this spline.

derivatives(x)
Return all derivatives of the spline at the point x.

g_coeffs()
Return spline coefficients.

g_knots()
Return positions of interior knots of the spline.

g_residual()
Return weighted sum of squared residuals of the spline approximation.

integral(a, b)
Return definite integral of the spline between two given points.

g_roots()
Return the zeros of the spline.

g_set_smoothing_factor(s)
Continue spline computation with the given smoothing factor s and with
the knots found at the last call.
```

UnivariateSpline.__call__(x, nu=0, ext=None)
Evaluate spline (or its nu-th derivative) at positions x.

**Parameters**

- **x** : array_like
A 1-D array of points at which to return the value of the smoothed spline or its derivatives. Note: x can be unordered but the evaluation is more efficient if x is (partially) ordered.

**nu** : int
The order of derivative of the spline to compute.

**ext** : int
Controls the value returned for elements of x not in the interval defined by the knot sequence.
- if ext=0 or ‘extrapolate’, return the extrapolated value.
- if ext=1 or ‘zeros’, return 0
- if ext=2 or ‘raise’, raise a ValueError
- if ext=3 or ‘const’, return the boundary value.

The default value is 0, passed from the initialization of UnivariateSpline.

**UnivariateSpline.**`antiderivative`(n=1)
Construct a new spline representing the antiderivative of this spline.

**Parameters**
- **n** : int, optional
  Order of antiderivative to evaluate. Default: 1

**Returns**
- **spline** : UnivariateSpline
  Spline of order k2=k+n representing the antiderivative of this spline.

**See also:**
splantider, derivative

**Notes**
New in version 0.13.0.

**Examples**

```python
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, np.pi/2, 70)
>>> y = 1 / np.sqrt(1 - 0.8*np.sin(x)**2)
>>> spl = UnivariateSpline(x, y, s=0)
```

The derivative is the inverse operation of the antiderivative, although some floating point error accumulates:

```python
>>> spl(1.7), spl.antiderivative().derivative()(1.7)
(array(2.1565429877197317), array(2.1565429877201865))
```

Antiderivative can be used to evaluate definite integrals:

```python
>>> ispl = spl.antiderivative()
>>> ispl(np.pi/2) - ispl(0)
2.2572053588768486
```

This is indeed an approximation to the complete elliptic integral $K(m) = \int_0^{\pi/2} [1 - m \sin^2 x]^{-1/2} dx$:

```python
>>> from scipy.special import ellipk
>>> ellipk(0.8)
2.2572053268208538
```

**UnivariateSpline.**`derivative`(n=1)
Construct a new spline representing the derivative of this spline.

**Parameters**
- **n** : int, optional
  Order of derivative to evaluate. Default: 1
Returns

spline : UnivariateSpline
Spline of order k2=k-n representing the derivative of this spline.

See also:

splder, antiderivative

Notes

New in version 0.13.0.

Examples

This can be used for finding maxima of a curve:

```python
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 10, 70)
>>> y = np.sin(x)
>>> spl = UnivariateSpline(x, y, k=4, s=0)
```

Now, differentiate the spline and find the zeros of the derivative. (NB: `sproot` only works for order 3 splines, so we fit an order 4 spline):

```python
>>> spl.derivative().roots() / np.pi
array([ 0.50000001, 1.5 , 2.49999998])
```

This agrees well with roots \(\pi/2 + n\pi\) of \(\cos(x) = \sin'(x)\).

UnivariateSpline.derivatives(x)

Return all derivatives of the spline at the point x.

Parameters

x : float
The point to evaluate the derivatives at.

Returns

der : ndarray, shape(k+1,)
Derivatives of the orders 0 to k.

Examples

```python
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 3, 11)
>>> y = x**2
>>> spl = UnivariateSpline(x, y)
>>> spl.derivatives(1.5)
array([2.25, 3.0, 2.0, 0])
```

UnivariateSpline.get_coeffs()

Return spline coefficients.

UnivariateSpline.get_knots()

Return positions of interior knots of the spline.

Internally, the knot vector contains 2*k additional boundary knots.

UnivariateSpline.get_residual()

Return weighted sum of squared residuals of the spline approximation.

This is equivalent to:

```python
sum((w[i] * (y[i]-spl(x[i])))**2, axis=0)
```

UnivariateSpline.integral(a, b)

Return definite integral of the spline between two given points.
Parameters

- **a**: float
  Lower limit of integration.
- **b**: float
  Upper limit of integration.

Returns

- **integral**: float
  The value of the definite integral of the spline between limits.

Examples

```python
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 3, 11)
>>> y = x**2
>>> spl = UnivariateSpline(x, y)
>>> spl.integral(0, 3)
9.0
```

which agrees with \( \int_0^3 x^2 \, dx = \frac{x^3}{3} \) between the limits of 0 and 3.

A caveat is that this routine assumes the spline to be zero outside of the data limits:

```python
>>> spl.integral(-1, 4)
9.0
>>> spl.integral(-1, 0)
0.0
```

UnivariateSpline.**roots**

- **roots()**: Return the zeros of the spline.

  Restriction: only cubic splines are supported by fitpack.

UnivariateSpline.**set_smoothing_factor**

- **set_smoothing_factor(s)**
  Continue spline computation with the given smoothing factor \( s \) and with the knots found at the last call.

  This routine modifies the spline in place.

**class** scipy.interpolate.InterpolatedUnivariateSpline(x, y, w=None, bbox=[None, None], k=3, ext=0, check_finite=False)

One-dimensional interpolating spline for a given set of data points.

Fits a spline \( y = spl(x) \) of degree \( k \) to the provided \( x, y \) data. Spline function passes through all provided points. Equivalent to UnivariateSpline with \( s=0 \).

Parameters

- **x**: (N,) array_like
  Input dimension of data points – must be increasing
- **y**: (N,) array_like
  input dimension of data points
- **w**: (N,) array_like, optional
  Weights for spline fitting. Must be positive. If None (default), weights are all equal.
- **bbox**: (2,) array_like, optional
  2-sequence specifying the boundary of the approximation interval. If None (default), \( bbox=[x[0], x[-1]] \).
- **k**: int, optional
  Degree of the smoothing spline. Must be 1 <= \( k <= 5 \).
- **ext**: int or str, optional
  Controls the extrapolation spline mode for elements not in the interval defined by the knot sequence.
  - If ext=0 or 'extrapolate', return the extrapolated value.
  - If ext=1 or 'zeros', return 0
  - If ext=2 or 'raise', raise a ValueError
  - If ext=3 or 'const', return the boundary value.
The default value 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 or non-sensical results) if the inputs do contain infinities or NaNs. Default is False.

See also:

- **UnivariateSpline**
  Superclass – allows knots to be selected by a smoothing condition

- **LSQUnivariateSpline**
  spline for which knots are user-selected

- **splev**
  An older, non object-oriented wrapping of FITPACK

- **sproot**, **splint**, **spalde**

- **BivariateSpline**
  A similar class for two-dimensional spline interpolation

**Notes**

The number of data points must be larger than the spline degree \( k \).

**Examples**

```python
import matplotlib.pyplot as plt
from scipy.interpolate import InterpolatedUnivariateSpline

x = np.linspace(-3, 3, 50)
y = np.exp(-x**2) + 0.1 * np.random.randn(50)
spl = InterpolatedUnivariateSpline(x, y)
plt.plot(x, y, 'ro', ms=5)
xs = np.linspace(-3, 3, 1000)
plt.plot(xs, spl(xs), 'g', lw=3, alpha=0.7)
plt.show()
```

Notice that the \( \text{spl}(x) \) interpolates \( y \):
>>> spl.get_residual()
0.0

Methods

__call__(x[, nu, ext])
Evaluate spline (or its nu-th derivative) at positions x.

antiderivative([n])
Construct a new spline representing the antiderivative of this spline.

derivative([n])
Construct a new spline representing the derivative of this spline.

derivatives(x)
Return all derivatives of the spline at the point x.

get_coeffs()
Return spline coefficients.

get_knots()
Return positions of interior knots of the spline.

get_residual()
Return weighted sum of squared residuals of the spline approximation.

integral(a, b)
Return definite integral of the spline between two given points.

roots()
Return the zeros of the spline.

set_smoothing_factor(s)
Continue spline computation with the given smoothing factor s and with the knots found at the last call.

InterpolatedUnivariateSpline.__call__(x, nu=0, ext=None)
Evaluate spline (or its nu-th derivative) at positions x.

Parameters

x : array_like
A 1-D array of points at which to return the value of the smoothed spline or its
derivatives. Note: x can be unordered but the evaluation is more efficient if x is
(partially) ordered.

nu : int
The order of derivative of the spline to compute.

ext : int
Controls the value returned for elements of x not in the interval defined by the
knot sequence.
•if ext=0 or ‘extrapolate’, return the extrapolated value.
•if ext=1 or ‘zeros’, return 0
•if ext=2 or ‘raise’, raise a ValueError
•if ext=3 or ‘const’, return the boundary value.
The default value is 0, passed from the initialization of UnivariateSpline.

InterpolatedUnivariateSpline.antiderivative(n=1)
Construct a new spline representing the antiderivative of this spline.

Parameters

n : int, optional
Order of antiderivative to evaluate. Default: 1

Returns

spline : UnivariateSpline
Spline of order k2=k+n representing the antiderivative of this spline.

See also:
splantider,derivative

Notes

New in version 0.13.0.

Examples

>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, np.pi/2, 70)
>>> y = 1 / np.sqrt(1 - 0.8*np.sin(x)**2)
>>> spl = UnivariateSpline(x, y, s=0)
The derivative is the inverse operation of the antiderivative, although some floating point error accumu-
lates:

```python
>>> spl(1.7), spl.antiderivative().derivative()(1.7)
(array(2.156429877197317), array(2.156429877201865))
```

Antiderivative can be used to evaluate definite integrals:

```python
>>> ispl = spl.antiderivative()
>>> ispl(np.pi/2) - ispl(0)
2.2572053588768486
```

This is indeed an approximation to the complete elliptic integral $K(m) = \int_{0}^{\pi/2}[1 - m \sin^2 x]^{-1/2}dx$:

```python
>>> from scipy.special import ellipk
>>> ellipk(0.8)
2.2572053268208538
```

**InterpolatedUnivariateSpline.derivative(n=1)**

Construct a new spline representing the derivative of this spline.

**Parameters**
- `n` : int, optional
  - Order of derivative to evaluate. Default: 1

**Returns**
- `spline` : UnivariateSpline
  - Spline of order k2=k-n representing the derivative of this spline.

**See also:**
- `splder`, `antiderivative`

**Notes**

New in version 0.13.0.

**Examples**

This can be used for finding maxima of a curve:

```python
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 10, 70)
>>> y = np.sin(x)
>>> spl = UnivariateSpline(x, y, k=4, s=0)

>>> spl.derivative().roots() / np.pi
array([ 0.50000001, 1.5 , 2.49999998])
```

This agrees well with roots $\pi/2 + n\pi$ of $\cos(x) = \sin'(x)$.

**InterpolatedUnivariateSpline. derivatives(x)**

Return all derivatives of the spline at the point x.

**Parameters**
- `x` : float
  - The point to evaluate the derivatives at.

**Returns**
- `der` : ndarray, shape=k+1.
  - Derivatives of the orders 0 to k.
Examples

```python
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 3, 11)
>>> y = x**2
>>> spl = UnivariateSpline(x, y)
>>> spl.derivatives(1.5)
array([2.25, 3.0, 2.0, 0])
```

InterpolatedUnivariateSpline.get_coeffs()
Return spline coefficients.

InterpolatedUnivariateSpline.get_knots()
Return positions of interior knots of the spline.
Internally, the knot vector contains 2*k additional boundary knots.

InterpolatedUnivariateSpline.get_residual()
Return weighted sum of squared residuals of the spline approximation.

This is equivalent to:

\[
\sum (w[i] \times (y[i]-\text{spl}(x[i])))^2, \text{axis=0}
\]

InterpolatedUnivariateSpline.integral(a, b)
Return definite integral of the spline between two given points.

Parameters

- **a**: float
  Lower limit of integration.

- **b**: float
  Upper limit of integration.

Returns

- **integral**: float
  The value of the definite integral of the spline between limits.

Examples

```python
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 3, 11)
>>> y = x**2
>>> spl = UnivariateSpline(x, y)
>>> spl.integral(0, 3)
9.0
```

which agrees with \( \int x^2 \, dx = x^3 / 3 \) between the limits of 0 and 3.

A caveat is that this routine assumes the spline to be zero outside of the data limits:

```python
>>> spl.integral(-1, 4)
9.0
>>> spl.integral(-1, 0)
0.0
```

InterpolatedUnivariateSpline.roots()
Return the zeros of the spline.

Restriction: only cubic splines are supported by fitpack.

InterpolatedUnivariateSpline.set_smoothing_factor(s)
Continue spline computation with the given smoothing factor \( s \) and with the knots found at the last call.
This routine modifies the spline in place.
class scipy.interpolate.LSQUnivariateSpline(x, y, t, w=None, bbox=[None, None], k=3, ext=0, check_finite=False)

One-dimensional spline with explicit internal knots.

Fits a spline \( y = \text{spl}(x) \) of degree \( k \) to the provided \( x, y \) data. \( t \) specifies the internal knots of the spline.

**Parameters**

- **x**: \((N,)\) array_like
  - Input dimension of data points – must be increasing
- **y**: \((N,)\) array_like
  - Input dimension of data points
- **t**: \((M,)\) array_like
  - interior knots of the spline. Must be in ascending order and:
    \[
    \bbox[0] < t[0] < \ldots < t[-1] < \bbox[-1]
    \]
- **w**: \((N,)\) array_like, optional
  - weights for spline fitting. Must be positive. If None (default), weights are all equal.
- **bbox**: \((2,)\) array_like, optional
  - 2-sequence specifying the boundary of the approximation interval. If None (default), \( \bbox = [x[0], x[-1]] \).
- **k**: int, optional
  - Degree of the smoothing spline. Must be 1 \( \leq k \leq 5 \). Default is \( k=3 \), a cubic spline.
- **ext**: int or str, optional
  - Controls the extrapolation mode for elements not in the interval defined by the knot sequence.
    - if ext=0 or 'extrapolate', return the extrapolated value.
    - if ext=1 or 'zeros', return 0
    - if ext=2 or 'raise', raise a ValueError
    - if ext=3 or 'const', return the boundary value.
  - The default value 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 or non-sensical results) if the inputs do contain infinities or NaNs. Default is False.

**Raises**

- **ValueError**
  - If the interior knots do not satisfy the Schoenberg-Whitney conditions

See also:

- **UnivariateSpline**
  - Superclass – knots are specified by setting a smoothing condition
- **InterpolatedUnivariateSpline**
  - spline passing through all points
- **splrep**
  - An older, non object-oriented wrapping of FITPACK
- **splev, sproot, splint, spalde**
- **BivariateSpline**
  - A similar class for two-dimensional spline interpolation

**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

```python
>>> from scipy.interpolate import LSQUnivariateSpline
>>> import matplotlib.pyplot as plt

>>> x = np.linspace(-3, 3, 50)

>>> y = np.exp(-x**2) + 0.1 * np.random.randn(50)

Fit a smoothing spline with a pre-defined internal knots:

>>> t = [-1, 0, 1]
>>> spl = LSQUnivariateSpline(x, y, t)

>>> xs = np.linspace(-3, 3, 1000)

>>> plt.plot(x, y, 'ro', ms=5)
>>> plt.plot(xs, spl(xs), 'g-', lw=3)
>>> plt.show()
```

Check the knot vector:

```python
>>> spl.get_knots()
array([-3., -1., 0., 1., 3.])
```

Methods

- `__call__(x[, nu, ext])`: Evaluate spline (or its nu-th derivative) at positions x.
- `antiderivative([n])`: Construct a new spline representing the antiderivative of this spline.
- `derivative([n])`: Construct a new spline representing the derivative of this spline.
- `derivatives(x)`: Return all derivatives of the spline at the point x.
- `get_coeffs()`: Return spline coefficients.
- `get_knots()`: Return positions of interior knots of the spline.
- `get_residual()`: Return weighted sum of squared residuals of the spline approximation.
- `integral(a, b)`: Return definite integral of the spline between two given points.
- `roots()`: Return the zeros of the spline.
- `set_smoothing_factor(s)`: Continue spline computation with the given smoothing factor s and with the knots found at the last fit.
\textbf{LSQUnivariateSpline.__call__}(x, nu=0, ext=None)
Evaluate spline (or its nu-th derivative) at positions x.

\textbf{Parameters}
\begin{itemize}
\item \texttt{x} : array_like
  A 1-D array of points at which to return the value of the smoothed spline or its
  derivatives. Note: x can be unordered but the evaluation is more efficient if x is
  (partially) ordered.
\item \texttt{nu} : int
  The order of derivative of the spline to compute.
\item \texttt{ext} : int
  Controls the value returned for elements of x not in the interval defined by the
  knot sequence.
  \begin{itemize}
  \item if \texttt{ext}=0 or 'extrapolate', return the extrapolated value.
  \item if \texttt{ext}=1 or 'zeros', return 0
  \item if \texttt{ext}=2 or 'raise', raise a ValueError
  \item if \texttt{ext}=3 or 'const', return the boundary value.
  \end{itemize}
\end{itemize}
The default value is 0, passed from the initialization of UnivariateSpline.

\textbf{LSQUnivariateSpline.antiderivative}(n=1)
Construct a new spline representing the antiderivative of this spline.

\textbf{Parameters}
\begin{itemize}
\item \texttt{n} : int, optional
  Order of antiderivative to evaluate. Default: 1
\end{itemize}

\textbf{Returns}
\begin{itemize}
\item \texttt{spline} : UnivariateSpline
  Spline of order k2=k+n representing the antiderivative of this spline.
\end{itemize}

\textbf{See also:}
splantider, derivative

\textbf{Notes}
New in version 0.13.0.

\textbf{Examples}
\begin{verbatim}
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, np.pi/2, 70)
>>> y = 1 / np.sqrt(1 - 0.8*np.sin(x)**2)
>>> spl = UnivariateSpline(x, y, s=0)

The derivative is the inverse operation of the antiderivative, although some floating point error accumu-
lates:

>>> spl(1.7), spl.antiderivative().derivative()(1.7)
(array(2.1565429877197317), array(2.1565429877201865))

Antiderivative can be used to evaluate definite integrals:

>>> ispl = spl.antiderivative()
>>> ispl(np.pi/2) - ispl(0)
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
\end{verbatim}

\textbf{LSQUnivariateSpline.derivative}(n=1)
Construct a new spline representing the derivative of this spline.
Parameters

\( n \) : int, optional
Order of derivative to evaluate. Default: 1

Returns

\( \text{spline} \) : UnivariateSpline
Spline of order \( k_2 = k - n \) representing the derivative of this spline.

See also:

\text{splder, antiderivative}

Notes

New in version 0.13.0.

Examples

This can be used for finding maxima of a curve:

```python
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 10, 70)
>>> y = np.sin(x)
>>> spl = UnivariateSpline(x, y, k=4, s=0)
```

Now, differentiate the spline and find the zeros of the derivative. (NB: \text{sproot} only works for order 3 splines, so we fit an order 4 spline):

```python
>>> spl.derivative().roots() / np.pi
array([ 0.50000001, 1.5, 2.49999998])
```

This agrees well with roots \( \pi / 2 + n \pi \) of \( \cos(x) = \sin'(x) \).

**LSQUnivariateSpline**.\text{derivatives}(x)

Return all derivatives of the spline at the point \( x \).

Parameters

\( x \) : float
The point to evaluate the derivatives at.

Returns

\( \text{der} \) : ndarray, shape(k+1,)
Derivatives of the orders 0 to k.

Examples

```python
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 3, 11)
>>> y = x**2
>>> spl = UnivariateSpline(x, y)
>>> spl.derivatives(1.5)
array([2.25, 3.0, 2.0, 0])
```

**LSQUnivariateSpline**.\text{get_coeffs}()

Return spline coefficients.

**LSQUnivariateSpline**.\text{get_knots}()

Return positions of interior knots of the spline.

Internally, the knot vector contains \( 2 \times k \) additional boundary knots.

**LSQUnivariateSpline**.\text{get_residual}()

Return weighted sum of squared residuals of the spline approximation.

This is equivalent to:

\[
\sum((w[i] \times (y[i]-\text{spl}(x[i])))^2, \text{axis}=0)
\]
LSQUnivariateSpline.integral(a, b)
Return definite integral of the spline between two given points.

Parameters
- a : float
  Lower limit of integration.
- b : float
  Upper limit of integration.

Returns
- integral : float
  The value of the definite integral of the spline between limits.

Examples
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 3, 11)
>>> y = x**2
>>> spl = UnivariateSpline(x, y)
>>> spl.integral(0, 3)
9.0
which agrees with \( \int x^2 dx = \frac{x^3}{3} \) between the limits of 0 and 3.

A caveat is that this routine assumes the spline to be zero outside of the data limits:

```python
>>> spl.integral(-1, 4)
9.0
>>> spl.integral(-1, 0)
0.0
```

LSQUnivariateSpline.roots()
Return the zeros of the spline.

Restriction: only cubic splines are supported by fitpack.

LSQUnivariateSpline.set_smoothing_factor(s)
Continue spline computation with the given smoothing factor s and with the knots found at the last call.
This routine modifies the spline in place.

Functional interface to FITPACK functions:

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>splrep(x, y[, w, xb, xe, k, task, s, t, ...])</td>
<td>Find the B-spline representation of 1-D curve.</td>
</tr>
<tr>
<td>splprep(x[, w, u, ub, ue, k, task, s, t, ...])</td>
<td>Find the B-spline representation of an N-dimensional curve.</td>
</tr>
<tr>
<td>splev(x, tck[, der, ext])</td>
<td>Evaluate a B-spline or its derivatives.</td>
</tr>
<tr>
<td>splint(a, b, tck[, full_output])</td>
<td>Evaluate the definite integral of a B-spline.</td>
</tr>
<tr>
<td>sproot(tck[, mest])</td>
<td>Find the roots of a cubic B-spline.</td>
</tr>
<tr>
<td>spalde(x, tck)</td>
<td>Evaluate all derivatives of a B-spline.</td>
</tr>
<tr>
<td>splder(tck[, n])</td>
<td>Compute the spline representation of the derivative of a given spline</td>
</tr>
<tr>
<td>splantider(tck[, n])</td>
<td>Compute the spline for the antiderivative (integral) of a given spline</td>
</tr>
</tbody>
</table>

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 \(xb \leq x \leq xe\).

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] and x[-1] respectively.

**k : int, optional**
The order of the spline fit. It is recommended to use cubic splines. Even order splines should be avoided especially with small s values. 1 <= k <= 5

**task : {1, 0, -1}, optional**
If task==0 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 (t will be stored and 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(2*m),m+sqrt(2*m)) where m is the number of datapoints in x, y, and w. default : s=m-sqrt(2*m) 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 automatically 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**
(t,c,k) a tuple 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, splev, sproot, splde, splint, bisplrep,bisplev

**Notes**
See splev for evaluation of the spline and its derivatives. Uses the FORTRAN routine curfit from FITPACK.
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 \( j=0, 1, \ldots, n-k-2 \).

References

Based on algorithms described in [R66], [R67], [R68], and [R69]:

[R66], [R67], [R68], [R69]

Examples

```python
>>> import matplotlib.pyplot as plt
>>> from scipy.interpolate import splev, splrep
>>> x = np.linspace(0, 10, 10)
>>> y = np.sin(x)
>>> tck = splrep(x, y)
>>> x2 = np.linspace(0, 10, 200)
>>> y2 = splev(x2, tck)
>>> plt.plot(x, y, 'o', x2, y2)
>>> plt.show()
```

scipy.interpolate.

splev(x, t=None, k=3, m=None, full_output=0, inpt=1, periodic=0)

Find the B-spline representation of a scalar-valued 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 parcuf 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 \( M = \text{len}(x[0]) \), where

5.7. Interpolation (scipy.interpolate)
SciPy Reference Guide, Release 0.16.0

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: \( \sum((w \times (y - g))^2, axis=0) \leq s \), 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 val-
ues 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.

t : int, optional
The knots needed for task=-1.

full_output : int, optional
If non-zero, then return optional outputs.

nest : 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.

per : 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.

quiet : int, 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.
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

384 Chapter 5. Reference
Notes

See `splev` for evaluation of the spline and its derivatives. The number of dimensions N must be smaller than 11.

References

[R63], [R64], [R65]

`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 splder 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 `splprep`, then the parameter values, `u` should be given.
- `tck`: tuple
  - A sequence of length 3 returned by `splrep` or `splprep` containing the knots, coefficients, and degree of the spline.
- `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`, `spalde`, `splint`, `bisplrep`, `bisplev`

References

[R58], [R59], [R60]

`scipy.interpolate.splint(a, b, tck, full_output=0)`

Evaluate the definite integral of a B-spline.

Given the knots and coefficients of a B-spline, evaluate the definite integral of the smoothing polynomial between two given points.

**Parameters**

- `a, b`: float
  - The end-points of the integration interval.
- `tck`: tuple
  - A tuple (t,c,k) 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

5.7. Interpolation (`scipy.interpolate`)
An array containing the integrals of the normalized B-splines defined on the set of knots.

See also:

splprep, splrep, sproot, spalde, splev, bisplrep, bisplev, UnivariateSpline, BivariateSpline

Notes

splint silently assumes that the spline function is zero outside the data interval (a, b).

References

[R61], [R62]

scipy.interpolate.sproot (tck, mest=10)

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
A tuple (t,c,k) 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, UnivariateSpline, BivariateSpline

References

[R70], [R71], [R72]

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.

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, UnivariateSpline, BivariateSpline
scipy.interpolate.splder(tck, n=1)

Compute the spline representation of the derivative of a given spline

**Parameters**
- `tck`: tuple of (t, c, k)
  - Spline whose derivative to compute
- `n`: int, optional
  - Order of derivative to evaluate. Default: 1

**Returns**
- `tck_der`: tuple of (t2, c2, k2)
  - Spline of order k2=k-n representing the derivative of the input spline.

See also:
- splantider, splev, spalde

**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: sproot only works for order 3 splines, so we fit an order 4 spline):

```python
>>> dspl = splder(spl)
>>> sproot(dspl) / np.pi
array([ 0.50000001, 1.5 , 2.49999998])
```

This agrees well with roots $\pi/2 + n\pi$ of $\cos(x) = \sin'(x)$.

scipy.interpolate.splantider(tck, n=1)

Compute the spline for the antiderivative (integral) of a given spline.

**Parameters**
- `tck`: tuple of (t, c, k)
  - Spline whose antiderivative to compute
- `n`: int, optional
  - Order of antiderivative to evaluate. Default: 1

**Returns**
- `tck_ader`: tuple of (t2, c2, k2)
  - Spline of order k2=k+n representing the antiderivative of the input spline.

See also:
- splder, splev, spalde

**Notes**

The `splder` function is the inverse operation of this function. Namely, `splder(splantider(tck))` is identical to `tck`, modulo rounding error.

New in version 0.13.0.
**Examples**

```python
>>> 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:

```python
>>> splev(1.7, spl), splev(1.7, splder(splantider(spl)))
(array(2.1565429877197317), array(2.1565429877201865))
```

Antiderivative can be used to evaluate definite integrals:

```python
>>> ispl = splantider(spl)
>>> splev(np.pi/2, ispl) - splev(0, ispl)
2.2572053588768486
```

This is indeed an approximation to the complete elliptic integral \( K(m) = \int_0^{\pi/2} [1 - m \sin^2 x]^{-1/2} dx \):

```python
>>> from scipy.special import ellipk
>>> ellipk(0.8)
2.2572053268208538
```

### 5.7.4 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.

**class scipy.interpolate.RectBivariateSpline**

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)]`.
- `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

**RectBivariateSpline.\_call\_**(x, y[, mth, dx, dy, grid])  
Evaluate the spline or its derivatives at given positions.

**RectBivariateSpline.ev**(xi, yi[, dx, dy])  
Evaluate the spline at points

**RectBivariateSpline.get_coeffs**()  
Return spline coefficients.

**RectBivariateSpline.get_knots**()  
Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable

**RectBivariateSpline.get_residual**()  
Return weighted sum of squared residuals of the spline

**RectBivariateSpline.integral**(xa, xb, ya, yb)  
Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

**5.7. Interpolation (scipy.interpolate)**  
389
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.

**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

**RectBivariateSpline.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**
- **integ** : float
  - The value of the resulting integral.

**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, and must lie within $(0, 2\pi)$.
- **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 $\text{sum}((r(i,j)-s(u(i),v(j)))**2)$ 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 $u.size \times v.size \times (0.1)^2$.

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
c = plt.figure()
s = [3e9, 2e9, 1e9, 1e8]
for ii in range(len(s)):
    lut = RectSphereBivariateSpline(lats, lons, data, s=3e9)
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 = %s" % s[ii])
c.show()
```
Methods

```python
.RectSphereBivariateSpline.__call__ (theta, phi[, dtheta, dphi, grid])
Evaluate the spline or its derivatives at given positions.
RectSphereBivariateSpline.ev (theta, phi[, dtheta, dphi])
Evaluate the spline at points
.RectSphereBivariateSpline.get_coeffs ()
Return spline coefficients.
.RectSphereBivariateSpline.get_knots ()
Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively.
.RectSphereBivariateSpline.get_residual ()
Return weighted sum of squared residuals of the spline
```

**RectSphereBivariateSpline.** __call__ (theta, phi[, dtheta, dphi, grid])
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.

**RectSphereBivariateSpline.ev (theta, phi[, dtheta, dphi])**
Evaluate the spline at points

Returns the interpolated value at (theta[i], phi[i]), i=0,...,len(theta)-1.

**Parameters**

- theta, phi : array_like
  Input coordinates. Standard Numpy broadcasting is obeyed.
- dtheta : int, optional

5.7. Interpolation (scipy.interpolate) 393
Order of theta-derivative
New in version 0.14.0.

\texttt{dphi} : int, optional
Order of phi-derivative
New in version 0.14.0.

RectSphereBivariateSpline.\texttt{get_coeffs}()
Return spline coefficients.

RectSphereBivariateSpline.\texttt{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.

RectSphereBivariateSpline.\texttt{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:

\begin{verbatim}
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.
\end{verbatim}

\textbf{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 \texttt{SmoothBivariateSpline} or \texttt{LSQBivariateSpline}.

\textbf{See also:}

\texttt{UnivariateSpline}
a similar class for univariate spline interpolation

\texttt{SmoothBivariateSpline}
to create a BivariateSpline through the given points

\texttt{LSQBivariateSpline}
to create a BivariateSpline using weighted least-squares fitting

\texttt{SphereBivariateSpline}
bivariate spline interpolation in spherical coordinates

\texttt{bisplrep} older wrapping of FITPACK
\texttt{bisplev} older wrapping of FITPACK

\textbf{Methods}

\begin{verbatim}
__call__ (x, y[, mth, 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.
\end{verbatim}
Table 5.50 – continued from previous page

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>get_knots()</td>
<td>Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable.</td>
</tr>
<tr>
<td>get_residual()</td>
<td>Return weighted sum of squared residuals of the spline</td>
</tr>
<tr>
<td>integral(xa, xb, ya, yb)</td>
<td>Evaluate the integral of the spline over area [xa,xb] x [ya,yb].</td>
</tr>
</tbody>
</table>

BivariateSpline.__call__(x, y, mth=None, 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.
  - 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.
  - mth : str
    - Deprecated argument. Has no effect.

BivariateSpline.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.

BivariateSpline.get_coeffs()

Return spline coefficients.

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.

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)

BivariateSpline.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.

5.7. Interpolation (scipy.interpolate)
ya, yb : float
    The end-points of the y integration interval.

Returns
    integ : float
    The value of the resulting integral.

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 approxima-
        tion 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:
        \sum((w[i]*(z[i]-s(x[i], y[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 z[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.

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) * (ky+1).

Methods

__call__(x, y[, mth, 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-vara-
get_residual() Return weighted sum of squared residuals of the spline
integral(xa, xb, ya, yb) Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

SmoothBivariateSpline.__call__(x, y, mth=None, 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.

\(dx\): 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.

\(mth\): str
Deprecated argument. Has no effect.

SmoothBivariateSpline.ev \((xi, yi, dx=0, dy=0)\)
Evaluate the spline at points

Returns the interpolated value at \((xi[i], yi[i]), i=0, \ldots,\) \(\text{len}(xi)-1\).

\(Parameters\)
\(xi, yi\): 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.

SmoothBivariateSpline.get_coeffs()
Return spline coefficients.

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 \(t[k+1:]\), \(t[-k-1:]\) and \(t[\text{len}(t)-k-1]=e\), respectively.

SmoothBivariateSpline.get_residual()
Return weighted sum of squared residuals of the spline approximation: sum \(((w[i]*(z[i]-s(x[i],y[i])))^2,\text{axis}=0)\)

SmoothBivariateSpline.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.

\(Returns\)
\(integ\): float
The value of the resulting integral.

class 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 condition: \( \sum\left((w(i)*(r(i) - s(\theta(i), \phi(i))))^2\right) \leq s \) Default \( s = \text{len}(w) \) 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. \( \epsilon \) 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,:], data[1:-1,1], data[1:-1,-1] = 0., 0., 0., 1., 1.
>>> data[1,1:-1], data[2:-2,2], data[2:-2,-2] = 2., 2.
>>> data[3,3:-2] = 3.
>>> data = np.roll(data, 4, 1)
```

We need to set up the interpolator object

```python
>>> 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

```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)
```

```python
>>> data_smth = lut(fine_lats, fine_lons)

```
```python
>>> ax3.imshow(data_smth, interpolation='nearest')
>>> plt.show()
```

### Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>__call__</code></td>
<td>Evaluate the spline or its derivatives at given positions.</td>
</tr>
<tr>
<td><code>ev</code></td>
<td>Evaluate the spline at points</td>
</tr>
<tr>
<td><code>get_coeffs</code></td>
<td>Return spline coefficients.</td>
</tr>
<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>
</tr>
<tr>
<td><code>get_residual</code></td>
<td>Return weighted sum of squared residuals of the spline</td>
</tr>
</tbody>
</table>

**SmoothSphereBivariateSpline.**

**__call__**(theta, phi[, dtheta, dphi, grid])

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.

**SmoothSphereBivariateSpline.**

**ev**(theta, phi[, dtheta=0, dphi=0, grid=True])

Evaluate the spline at points

Returns the interpolated value at \((\theta[i], \phi[i]), i=0, \ldots, \text{len}(\theta)-1\).
Parameters

theta, phi : array_like
Input coordinates. Standard Numpy broadcasting is obeyed.
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.

SmoothSphereBivariateSpline.get_coeffs()
Return spline coefficients.

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 tk[+1:-1] and tk[+1]=b, tk[-1]=e, respectively.

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)

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) * (ky+1).

Methods
__call__(x, y[, mth, 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

integral(xa, xb, ya, yb)  Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

LSQBivariateSpline.__call__(x, y, mth=None, 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.

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.

mth : str  
Deprecated argument. Has no effect.

LSQBivariateSpline.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.

LSQBivariateSpline.get_coeffs()  Return spline coefficients.

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.

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)

5.7. Interpolation (scipy.interpolate)
LSQBivariateSpline.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.

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.
>>> 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. 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] += .0001
>>> knotst[-1] -= .0001
>>> knotsp[0] += .0001
>>> knotsp[-1] -= .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

- **__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
- **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

#### LSQSphereBivariateSpline.__call__(theta, phi[, dtheta=0, dphi=0, grid=True])
Evaluate the spline or its derivatives at given positions.

- **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.

**LSQSphereBivariateSpline.ev**(theta, phi, dtheta=0, dphi=0)

Evaluate the spline at points

Returns the interpolated value at \((\text{theta}[i], \text{phi}[i]), i=0,...,\text{len(theta)}-1\).

**Parameters**

- **theta, phi**: array_like
  - Input coordinates. Standard Numpy broadcasting is obeyed.

- **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.

**LSQSphereBivariateSpline.get_coeffs**()

Return spline coefficients.

**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 \([k+1:-k-1]\) and \([k+1]=b, t[-k-1]:=e\), respectively.

**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:

- **bisplrep**(x, y, z, w=None, xb=None, xe=None, yb=None, ye=None, kx=3, ky=3, task=0, s=None, eps=1e-16, tx=None, ty=None, full_output=0, nxest=None, nyest=None, quiet=1)  
  Find a bivariate B-spline representation of a surface.

- **bisplev**(x, y, tck[, dx, dy])  
  Evaluate a bivariate B-spline and its derivatives.

**scipy.interpolate.bisplrep**(x, y, z, w=None, xb=None, xe=None, yb=None, ye=None, kx=3, ky=3, task=0, s=None, eps=1e-16, tx=None, ty=None, full_output=0, nxest=None, nyest=None, quiet=1)  

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 \(w=np.ones(\text{len}(x))\).

- **xb, xe**: float, optional
End points of approximation interval in x. By default \( x_b = \text{min}(x), \)
\( x_e = \text{max}(x) \).
yb, ye : float, optional
End points of approximation interval in y. By default \( y_b = \text{min}(y), \)
\( y_e = \text{max}(y) \).
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 \( m = \text{len}(x) \).
eps : float, optional
A threshold for determining the effective rank of an over-determined linear system of
equations (0 < eps < 1). eps is not likely to need changing.
full_output : int, optional
Non-zero to return optional outputs.
xest, yest : int, optional
Over-estimates of the total number of knots. If None
then \( n_{xest} = \text{max}(kx+\sqrt{m}/2, 2*kx+3), \)
\( n_{yest} = \text{max}(ky+\sqrt{m}/2, 2*ky+3) \).
quiet : int, optional
Non-zero to suppress printing of messages. This parameter is deprecated; use standard
Python warning filters instead.

Returns

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
[R52], [R53], [R54]
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**
- [R49], [R50], [R51]

### 5.7.5 Additional tools

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<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>
</tr>
</tbody>
</table>

**scipy.interpolate.lagrange**

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.

**scipy.interpolate.approximate_taylor_polynomial**

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 \(\text{order}+1\) times. If None, use \text{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.

See also:

5.8 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)

5.8.1 MATLAB® files

loadmat(file_name[, mdict, appendmat]) 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).

See also:
scipy.io.loadmat (file_name, mdict=None, appendmat=True, **kwargs) Load MATLAB file
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.

**scipy.io.savemat**

Save a dictionary of names and arrays into 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(file_name, appendmat=True, **kwargs)
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
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.

5.8.2 IDL® files

readsav(file_name[, idict, python_dict, ...])  Read an IDL .sav file

scipy.io.readsav(file_name, idict=None, python_dict=False, uncompressed_file_name=None, verb-
bose=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.

5.8.3 Matrix Market files

mminfo(source)  Queries the contents of the Matrix Market file ‘filename’ to extract size and storage information.

Parameters

   source : file
    Matrix Market filename (extension .mtx) or open file object

Returns

   rows,cols : int
    Number of matrix rows and 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’.

   field : str

   symm : str

mmread(source)  Reads the contents of a Matrix Market file ‘filename’ into a matrix.

Parameters

   source : file
    Matrix Market filename (extensions .mtx, .mtz.gz) or open file object.

Returns

   a:
    Sparse or full matrix

mmwrite(target, a[, comment, field, precision])  Writes the sparse or dense array a to a Matrix Market formatted file.

scipy.io.mminfo(source)
    Queries the contents of the Matrix Market file ‘filename’ to extract size and storage information.

Parameters

   source : file
    Matrix Market filename (extension .mtx) or open file object

Returns

   rows,cols : int
    Number of matrix rows and 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’.

   field : str

   symm : str

scipy.io.mmread(source)
    Reads the contents of a Matrix Market file ‘filename’ into a matrix.

Parameters

   source : file
    Matrix Market filename (extensions .mtx, .mtz.gz) or open file object.

Returns

   a:
    Sparse or full matrix

scipy.io.mmwrite(target, a[, comment=", field=None, precision=None])
    Writes the sparse or dense array a to a Matrix Market formatted file.
**Parameters**

- **target**: file
  - Matrix Market filename (extension .mtx) or open file 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.

### 5.8.4 Unformatted Fortran files

**FortranFile**(filename[, mode, header_dtype]) A file object for unformatted sequential files from Fortran code.

**class** scipy.io.FortranFile (filename, mode='r', header_dtype=<type 'numpy.uint32'>)

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:

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,-1)))
>>> f.close()
```

To read this file:
```python
from scipy.io import FortranFile
f = FortranFile('test.unf', 'r')
print(f.read_ints(dtype=np.int32))
[1 2 3 4 5]
print(f.read_reals(dtype=np.float).reshape((5,-1)))
[[ 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. ]]
```

Methods

- close() Closes the file.
- 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.
- 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.
- read_record(dtype=None) Reads a record of a given type from the file.
  - 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_ints

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.

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

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

FortranFile.read_record(dtype=None) Reads a record of a given type from the file.

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_ints
Notes

If the record contains a multi-dimensional array, calling reshape or resize will restructure the array to the correct size. Since Fortran multidimensional arrays are stored in column-major format, this may have some non-intuitive consequences. If the variable was declared as `INTEGER var(5,4)`, for example, var could be read with `read_record(dtype=np.integer).reshape((4,5))` since Python uses row-major ordering of indices.

One can transpose to obtain the indices in the same order as in Fortran.

For records that contain several variables or mixed types (as opposed to single scalar or array types), it is possible to specify a dtype with mixed types:

```python
>>> record = f.read_record([('a', '<f4'), ('b', '<i4')])
```

```python
>>> record['a'] # access the variable 'a'
5.6
```

and if any of the variables are arrays, the shape can be specified as the third item in the relevant tuple:

```python
>>> record = f.read_record([('a', '<f4'), ('b', '<i4', (3,3))])
```

Numpy also supports a short syntax for this kind of type:

```python
>>> record = f.read_record('<f4,(3,3)<i4')
```

```python
>>> record['f0'] # variables are called f0, f1, ...
5.6
```

FortranFile.write_record(s)

Write a record (including sizes) to the file.

Parameters

- s : array_like
  The data to write.

5.8.5 Wav sound files (scipy.io.wavfile)

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>read(filename[, mmap])</td>
<td>Return the sample rate (in samples/sec) and data from a WAV file</td>
</tr>
<tr>
<td>write(filename, rate, data)</td>
<td>Write a numpy array as a WAV file</td>
</tr>
</tbody>
</table>

scipy.io.wavfile.read(filename, mmap=False)

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

Notes

- The file can be an open file or a filename.
- The returned sample rate is a Python integer.
- The data is returned as a numpy array with a data-type determined from the file.
• This function cannot read wav files with 24 bit data.

```python
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**
- The file can be an open file or a filename.
- Writes a simple uncompressed WAV file.
- The bits-per-sample will be determined by the data-type.
- To write multiple-channels, use a 2-D array of shape (Nsamples, Nchannels).

### 5.8.6 Arff files (scipy.io.arff)

```python
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.
5.8.7 Netcdf (scipy.io.netcdf)

```python
class scipy.io.netcdf.netcdf_file(filename[, mode, mmap, version])
```
A file object for NetCDF data.

```python
class scipy.io.netcdf.netcdf_variable(data, typecode, size, shape, ...)
```
A data object for the netcdf module.

The `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
- `mode` : {'r', 'w', 'a'}, optional
- `mmap` : None or bool, optional
- `version` : {1, 2}, optional

**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)
time = f.createVariable('time', 'i', ('time',))
time[:] = np.arange(10)
time.units = 'days since 2008-01-01'
f.close()
```

Note the assignment of `range(10)` to `time[:].` Exposing the slice of the time variable allows for the data to be set in the object, rather than letting `range(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)
Created for a test
time = f.variables['time']
print(time.units)
days since 2008-01-01
time.shape
(10,)
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 0x7fe7b3763180>
```

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()
```

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)
Created for a test
```

**Methods**

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>close()</td>
<td>Closes the NetCDF file.</td>
</tr>
<tr>
<td>createDimension(name, length)</td>
<td>Adds a dimension to the Dimension section of the NetCDF data structure.</td>
</tr>
<tr>
<td>createVariable(name, type, dimensions)</td>
<td>Create an empty variable for the <code>netcdf_file</code> object, specifying its data type and dimensions.</td>
</tr>
</tbody>
</table>
Table 5.65 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<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>
<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
netcdf_file.close()
```
Closes the NetCDF file.

```python
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
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
netcdf_file.flush()
```
Perform a sync-to-disk flush if the `netcdf_file` object is in write mode.

**See also:**

`sync` Identical function

```python
netcdf_file.sync()
```
Perform a sync-to-disk flush if the `netcdf_file` object is in write mode.

**See also:**

`sync` Identical function
class scipy.io.netcdf.netcdf_variable(data, typecode, size, shape, dimensions, attributes=None)

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.

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.

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.

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.

netcdf_variable.itemsize()

Return the itemsize of the variable.

Returns

itemsize : int

The element size of the variable (eg, 8 for float64).

netcdf_variable.typecode()

Return the typecode of the variable.

Returns

typecode : char

The character typecode of the variable (eg, ‘i’ for int).

5.9 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.

5.9.1 Basics

```python
inv(a[, overwrite_a, check_finite])
```

Compute the inverse of a matrix.

Parameters

- a : array_like
  Square matrix to be inverted.

- overwrite_a : bool, optional

```python
solve(a, b[, sym_pos, lower, overwrite_a, ...])
```

Solve the equation $a \times x = b$ for $x$.

```python
solve_banded(l_and_u, ab, b[, overwrite_ab, ...])
```

Solve the equation $a \times x = b$ for $x$, assuming $a$ is a banded matrix.

```python
solve_triangular(a, b[, trans, lower, ...])
```

Solve the equation $a \times x = b$ for $x$, assuming $a$ is a triangular matrix.

```python
det(a[, overwrite_a, check_finite])
```

Compute the determinant of a matrix.

```python
lstsq(a, b[, cond, overwrite_a, ...])
```

Compute least-squares solution to equation $A \times x = b$.

```python
pinv(a[, cond, rcond, return_rank, check_finite])
```

Compute the (Moore-Penrose) pseudo-inverse of a matrix.

```python
pinvh(a[, cond, rcond, lower, return_rank, ...])
```

Compute the (Moore-Penrose) pseudo-inverse of a Hermitian matrix.

```python
kron(a, b)
```

Kronecker product.

```python
tril(m[, k])
```

Make a copy of a matrix with elements above the k-th diagonal zeroed.

```python
triu(m[, k])
```

Make a copy of a matrix with elements below the k-th diagonal zeroed.

```python
orthogonal_procrustes(A, B[, check_finite])
```

Compute the matrix solution of the orthogonal Procrustes problem.

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**

\( \text{ainv} \) : ndarray
Inverse of the matrix \( a \).

**Raises**

\[ \text{LinAlgError} \] :
If \( a \) is singular.

\[ \text{ValueError} \] :
If \( a \) is not square, or not 2-dimensional.

**Examples**

```python
given
```

```python
>>> from scipy import linalg
>>> a = np.array([[1., 2.], [3., 4.]])
>>> linalg.inv(a)
array([[-2., 1. ],
       [ 1.5, -0.5]])
```

```python
scipy.linalg.solve(a, b, sym_pos=False, lower=False, overwrite_a=False, overwrite_b=False, check_finite=True)
```

```python
Solve the equation \( a \ x = b \) for \( x \).
```

**Parameters**

\( a \) : (M, M) array_like
A square matrix.

\( b \) : (M,) or (M, N) array_like
Right-hand side matrix in \( a \ x = b \).

**sym_pos** : bool, optional
Assume \( a \) is symmetric and positive definite.

**lower** : bool, optional
Use only data contained in the lower triangle of \( a \), if \( sym \_pos \) is true. Default is to use upper triangle.

**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.

**Returns**

\( x \) : (M,) or (M, N) ndarray
Solution to the system \( a \ x = b \). Shape of the return matches the shape of \( b \).

**Raises**

\[ \text{LinAlgError} \] :
If \( a \) is singular.

**Examples**

Given \( a \) and \( b \), solve for \( x \):

```python
given
```
\[ x = \begin{bmatrix} 2 & -2 & 9 \end{bmatrix} \]

\[ np.dot(a, x) == b \]

\[ \begin{bmatrix} True, True, True \end{bmatrix}, \text{dtype=boolean} \]

```python
scipy.linalg.solve_banded(l_and_u, ab, b, overwrite_ab=False, overwrite_b=False, debug=False, check_finite=True)
```

Solve the equation \( a x = b \) for \( x \), assuming \( a \) is a banded matrix.

The matrix \( a \) is stored in \( ab \) using the matrix diagonal ordered form:

\[ ab[u + i - j, j] == a[i, j] \]

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>
</tr>
<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 \( b \).

```python
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:

\[ ab[u + i - j, j] == a[i, j] \] (if upper form; \( i <= j \))

\[ ab[i - j, j] == a[i, j] \] (if lower form; \( i >= j \))

Example of \( ab \) (shape of \( a \) is (6, 6), \( u = 2 \)):

**upper form:**

<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>*</td>
<td>a02</td>
<td>a13</td>
<td>a24</td>
<td>a35</td>
<td></td>
</tr>
<tr>
<td>*</td>
<td>a01</td>
<td>a12</td>
<td>a23</td>
<td>a34</td>
<td>a45</td>
</tr>
<tr>
<td>a00</td>
<td>a11</td>
<td>a22</td>
<td>a33</td>
<td>a44</td>
<td>a55</td>
</tr>
</tbody>
</table>

**lower form:**

<table>
<thead>
<tr>
<th></th>
<th>a01</th>
<th>a12</th>
<th>a23</th>
<th>a33</th>
<th>a44</th>
<th>a55</th>
</tr>
</thead>
<tbody>
<tr>
<td>a10</td>
<td>a21</td>
<td>a32</td>
<td>a43</td>
<td>a54</td>
<td></td>
<td></td>
</tr>
<tr>
<td>a20</td>
<td>a31</td>
<td>a42</td>
<td>a53</td>
<td></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 \( b \).

**scipy.linalg.solve_circulant\( (c, b, singular=\text{\textquoteleft}raise\text{\textquoteright}, tol=None, caxis=-1, baxis=0, outaxis=0)\)**

Solve \( C x = b \) for \( x \), where \( C \) is a 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:

\[ x = \text{ifft}\left(\frac{\text{fft}(b)}{\text{fft}(c)}\right) \]

where \( \text{fft} \) and \( \text{ifft} \) 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:
  \[ tol = \text{abs}\_eigs\text{.max()} \times \text{abs}\_eigs\text{.size} \times \text{np}\text{.finfo}(\text{np}\text{.float64})\text{.eps} \]
  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 \( \text{solve\_circulant} \) 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`

**Notes**
For a one-dimensional vector \( c \) with length \( m \), and an array \( b \) with shape \((m, \ldots)\),

\[
\text{solve}_\text{circulant}(c, b)
\]

returns the same result as

\[
\text{solve}(\text{circulant}(c), b)
\]

where \( \text{solve} \) and \( \text{circulant} \) are from \texttt{scipy.linalg}.

New in version 0.16.0.

**Examples**

```python
>>> 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 \texttt{scipy.linalg.solve}:

```python
>>> solve(circulant(c), b)
array([ 0.75, -0.25, 0.25])
```

A singular example:

```python
>>> c = np.array([1, 1, 0, 0])
>>> b = np.array([1, 2, 3, 4])
```

Calling \( \text{solve}_\text{circulant}(c, b) \) will raise a \texttt{LinAlgError}. For the least square solution, use the option \texttt{singular='lstsq'}:

```python
>>> solve_circulant(c, b, singular='lstsq')
array([ 0.25, 1.25, 2.25, 1.25])
```

Compare to \texttt{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 \( c \): \( c[:, \text{np.newaxis}, :] \) 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)
```

```python
>>> 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(a, b, trans=0, lower=False, unit_diagonal=False, overwrite_b=False, debug=False, 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:
  - `trans` system
    - 0 or ‘N’ : $a x = b$
    - 1 or ‘T’ : $a^T x = b$
    - 2 or ‘C’ : $a^H x = b$
- **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.

`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, \( r = \text{conjugate}(c) \) 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, \( r = \text{conjugate}(c) \) 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 \( T \times x = b \).

- **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 (result entirely NaNs) if the inputs do contain infinities or NaNs.

**Returns**

- **x** : (M,) or (M, K) ndarray
  The solution to the system \( T \times x = b \). Shape of return matches shape of \( b \).

**Notes**

The solution is computed using Levinson-Durbin recursion, which is faster than generic least-squares methods, but can be less numerically stable.

```python
scipy.linalg.det(a, overwrite_a=False, 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.

For a 3x3 matrix, for example, the determinant is computed as follows:

\[
\begin{vmatrix}
  a & b & c \\
  d & e & f \\
  g & h & i \\
\end{vmatrix}
\]

\[
\text{det}(A) = a \times e \times i + b \times f \times g + c \times d \times h - c \times e \times g - b \times d \times i - a \times f \times h
\]

**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]])
>>> linalg.det(a)
0.0
>>> a = np.array([[0, 0], [0, 0]])
```
scipy.linalg.det(a)
3.0

scipy.linalg.norm(a, ord=None)
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.

ord : {non-zero int, inf, -inf, ‘fro’}, optional
Order of the norm (see table under Notes). inf means numpy’s inf object.

Returns

norm : float
Norm of the matrix or vector.

Notes

For values of ord <= 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 [R86]:

\[ ||A||_F = \left[ \sum_{i,j} \text{abs}(a_{i,j})^2 \right]^{1/2} \]

References

[R86]

Examples

>>> from scipy.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]])

>>> norm(a)
7.74596692414834
>>> norm(b)
7.74596692414834
```python
>>> 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
>>> 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)
7.3484692283495345
>>> norm(a, -2)
nan
>>> norm(b, -2)
1.8570331885190563e-016
>>> norm(a, 3)
5.8480354764257312
>>> norm(a, -3)
nan
```

```python
scipy.linalg.lstsq(a, b, cond=None, overwrite_a=False, overwrite_b=False, check_finite=True)
```

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 $rcond * \text{largest}_\text{singular}_\text{value}$ 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.

**Returns**
- **x**: $(N,)$ or $(N, K)$ ndarray
- **residues**: () or $(1,)$ or $(K,)$ ndarray
Sums of residues, squared 2-norm for each column in \( b - a x \). If rank of matrix \( a \) is \(< N \) or \( > M \) this is an empty array. If \( b \) was 1-D, this is an (1,) shape array, otherwise the shape is (K,).

**rank**: int
  Effective rank of matrix \( a \).

**s**: (min(M,N),) ndarray
  Singular values of \( a \). The condition number of \( a \) is \( \text{abs}(s[0]/s[-1]) \).

**Raises**

LinAlgError :
  If computation does not converge.

**See also:**

* optimize.nnls
  linear least squares with non-negativity constraint

* scipy.linalg.pinv2
  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.

\( \text{cond, rcond} \) : float, optional
  Cutoff for 'small' singular values in the least-squares solver. Singular values smaller than \( \text{rcond} \times \text{largest_singular_value} \) are considered zero.

\( \text{return_rank} \) : bool, optional
  If True, return the effective rank of the matrix

\( \text{check_finite} \) : 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 \( a \).

\( \text{rank} \) : int
  The effective rank of the matrix. Returned if \( \text{return_rank} == \text{True} \)

**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
  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.

\( \text{cond, rcond} \) : float or None
  Cutoff for 'small' singular values in the least-squares solver. Singular values smaller than \( \text{rcond} \times \text{largest_singular_value} \) are considered zero.
Cutoff for ‘small’ singular values. Singular values smaller than 
\( rcond \times \text{largest}_\text{singular}_\text{value} \) 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
>>> 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(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 * 
\text{largest}_\text{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. (De-
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
B : (N, N) ndarray
The pseudo-inverse of matrix a.
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
```

cipy.linalg.kron(a, b)
Kronecker product.

The result is the block matrix:

```
  b[0,0]*a[0,0]  b[0,1]*a[0,1] ... b[0,-1]*a[0,-1]
  b[1,0]*a[1,0]  b[1,1]*a[1,1] ... b[1,-1]*a[1,-1]
  ...
  b[-1,0]*a[-1,0] b[-1,1]*a[-1,1] ... b[-1,-1]*a[-1,-1]
```

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]]))
array([[1, 1, 2, 2, 3, 3, 4, 4]])
```

cipy.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]])
```

cipy.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's `orthogonal_procrustes` function

```python
scipy.linalg.orthogonal_procrustes(A, B, check_finite=True)
```

- **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 $\text{dot}(A, R) - B$, subject to $\text{dot}(R^T, R) = I$. 
  - **scale**: float
    - Sum of the singular values of $\text{dot}(A^T, B)$.

- ** Raises**

  - **ValueError**
    - If the input arrays are incompatibly shaped. This may also be raised if matrix A or B contains an inf or nan and check_finite is True, or if the matrix product AB contains an inf or nan.

Notes

- New in version 0.15.0.

References

- [R87] 5.9.2 Eigenvalue Problems

SciPy's `eig` function

```python
scipy.linalg.eig(a[, b, left, right, overwrite_a, ...])
```

Solve an ordinary or generalized eigenvalue problem of a square matrix.

5.9. Linear algebra (scipy.linalg)
Table 5.68 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>eigvals(a, b, overwrite_a, check_finite)</code></td>
<td>Compute eigenvalues from an ordinary or generalized eigenvalue problem.</td>
</tr>
<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>eigvalsh(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>
</tbody>
</table>

```python
scipy.linalg.eig(a, b=None, left=False, right=True, overwrite_a=False, overwrite_b=False, check_finite=True)
```

Solve an ordinary or generalized eigenvalue problem of a square matrix.

Find eigenvalues \( w \) and right or left eigenvectors of a general matrix:

\[
a \ v_r[:,i] = w[i] \ b \ v_r[:,i]
\]

\[
a.H \ v_l[:,i] = w[i].conj() \ b.H \ v_l[:,i]
\]

where \( .H \) 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.

**Returns**
- `w` : (M,) double or complex ndarray
  The eigenvalues, each repeated according to its multiplicity.
- `vl` : (M, M) double or complex ndarray
  The normalized left eigenvector corresponding to the eigenvalue \( w[i] \) is the column \( v_l[:,i] \). 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 \( v_r[:,i] \). Only returned if \( right=True \).

**Raises**
- LinAlgError
  If eigenvalue computation does not converge.

**See also:**
- `eigh`
  Eigenvalues and right eigenvectors for symmetric/Hermitian arrays.

```python
scipy.linalg.eigvals(a, b=None, overwrite_a=False, check_finite=True)
```

Compute eigenvalues from an ordinary or generalized eigenvalue problem.

Find eigenvalues of a general matrix:
SciPy Reference Guide, Release 0.16.0

\[ a \cdot \text{vr}[:,i] = w[i] \cdot b \cdot \text{vr}[:,i] \]

**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. If omitted, identity matrix is assumed.
- \( \text{overwrite}_a \) : bool, optional
  Whether to overwrite data in \( a \) (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**
- \( w \) : (M,) double or complex ndarray
  The eigenvalues, each repeated according to its multiplicity, but not in any specific order.

**Raises**
- LinAlgError
  If eigenvalue computation does not converge

See also:
- \( \text{eigvalsh} \)
  eigenvalues of symmetric or Hermitian arrays,
- \( \text{eig} \)
  eigenvalues and right eigenvectors of general arrays.
- \( \text{eigh} \)
  eigenvalues and eigenvectors of symmetric/Hermitian arrays.

```python
scipy.linalg.eigh(a, b=None, lower=True, eigvals_only=False, 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 \( w \) and optionally eigenvectors \( v \) of matrix \( a \), where \( b \) is positive definite:

\[ a \cdot v[:,i] = w[i] \cdot b \cdot v[:,i] \]

\[ v[i,:,\text{conj}()] \cdot a \cdot v[:,i] = w[i] \]

\[ v[i,:,\text{conj}()] \cdot b \cdot v[:,i] = 1 \]

**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.
- \( \text{lower} \) : bool, optional
  Whether the pertinent array data is taken from the lower or upper triangle of \( a \). (Default: lower)
- \( \text{eigvals}_\text{only} \) : bool, optional
  Whether to calculate only eigenvalues and no eigenvectors. (Default: both are calculated)
- \( \text{turbo} \) : bool, optional
  Use divide and conquer algorithm (faster but expensive in memory, only for generalized eigenvalue problem and if eigvals=\( \text{None} \))
- \( \text{eigvals} \) : tuple (lo, hi), optional

5.9. Linear algebra (scipy.linalg) 433
Indexes of the smallest and largest (in ascending order) eigenvalues and corresponding eigenvectors to be returned: \( 0 \leq lo \leq hi \leq M-1 \). 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:**
- \( \textit{eig} \)
eigenvalues and right eigenvectors for non-symmetric arrays

**scipy.linalg.eigvalsh**
\((a, b=None, lower=True, overwrite_a=False, overwrite_b=False, turbo=True,\)
\( \textit{eigvals}=None, \textit{type}=1, \textit{check_finite}=True)\)
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.
- \( \textit{lower} \) : 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: \( 0 \leq lo < hi \leq M-1 \). 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 \( N (1 \leq N \leq M) \) 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:

- **eigvals** eigenvalues of general arrays
- **eigh** eigenvalues and right eigenvectors for symmetric/Hermitian arrays
- **eig** eigenvalues and right eigenvectors for non-symmetric arrays

`scipy.linalg.eig_banded`(a_band, lower=False, eigvals_only=False, overwrite_a_band=False, select='a', select_range=None, max_ev=0, check_finite=True)
Solve real symmetric or complex hermitian band matrix eigenvalue problem.

Find eigenvalues \( w \) and optionally right eigenvectors \( v \) of \( a \):

\[
a v[:,i] = w[i] v[:,i] \\
v.H v = \text{identity}
\]

The matrix \( a \) is stored in a_band either in lower diagonal or upper diagonal ordered form:

\[
a\_band[u + i - j, j] == a[i,j] \text{ (if upper form; i <= j) } a\_band[i - j, j] == a[i,j] \text{ (if lower form; i >= j) }
\]

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
```

5.9. Linear algebra (`scipy.linalg`) 435
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

**scipy.linalg.eigvals_banded**

Solve real symmetric or complex hermitian band matrix eigenvalue problem.

Find eigenvalues w 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)
- **overwrite_a_band**: bool, optional
  - Discard data in a_band (may enhance performance)
- **select**: {'a', 'v', 'i'}, optional
  - Which eigenvalues to calculate
    - 'a': All eigenvalues
    - 'v': Eigenvalues in the interval (min, max]
    - 'i': Eigenvalues with indices min <= i <= max
- **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
- **eigvals**: eigenvalues of general arrays
- **eigh**: eigenvalues and right eigenvectors for symmetric/Hermitian arrays
- **eig**: eigenvalues and right eigenvectors for non-symmetric arrays

### 5.9.3 Decompositions

- **lu(a, permute_l, overwrite_a, check_finite)**: Compute pivoted LU decomposition of a matrix.
- **lu_factor(a, overwrite_a, check_finite)**: Compute pivoted LU decomposition of a matrix.
- **lu_solve(lu_and_piv, b[, trans, ...])**: Solve an equation system, a x = b, given the LU factorization of a
- **svd(a[, full_matrices, compute_uv, ...])**: Singular Value Decomposition.
- **svdvals(a[, overwrite_a, check_finite])**: Compute singular values of a matrix.
- **diagsvd(s, M, N)**: Construct the sigma matrix in SVD from singular values and size M, N.
- **orth(A)**: Construct an orthonormal basis for the range of A using SVD
- **cholesky(a[, lower, overwrite_a, check_finite])**: Compute the Cholesky decomposition of a matrix.

Continued on next page
SciPy Reference Guide, Release 0.16.0

Table 5.69 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>cholesky_banded(ab[, overwrite_ab, lower, ...])</code></td>
<td>Cholesky decompose a banded Hermitian positive-definite matrix</td>
</tr>
<tr>
<td><code>cho_factor(a[, lower, overwrite_a, check_finite])</code></td>
<td>Compute the Cholesky decomposition of a matrix, to use in cho_solve</td>
</tr>
<tr>
<td><code>cho_solve(c_and_lower, b[, overwrite_b, ...])</code></td>
<td>Solve the linear equations $A x = b$, given the Cholesky factorization of $A$.</td>
</tr>
<tr>
<td><code>cho_solve_banded(cb_and_lower, b[, ...])</code></td>
<td>Solve the linear equations $A x = b$, given the Cholesky factorization of $A$.</td>
</tr>
<tr>
<td><code>polar(a[, side])</code></td>
<td>Compute the polar decomposition.</td>
</tr>
<tr>
<td><code>qr(a[, overwrite_a, lwork, mode, pivoting, ...])</code></td>
<td>Compute QR decomposition of a matrix.</td>
</tr>
<tr>
<td><code>qr_multiply(a, c[, mode, pivoting, ...])</code></td>
<td>Calculate the QR decomposition and multiply $Q$ with a matrix.</td>
</tr>
<tr>
<td><code>qr_update(Q, R, u, v[, overwrite_qruv, ...])</code></td>
<td>Rank-k QR update</td>
</tr>
<tr>
<td><code>qr_delete(Q, R, k[, p, which, overwrite_qr, ...])</code></td>
<td>QR downdate on row or column deletions</td>
</tr>
<tr>
<td><code>qr_insert(Q, R, k[, which, rcond, ...])</code></td>
<td>QR update on row or column insertions</td>
</tr>
<tr>
<td><code>rq(a[, overwrite_a, lwork, mode, check_finite])</code></td>
<td>Compute RQ decomposition of a matrix.</td>
</tr>
<tr>
<td><code>schur(a[, output, lwork, overwrite_a, sort, ...])</code></td>
<td>Compute Schur decomposition of a matrix.</td>
</tr>
<tr>
<td><code>rsf2csf(T, Z[, check_finite])</code></td>
<td>Convert real Schur form to complex Schur form.</td>
</tr>
<tr>
<td><code>hessenberg(a[, calc_q, overwrite_a, ...])</code></td>
<td>Compute Hessenberg form of a matrix.</td>
</tr>
</tbody>
</table>

**scipy.linalg.lu**

```python
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 $P L$ (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

**Notes**

This is a LU factorization routine written for Scipy.

**scipy.linalg.lu_factor**

```python
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 \( \text{piv}[i] \).

**See also:**

- **lu_solve**: solve an equation system using the LU factorization of a matrix

**Notes**

This is a wrapper to the \(*\text{GETRF}\) routines from LAPACK.

```python
scipy.linalg.lu_solve(lu_and_piv, b, trans=0, overwrite_b=False, check_finite=True)
```

Solve an equation system, \( a \times b \), given the LU factorization of \( a \)

**Parameters**

- **(lu, piv)**
  - Factorization of the coefficient matrix \( a \), as given by \text{lu_factor}
- **b**: array
  - Right-hand side
- **trans**: \{0, 1, 2\}, optional
  - Type of system to solve:
    | trans | system      |
    |-------|-------------|
    | 0     | \( a \times b \) |
    | 1     | \( a^T \times b \) |
    | 2     | \( a^H \times b \) |
- **overwrite_b**: bool, optional
  - Whether to overwrite data in \( b \) (may increase 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**: array
  - Solution to the system

**See also:**

- **lu_factor**: LU factorize a matrix
scipy.linalg.svd(a, full_matrices=True, compute_uv=True, overwrite_a=False, check_finite=True)

Singular Value Decomposition.

Factorizes the matrix a into two unitary matrices U and Vh, and a 1-D array s of singular values (real, non-negative) such that \( a = U \times S \times Vh \), 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, 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.

**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
generate code here from examples
```

```python
generate code here
```
scipy.linalg.svdvals(a, overwrite_a=False, check_finite=True)

Compute singular values of a matrix.

Parameters

- **a**: (M, N) array_like
  - Matrix to decompose.
- **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.

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)
```

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

scipy.linalg.orth(A)

Construct an orthonormal basis for the range of A using SVD

Parameters

- **A**: (M, N) array_like
  - Input array

Returns

- **Q**: (M, K) ndarray
  - Orthonormal basis for the range of A. K = effective rank of A, as determined by automatic cutoff

See also:

- **svd**
  - Singular value decomposition of a matrix
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

```python
>>> from scipy import array, linalg, dot
>>> a = array([[1,-2j],[2j,5]])
>>> L = linalg.cholesky(a, lower=True)
>>> L
array([[ 1.+0.j, 0.+0.j],
       [ 0.+2.j, 1.+0.j]])
>>> dot(L, L.T.conj())
array([[ 1.+0.j, 0.-2.j],
       [ 0.+2.j, 5.+0.j]])
```

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:

\[ ab[u + i - j, j] == a[i,j] \quad (\text{if upper form; } i \leq j) \]
\[ ab[i - j, j] == a[i,j] \quad (\text{if lower form; } i \geq j) \]

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

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 decom-
position. 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.

scipy.linalg.cho_solve(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, lower) : tuple, (array, bool)
  Cholesky factorization of \( a \), as given by cho_factor
- b : array
  Right-hand side
- 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
- x : array
  The solution to the system \( A x = b \)

See also:
cho_factor

Cholesky factorization of a matrix

scipy.linalg.cho_solve_banded(cb_and_lower, b, overwrite_b=False, check_finite=True)

Solve the linear equations A x = b, given the Cholesky factorization of A.

Parameters

- (cb, lower) : tuple, (array, bool)
  - cb is the Cholesky factorization of A, as given by cholesky_banded. lower must be the same value that was given to cholesky_banded.
- b : array
  - 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.

scipy.linalg.polar(a, side='right')

Compute the polar decomposition.

Returns the factors of the polar decomposition [R88] 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” [R89] 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

[R88], [R89]

Examples

```python
c from scipy.linalg import polar

c = np.array([[1, -1], [2, 4]])
c, p = polar(a)
```
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],
       [-0.42393237, 0.78757942],
       [ 0.88054056, 0.4739708 ]])
```

```python
>>> p
array([[ 0.48470147, 0.96940295, 1.15122648],
       [ 0.96940295, 1.9388059 , 2.30245295],
       [ 1.15122648, 2.30245295, 3.65696431]])
```

```python
>>> u.dot(p)  # Verify the decomposition.
array([[ 0.5, 1. , 2. ],
       [ 1.5, 3. , 4. ]])
```

```python
>>> u.T.dot(u)  # The rows of u are orthonormal.
array([[ 1.00000000e+00, -2.07353665e-17],
       [ -2.07353665e-17, 1.00000000e+00]])
```

Another non-square example, with \( m > n \):

```python
>>> c = b.T
>>> u, p = polar(c)
>>> u
array([[-0.21196618, 0.39378971],
       [-0.42393237, 0.78757942],
       [ 0.88054056, 0.4739708 ]])
```

```python
>>> p
array([[ 1.23116567, 1.93241587],
       [ 1.93241587, 4.84930602]])
```

```python
>>> u.dot(p)  # Verify the decomposition.
array([[ 0.5, 1.5],
       [ 1. , 3. ],
       [ 2. , 4. ]])
```

```python
>>> 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** *(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 \( \geq \) 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).
SciPy Reference Guide, Release 0.16.0

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'. $K = \min(M, N)$.
- **P** : int ndarray
  Of shape (N,) for pivoting=True. Not returned if pivoting=False.

**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))

>>> 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,))

>>> 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(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 $A = QR$ where Q is unitary/orthogonal and R upper triangular. Multiply Q with a vector or a matrix c.

**Parameters**

- **a**: array_like, shape (M, N)
  - Matrix to be decomposed
- **c**: array_like, one- or two-dimensional
  - Calculate the product of c and q, depending on the mode:
  - **mode**: {'left', 'right'}, optional
    - `dot(Q, c)` is returned if mode is 'left', `dot(c, 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**: float or complex ndarray
  - the product of Q and c, as defined in mode
- **R**: float or complex ndarray
  - Of shape (K, N), $K = \min(M, N)$.
- **P**: ndarray of ints
  - Of shape (N,) for pivoting=True. Not returned if pivoting=False.

**Raises**

- **LinAlgError**: Raised if decomposition fails

**Notes**

This is an interface to the LAPACK routines dgeqrf, zgeqrf, dormqr, zunmqr, dgeqp3, and zgeqp3.

New in version 0.11.0.

scipy.linalg.qr_update(Q, R, u, v, overwrite_qruv=False, check_finite=True)

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

**See also:**

qr, qr_multiply, qr_delete, qr_insert

**Notes**

This routine does not guarantee that the diagonal entries of \(R1\) are real or positive.

New in version 0.16.0.

**References**

[R96], [R97], [R98]

**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 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)
>>> q_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, -0.30466718, -0.27487277, -0.77079214, 0.0256951 ],
       [ 0.64888568, 0.23001 , -0.4859845 , 0.49883891, 0.20253783]])
```

```python
>>> r_up
array([[ 18.49324201, 24.11691794, -44.98940746],
       [ 0. , 31.95894662, -27.40998201],
       [ 0. , 0. , -9.25451794],
       [ 0. , 0. , 0. ],
       [ 0. , 0. , 0. ]])
```

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:
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)
>>> np.allclose(np.dot(qe_up, re_up), a_up)
True
>>> np.allclose(np.dot(qe_up.T, qe_up), np.eye(3))
True
```

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, u, v, False)
>>> np.allclose(a_up2, np.dot(q_up2, r_up2))
True
>>> np.allclose(np.dot(q_up2.T, q_up2), np.eye(5))
True
```

This update is also a valid qr decomposition of $A + U V^T$. 

```python
>>> a_up2 = a + np.dot(u2, v2.T)
>>> np.allclose(a_up2, np.dot(q_up2, r_up2))
True
>>> np.allclose(np.dot(q_up2.T, q_up2), np.eye(5))
True
```

```
scipy.linalg.qr_delete(Q, R, k, p=1, which='row', overwrite_qr=False, check_finite=True)
```
QR downdate on row or column deletions

If $A = QR$ is the QR factorization of $A$, return the QR factorization of $A$ where $p$ rows or columns have been removed starting at row or column $k$.

**Parameters**

- $Q$: (M, M) or (M, N) array_like
  
  Unitary/orthogonal matrix from QR decomposition.

- $R$: (M, N) or (N, N) array_like
  
  Upper triangular matrix from QR decomposition.

- $k$: int
  
  Index of the first row or column to delete.

- $p$: 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 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

**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**

[R90], [R91], [R92]

**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)
```

```python
>>> q1
array([[ 0.30942637, 0.15347579, 0.93845645],
       [ 0.61885275, 0.71680171, -0.32127338],
       [ 0.72199487, -0.68017681, -0.12681844]])
```

```python
>>> r1
array([[ 9.69535971, -0.4125685 , -6.80738023],
```
The update is equivalent, but faster than the following.

```python
>>> al = np.delete(a, slice(2,4), 0)
>>> al
array([[ 3., -2., -2.],
       [ 6., -9., -3.],
       [ 7., 8., -6.]])
```

```python
>>> q_direct, r_direct = linalg.qr(al)
```

Check that we have equivalent results:

```python
>>> np.dot(q1, r1)
array([[ 3., -2., -2.],
       [ 6., -9., -3.],
       [ 7., 8., -6.]])
```

```python
>>> np.allclose(np.dot(q1, r1), al)
True
```

And the updated Q is still unitary:

```python
>>> np.allclose(np.dot(q1.T, q1), np.eye(3))
True
```

scipy.linalg.qr_insert(Q, R, u, k, which='row', rcond=None, overwrite_qru=False, check_finite=True)

QR update on row or column insertions

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**

- \( Q_1 \): ndarray
  - Updated unitary/orthogonal factor
- \( R_1 \): 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 \( R1 \) are positive.
New in version 0.16.0.

References
[R93], [R94], [R95]

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.
```  
```
>>> u = np.array([[ 6., -9., -3.],
... [-3., 10., 1.]]
>>> q1, r1 = linalg.qr_insert(q, r, u, 2, 'row')
>>> 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])
>>> r1
array([-11.78986216, 6.44623587, 3.81685018],
      [-0. , -16.01393278, 3.72202865],
      [ 0. , -6.13010256, 0.16065817, -0.0063658 ],
      [ 0. , 0. , 0. , 0. ),
      [ 0. , 0. , 0. , 0. )])
The update is equivalent, but faster than the following.
```  
```
>>> 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:
```  
```
>>> np.dot(q1, r1)
array([[ 3., -2., -2.],
       [ 6., -7., 4.],
       [ 6., -9., -3.],
       [ 6., -7., 4.],
       [ 7., 8., -6.]])
```
[[-3., 10.,  1.],
 [ 7.,  8., -6.]]

```python
>>> 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(5))
True
```

**scipy.linalg.rq**

```
Compute RQ decomposition of a matrix.

Calculate the decomposition $A = R Q$ 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'}, 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).
- **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

- **R** : float or complex ndarray
  Of shape (M, N) or (M, K) for mode='economic'. K = min(M, N).
- **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, sorgrq, dorgrq, cungrq and zungrq.

If mode=economic, the shapes of Q and 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
>>> from numpy import random, dot, allclose

>>> a = random.randn(6, 9)
>>> r, q = linalg.rq(a)
>>> allclose(a, dot(r, q))
True

```

```python
>>> r.shape, q.shape
((6, 9), (9, 9))

```

```python
>>> r2 = linalg.rq(a, mode='r')
>>> allclose(r, r2)
True
```

```python
>>> r3, q3 = linalg.rq(a, mode='economic')
>>> r3.shape, q3.shape
((6, 6), (6, 9))
```
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
- output : {'real', 'complex'}, optional
  Construct the real or complex QZ decomposition for real matrices. Default is 'real'.
- 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, IT DOESN'T WORK WELL ON WINDOWS.
  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 \( x = (\text{alphar} + \text{alphai} \times 1j)/\text{beta} \). 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.
sdim : int, optional
If sorting was requested, a fifth return value will contain the number of eigenvalues for which the sort condition was True.

Notes
Q is transposed versus the equivalent function in Matlab.
New in version 0.11.0.

Examples
```python
c>>> from scipy import linalg
c>>> np.random.seed(1234)
c>>> A = np.arange(9).reshape((3,3))
c>>> B = np.random.randn(3,3)
c>>> AA, BB, Q, Z = linalg.qz(A, B)
c>>> AA
array([[-13.40928183, -4.62471562, 1.09215523],
       [ 0.00000000,  0.00000000,  1.22805978],
       [ 0.00000000,  0.00000000,  0.31973817]])
c>>> BB
array([[ 0.33362547, -1.37393632, 0.02179805],
       [ 0.00000000,  1.68144922, 0.74683866],
       [ 0.00000000,  0.00000000,  0.92582940]])
c>>> Q
array([[ 0.14134727, -0.97562773, 0.16784365],
       [ 0.49835904, -0.07636948, -0.86360059],
       [ 0.85537081,  0.20571399,  0.47541828]])
c>>> Z
array([[-0.24900855, -0.51772687, 0.81850696],
       [-0.79813178,  0.58842606, 0.12938478],
       [-0.54861681, -0.62105853, -0.55973739]])
```

```
scipy.linalg.schur(a, output=’real’, lwork=None, overwrite_a=False, sort=None, check_finite=True)

Compute Schur decomposition of a matrix.

The Schur decomposition is:

A = Z T Z^H

where Z is unitary and 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 \((x.\text{real} < 0.0)\)
- 'rhp' Right-hand plane \((x.\text{real} > 0.0)\)
- 'iuc' Inside the unit circle \((x*x.\text{conjugate()} \leq 1.0)\)
- 'ouc' Outside the unit circle \((x*x.\text{conjugate()} > 1.0)\)

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
- **scipy.linalg.rsf2csf** Convert real Schur form to complex Schur form.
  Convert a quasi-diagonal real-valued Schur form to the upper triangular complex-valued Schur form.

**Parameters**

- \(T\) : \((M, M)\) array_like
  Real Schur form of the original matrix
- \(Z\) : \((M, M)\) array_like
  Schur transformation 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**

- \(T\) : \((M, M)\) ndarray
  Complex Schur form of the original matrix
- \(Z\) : \((M, M)\) ndarray
  Schur transformation matrix corresponding to the complex form

**See also:**

- **schur** Schur decompose a matrix
`scipy.linalg.hessenberg(a, calc_q=False, overwrite_a=False, check_finite=True)`

Compute Hessenberg form of a matrix.

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 `calc_q=True`.

See also:

- `scipy.linalg.interpolative` – Interpolative matrix decompositions

### 5.9.4 Matrix Functions

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>expm(A[, q])</code></td>
<td>Compute the matrix exponential using Pade approximation.</td>
</tr>
<tr>
<td><code>logm(A[, disp])</code></td>
<td>Compute matrix logarithm.</td>
</tr>
<tr>
<td><code>cosm(A)</code></td>
<td>Compute the matrix cosine.</td>
</tr>
<tr>
<td><code>sinm(A)</code></td>
<td>Compute the matrix sine.</td>
</tr>
<tr>
<td><code>tanhm(A)</code></td>
<td>Compute the matrix tangent.</td>
</tr>
<tr>
<td><code>coshm(A)</code></td>
<td>Compute the hyperbolic matrix cosine.</td>
</tr>
<tr>
<td><code>sinhm(A)</code></td>
<td>Compute the hyperbolic matrix sine.</td>
</tr>
<tr>
<td><code>tanhm(A)</code></td>
<td>Compute the hyperbolic matrix tangent.</td>
</tr>
<tr>
<td><code>signm(A[, disp])</code></td>
<td>Matrix sign function.</td>
</tr>
<tr>
<td><code>sqrtm(A[, disp, blocksize])</code></td>
<td>Matrix square root.</td>
</tr>
<tr>
<td><code>funm(A, func[, disp])</code></td>
<td>Evaluate a matrix function specified by a callable.</td>
</tr>
<tr>
<td><code>expm_frechet(A, E[, method, compute_expm, ...])</code></td>
<td>Frechet derivative of the matrix exponential of A in the direction E.</td>
</tr>
<tr>
<td><code>expm_cond(A[, check_finite])</code></td>
<td>Relative condition number of the matrix exponential in the Frobenius norm.</td>
</tr>
<tr>
<td><code>fractional_matrix_power(A, t)</code></td>
<td>Compute the fractional power of a matrix.</td>
</tr>
</tbody>
</table>

### scipy.linalg.expm

`scipy.linalg.expm(A, q=None)`

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 \( A \).
References

[R75]

Examples

```python
>>> from scipy.linalg import expm, sinm, cosm
```

Matrix version of the formula exp(0) = 1:

```python
>>> expm(np.zeros((2,2))
array([[ 1., 0.],
       [ 0., 1.]])
```

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]])
>>> cosm(a) + 1j*sinm(a)
array([[ 0.42645930+1.89217551j, -2.13721484-0.97811252j],
       [ 1.06860742+0.48905626j, -1.71075555+0.91406299j]])
```

```python
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

References

[R83], [R84], [R85]

Examples

```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])
>>> expm(b)  # Verify expm(logm(a)) returns a
array([[ 1., 3.],
       [1., 4.]])
```

```python
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],
       [ 1.06835472+0.48905626j, -1.71075555+0.91406299j]])
```

```python
cosm(a) + 1j*sinm(a)
array([[ 0.42645930+1.89217551j, -2.13721484-0.97811252j],
       [ 1.06835472+0.48905626j, -1.71075555+0.91406299j]])
```

**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 cosine of $A$.

**Examples**

```python
from scipy.linalg import expm, sinm, cosm

cosm(a) + 1j*sinm(a)
```

**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**

```python
t = tanm(a)
t
```

5.9. Linear algebra (`scipy.linalg`)
array([[ -2.00876993, -8.41880636],
        [ -2.80626879, -10.42757629]])

Verify $\tan m(a) = \sin m(a) \cdot \text{inv}(\cos m(a))$

```python
>>> s = sinm(a)
>>> c = cosm(a)
>>> s.dot(np.linalg.inv(c))
array([[ -2.00876993, -8.41880636],
        [ -2.80626879, -10.42757629]])
```

**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**

```python
>>> 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 $\tan hm(a) = \sin hm(a) \cdot \text{inv}(\coshm(a))$

```python
>>> t = tanhm(a)
>>> s = sinhm(a)
>>> t - s.dot(np.linalg.inv(c))
array([[ 2.72004641e-15, 4.55191440e-15],
        [ 0.00000000e+00, -5.55111512e-16]])
```

**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**

- *sinhm* : (N, N) ndarray
  Hyperbolic matrix sine of *A*

**Examples**

```python
>>> from scipy.linalg import tanhm, sinhm, coshm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> s = sinhm(a)
>>> s
array([[ 10.57300653, 39.28826594],
        [ 13.09608865, 49.86127247]])

Verify $\tan hm(a) = \sin hm(a) \cdot \text{inv}(\coshm(a))$

```python
>>> t = tanhm(a)
>>> s = sinhm(a)
>>> t - s.dot(np.linalg.inv(c))
array([[ 2.72004641e-15, 4.55191440e-15],
        [ 0.00000000e+00, -5.55111512e-16]])
```
```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(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, sinhm, 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)))`

```python
>>> s = sinhm(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.signm(A, disp=True)**

Matrix sign function.

Extension of the scalar sign(x) to matrices.

**Parameters**

- `A` : (N, N) array_like
  Matrix at which to evaluate the sign function
- `disp` : bool, optional
  Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)

**Returns**

- `signm` : (N, N) ndarray
  Value of the sign function at A
- `errest` : float
  (if disp == False)
  1-norm of the estimated error, `||err||_1 / ||A||_1`

**Examples**

```python
>>> from scipy.linalg import signm, eigvals
>>> a = [[1,2,3], [1,2,1], [1,1,1]]
>>> eigvals(a)
array([ 4.12488542+0.j, -0.76155718+0.j,  0.63667176+0.j])
>>> eigvals(signm(a))
array([-1.+0.j,  1.+0.j,  1.+0.j])
```
scipy.linalg.sqrtm(A, disp=True, blocksize=64)

Matrix square root.

**Parameters**
- A : (N, N) array_like
  Matrix whose square root to evaluate
- disp : bool, optional
  Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)
- blocksize : integer, optional
  If the blocksize is not degenerate with respect to the size of the input array, then use a blocked algorithm. (Default: 64)

**Returns**
- 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**

[R101]

**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(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 (eg. 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 [R78]).

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
[R78]
```

```
Examples
```ipython
>>> 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.]])
```

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 [R76]. 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

[R76]

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))

>>> 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, 3:] = E; M[3:, 3:] = A
>>> expm_M = scipy.linalg.expm(M)
>>> np.allclose(expm_A, expm_M[:3, :3])
True
>>> np.allclose(expm_frechet_AE, expm_M[:3, 3:])
True
```

scipy.linalg.expm_cond(A, check_finite=True)

Relative condition number of the matrix exponential in the Frobenius norm.

**Parameters**

A : 2d array_like

Square input matrix with shape (N, N).

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.

scipy.linalg.fractional_matrix_power(A, t)

Compute the fractional power of a matrix.

Proceeds according to the discussion in section (6) of [R77].

**Parameters**

A : (N, N) array_like
Matrix whose fractional power to evaluate.

\[ t : \text{float} \]
Fractional power.

**Returns**

\[ X : (N, N) \text{array_like} \]
The fractional power of the matrix.

**References**

[R77]

**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.]])
```

### 5.9.5 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, r)`  Solves the continuous algebraic Riccati equation, or CARE, defined as (A'X + XA - XBR^-1B'X+Q=0) directly using a Schur decomposition method.

- `solve_discrete_are(a, b, q, r)`  Solves the discrete algebraic Riccati equation, or DARE, defined as (X = A'XA - (A'XB)(R+B'XB)^-1(B'XA)+Q), directly using a Schur decomposition method.

- `solve_discrete_lyapunov(a, q[, method])`  Solves the discrete Lyapunov equation (A'XA - X = -Q)

- `solve_lyapunov(a, q)`  Solves the continuous Lyapunov equation (AX + XA' = Q) given the values of A and Q using the Bartels-Stewart algorithm.

**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' = 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.

**scipy.linalg.solve_continuous_are**(a, b, q, r)  Solves the continuous algebraic Riccati equation, or CARE, defined as (A'X + XA - XBR^-1B'X+Q=0) directly.
using a Schur decomposition method.

**Parameters**
- **a**: (M, M) array_like
  
  Input
- **b**: (M, N) array_like
  
  Input
- **q**: (M, M) array_like
  
  Input
- **r**: (N, N) array_like
  
  Non-singular, square matrix

**Returns**
- **x**: (M, M) ndarray
  
  Solution to the continuous algebraic Riccati equation

See also:

**solve_discrete_are**

Solves the discrete algebraic Riccati equation

**Notes**


http://dspace.mit.edu/bitstream/handle/1721.1/1301/R-0859-05666488.pdf

New in version 0.11.0.

```python
scipy.linalg.solve_discrete_are(a, b, q, r)
```

Solves the discrete algebraic Riccati equation, or DARE, defined as 

\[ \begin{align*} 
X &= A'XA - (A'XB)(R + B'XB)^{-1}(B'XA) + Q 
\end{align*} \]

**Parameters**
- **a**: (M, M) array_like
  
  Non-singular, square matrix
- **b**: (M, N) array_like
  
  Input
- **q**: (M, M) array_like
  
  Input
- **r**: (N, N) array_like
  
  Non-singular, square matrix

**Returns**
- **x**: ndarray
  
  Solution to the continuous Lyapunov equation

See also:

**solve_continuous_are**

Solves the continuous algebraic Riccati equation

**Notes**


http://dspace.mit.edu/bitstream/handle/1721.1/1301/R-0859-05666488.pdf

New in version 0.11.0.

```python
scipy.linalg.solve_discrete_lyapunov(a, q, method=None)
```

Solves the discrete Lyapunov equation 

\[ \begin{align*} 
A'XA - X &= -Q 
\end{align*} \]

**Parameters**
- **a**: (M, M) array_like
  
  A square matrix
q : (M, M) array_like
    Right-hand side square matrix

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_lyapunov
    computes the solution to the continuous 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, [R99]. 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 $(B'X + XB = -C)$ 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 [R100].

New in version 0.11.0.

References
[R99], [R100]

scipy.linalg.solve_lyapunov(a, q)
Solves the continuous Lyapunov equation $(AX + XA^H = Q)$ given the values of A and Q using the Bartels-Stewart algorithm.

Parameters a : array_like
    A square matrix
q : array_like
    Right-hand side square matrix

Returns x : array_like
    Solution to the continuous Lyapunov equation

See also:

solve_sylvester
    computes the solution to the Sylvester equation

Notes
Because the continuous Lyapunov equation is just a special form of the Sylvester equation, this solver relies entirely on solve_sylvester for a solution.

New in version 0.11.0.

5.9.6 Special Matrices
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**

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) are ignored.

**Examples**

```python
>>> from scipy.linalg import block_diag
>>> A = [[1, 0],
...     [0, 1]]
>>> B = [[3, 4, 5],
...     [6, 7, 8]]
>>> C = [[7]]
>>> block_diag(A, B, C)
array([[1, 0, 0, 0, 0],
       [0, 1, 0, 0, 0],
       [0, 0, 3, 4, 5],
       [0, 0, 6, 7, 8],
       [0, 0, 0, 0, 7]])
```

```python
>>> block_diag(1.0, [2, 3], [[4, 5], [6, 7]])
array([[1., 0., 0., 0., 0.],
       [0., 2., 3., 0., 0.],
       [0., 0., 0., 4., 5.],
       [0., 0., 0., 6., 7.]])
```
**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

**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(a)**
Create a companion matrix.

Create the companion matrix [R73] 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**
[R73]

**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(n, scale=None)**
Discrete Fourier transform matrix.
Create the matrix that computes the discrete Fourier transform of a sequence [R74]. 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, ‘sqrt(n)’, or ‘n’. If `scale` is ‘sqrt(n)’, 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**

[R74]

**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**

Construct a Hadamard matrix.

**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]])
```

**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**(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, -0.81649658,   0. ,           0. ],
       [ 0.2236068 ,  0.2236068 ,  0.2236068 ,  0.2236068 , -0.89442719]])
```

**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**\((n, exact=False)\)

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]
4.2475099528537506e+19

>>> invhilbert(16, exact=True)[7,7]
4247509952853737856L
```

`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 [R81] [R82]. 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

[R81], [R82]

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. ]])
```
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.uint64` (if n < 35) or an object array of Python long 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 the values in the array will not be the exact coefficients, but this version is much faster than `exact=True`.

**Returns**

- **p**: (n, n) ndarray
  - The Pascal matrix.

**See also:**

- `invpascal`

**Notes**


New in version 0.11.0.

**Examples**

```python
>>> from scipy.linalg import pascal
>>> pascal(4)
dtype=uint64)
array([[ 1,  1,  1,  1],
       [ 1,  2,  3,  4],
       [ 1,  3,  6, 10],
       [ 1,  4, 10, 20]], dtype=uint64)
>>> pascal(4, kind='lower')
dtype=uint64)
array([[ 1,  0,  0,  0],
       [ 1,  1,  0,  0],
       [ 1,  2,  1,  0],
       [ 1,  3,  3,  1]], dtype=uint64)
```

```
>>> pascal(50)[-1, -1]
25477612258980856902730428600L
>>> from scipy.special import comb
>>> comb(98, 49, exact=True)
25477612258980856902730428600L
```

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 long 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**

[R79], [R80]

**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.,  1.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  1.,  0.],
       [ 0.,  0.,  0.,  0.,  1.]])
```

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**

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, `c == 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`, 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

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, 4, 5, 6],
       [2, 1, 4, 5],
       [3, 2, 1, 4]])
>>> 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\((N, M=None, k=0, dtype=None)\)
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

```python
>>> 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]])
```

5.9.7 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(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.

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} respectevely, and are stored in attribute typecode of the returned functions.

scipy.linalg.find_best_blas_type([arrays=(), dtype=None])
Find best-matching BLAS/LAPACK type.

5.9. Linear algebra (scipy.linalg) 477
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.

See also:
- `scipy.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

### 5.10 Low-level BLAS functions

This module contains low-level functions from the BLAS library.

New in version 0.12.0.

**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`.

### 5.11 Finding functions

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>get_blas_funcs(names[, arrays, dtype])</code></td>
<td>Return available BLAS function objects from names.</td>
</tr>
<tr>
<td><code>find_best_blas_type([arrays, dtype])</code></td>
<td>Find best-matching BLAS/LAPACK type.</td>
</tr>
</tbody>
</table>

**Scipy**

- **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.

```
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.
```

5.12 BLAS Level 1 functions

Continued on next page
### Table 5.75 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dzasum(x,[n,offx,incx])</td>
<td>Wrapper for dzasum.</td>
</tr>
<tr>
<td>dznrm2(x,[n,offx,incx])</td>
<td>Wrapper for dznrm2.</td>
</tr>
<tr>
<td>icamax(x,[n,offx,incx])</td>
<td>Wrapper for icamax.</td>
</tr>
<tr>
<td>idamax(x,[n,offx,incx])</td>
<td>Wrapper for idamax.</td>
</tr>
<tr>
<td>isamax(x,[n,offx,incx])</td>
<td>Wrapper for isamax.</td>
</tr>
<tr>
<td>izamax(x,[n,offx,incx])</td>
<td>Wrapper for izamax.</td>
</tr>
<tr>
<td>sasum(x,[n,offx,incx])</td>
<td>Wrapper for sasum.</td>
</tr>
<tr>
<td>saxpy(x,y,[n,a,offx,incx,offy,incy])</td>
<td>Wrapper for saxpy.</td>
</tr>
<tr>
<td>scasum(x,[n,offx,incx])</td>
<td>Wrapper for scasum.</td>
</tr>
<tr>
<td>scnrm2(x,[n,offx,incx])</td>
<td>Wrapper for scnrm2.</td>
</tr>
<tr>
<td>scopy(x,y,[n,offx,incx,offy,incy])</td>
<td>Wrapper for scopy.</td>
</tr>
<tr>
<td>sdot(x,y,[n,offx,incx,offy,incy])</td>
<td>Wrapper for sdot.</td>
</tr>
<tr>
<td>snrm2(x,[n,offx,incx])</td>
<td>Wrapper for snrm2.</td>
</tr>
<tr>
<td>srot(...)</td>
<td>Wrapper for srot.</td>
</tr>
<tr>
<td>srotg(a,b)</td>
<td>Wrapper for srotg.</td>
</tr>
<tr>
<td>srotm(...)</td>
<td>Wrapper for srotm.</td>
</tr>
<tr>
<td>srotmg(d1,d2,x1,y1)</td>
<td>Wrapper for srotmg.</td>
</tr>
<tr>
<td>sscal(a,x,[n,offx,incx])</td>
<td>Wrapper for sscal.</td>
</tr>
<tr>
<td>ssaxpy(x,y,[n,a,offx,incx,offy,incy])</td>
<td>Wrapper for ssaxpy.</td>
</tr>
<tr>
<td>zaxpy(x,y,[n,a,offx,incx,offy,incy])</td>
<td>Wrapper for zaxpy.</td>
</tr>
<tr>
<td>zcopy(x,y,[n,offx,incx,offy,incy])</td>
<td>Wrapper for zcopy.</td>
</tr>
<tr>
<td>zdotc(x,y,[n,offx,incx,offy,incy])</td>
<td>Wrapper for zdotc.</td>
</tr>
<tr>
<td>zdrot(...)</td>
<td>Wrapper for zdrot.</td>
</tr>
<tr>
<td>zdscal(a,x,[n,offx,incx,overwrite_x])</td>
<td>Wrapper for zdscal.</td>
</tr>
<tr>
<td>zrotg(a,b)</td>
<td>Wrapper for zrotg.</td>
</tr>
<tr>
<td>zswap(x,y,[n,offx,incx,offy,incy])</td>
<td>Wrapper for zswap.</td>
</tr>
</tbody>
</table>

```python
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`: rank-1 array('F') 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

```python
scipy.linalg.blas.ccopy (x, y[, n, offx, incx, offy, incy]) = <fortran object>
Wrapper for ccopy.
```

**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)
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.cdotc(x, y[, n, offx, incx, offy, incy]) = <fortran cdotc>
Wrapper for cdotc.

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.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(a, b) = <fortran crotg>
Wrapper for crotg.

Parameters
   a : input complex
   b : input complex

Returns
   c : complex
   s : complex
scipy.linalg.blas.cscal \((a, x[n, offx, incx]) = \text{<fortran object>}\)

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: \((\text{len}(x)) - \text{offx})/\text{abs}(\text{incx})\)
- \(offx\) : input int, optional
  - Default: 0
- \(incx\) : input int, optional
  - Default: 1

scipy.linalg.blas.csrot \((x, y, c[n, offx, incx, offy, incy, overwrite_x, overwrite_y]) = \text{<fortran object>}\)

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: \((\text{len}(x)) - 1 - \text{offx})/\text{abs}(\text{incx}) + 1\)
- \(overwrite_x\) : 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 \((a, x[n, offx, incx, overwrite_x]) = \text{<fortran object>}\)

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: \((\text{len}(x)) - \text{offx})/\text{abs}(\text{incx})\)
- \(overwrite_x\) : input int, optional
  - Default: 0
- \(offx\) : input int, optional
  - Default: 0
- \(incx\) : input int, optional
  - Default: 1
scipy.linalg.blas.cswap (x[, 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 : 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.dasum (x[, n, offx, 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: (len(x)-offx)/abs(incx)
    offx : input int, optional
        Default: 0
    incx : input int, optional
        Default: 1

scipy.linalg.blas.daxpy (x, y[, n, a, offx, incx, offy, 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: (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.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 (*)
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(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(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
\texttt{overwrite\_x} : input int, optional  
    Default: 0
\texttt{offx} : input int, optional  
    Default: 0
\texttt{incx} : input int, optional  
    Default: 1
\texttt{overwrite\_y} : input int, optional  
    Default: 0
\texttt{offy} : input int, optional  
    Default: 0
\texttt{incy} : input int, optional  
    Default: 1

\texttt{scipy.linalg.blas.drotg}(a, b) = <fortran object>  
Wrapper for \texttt{drotg}.

\textbf{Parameters}  
\texttt{a} : input float  
\texttt{b} : input float

\textbf{Returns}  
\texttt{c} : float  
\texttt{s} : float

\texttt{scipy.linalg.blas.drotm}(x, y, param[, n, offx, incx, offy, incy, overwrite\_x, overwrite\_y]) = <fortran object>  
Wrapper for \texttt{drotm}.

\textbf{Parameters}  
\texttt{x} : input rank-1 array(\texttt{d}) with bounds (*)  
\texttt{y} : input rank-1 array(\texttt{d}) with bounds (*)  
\texttt{param} : input rank-1 array(\texttt{d}) with bounds (5)

\textbf{Returns}  
\texttt{x} : rank-1 array(\texttt{d}) with bounds (*)  
\texttt{y} : rank-1 array(\texttt{d}) with bounds (*)

\textbf{Other Parameters}  
\texttt{n} : input int, optional  
    Default: (len(x)-offx)/abs(incx)
\texttt{overwrite\_x} : input int, optional  
    Default: 0
\texttt{offx} : input int, optional  
    Default: 0
\texttt{incx} : input int, optional  
    Default: 1
\texttt{overwrite\_y} : input int, optional  
    Default: 0
\texttt{offy} : input int, optional  
    Default: 0
\texttt{incy} : input int, optional  
    Default: 1

\texttt{scipy.linalg.blas.drotmg}(d1, d2, x1, y1) = <fortran object>  
Wrapper for \texttt{drotmg}.

\textbf{Parameters}  
\texttt{d1} : input float  
\texttt{d2} : input float  
\texttt{x1} : input float  
\texttt{y1} : input float

\textbf{Returns}  
\texttt{param} : rank-1 array(\texttt{d}) with bounds (5)

\texttt{scipy.linalg.blas.dscal}(a, x[, n, offx, incx]) = <fortran object>  
Wrapper for \texttt{dscal}.

5.12. BLAS Level 1 functions
**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 (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

`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

`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
scipy.linalg.blas.\texttt{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.\texttt{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.\texttt{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.\texttt{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

scipy.linalg.blas.\texttt{sasum}(x[, n, offx, incx]) = <fortran sasum>
Wrapper for sasum.

**Parameters**
- x : input rank-1 array(‘F’) with bounds (*)

**Returns**
- s : float

5.12. BLAS Level 1 functions
**SciPy Reference Guide, Release 0.16.0**

### scipy.linalg.blas.saxpy

```python
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

```python
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

```python
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)
- **offx**: input int, optional
  - Default: 0
- **incx**: input int, optional
  - Default: 1

### scipy.linalg.blas.scopy

```python
scipy.linalg.blas.scopy(x, y, [n, offx, incx, offy, incy]) = <fortran object>
```

**Wrapper for scopy.**

---

488 Chapter 5. Reference
**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)`
- `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.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)`
- `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.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

```python
scipy.linalg.blas.srot(x, y, c[, s, 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: \( (\text{len}(x) - \text{offx}) / \text{abs}(\text{incx}) + 1 \)
- **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

```python
scipy.linalg.blas.srotg(a, b) = <fortran object>
```
Wrapper for srotg.

**Parameters**
- **a**: input float
- **b**: input float

**Returns**
- **c**: float
- **s**: float

```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: \( (\text{len}(x) - \text{offx}) / \text{abs}(\text{incx}) \)
- **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

```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 (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 (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 (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 (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

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

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

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 of `D` with bounds (*)
- `y`: input rank-1 array of `D` with bounds (*)
- `c`: input float
- `s`: input float

**Returns**

- `x`: rank-1 array of `D` with bounds (*)
- `y`: rank-1 array of `D` with bounds (*)

**Other Parameters**

- `n`: input int, optional
- `overwrite_x`: input int, optional
- `offx`: input int, optional
- `incx`: input int, optional
- `overwrite_y`: input int, optional
- `offy`: input int, optional
- `incy`: input int, optional

```python
scipy.linalg.blas.zdscal(a, x[, n, offx, incx, overwrite_x]) = <fortran object>
```

Wrapper for `zdscal`.

**Parameters**

- `a`: input float
- `x`: input rank-1 array of `D` with bounds (*)

**Returns**

- `x`: rank-1 array of `D` with bounds (*)

**Other Parameters**

- `n`: input int, optional
- `overwrite_x`: input int, optional
- `offx`: input int, optional
- `incx`: input int, optional

```python
scipy.linalg.blas.zrotg(a, b) = <fortran object>
```

Wrapper for `zrotg`.

**Parameters**

- `a`: input complex
- `b`: input complex

**Returns**

- `c`: complex
- `s`: complex

```python
scipy.linalg.blas.zscal(a, x[, n, offx, incx]) = <fortran object>
```

Wrapper for `zscal`.

**Parameters**

- `a`: input complex
- `x`: input rank-1 array of `D` with bounds (*)

**Returns**

- `x`: rank-1 array of `D` with bounds (*)

**Other Parameters**

- `n`: input int, optional
- `offx`: input int, optional

5.12. BLAS Level 1 functions
The function `scipy.linalg.blas.zswap` wraps the zswap function.

**Parameters**
- `x`: input rank-1 array of `D` type with bounds (*)
- `y`: input rank-1 array of `D` type with bounds (*)

**Returns**
- `x`: rank-1 array of `D` type with bounds (*)
- `y`: rank-1 array of `D` type 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

### 5.13 BLAS Level 2 functions

- `cgemv(...)` Wrapper for `cgemv`
- `cgerc(...)` Wrapper for `cgerc`
- `cgeru(...)` Wrapper for `cgeru`
- `chemv(...)` Wrapper for `chemv`
- `ctrmv(...)` Wrapper for `ctrmv`
- `csyr(alpha,x,[lower,incx,offx,n,a,overwrite_a])` Wrapper for `csyr`
- `cher(alpha,x,[lower,incx,offx,n,a,overwrite_a])` Wrapper for `cher`
- `cher2(...)` Wrapper for `cher2`
- `dgemv(...)` Wrapper for `dgemv`
- `dger(...)` Wrapper for `dger`
- `dsymv(...)` Wrapper for `dsymv`
- `dtrmv(...)` Wrapper for `dtrmv`
- `dsyr(alpha,x,[lower,incx,offx,n,a,overwrite_a])` Wrapper for `dsyr`
- `dsyr2(...)` Wrapper for `dsyr2`
- `sgemv(...)` Wrapper for `sgemv`
- `sger(...)` Wrapper for `sger`
- `ssymv(...)` Wrapper for `ssymv`
- `strmv(...)` Wrapper for `strmv`
- `ssyr(alpha,x,[lower,incx,offx,n,a,overwrite_a])` Wrapper for `ssyr`
- `ssyr2(...)` Wrapper for `ssyr2`
- `zgemv(...)` Wrapper for `zgemv`
- `zgerc(...)` Wrapper for `zgerc`
- `zgeru(...)` Wrapper for `zgeru`
- `zhemv(...)` Wrapper for `zhemv`
- `ztrmv(...)` Wrapper for `ztrmv`
- `zsy2(alpha,x,[lower,incx,offx,n,a,overwrite_a])` Wrapper for `zsy2`

Continued on next page
Table 5.76 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>zher</td>
<td>Wrapper for zher.</td>
</tr>
<tr>
<td>zher2</td>
<td>Wrapper for zher2.</td>
</tr>
</tbody>
</table>

```python
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

```python
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
- `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
scipy.linalg.blas.cgeru(alpha, x, y[, incx, incy, a, overwrite_x, overwrite_y, overwrite_a]) = <fortran object>
```
Wrapper for cgeru.

5.13. BLAS Level 2 functions
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

```
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.ctrmv (a, x[, offx, incx, lower, trans, unitdiag, 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
SciPy Reference Guide, Release 0.16.0

lower : input int, optional
Default: 0
trans : input int, optional
Default: 0
unitdiag : input int, optional
Default: 0

scipy.linalg.blas.csyr (alpha, x[, lower, incx, offx, n, 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
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

scipy.linalg.blas.cher (alpha, x[, lower, incx, offx, n, 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

scipy.linalg.blas.cher2 (alpha, x, y[, lower, incx, offx, incy, offy, n, 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

5.13. BLAS Level 2 functions 497
Default: 1

\texttt{offx} : input int, optional
 Default: 0

\texttt{incy} : input int, optional
 Default: 1

\texttt{offy} : input int, optional
 Default: 0

\texttt{n} : input int, optional
 Default: 

\texttt{a} : input rank-2 array('F') with bounds (n,n)

\texttt{overwrite_a} : input int, optional
 Default: 0

\begin{verbatim}
scipy.linalg.blas.dgemv(alpha, a, x[, beta, y, offx, incx, offy, incy, trans, overwrite_y]) = <fortran object>
\end{verbatim}

Wrapper for dgemv.

**Parameters**

\texttt{alpha} : input float
 \texttt{a} : input rank-2 array('d') with bounds (m,n)
 \texttt{x} : input rank-1 array('d') with bounds (*)

**Returns**

\texttt{y} : rank-1 array('d') with bounds (ly)

**Other Parameters**

\texttt{beta} : input float, optional
 Default: 0.0

\texttt{y} : input rank-1 array('d') with bounds (ly)

\texttt{overwrite_y} : input int, optional
 Default: 0

\texttt{offx} : input int, optional
 Default: 0

\texttt{incx} : input int, optional
 Default: 1

\texttt{offy} : input int, optional
 Default: 0

\texttt{incy} : input int, optional
 Default: 0

\texttt{trans} : input int, optional
 Default: 0

scipy.linalg.blas.dger(alpha, x, y[, incx, incy, a, overwrite_x, overwrite_y, overwrite_a]) = <fortran object>

Wrapper for dger.

**Parameters**

\texttt{alpha} : input float
 \texttt{x} : input rank-1 array('d') with bounds (m)
 \texttt{y} : input rank-1 array('d') with bounds (n)

**Returns**

\texttt{a} : rank-2 array('d') with bounds (m,n)

**Other Parameters**

\texttt{overwrite_x} : input int, optional
 Default: 1

\texttt{incx} : input int, optional
 Default: 1

\texttt{overwrite_y} : input int, optional
 Default: 1

\texttt{incy} : input int, optional
 Default: 1
SciPy Reference Guide, Release 0.16.0

\begin{verbatim}
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: 0
- lower : input int, optional
  Default: 0

scipy.linalg.blas.dtrmv(a, x[, offx, incx, lower, trans, unitdiag, 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
- unitdiag : input int, optional
  Default: 0

scipy.linalg.blas.dsyx(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)
\end{verbatim}

5.13. BLAS Level 2 functions
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: \((\text{len}(x)-1-\text{offx})/\text{abs}(\text{incx})+1\)
- a : input rank-2 array(‘d’) with bounds (n,n)
- overwrite_a : input int, optional
  Default: 0

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: \((\text{len}(y)-1-\text{offy})/\text{abs}(\text{incy})+1\)
- a : input rank-2 array(‘d’) with bounds (n,n)
- overwrite_a : input int, optional
  Default: 0

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
scipy.linalg.blas.sger (alpha, x, y[, incx, incy, a, overwrite_x, overwrite_y, overwrite_a]) = <fortran object>
Wrapper for sger.

Parameters
- alpha : input float
- 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
- overwrite_a : input int, optional
  Default: 0

scipy.linalg.blas.ssymv (alpha, a, x[, beta, y, offx, incx, offy, incy, lower, overwrite_y]) = <fortran object>
Wrapper for ssymv.

Parameters
- alpha : input float
- 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
- 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.strmv (a, x[, offx, incx, lower, trans, unitdiag, overwrite_x]) = <fortran object>
Wrapper for strmv.

5.13. BLAS Level 2 functions
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

\(\text{overwrite}_x\) : input int, optional
  Default: 0
\(\text{offx}\) : input int, optional
  Default: 0
\(\text{incx}\) : input int, optional
  Default: 1
\(\text{lower}\) : input int, optional
  Default: 0
\(\text{trans}\) : input int, optional
  Default: 0
\(\text{unitdiag}\) : input int, optional
  Default: 0

```
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

\(\text{lower}\) : input int, optional
  Default: 0
\(\text{incx}\) : input int, optional
  Default: 1
\(\text{offx}\) : input int, optional
  Default: 0
\(\text{n}\) : input int, optional
  Default: (len(x)-1-offx)/abs(incx)+1
\(\text{a}\) : input rank-2 array('f') with bounds (n,n)
\(\text{overwrite}_a\) : input int, optional
  Default: 0

```
scipy.linalg.blas.ssyr2 (alpha, x[, 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

\(\text{lower}\) : input int, optional
  Default: 0
\(\text{incx}\) : 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
\(\text{n}\) : input int, optional
Default: \((\text{len}(x)-1-\text{offx})/\text{abs}(\text{incx})+1 \leq (\text{len}(y)-1-\text{offy})/\text{abs}(\text{incy})+1\)  
\(a\) : input rank-2 array('f') with bounds (n,n)  
\text{overwrite}_a\) : input int, optional  
Default: 0

\text{scipy.linalg.blas.\text{zgemv}}(\text{alpha}, a[, \text{beta}, y, \text{offx}, \text{incy}, \text{trans}, \text{overwrite}_y]) = \langle\text{fortran object}\rangle

Wrapper for \text{zgemv}.

\textbf{Parameters}  
\text{alpha} : input complex  
a : input rank-2 array('D') with bounds (m,n)  
x : input rank-1 array('D') with bounds (*)  
\text{Returns}  
y : rank-1 array('D') with bounds (ly)  
\text{Other Parameters}  
\text{beta} : input complex, optional  
Default: \((0.0, 0.0)\)  
y : input rank-1 array('D') with bounds (ly)  
\text{overwrite}_y\) : input int, optional  
Default: 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  
\text{trans} : input int, optional  
Default: 0

\text{scipy.linalg.blas.\text{zgerc}}(\text{alpha}, x[, \text{incx}, \text{incy}, a, \text{overwrite}_x, \text{overwrite}_y, \text{overwrite}_a]) = \langle\text{fortran object}\rangle

Wrapper for \text{zgerc}.

\textbf{Parameters}  
\text{alpha} : input complex  
x : input rank-1 array('D') with bounds (m)  
y : input rank-1 array('D') with bounds (n)  
\text{Returns}  
a : rank-2 array('D') with bounds (m,n)  
\text{Other Parameters}  
\text{overwrite}_x\) : input int, optional  
Default: 1  
\text{incx} : input int, optional  
Default: 1  
\text{overwrite}_y\) : input int, optional  
Default: 1  
\text{incy} : input int, optional  
Default: 1  
a : input rank-2 array('D') with bounds (m,n), optional  
Default: \((0.0,0.0,0.0)\)  
\text{overwrite}_a\) : input int, optional  
Default: 0

\text{scipy.linalg.blas.\text{zgeru}}(\text{alpha}, x[, \text{incx}, \text{incy}, a, \text{overwrite}_x, \text{overwrite}_y, \text{overwrite}_a]) = \langle\text{fortran object}\rangle

Wrapper for \text{zgeru}.

5.13. BLAS Level 2 functions 503
**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
- **incx**: 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

The function call is:

```python
scipy.linalg.blas.zhemv(alpha, a, x, beta, y, offx, incx, offy, incy, lower, overwrite_y)
```

This is a wrapper for the BLAS function `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
- **incx**: input int, optional
  - Default: 1
- **offy**: input int, optional
  - Default: 0
- **incy**: input int, optional
  - Default: 1
- **lower**: input int, optional
  - Default: 0

The function call is:

```python
scipy.linalg.blas.ztrmv(a, x, offx, incx, lower, trans, unitdiag, overwrite_x)
```

This is a wrapper for the BLAS function `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
unitdiag : input int, optional
  Default: 0

scipy.linalg.blas.zsyr (alpha, x[, lower, incx, offx, n, a, overwrite_a]) = <fortran object>
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

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
  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.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

5.13. BLAS Level 2 functions 505
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
```

### 5.14 BLAS Level 3 functions

#### cgemm

Wrapper for `cgemm`.

```
cgemm(...)  Wrapper for cgemm.
```

#### chemm

Wrapper for `chemm`.

```
chemm(alpha,a,b,[beta,c,side,lower,overwrite_c])  Wrapper for chemm.
```

#### cherk

Wrapper for `cherk`.

```
cherk(alpha,a,[beta,c,trans,lower,overwrite_c])  Wrapper for cherk.
```

#### cher2k

Wrapper for `cher2k`.

```
cher2k(...)  Wrapper for cher2k.
```

#### csymm

Wrapper for `csymm`.

```
csymm(alpha,a,b,[beta,c,side,lower,overwrite_c])  Wrapper for csymm.
```

#### csyrk

Wrapper for `csyrk`.

```
csyrk(alpha,a,[beta,c,trans,lower,overwrite_c])  Wrapper for csyrk.
```

#### csyr2k

Wrapper for `csyr2k`.

```
csyr2k(...)  Wrapper for csyr2k.
```

#### dgemm

Wrapper for `dgemm`.

```
dgemm(...)  Wrapper for dgemm.
```

#### dsymm

Wrapper for `dsymm`.

```
dsymm(alpha,a,b,[beta,c,side,lower,overwrite_c])  Wrapper for dsymm.
```

#### dsyrk

Wrapper for `dsyrk`.

```
dsyrk(alpha,a,[beta,c,trans,lower,overwrite_c])  Wrapper for dsyrk.
```

#### dsyr2k

Wrapper for `dsyr2k`.

```
dsyr2k(...)  Wrapper for dsyr2k.
```

#### sgemm

Wrapper for `sgemm`.

```
sgemm(...)  Wrapper for sgemm.
```

#### ssymm

Wrapper for `ssymm`.

```
ssymm(alpha,a,b,[beta,c,side,lower,overwrite_c])  Wrapper for ssymm.
```

#### ssyrk

Wrapper for `ssyrk`.

```
ssyrk(alpha,a,[beta,c,trans,lower,overwrite_c])  Wrapper for ssyrk.
```

#### ssyr2k

Wrapper for `ssyr2k`.

```
ssyr2k(...)  Wrapper for ssyr2k.
```

#### zgemm

Wrapper for `zgemm`.

```
zgemm(...)  Wrapper for zgemm.
```

#### zhemm

Wrapper for `zhemm`.

```
zhemm(alpha,a,b,[beta,c,side,lower,overwrite_c])  Wrapper for zhemm.
```

#### zherk

Wrapper for `zherk`.

```
zherk(alpha,a,[beta,c,trans,lower,overwrite_c])  Wrapper for zherk.
```

#### zher2k

Wrapper for `zher2k`.

```
zher2k(...)  Wrapper for zher2k.
```

#### zsymm

Wrapper for `zsymm`.

```
zsymm(alpha,a,b,[beta,c,side,lower,overwrite_c])  Wrapper for zsymm.
```

#### zsyrk

Wrapper for `zsyrk`.

```
zsyrk(alpha,a,[beta,c,trans,lower,overwrite_c])  Wrapper for zsyrk.
```

#### zsyr2k

Wrapper for `zsyr2k`.

```
zsyr2k(...)  Wrapper for zsyr2k.
```

```python
scipy.linalg.blas.cgemm(alpha, a, b[, 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)
- `c` : rank-2 array('F') with bounds (m,n)

**Returns**

**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
scipy.linalg.blas.

scipy.linalg.blas.

scipy.linalg.blas.

5.14. BLAS Level 3 functions
Default: 0

```
scipy.linalg.blas.csymm(alpha, a, b[, beta, c, side, lower, overwrite_c]) = <fortran object>
```

**Wrapper for csymm.**

**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.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.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**
- **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.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

```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)
- **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

```python
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

```python
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)
SciPy Reference Guide, Release 0.16.0

**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

```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

```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

```python
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
SciPy Reference Guide, Release 0.16.0

scipy.linalg.blas.ssyr2k (alpha, a[, 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.zgemm (alpha, a[, 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 (alpha, a[, 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
  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.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.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.zsymm(alpha, a, b[, beta, c, side, lower, overwrite_c]) = <fortran object>
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.zsyrk (alpha[, beta, c, trans, lower, overwrite_c]) = <fortran object>

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
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.zsyr2k (alpha, a[, b[, beta, c, trans, lower, overwrite_c]]) = <fortran object>

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

5.15 Low-level LAPACK functions

This module contains low-level functions from the LAPACK library.

New in version 0.12.0.

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.

5.16 Finding functions

get_lapack_funcs(names[, arrays, dtype]) Return available LAPACK function objects from names.

5.17 All functions

5.17. All functions
<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>sgbsv(kl,ku,ab,b,[overwrite_ab,overwrite_b])</td>
<td>Wrapper for sgbsv.</td>
</tr>
<tr>
<td>dgbsv(kl,ku,ab,b,[overwrite_ab,overwrite_b])</td>
<td>Wrapper for dgbsv.</td>
</tr>
<tr>
<td>cgbsv(kl,ku,ab,b,[overwrite_ab,overwrite_b])</td>
<td>Wrapper for cgbsv.</td>
</tr>
<tr>
<td>zgbsv(kl,ku,ab,b,[overwrite_ab,overwrite_b])</td>
<td>Wrapper for zgbsv.</td>
</tr>
<tr>
<td>sgbrtf(ab,kl,ku,[m,n,ldab,overwrite_ab])</td>
<td>Wrapper for sgbrtf.</td>
</tr>
<tr>
<td>dgbbrtf(ab,kl,ku,[m,n,ldab,overwrite_ab])</td>
<td>Wrapper for dgbbrtf.</td>
</tr>
<tr>
<td>cgbbrtf(ab,kl,ku,[m,n,ldab,overwrite_ab])</td>
<td>Wrapper for cgbbrtf.</td>
</tr>
<tr>
<td>zgbbrtf(ab,kl,ku,[m,n,ldab,overwrite_ab])</td>
<td>Wrapper for zgbbrtf.</td>
</tr>
<tr>
<td>sgbrts(…)</td>
<td>Wrapper for sgbrts.</td>
</tr>
<tr>
<td>dgbbrts(…)</td>
<td>Wrapper for dgbbrts.</td>
</tr>
<tr>
<td>cgbbrts(…)</td>
<td>Wrapper for cgbbrts.</td>
</tr>
<tr>
<td>zgbbrts(…)</td>
<td>Wrapper for zgbbrts.</td>
</tr>
<tr>
<td>sgeba1(a,[scale,permute,overwrite_a])</td>
<td>Wrapper for sgeba1.</td>
</tr>
<tr>
<td>dgeba1(a,[scale,permute,overwrite_a])</td>
<td>Wrapper for dgeba1.</td>
</tr>
<tr>
<td>cgeba1(a,[scale,permute,overwrite_a])</td>
<td>Wrapper for cgeba1.</td>
</tr>
<tr>
<td>zgeba1(a,[scale,permute,overwrite_a])</td>
<td>Wrapper for zgeba1.</td>
</tr>
<tr>
<td>sgees(…)</td>
<td>Wrapper for sgees.</td>
</tr>
<tr>
<td>dgees(…)</td>
<td>Wrapper for dgees.</td>
</tr>
<tr>
<td>cgees(…)</td>
<td>Wrapper for cgees.</td>
</tr>
<tr>
<td>zgees(…)</td>
<td>Wrapper for zgees.</td>
</tr>
<tr>
<td>sgeev(…)</td>
<td>Wrapper for sgeev.</td>
</tr>
<tr>
<td>dgeev(…)</td>
<td>Wrapper for dgeev.</td>
</tr>
<tr>
<td>cgeev(…)</td>
<td>Wrapper for cgeev.</td>
</tr>
<tr>
<td>zgeev(…)</td>
<td>Wrapper for zgeev.</td>
</tr>
<tr>
<td>sgeev_lwork(n,[compute_vl,compute_vr])</td>
<td>Wrapper for sgeev_lwork.</td>
</tr>
<tr>
<td>dgeev_lwork(n,[compute_vl,compute_vr])</td>
<td>Wrapper for dgeev_lwork.</td>
</tr>
<tr>
<td>cgeev_lwork(n,[compute_vl,compute_vr])</td>
<td>Wrapper for cgeev_lwork.</td>
</tr>
<tr>
<td>zgeev_lwork(n,[compute_vl,compute_vr])</td>
<td>Wrapper for zgeev_lwork.</td>
</tr>
<tr>
<td>sgegov(…)</td>
<td>Wrapper for sgegov.</td>
</tr>
<tr>
<td>dgegov(…)</td>
<td>Wrapper for dgegov.</td>
</tr>
<tr>
<td>cgegov(…)</td>
<td>Wrapper for cgegov.</td>
</tr>
<tr>
<td>zgegov(…)</td>
<td>Wrapper for zgegov.</td>
</tr>
<tr>
<td>sgehrd(a,[lo,hi,lwork,overwrite_a])</td>
<td>Wrapper for sgehrd.</td>
</tr>
<tr>
<td>dgehrd(a,[lo,hi,lwork,overwrite_a])</td>
<td>Wrapper for dgehrd.</td>
</tr>
<tr>
<td>cgehrd(a,[lo,hi,lwork,overwrite_a])</td>
<td>Wrapper for cgehrd.</td>
</tr>
<tr>
<td>zgehrd(a,[lo,hi,lwork,overwrite_a])</td>
<td>Wrapper for zgehrd.</td>
</tr>
<tr>
<td>sgehrd_lwork(n,[lo,hi])</td>
<td>Wrapper for sgehrd_lwork.</td>
</tr>
<tr>
<td>dgehrd_lwork(n,[lo,hi])</td>
<td>Wrapper for dgehrd_lwork.</td>
</tr>
<tr>
<td>cgehrd_lwork(n,[lo,hi])</td>
<td>Wrapper for cgehrd_lwork.</td>
</tr>
<tr>
<td>zgehrd_lwork(n,[lo,hi])</td>
<td>Wrapper for zgehrd_lwork.</td>
</tr>
<tr>
<td>sgelss(a,b,[cond,lwork,overwrite_a,overwrite_b])</td>
<td>Wrapper for sgelss.</td>
</tr>
<tr>
<td>dgelss(a,b,[cond,lwork,overwrite_a,overwrite_b])</td>
<td>Wrapper for dgelss.</td>
</tr>
<tr>
<td>cgelss(a,b,[cond,lwork,overwrite_a,overwrite_b])</td>
<td>Wrapper for cgelss.</td>
</tr>
<tr>
<td>zgelss(a,b,[cond,lwork,overwrite_a,overwrite_b])</td>
<td>Wrapper for zgelss.</td>
</tr>
<tr>
<td>sgelss_lwork(m,n,nrhs,[cond,lwork])</td>
<td>Wrapper for sgelss_lwork.</td>
</tr>
<tr>
<td>dgelss_lwork(m,n,nrhs,[cond,lwork])</td>
<td>Wrapper for dgelss_lwork.</td>
</tr>
<tr>
<td>cgelss_lwork(m,n,nrhs,[cond,lwork])</td>
<td>Wrapper for cgelss_lwork.</td>
</tr>
<tr>
<td>zgelss_lwork(m,n,nrhs,[cond,lwork])</td>
<td>Wrapper for zgelss_lwork.</td>
</tr>
<tr>
<td>sgelss_lwork(m,n,nrhs,[cond,lwork])</td>
<td>Wrapper for sgelss_lwork.</td>
</tr>
<tr>
<td>dgelss_lwork(m,n,nrhs,[cond,lwork])</td>
<td>Wrapper for dgelss_lwork.</td>
</tr>
<tr>
<td>cgelss_lwork(m,n,nrhs,[cond,lwork])</td>
<td>Wrapper for cgelss_lwork.</td>
</tr>
<tr>
<td>zgelss_lwork(m,n,nrhs,[cond,lwork])</td>
<td>Wrapper for zgelss_lwork.</td>
</tr>
<tr>
<td>sgelsd(…)</td>
<td>Wrapper for sgelsd.</td>
</tr>
<tr>
<td>dgelss(…)</td>
<td>Wrapper for dgelss.</td>
</tr>
<tr>
<td>Function</td>
<td>Description</td>
</tr>
<tr>
<td>----------</td>
<td>-------------</td>
</tr>
<tr>
<td>cgelsd(...)</td>
<td>Wrapper for cgelsd.</td>
</tr>
<tr>
<td>zgelsd(...)</td>
<td>Wrapper for zgelsd.</td>
</tr>
<tr>
<td>sgelsd_lwork(m,n,nrhs,[cond,lwork])</td>
<td>Wrapper for sgelsd_lwork.</td>
</tr>
<tr>
<td>dgelsd_lwork(m,n,nrhs,[cond,lwork])</td>
<td>Wrapper for dgelsd_lwork.</td>
</tr>
<tr>
<td>cgelsd_lwork(m,n,nrhs,[cond,lwork])</td>
<td>Wrapper for cgelsd_lwork.</td>
</tr>
<tr>
<td>zgelsd_lwork(m,n,nrhs,[cond,lwork])</td>
<td>Wrapper for zgelsd_lwork.</td>
</tr>
<tr>
<td>sgeqpf(...)</td>
<td>Wrapper for sgeqpf.</td>
</tr>
<tr>
<td>dgeqpf(...)</td>
<td>Wrapper for dgeqpf.</td>
</tr>
<tr>
<td>cgeqpf(...)</td>
<td>Wrapper for cgeqpf.</td>
</tr>
<tr>
<td>zgeqpf(...)</td>
<td>Wrapper for zgeqpf.</td>
</tr>
<tr>
<td>sgeqrf(...)</td>
<td>Wrapper for sgeqrf.</td>
</tr>
<tr>
<td>dgeqrf(...)</td>
<td>Wrapper for dgeqrf.</td>
</tr>
<tr>
<td>cgeqrf(...)</td>
<td>Wrapper for cgeqrf.</td>
</tr>
<tr>
<td>zgeqrf(...)</td>
<td>Wrapper for zgeqrf.</td>
</tr>
<tr>
<td>sgelsy(...)</td>
<td>Wrapper for sgelsy.</td>
</tr>
<tr>
<td>dgelsy(...)</td>
<td>Wrapper for dgelsy.</td>
</tr>
<tr>
<td>cgelsy(...)</td>
<td>Wrapper for cgelsy.</td>
</tr>
<tr>
<td>zgelsy(...)</td>
<td>Wrapper for zgelsy.</td>
</tr>
<tr>
<td>sgelsy_lwork(m,n,nrhs,cond,[lwork])</td>
<td>Wrapper for sgelsy_lwork.</td>
</tr>
<tr>
<td>dgelsy_lwork(m,n,nrhs,cond,[lwork])</td>
<td>Wrapper for dgelsy_lwork.</td>
</tr>
<tr>
<td>cgelsy_lwork(m,n,nrhs,cond,[lwork])</td>
<td>Wrapper for cgelsy_lwork.</td>
</tr>
<tr>
<td>zgelsy_lwork(m,n,nrhs,cond,[lwork])</td>
<td>Wrapper for zgelsy_lwork.</td>
</tr>
<tr>
<td>sgeqp3(a,[lwork,overwrite_a])</td>
<td>Wrapper for sgeqp3.</td>
</tr>
<tr>
<td>dgeqp3(a,[lwork,overwrite_a])</td>
<td>Wrapper for dgeqp3.</td>
</tr>
<tr>
<td>cgeqp3(a,[lwork,overwrite_a])</td>
<td>Wrapper for cgeqp3.</td>
</tr>
<tr>
<td>zgeqp3(a,[lwork,overwrite_a])</td>
<td>Wrapper for zgeqp3.</td>
</tr>
<tr>
<td>sgeqrf(...)</td>
<td>Wrapper for sgeqrf.</td>
</tr>
<tr>
<td>dgeqrf(...)</td>
<td>Wrapper for dgeqrf.</td>
</tr>
<tr>
<td>cgeqrf(...)</td>
<td>Wrapper for cgeqrf.</td>
</tr>
<tr>
<td>zgeqrf(...)</td>
<td>Wrapper for zgeqrf.</td>
</tr>
<tr>
<td>sgsvd(...)</td>
<td>Wrapper for sgsvd.</td>
</tr>
<tr>
<td>dgsvd(...)</td>
<td>Wrapper for dgsvd.</td>
</tr>
<tr>
<td>cgsvd(...)</td>
<td>Wrapper for cgsvd.</td>
</tr>
<tr>
<td>zgsvd(...)</td>
<td>Wrapper for zgsvd.</td>
</tr>
<tr>
<td>sgetrf(...)</td>
<td>Wrapper for sgetrf.</td>
</tr>
<tr>
<td>dgetrf(...)</td>
<td>Wrapper for dgetrf.</td>
</tr>
<tr>
<td>cgetrf(...)</td>
<td>Wrapper for cgetrf.</td>
</tr>
<tr>
<td>zgetrf(...)</td>
<td>Wrapper for zgetrf.</td>
</tr>
<tr>
<td>sgetri(...)</td>
<td>Wrapper for sgetri.</td>
</tr>
<tr>
<td>dgetri(...)</td>
<td>Wrapper for dgetri.</td>
</tr>
<tr>
<td>cgetri(...)</td>
<td>Wrapper for cgetri.</td>
</tr>
<tr>
<td>zgetri(...)</td>
<td>Wrapper for zgetri.</td>
</tr>
</tbody>
</table>
Table 5.79 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>sgetrs(lu,piv,b,[trans,overwrite_b])</td>
<td>Wrapper for sgetrs.</td>
</tr>
<tr>
<td>dgetrs(lu,piv,b,[trans,overwrite_b])</td>
<td>Wrapper for dgetrs.</td>
</tr>
<tr>
<td>cgetrs(lu,piv,b,[trans,overwrite_b])</td>
<td>Wrapper for cgetrs.</td>
</tr>
<tr>
<td>zgetrs(lu,piv,b,[trans,overwrite_b])</td>
<td>Wrapper for zgetrs.</td>
</tr>
<tr>
<td>sgges(...)</td>
<td>Wrapper for sgges.</td>
</tr>
<tr>
<td>dgges(...)</td>
<td>Wrapper for dgges.</td>
</tr>
<tr>
<td>cgges(...)</td>
<td>Wrapper for cgges.</td>
</tr>
<tr>
<td>zgges(...)</td>
<td>Wrapper for zgges.</td>
</tr>
<tr>
<td>sggev(...)</td>
<td>Wrapper for sggev.</td>
</tr>
<tr>
<td>dggev(...)</td>
<td>Wrapper for dggev.</td>
</tr>
<tr>
<td>cggev(...)</td>
<td>Wrapper for cggev.</td>
</tr>
<tr>
<td>zggev(...)</td>
<td>Wrapper for zggev.</td>
</tr>
<tr>
<td>chbevd(...)</td>
<td>Wrapper for chbevd.</td>
</tr>
<tr>
<td>zhbevd(...)</td>
<td>Wrapper for zhbevd.</td>
</tr>
<tr>
<td>cheev(a,[compute_v,lower,lwork,overwrite_a])</td>
<td>Wrapper for cheev.</td>
</tr>
<tr>
<td>zheev(a,[compute_v,lower,lwork,overwrite_a])</td>
<td>Wrapper for zheev.</td>
</tr>
<tr>
<td>cheevd(a,[compute_v,lower,lwork,overwrite_a])</td>
<td>Wrapper for cheevd.</td>
</tr>
<tr>
<td>zheevd(a,[compute_v,lower,lwork,overwrite_a])</td>
<td>Wrapper for zheevd.</td>
</tr>
<tr>
<td>cheevr(...)</td>
<td>Wrapper for cheevr.</td>
</tr>
<tr>
<td>zheevr(...)</td>
<td>Wrapper for zheevr.</td>
</tr>
<tr>
<td>chegv(...)</td>
<td>Wrapper for chegv.</td>
</tr>
<tr>
<td>zhegv(...)</td>
<td>Wrapper for zhegv.</td>
</tr>
<tr>
<td>chegvx(...)</td>
<td>Wrapper for chegvx.</td>
</tr>
<tr>
<td>zhegvx(...)</td>
<td>Wrapper for zhegvx.</td>
</tr>
<tr>
<td>slarf(v,tau,c,work,[side,incv,overwrite_c])</td>
<td>Wrapper for slarf.</td>
</tr>
<tr>
<td>dlarf(v,tau,c,work,[side,incv,overwrite_c])</td>
<td>Wrapper for dlarf.</td>
</tr>
<tr>
<td>clarf(v,tau,c,work,[side,incv,overwrite_c])</td>
<td>Wrapper for clarf.</td>
</tr>
<tr>
<td>zlarf(v,tau,c,work,[side,incv,overwrite_c])</td>
<td>Wrapper for zlarf.</td>
</tr>
<tr>
<td>slarfg(n,alpha,x,[incx,overwrite_x])</td>
<td>Wrapper for slarfg.</td>
</tr>
<tr>
<td>dlarfg(n,alpha,x,[incx,overwrite_x])</td>
<td>Wrapper for dlarfg.</td>
</tr>
<tr>
<td>clarfg(n,alpha,x,[incx,overwrite_x])</td>
<td>Wrapper for clarfg.</td>
</tr>
<tr>
<td>zlarfg(n,alpha,x,[incx,overwrite_x])</td>
<td>Wrapper for zlarfg.</td>
</tr>
<tr>
<td>slartg(f,g)</td>
<td>Wrapper for slartg.</td>
</tr>
<tr>
<td>dlartg(f,g)</td>
<td>Wrapper for dlartg.</td>
</tr>
<tr>
<td>clartg(f,g)</td>
<td>Wrapper for clartg.</td>
</tr>
<tr>
<td>zlartg(f,g)</td>
<td>Wrapper for zlartg.</td>
</tr>
<tr>
<td>dlassd(i,d,z,[rho])</td>
<td>Wrapper for dlassd.</td>
</tr>
<tr>
<td>slassd(i,d,z,[rho])</td>
<td>Wrapper for slassd.</td>
</tr>
<tr>
<td>slaswp(a,piv,[k1,k2,off,inc,overwrite_a])</td>
<td>Wrapper for slaswp.</td>
</tr>
<tr>
<td>dlaswp(a,piv,[k1,k2,off,inc,overwrite_a])</td>
<td>Wrapper for dlaswp.</td>
</tr>
<tr>
<td>claswp(a,piv,[k1,k2,off,inc,overwrite_a])</td>
<td>Wrapper for claswp.</td>
</tr>
<tr>
<td>zlaswp(a,piv,[k1,k2,off,inc,overwrite_a])</td>
<td>Wrapper for zlaswp.</td>
</tr>
<tr>
<td>slauum(c,[lower,overwrite_c])</td>
<td>Wrapper for slauum.</td>
</tr>
<tr>
<td>dlauum(c,[lower,overwrite_c])</td>
<td>Wrapper for dlauum.</td>
</tr>
<tr>
<td>clauum(c,[lower,overwrite_c])</td>
<td>Wrapper for clauum.</td>
</tr>
<tr>
<td>zlauum(c,[lower,overwrite_c])</td>
<td>Wrapper for zlauum.</td>
</tr>
</tbody>
</table>

Continued on next page
Table 5.79 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>spbsv</code></td>
<td>Wrapper for <code>spbsv</code>.</td>
</tr>
<tr>
<td><code>dpbsv</code></td>
<td>Wrapper for <code>dpbsv</code>.</td>
</tr>
<tr>
<td><code>cpbsv</code></td>
<td>Wrapper for <code>cpbsv</code>.</td>
</tr>
<tr>
<td><code>zpbsv</code></td>
<td>Wrapper for <code>zpbsv</code>.</td>
</tr>
<tr>
<td><code>spbtrf</code></td>
<td>Wrapper for <code>spbtrf</code>.</td>
</tr>
<tr>
<td><code>dpbtrf</code></td>
<td>Wrapper for <code>dpbtrf</code>.</td>
</tr>
<tr>
<td><code>cpbtrf</code></td>
<td>Wrapper for <code>cpbtrf</code>.</td>
</tr>
<tr>
<td><code>zpbtrf</code></td>
<td>Wrapper for <code>zpbtrf</code>.</td>
</tr>
<tr>
<td><code>spbtrs</code></td>
<td>Wrapper for <code>spbtrs</code>.</td>
</tr>
<tr>
<td><code>dpbtrs</code></td>
<td>Wrapper for <code>dpbtrs</code>.</td>
</tr>
<tr>
<td><code>cpbtrs</code></td>
<td>Wrapper for <code>cpbtrs</code>.</td>
</tr>
<tr>
<td><code>zpbtrs</code></td>
<td>Wrapper for <code>zpbtrs</code>.</td>
</tr>
<tr>
<td><code>sposv</code></td>
<td>Wrapper for <code>sposv</code>.</td>
</tr>
<tr>
<td><code>dposv</code></td>
<td>Wrapper for <code>dposv</code>.</td>
</tr>
<tr>
<td><code>cposv</code></td>
<td>Wrapper for <code>cposv</code>.</td>
</tr>
<tr>
<td><code>zposv</code></td>
<td>Wrapper for <code>zposv</code>.</td>
</tr>
<tr>
<td><code>spotrf</code></td>
<td>Wrapper for <code>spotrf</code>.</td>
</tr>
<tr>
<td><code>dpotrf</code></td>
<td>Wrapper for <code>dpotrf</code>.</td>
</tr>
<tr>
<td><code>cpotrf</code></td>
<td>Wrapper for <code>cpotrf</code>.</td>
</tr>
<tr>
<td><code>zpotrf</code></td>
<td>Wrapper for <code>zpotrf</code>.</td>
</tr>
<tr>
<td><code>spotri</code></td>
<td>Wrapper for <code>spotri</code>.</td>
</tr>
<tr>
<td><code>dpotri</code></td>
<td>Wrapper for <code>dpotri</code>.</td>
</tr>
<tr>
<td><code>cpotri</code></td>
<td>Wrapper for <code>cpotri</code>.</td>
</tr>
<tr>
<td><code>zpotri</code></td>
<td>Wrapper for <code>zpotri</code>.</td>
</tr>
<tr>
<td><code>spotrs</code></td>
<td>Wrapper for <code>spotrs</code>.</td>
</tr>
<tr>
<td><code>dpotrs</code></td>
<td>Wrapper for <code>dpotrs</code>.</td>
</tr>
<tr>
<td><code>cpotrs</code></td>
<td>Wrapper for <code>cpotrs</code>.</td>
</tr>
<tr>
<td><code>zpotrs</code></td>
<td>Wrapper for <code>zpotrs</code>.</td>
</tr>
<tr>
<td><code>crot</code></td>
<td>Wrapper for <code>crot</code>.</td>
</tr>
<tr>
<td><code>zrot</code></td>
<td>Wrapper for <code>zrot</code>.</td>
</tr>
<tr>
<td><code>strsyl</code></td>
<td>Wrapper for <code>strsyl</code>.</td>
</tr>
<tr>
<td><code>dtrsyi</code></td>
<td>Wrapper for <code>dtrsyi</code>.</td>
</tr>
<tr>
<td><code>ctrsyi</code></td>
<td>Wrapper for <code>ctrsyi</code>.</td>
</tr>
<tr>
<td><code>ztrsyi</code></td>
<td>Wrapper for <code>ztrsyi</code>.</td>
</tr>
<tr>
<td><code>strtri</code></td>
<td>Wrapper for <code>strtri</code>.</td>
</tr>
<tr>
<td><code>dtrtri</code></td>
<td>Wrapper for <code>dtrtri</code>.</td>
</tr>
<tr>
<td><code>ctrtri</code></td>
<td>Wrapper for <code>ctrtri</code>.</td>
</tr>
<tr>
<td><code>ztrtri</code></td>
<td>Wrapper for <code>ztrtri</code>.</td>
</tr>
<tr>
<td><code>strtrs</code></td>
<td>Wrapper for <code>strtrs</code>.</td>
</tr>
<tr>
<td><code>dtrtrs</code></td>
<td>Wrapper for <code>dtrtrs</code>.</td>
</tr>
<tr>
<td><code>ctrtrs</code></td>
<td>Wrapper for <code>ctrtrs</code>.</td>
</tr>
<tr>
<td><code>ztrtrs</code></td>
<td>Wrapper for <code>ztrtrs</code>.</td>
</tr>
</tbody>
</table>
Table 5.79 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>sgtsv(...)</td>
<td>Wrapper for sgtsv.</td>
</tr>
<tr>
<td>dgtsv(...)</td>
<td>Wrapper for dgtsv.</td>
</tr>
<tr>
<td>cgtsv(...)</td>
<td>Wrapper for cgtsv.</td>
</tr>
<tr>
<td>zgtsv(...)</td>
<td>Wrapper for zgtsv.</td>
</tr>
<tr>
<td>sptsv(...)</td>
<td>Wrapper for sptsv.</td>
</tr>
<tr>
<td>dptsv(...)</td>
<td>Wrapper for dptsv.</td>
</tr>
<tr>
<td>cptsv(...)</td>
<td>Wrapper for cptsv.</td>
</tr>
<tr>
<td>zptsv(...)</td>
<td>Wrapper for zptsv.</td>
</tr>
<tr>
<td>slamch(cmach)</td>
<td>Wrapper for slamch.</td>
</tr>
<tr>
<td>dlamch(cmach)</td>
<td>Wrapper for dlamch.</td>
</tr>
<tr>
<td>sorghr(a,tau,[lo,hi,lwork,overwrite_a])</td>
<td>Wrapper for sorghr.</td>
</tr>
<tr>
<td>dorghr(a,tau,[lo,hi,lwork,overwrite_a])</td>
<td>Wrapper for dorghr.</td>
</tr>
<tr>
<td>sorgqr(a,tau,[lwork,overwrite_a])</td>
<td>Wrapper for sorgqr.</td>
</tr>
<tr>
<td>dorgqr(a,tau,[lwork,overwrite_a])</td>
<td>Wrapper for dorgqr.</td>
</tr>
<tr>
<td>slange(norm,a)</td>
<td>Wrapper for slange.</td>
</tr>
<tr>
<td>dlange(norm,a)</td>
<td>Wrapper for dlange.</td>
</tr>
<tr>
<td>clange(norm,a)</td>
<td>Wrapper for clange.</td>
</tr>
<tr>
<td>zlange(norm,a)</td>
<td>Wrapper for zlange.</td>
</tr>
</tbody>
</table>

```
sctsv(...)  Wrapper for sctsv.
dtstsv(...)  Wrapper for dtstsv.
cctsv(...)  Wrapper for cctsv.
zctsv(...)  Wrapper for zctsv.
sptstsv(...)  Wrapper for sptstsv.
dptstsv(...)  Wrapper for dptstsv.
cptstsv(...)  Wrapper for cptstsv.
zptstsv(...)  Wrapper for zptstsv.
slamch(cmach)  Wrapper for slamch.
dlamch(cmach)  Wrapper for dlamch.
sorghr(a,tau,[lo,hi,lwork,overwrite_a])  Wrapper for sorghr.
dorghr(a,tau,[lo,hi,lwork,overwrite_a])  Wrapper for dorghr.
sorgqr(a,tau,[lwork,overwrite_a])  Wrapper for sorgqr.
dorgqr(a,tau,[lwork,overwrite_a])  Wrapper for dorgqr.
sorgqr(...)  Wrapper for sorgqr.
dorgqr(...)  Wrapper for dorgqr.
sorgqr(...)  Wrapper for sorgqr.
dorgqr(...)  Wrapper for dorgqr.
sormqr(...)  Wrapper for sormqr.
dormqr(...)  Wrapper for dormqr.
ssbev(ab,[compute_v,lower,ldab,overwrite_ab])  Wrapper for ssbev.
dsbev(ab,[compute_v,lower,ldab,overwrite_ab])  Wrapper for dsbev.
ssbev(...)  Wrapper for ssbev.
ssbev(...)  Wrapper for ssbev.
ssbev(...)  Wrapper for ssbev.
ssbev(...)  Wrapper for ssbev.
ssbev(...)  Wrapper for ssbev.
ssyev(...)  Wrapper for ssyev.
ssyev(...)  Wrapper for ssyev.
ssyev(...)  Wrapper for ssyev.
ssyev(...)  Wrapper for ssyev.
ssyev(...)  Wrapper for ssyev.
ssyev(...)  Wrapper for ssyev.
ssyev(...)  Wrapper for ssyev.
slange(norm,a)  Wrapper for slange.
dlange(norm,a)  Wrapper for dlange.
clange(norm,a)  Wrapper for clange.
zlange(norm,a)  Wrapper for zlange.
```

scipy.linalg.lapack. **sgbsv** (kl, ku, ab[, overwrite_ab, overwrite_b]) = <fortran object>

**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 (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 (kl, ku, ab[, overwrite_ab, overwrite_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 (kl, ku, ab[, overwrite_ab, overwrite_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(ab, kl, ku[, m, n, ldab, overwrite_ab]) = <fortran object>
Wrapper for sgbtrf.

Parameters

- **ab**: input rank-2 array('f') with bounds (ldab,*)
- **kl**: input int
- **ku**: input int

Returns

- **lu**: rank-2 array('f') with bounds (ldab,*) 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: shape(ab,0)

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,*)
- **kl**: input int
- **ku**: input int

Returns

- **lu**: rank-2 array('d') with bounds (ldab,*) 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: shape(ab,0)

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,*)
- **kl**: input int
- **ku**: input int

Returns

- **lu**: rank-2 array('F') with bounds (ldab,*) 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: shape(ab,0)
scipy.linalg.lapack.

\texttt{zgbtrf}(ab, kl, ku[, m, n, ldab, overwrite\_ab]) = \texttt{<fortran object>}

Wrapper for \texttt{zgbtrf}.

**Parameters**

- \texttt{ab} : input rank-2 array('D') with bounds (ldab,*)
- \texttt{kl} : input int
- \texttt{ku} : input int

**Returns**

- \texttt{lu} : rank-2 array('D') with bounds (ldab,*) and ab storage
- \texttt{ipiv} : rank-1 array('i') with bounds (MIN(m,n))
- \texttt{info} : int

**Other Parameters**

- \texttt{m} : input int, optional
- Default: shape(ab,1)
- \texttt{n} : input int, optional
- Default: shape(ab,1)
- \texttt{overwrite\_ab} : input int, optional
- Default: 0
- \texttt{ldab} : input int, optional
- Default: shape(ab,0)

scipy.linalg.lapack.

\texttt{sgbtrs}(ab, kl, ku, b, ipiv[, trans, n, ldab, ldb, overwrite\_b]) = \texttt{<fortran object>}

Wrapper for \texttt{sgbtrs}.

**Parameters**

- \texttt{ab} : input rank-2 array('f') with bounds (ldab,*)
- \texttt{kl} : input int
- \texttt{ku} : input int
- \texttt{b} : input rank-2 array('f') with bounds (ldb,*)
- \texttt{ipiv} : input rank-1 array('i') with bounds (n)

**Returns**

- \texttt{x} : rank-2 array('f') with bounds (ldb,*) and b storage
- \texttt{info} : int

**Other Parameters**

- \texttt{overwrite\_b} : input int, optional
- Default: 0
- \texttt{trans} : input int, optional
- Default: 0
- \texttt{n} : input int, optional
- Default: shape(ab,1)
- \texttt{ldab} : input int, optional
- Default: shape(ab,0)
- \texttt{ldb} : input int, optional
- Default: shape(b,0)

scipy.linalg.lapack.

\texttt{dgbtrs}(ab, kl, ku, b, ipiv[, trans, n, ldab, ldb, overwrite\_b]) = \texttt{<fortran object>}

Wrapper for \texttt{dgbtrs}.

**Parameters**

- \texttt{ab} : input rank-2 array('d') with bounds (ldab,*)
- \texttt{kl} : input int
- \texttt{ku} : input int
- \texttt{b} : input rank-2 array('d') with bounds (ldb,*)
- \texttt{ipiv} : input rank-1 array('i') with bounds (n)

**Returns**

- \texttt{x} : rank-2 array('d') with bounds (ldb,*) and b storage
- \texttt{info} : int

**Other Parameters**

- \texttt{overwrite\_b} : input int, optional
- Default: 0
- \texttt{trans} : input int, optional

5.17. All functions
SciPy Reference Guide, Release 0.16.0

```python
def 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,*)
- **kl**: input int
- **ku**: input int
- **b**: input rank-2 array('F') with bounds (ldb,*)
- **ipiv**: input rank-1 array('i') with bounds (n)

Returns
- **x**: rank-2 array('F') with bounds (ldb,*) 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)
```

```python
def zgbtrs(ab, kl, ku, b, ipiv[, trans, n, ldab, ldb, overwrite_b]) = <fortran object>
Wrapper for zgbtrs.

Parameters
- **ab**: input rank-2 array('D') with bounds (ldab,*)
- **kl**: input int
- **ku**: input int
- **b**: input rank-2 array('D') with bounds (ldb,*)
- **ipiv**: input rank-1 array('i') with bounds (n)

Returns
- **x**: rank-2 array('D') with bounds (ldb,*) 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)
```

```python
def sgebal(a[, scale, permute, overwrite_a]) = <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(a, scale, permute, overwrite_a) = <fortran object>
```

Wrapper for dgebal.

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.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(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

5.17. All functions
**Other Parameters**

- **scale**: input int, optional
  - Default: 0
- **permute**: input int, optional
  - Default: 0
- **overwrite_a**: input int, optional
  - Default: 0

```python
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: 3*n

**Notes**

Call-back functions:

```python
def sselect(arg1, arg2):
    return sselect
```

Required arguments:
- **arg1**: input float
- **arg2**: input float

Return objects:
- **sselect**: int

```python
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: 3*n

Notes

Call-back functions:

```python
def dselect(arg1, arg2): return dselect
```

Required arguments:
- `arg1`: input float
- `arg2`: input float

Return objects:
- `dselect`: int

Python function:

```python
scipy.linalg.lapack.cgees(cselect, a[, compute_v, sort_t, lwork, cselect_extra_args, overwrite_a]) = <fortran object>
```

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: 3*n

Notes

Call-back functions:

```python
def cselect(arg): return cselect
```

Required arguments:
- `arg`: input complex

Return objects:
- `cselect`: int
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: 3*n

**Notes**

Call-back functions:

def zselect(arg): return zselect

Required arguments:
- arg : input complex

Return objects:
- zselect : int

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**

- **wr**: rank-1 array('f') with bounds (n)
- **wi**: 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
- **lwork**: input int, optional
  Default: 4*n

scipy.linalg.lapack.dgeev (a[, compute_vl, compute_vr, lwork, overwrite_a]) = <fortran object>

Wrapper for dgeev.

**Parameters**

- **a**: input rank-2 array('d') with bounds (n,n)
Returns

- \( wr \) : rank-1 array('d') with bounds (n)
- \( wi \) : 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
- \( lwork \) : input int, optional
  Default: 4*n

```
scipy.linalg.lapack.cgeev(a[, compute_vl, compute_vr, lwork, overwrite_a]) = <fortran object>
```

Wrapper for cgeev.

Parameters

- \( a \) : input rank-2 array('F') with bounds (n,n)

Returns

- \( w \) : 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
- \( lwork \) : input int, optional
  Default: 2*n

```
scipy.linalg.lapack.zgeev(a[, compute_vl, compute_vr, lwork, overwrite_a]) = <fortran object>
```

Wrapper for zgeev.

Parameters

- \( a \) : input rank-2 array('D') with bounds (n,n)

Returns

- \( w \) : 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
- \( lwork \) : input int, optional
  Default: 2*n

```
scipy.linalg.lapack.sgeev_lwork(n[, compute_vl, compute_vr]) = <fortran object>
```

Wrapper for sgeev_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

```python
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

```python
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

```python
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

```python
scipy.linalg.lapack.sgegv(a, b[, compute_vl, compute_vr, lwork, overwrite_a, overwrite_b]) = <fortran object>
```
Wrapper for `sg eigv`.

**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
SciPy Reference Guide, Release 0.16.0

.. _dgegv:

.. code-block::

   scipy.linalg.lapack.dgegv(a, b[, compute_vl, compute_vr, lwork, overwrite_a, overwrite_b]) =
   <fortran object>

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: 8*n

.. _cgegv:

.. code-block::

   scipy.linalg.lapack.cgegv(a, b[, compute_vl, compute_vr, lwork, overwrite_a, overwrite_b]) =
   <fortran object>

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: 2*n

5.17. All functions 529
scipy.linalg.lapack.zgegv\( (a, b[, compute_vl, compute_vr, lwork, overwrite_a, overwrite_b]) \) =
<fortran object>

Wrapper for zgegv.

**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)
- \( \text{info} \) : int

**Other Parameters**
- \( \text{compute_vl} \) : input int, optional
  Default: 1
- \( \text{compute_vr} \) : input int, optional
  Default: 1
- \( \text{overwrite_a} \) : input int, optional
  Default: 0
- \( \text{overwrite_b} \) : input int, optional
  Default: 0
- \( \text{lwork} \) : input int, optional
  Default: 2*n

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**
- \( h \) : rank-2 array('f') with bounds (n,n) and a storage
- \( \tau \) : rank-1 array('f') with bounds (n - 1)
- \( \text{info} \) : int

**Other Parameters**
- \( \text{lo} \) : input int, optional
  Default: 0
- \( \text{hi} \) : input int, optional
  Default: n-1
- \( \text{overwrite_a} \) : input int, optional
  Default: 0
- \( \text{lwork} \) : input int, optional
  Default: MAX(n,1)

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**
- \( h \) : rank-2 array('d') with bounds (n,n) and a storage
- \( \tau \) : rank-1 array('d') with bounds (n - 1)
- \( \text{info} \) : int

**Other Parameters**
- \( \text{lo} \) : input int, optional
  Default: 0
- \( \text{hi} \) : input int, optional
  Default: n-1
- \( \text{overwrite_a} \) : input int, optional
  Default: 0
- \( \text{lwork} \) : input int, optional
  Default: MAX(n,1)
scipy.linalg.lapack.cgehrd(a[, lo, hi, lwork, overwrite_a]) = <fortran object>
Wrapper for cgehrd.

Parameters
- a : input rank-2 array('F') with bounds (n,n)

Returns
- h : 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(a[, lo, hi, lwork, overwrite_a]) = <fortran object>
Wrapper for zgehrd.

Parameters
- a : input rank-2 array('D') with bounds (n,n)

Returns
- h : 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)

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(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(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(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(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: 3*minmn+MAX(2*minmn,MAX(maxmn,nrhs))

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)
  rank : int
  work : rank-1 array('d') with bounds (MAX(lwork,1))
  info : int
SciPy Reference Guide, Release 0.16.0

5.17. All functions

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: 3*minmn+MAX(2*minmn,MAX(maxmn,nrhs))

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: 2*minmn+MAX(maxmn,nrhs)

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: 2*minmn+MAX(maxmn,nrhs)

scipy.linalg.lapack.sgelss_lwork (m, n, nrhs[, cond, lwork]) = <fortran object>
Wrapper for sgelss_lwork.
\begin{verbatim}
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(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(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(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(a, b, lwork, size_iwork[, cond, overwrite_a, overwrite_b]) = <fortran object>
Wrapper for sgelsd.
\end{verbatim}
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(a, b, lwork, size_iwork[, cond, overwrite_a, overwrite_b]) = <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(a, b, lwork, size_iwork[, cond, overwrite_a, overwrite_b]) = <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 Reference Guide, Release 0.16.0

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)
- **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.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(m, n, nrhs[, cond, lwork]) = <fortran object>

Wrapper for dgelsd_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.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(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(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(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
**SciPy Reference Guide, Release 0.16.0**

**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(a, b, jptv, cond, lwork[[], overwrite_a, overwrite_b]) = <fortran object>

Wrapper for cgelsy.

**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.zgelsy(a, b, jptv, cond, lwork[[], overwrite_a, overwrite_b]) = <fortran object>

Wrapper for zgelsy.

**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.sgelss_lwork(m, n, nrhs, cond[, lwork]) = <fortran object>

Wrapper for sgelss_lwork.

**Parameters**
- `m`: input int
- `n`: input int
- `nrhs`: input int
```
cond : input float

Returns
  work : float
  info : int

Other Parameters
  lwork : input int, optional
          Default: -1

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
  work : float
  info : int

Other Parameters
  lwork : input int, optional
          Default: -1

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
  work : complex
  info : int

Other Parameters
  lwork : input int, optional
          Default: -1

scipy.linalg.lapack.zgelsy_lwork(m, n, nrhs, cond[, lwork]) = <fortran object>
Wrapper for zgelsy_lwork.

Parameters
  m : input int
  n : input int
  nrhs : input int
  cond : input float

Returns
  work : complex
  info : int

Other Parameters
  lwork : input int, optional
          Default: -1

scipy.linalg.lapack.sgeqp3(a[, lwork, overwrite_a]) = <fortran object>
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: 3*(n+1)

scipy.linalg.lapack.dgeqp3 (a[, lwork, overwrite_a]) = <fortran object>
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: 3*(n+1)

scipy.linalg.lapack.cgeqp3 (a[, lwork, overwrite_a]) = <fortran object>
Wrapper for cgeqp3.

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: 3*(n+1)

scipy.linalg.lapack.zgeqp3 (a[, lwork, overwrite_a]) = <fortran object>
Wrapper for zgeqp3.

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: 3*(n+1)

scipy.linalg.lapack.sgeqrf (a[, lwork, overwrite_a]) = <fortran object>
Wrapper for sgeqrf.

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
**SciPy Reference Guide, Release 0.16.0**

Default: 0

**lwork** : input int, optional
Default: 3*n

```python
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: 3*n

```python
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: 3*n

```python
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: 3*n

```python
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: 3*n

5.17. All functions 541
Default: 3*m

\texttt{scipy.linalg.lapack.dgerqf}(a[, lwork, overwrite_a]) = <fortran object>

Wrapper for \texttt{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 (\text{MIN}(m,n))
- \(work\) : rank-1 array(‘d’) with bounds (\text{MAX}(lwork,1))
- \(info\) : int

**Other Parameters**
- \(overwrite_a\) : input int, optional
  Default: 0
- \(lwork\) : input int, optional
  Default: 3*m

\texttt{scipy.linalg.lapack.cgerqf}(a[, lwork, overwrite_a]) = <fortran object>

Wrapper for \texttt{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 (\text{MIN}(m,n))
- \(work\) : rank-1 array(‘F’) with bounds (\text{MAX}(lwork,1))
- \(info\) : int

**Other Parameters**
- \(overwrite_a\) : input int, optional
  Default: 0
- \(lwork\) : input int, optional
  Default: 3*m

\texttt{scipy.linalg.lapack.zgerqf}(a[, lwork, overwrite_a]) = <fortran object>

Wrapper for \texttt{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 (\text{MIN}(m,n))
- \(work\) : rank-1 array(‘D’) with bounds (\text{MAX}(lwork,1))
- \(info\) : int

**Other Parameters**
- \(overwrite_a\) : input int, optional
  Default: 0
- \(lwork\) : input int, optional
  Default: 3*m

\texttt{scipy.linalg.lapack.sgesdd}(a[, compute_uv, full_matrices, lwork, overwrite_a]) = <fortran object>

Wrapper for \texttt{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 (\text{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
SciPy Reference Guide, Release 0.16.0

```python
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: (compute_uv?4*minmn*minmn+MAX(m,n)+9*minmn:MAX(14*minmn+4,10*minmn+2+25*(25+8))+MAX(m,n))
```

```python
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: (compute_uv?2*minmn*minmn+MAX(m,n)+2*minmn:2*minmn+MAX(m,n))
```

```python
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
```

5.17. All functions 543
SciPy Reference Guide, Release 0.16.0

```python
cscipy.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

cscipy.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

cscipy.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

cscipy.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.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(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
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(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(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

5.17. All functions 545
overwrite_b : input int, optional
    Default: 0

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 (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
    Other Parameters
        overwrite_a : input int, optional
            Default: 0

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 (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 (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: 3*n
SciPy Reference Guide, Release 0.16.0

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: 3*n

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: 3*n

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
    overwrite_lu : input int, optional
        Default: 0
    lwork : input int, optional
        Default: 3*n

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(n) = <fortran object>
Wrapper for dgetri_lwork.

Parameters
    n : input int
Returns
    work : float
    info : int

scipy.linalg.lapack.cgetri_lwork(n) = <fortran object>
Wrapper for cgetri_lwork.

Parameters
    n : input int
Returns
    work : complex
    info : int

5.17. All functions

547
Wrapper for `zgetri_lwork`.

Parameters

- `n`: input int

Returns

- `work`: complex
- `info`: int

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

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

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

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

```python
cipy.linalg.lapack.sgges(sselect, a, b[, jobvsl, jobvsr, sort_t, ldvs, ldvsr, lwork, sselect_extra_args, overwrite_a, overwrite_b]) = <fortran object>
```

Wrapper for `sgges`.

**Parameters**

- `sselect` : call-back function
  - `a` : input rank-2 array('f') with bounds (lda,*)
  - `b` : input rank-2 array('f') with bounds (ldb,*)

**Returns**

- `a` : rank-2 array('f') with bounds (lda,*)
- `b` : rank-2 array('f') with bounds (ldb,*)
- `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)
- `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
- `sselect_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: 8*n+16

**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(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,*)
b : input rank-2 array('d') with bounds (ldb,*)

Returns

a : rank-2 array('d') with bounds (lda,*)
b : rank-2 array('d') with bounds (ldb,*)
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)
vl : rank-2 array('d') with bounds (ldvsl,n)
vr : 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: 8*n+16

Notes

Call-back functions:

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(cselect, a, b[, jobvsl, jobvsr, sort_t, ldvsl, ldvsr, lwork, cselect_extra_args, overwrite_a, overwrite_b]) = <fortran object>

Wrapper for cgges.

Parameters

cselect : call-back function
a : input rank-2 array('F') with bounds (lda,*)
b : input rank-2 array('F') with bounds (ldb,*)
Returns

- **a** : rank-2 array('F') with bounds (lda,*)
- **b** : rank-2 array('F') with bounds (ldb,*)
- **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: 2*n

Notes

Call-back functions:

```python
def cselect(alpha,beta): return cselect
```

Required arguments:

- **alpha** : input complex
- **beta** : input complex

Return objects:

- **cselect** : int

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,*)
  - **b** : input rank-2 array('D') with bounds (ldb,*)

Returns

- **a** : rank-2 array('D') with bounds (lda,*)
- **b** : rank-2 array('D') with bounds (ldb,*)
- **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: 2*n

Notes

Call-back functions:

```python
def zselect(alpha,beta): return zselect
```

Required arguments:

- alpha : input complex
- beta : input complex

Return objects:

- zselect : int

scipy.linalg.lapack.sgeev(a, b[, compute_vl, compute_vr, lwork, overwrite_a, overwrite_b]) =
    <fortran object>

Wrapper for sgeev.

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: 8*n
```python
scipy.linalg.lapack.dggev(a, b[, compute_vl, compute_vr, lwork, overwrite_a, overwrite_b]) =
<fortran object>

Wrapper for dggev.

**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
- **overwrite_a**: input int, optional
  Default: 0
- **overwrite_b**: input int, optional
  Default: 0
- **lwork**: input int, optional
  Default: 8*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

- **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: 2*n

```
scipy.linalg.lapack.chbevd(ab, compute_v, lower, ldab, lwork, liwork, overwrite_ab)
```

Wrapper for chbevd.

Parameters

- **ab**: input rank-2 array(‘F’) with bounds (ldab,*)

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)
- **lwork**: 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(ab, compute_v, lower, ldab, lwork, liwork, overwrite_ab)
```

Wrapper for zhbevd.

Parameters

- **ab**: input rank-2 array(‘D’) with bounds (ldab,*)

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: 0
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,*)
- **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: 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.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,*)
- **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: \((\text{compute}_v?(\text{range}==2?((i-\text{il}+1):n):1))\)

```
scipy.linalg.lapack.cheev(a[ , compute_v , lower , lwork , overwrite_a ]) = <fortran object>
```

**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: 2\*n-1

```
scipy.linalg.lapack.zheev(a[ , compute_v , lower , lwork , overwrite_a ]) = <fortran object>
```

**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: 2\*n-1

```
scipy.linalg.lapack.cheevd(a[ , compute_v , lower , lwork , overwrite_a ]) = <fortran object>
```

**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
SciPy Reference Guide, Release 0.16.0

Default: 0

**lwork**: input int, optional
Default: (compute_v?2*n+n*n:n+1)

`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: (compute_v?2*n+n*n:n+1)

`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: 18*n

`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’
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(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(a, b[, itype, jobz, uplo, lwork, overwrite_a, overwrite_b]) = <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)

Other Parameters
   lwork : input int, optional
           Default: 18*n
   overwrite_a : input int, optional
                 Default: 0
   overwrite_b : input int, optional
                 Default: 0
 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: \(2*n+n*n\)

```
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: \(2*n+n*n\)

```
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’
**SciPy Reference Guide, Release 0.16.0**

```python
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: 18*n-1

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: 18*n-1

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 (*)
   tau : input float
   c : input rank-2 array(‘F’) with bounds (m,n)
   work : input rank-1 array(‘F’) with bounds (*)

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(v, tau, c[, side, incv, overwrite_c]) = <fortran object>

Wrapper for dlarf.
```
**Parameters**

\- \(v\): input rank-1 array('d') with bounds (*)
\- \(\tau\): input float
\- \(c\): input rank-2 array('d') with bounds (m,n)
\- \(\text{work}\): input rank-1 array('d') with bounds (*)

**Returns**

\(c\): rank-2 array('d') with bounds (m,n)

**Other Parameters**

\- \(\text{side}\): input string(len=1), optional
  
  Default: ‘L’
\- \(\text{incv}\): input int, optional
  
  Default: 1
\- \(\text{overwrite}_c\): input int, optional
  
  Default: 0

```python
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 (*)
\- \(\tau\): input complex
\- \(c\): input rank-2 array('F') with bounds (m,n)
\- \(\text{work}\): input rank-1 array('F') with bounds (*)

**Returns**

\(c\): rank-2 array('F') with bounds (m,n)

**Other Parameters**

\- \(\text{side}\): input string(len=1), optional
  
  Default: ‘L’
\- \(\text{incv}\): input int, optional
  
  Default: 1
\- \(\text{overwrite}_c\): input int, optional
  
  Default: 0

```python
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 (*)
\- \(\tau\): input complex
\- \(c\): input rank-2 array('D') with bounds (m,n)
\- \(\text{work}\): input rank-1 array('D') with bounds (*)

**Returns**

\(c\): rank-2 array('D') with bounds (m,n)

**Other Parameters**

\- \(\text{side}\): input string(len=1), optional
  
  Default: ‘L’
\- \(\text{incv}\): input int, optional
  
  Default: 1
\- \(\text{overwrite}_c\): input int, optional
  
  Default: 0

```python
scipy.linalg.lapack.slarf(n, alpha, x[, incx, overwrite_x]) = <fortran object>
```

Wrapper for slarf.

**Parameters**

\- \(n\): input int
\- \(\alpha\): input float
\- \(x\): input rank-1 array('f') with bounds (*)

**Returns**

\(\alpha\): float
\(x\): rank-1 array('f') with bounds (*)
\(\tau\): float

**Other Parameters**

\(\text{overwrite}_x\): input int, optional
  
  Default: 0
incx : input int, optional
    Default: 1

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 (*)

Returns
alpha : float
x : rank-1 array('d') with bounds (*)
tau : float

Other Parameters
overwrite_x : input int, optional
    Default: 0
incx : input int, optional
    Default: 1

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 (*)

Returns
alpha : complex
x : rank-1 array('F') with bounds (*)
tau : complex

Other Parameters
overwrite_x : input int, optional
    Default: 0
incx : input int, optional
    Default: 1

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 (*)

Returns
alpha : complex
x : rank-1 array('D') with bounds (*)
tau : complex

Other Parameters
overwrite_x : input int, optional
    Default: 0
incx : input int, optional
    Default: 1

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 $(f, g) = \langle\text{fortran object}\rangle$
Wrapper for dlartg.

**Parameters**
- $f$: input float
- $g$: input float

**Returns**
- $cs$: float
- $sn$: float
- $r$: float

scipy.linalg.lapack.clartg $(f, g) = \langle\text{fortran object}\rangle$
Wrapper for clartg.

**Parameters**
- $f$: input complex
- $g$: input complex

**Returns**
- $cs$: float
- $sn$: complex
- $r$: complex

scipy.linalg.lapack.zlartg $(f, g) = \langle\text{fortran object}\rangle$
Wrapper for zlartg.

**Parameters**
- $f$: input complex
- $g$: input complex

**Returns**
- $cs$: float
- $sn$: complex
- $r$: complex

scipy.linalg.lapack.dlasd4 $(i, d, z[, rho]) = \langle\text{fortran object}\rangle$
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.slasd4 $(i, d, z[, rho]) = \langle\text{fortran object}\rangle$
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.slaswp $(a, piv[, k1, k2, off, inc, overwrite_a]) = \langle\text{fortran object}\rangle$
Wrapper for slaswp.
**Parameters**

- `a`: input rank-2 array('f') with bounds (nrows,n)
- `piv`: input rank-1 array('i') with bounds (*)

**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: len(piv)-1
- `off` : input int, optional
  - Default: 0
- `inc` : input int, optional
  - Default: 1

```python
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 (*)

**Returns**

- `a`: rank-2 array('d') with bounds (nrows,n)

**Other Parameters**

- `overwrite_a`: input int, optional
  - Default: 0
- `k1` : input int, optional
  - Default: 0
- `k2` : input int, optional
  - Default: len(piv)-1
- `off` : input int, optional
  - Default: 0
- `inc` : input int, optional
  - Default: 1

```python
scipy.linalg.lapack.claswp(a, piv[, k1, k2, off, inc, overwrite_a]) = <fortran object>
```

Wrapper for `claswp`.

**Parameters**

- `a`: input rank-2 array('F') with bounds (nrows,n)
- `piv`: input rank-1 array('i') with bounds (*)

**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: len(piv)-1
- `off` : input int, optional
  - Default: 0
- `inc` : input int, optional
  - Default: 1

```python
scipy.linalg.lapack.zlaswp(a, piv[, k1, k2, off, inc, overwrite_a]) = <fortran object>
```

Wrapper for `zlaswp`.

**Parameters**

- `a`: input rank-2 array('D') with bounds (nrows,n)
- `piv`: input rank-1 array('i') with bounds (*)

**Returns**

- `a`: rank-2 array('D') with bounds (nrows,n)
**Other Parameters**

- `overwrite_a` : input int, optional
  Default: 0
- `k1` : input int, optional
  Default: 0
- `k2` : input int, optional
  Default: len(piv)-1
- `off` : input int, optional
  Default: 0
- `inc` : input int, optional
  Default: 1

```python
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

```python
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

```python
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

```python
scipy.linalg.lapack.zlaum(c[, lower, overwrite_c]) = <fortran object>
```

Wrapper for zlaum.

**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

```python
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

```python
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

```python
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 Reference Guide, Release 0.16.0

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 (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 (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 (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

5.17. All functions 567
SciPy Reference Guide, Release 0.16.0

```
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
  ldab : input int, optional
    Default: shape(ab,0)
  overwrite_ab : input int, optional
    Default: 0

Returns
  c : rank-2 array('D') with bounds (ldab,n) and ab storage
  info : int

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
  ldab : input int, optional
    Default: shape(ab,0)
  overwrite_b : input int, optional
    Default: 0

Returns
  x : rank-2 array('f') with bounds (ldb,nrhs) and b storage
  info : int

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)
  overwrite_b : input int, optional
    Default: 0

Returns
  x : rank-2 array('d') with bounds (ldb,nrhs) and b storage
  info : int

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)
  lower : input int, optional
    Default: 0
  ldab : input int, optional
    Default: shape(ab,0)
```

568 Chapter 5. Reference
```
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(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(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(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
```
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(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.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(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(a, lower, clean, overwrite_a) = <fortran object>

Wrapper for cpotrf.
SciPy Reference Guide, Release 0.16.0

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(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(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(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(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

5.17. All functions
SciPy Reference Guide, Release 0.16.0

572 Chapter 5. Reference

\texttt{scipy.linalg.lapack.zpotri}(c, lower, overwrite_c) = \texttt{<fortran object>}

Wrapper for \texttt{zpotri}.

**Parameters**
- \texttt{c} : input rank-2 array(‘D’) with bounds (n,n)
- \texttt{lower} : input int, optional
  Default: 0

**Returns**
- \texttt{inv_a} : rank-2 array(‘D’) with bounds (n,n) and c storage
- \texttt{info} : int

**Other Parameters**
- \texttt{overwrite_c} : input int, optional
  Default: 0
- \texttt{lower} : input int, optional
  Default: 0

\texttt{scipy.linalg.lapack.spotrs}(c, b, lower, overwrite_b) = \texttt{<fortran object>}

Wrapper for \texttt{spotrs}.

**Parameters**
- \texttt{c} : input rank-2 array(‘f’) with bounds (n,n)
- \texttt{b} : input rank-2 array(‘f’) with bounds (n,nrhs)
- \texttt{lower} : input int, optional
  Default: 0

**Returns**
- \texttt{x} : rank-2 array(‘f’) with bounds (n,nrhs) and b storage
- \texttt{info} : int

**Other Parameters**
- \texttt{overwrite_b} : input int, optional
  Default: 0
- \texttt{lower} : input int, optional
  Default: 0

\texttt{scipy.linalg.lapack.dpotrs}(c, b, lower, overwrite_b) = \texttt{<fortran object>}

Wrapper for \texttt{dpotrs}.

**Parameters**
- \texttt{c} : input rank-2 array(‘d’) with bounds (n,n)
- \texttt{b} : input rank-2 array(‘d’) with bounds (n,nrhs)
- \texttt{lower} : input int, optional
  Default: 0

**Returns**
- \texttt{x} : rank-2 array(‘d’) with bounds (n,nrhs) and b storage
- \texttt{info} : int

**Other Parameters**
- \texttt{overwrite_b} : input int, optional
  Default: 0
- \texttt{lower} : input int, optional
  Default: 0

\texttt{scipy.linalg.lapack.cpotrs}(c, b, lower, overwrite_b) = \texttt{<fortran object>}

Wrapper for \texttt{cpotrs}.

**Parameters**
- \texttt{c} : input rank-2 array(‘F’) with bounds (n,n)
- \texttt{b} : input rank-2 array(‘F’) with bounds (n,nrhs)
- \texttt{lower} : input int, optional
  Default: 0

**Returns**
- \texttt{x} : rank-2 array(‘F’) with bounds (n,nrhs) and b storage
- \texttt{info} : int

**Other Parameters**
- \texttt{overwrite_b} : input int, optional
  Default: 0
- \texttt{lower} : input int, optional
  Default: 0

\texttt{scipy.linalg.lapack.zpotrs}(c, b, lower, overwrite_b) = \texttt{<fortran object>}

Wrapper for \texttt{zpotrs}.

**Parameters**
- \texttt{c} : input rank-2 array(‘D’) with bounds (n,n)
- \texttt{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 (x, y, c[, n, offx, incx, offy, incy, overwrite_x, overwrite_y]) = <fortran object>

Wrapper for crot.

Parameters

x : input rank-1 array('F') with bounds (*)

y : input rank-1 array('F') with bounds (*)

c : input float

s : input complex

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

incy : input int, optional
    Default: 1

scipy.linalg.lapack.zrot (x, y, c[, n, offx, incx, offy, incy, overwrite_x, overwrite_y]) = <fortran object>

Wrapper for zrot.

Parameters

x : input rank-1 array('D') with bounds (*)

y : input rank-1 array('D') with bounds (*)

c : input float

s : input complex

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

5.17. All functions 573
Default: 0

\[ \text{incy} : \text{input int, optional} \]
Default: 1

```
scipy.linalg.lapack.strsyl(a, b, c[, trana, tranb, isgn, overwrite_c]) = <fortran object>
```

Wrapper for \texttt{strsyl}.

**Parameters**
\[ a : \text{input rank-2 array('f') with bounds (m,m)} \]
\[ b : \text{input rank-2 array('f') with bounds (n,n)} \]
\[ c : \text{input rank-2 array('f') with bounds (m,n)} \]

**Returns**
\[ x : \text{rank-2 array('f') with bounds (m,n) and c storage} \]
\[ \text{scale} : \text{float} \]
\[ \text{info} : \text{int} \]

**Other Parameters**
\[ \text{trana} : \text{input string(len=1), optional} \]
Default: ‘N’
\[ \text{tranb} : \text{input string(len=1), optional} \]
Default: ‘N’
\[ \text{isgn} : \text{input int, optional} \]
Default: 1
\[ \text{overwrite_c} : \text{input int, optional} \]
Default: 0

```
scipy.linalg.lapack.dtrsyl(a, b, c[, trana, tranb, isgn, overwrite_c]) = <fortran object>
```

Wrapper for \texttt{dtrsyl}.

**Parameters**
\[ a : \text{input rank-2 array('d') with bounds (m,m)} \]
\[ b : \text{input rank-2 array('d') with bounds (n,n)} \]
\[ c : \text{input rank-2 array('d') with bounds (m,n)} \]

**Returns**
\[ x : \text{rank-2 array('d') with bounds (m,n) and c storage} \]
\[ \text{scale} : \text{float} \]
\[ \text{info} : \text{int} \]

**Other Parameters**
\[ \text{trana} : \text{input string(len=1), optional} \]
Default: ‘N’
\[ \text{tranb} : \text{input string(len=1), optional} \]
Default: ‘N’
\[ \text{isgn} : \text{input int, optional} \]
Default: 1
\[ \text{overwrite_c} : \text{input int, optional} \]
Default: 0

```
scipy.linalg.lapack.ctrsyl(a, b, c[, trana, tranb, isgn, overwrite_c]) = <fortran object>
```

Wrapper for \texttt{ctrsyl}.

**Parameters**
\[ a : \text{input rank-2 array('F') with bounds (m,m)} \]
\[ b : \text{input rank-2 array('F') with bounds (n,n)} \]
\[ c : \text{input rank-2 array('F') with bounds (m,n)} \]

**Returns**
\[ x : \text{rank-2 array('F') with bounds (m,n) and c storage} \]
\[ \text{scale} : \text{float} \]
\[ \text{info} : \text{int} \]

**Other Parameters**
\[ \text{trana} : \text{input string(len=1), optional} \]
Default: ‘N’
\[ \text{tranb} : \text{input string(len=1), optional} \]
Default: ‘N’
\[ \text{isgn} : \text{input int, optional} \]
Default: 1
`overwrite_c` : input int, optional
Default: 0

scipy.linalg.lapack.ztrsyl(a, b, c[, trana, tranb, isgn, overwrite_c]) = <fortran object>
Wrapper for ztrsyl.

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.strtri(c[, lower, unitdiag, overwrite_c]) = <fortran object>
Wrapper for strtri.

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.dtrtri(c[, lower, unitdiag, overwrite_c]) = <fortran object>
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(c[, lower, unitdiag, overwrite_c]) = <fortran object>
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

5.17. All functions
SciPy Reference Guide, Release 0.16.0

Other Parameters

overwrite_c : input int, optional
  Default: 0
lower : input int, optional
  Default: 0
unitdiag : input int, optional
  Default: 0

scipy.linalg.lapack.zhptri(c[, lower, unitdiag, overwrite_c]) = <fortran object>
Wrapper for zhptri.

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.ztrtrs(a, b[, lower, trans, unitdiag, lda, overwrite_b]) = <fortran object>
Wrapper for ztrtrs.

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(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(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

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(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.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: hi-lo

5.17. All functions
577
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
  h : 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: hi-lo

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: 3*n

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: 3*n

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: 3*n
Default: 3*m

```python
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))
- `info`: int

**Other Parameters**
- `overwrite_a`: input int, optional
  - Default: 0
- `lwork`: input int, optional
  - Default: 3*m

```python
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

```python
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

```python
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 (*)
- `du`: input rank-1 array('f') with bounds (n - 1)
- `b`: input rank-2 array('f') with bounds (,)

---

5.17. All functions 579
**Returns**

- \( \text{du2} \) : rank-1 array('f') with bounds (n - 1) and dl storage
- \( \text{d} \) : rank-1 array('f') with bounds (*)
- \( \text{du} \) : rank-1 array('f') with bounds (n - 1)
- \( \text{x} \) : rank-2 array('f') with bounds (n) and b storage
- \( \text{info} \) : int

**Other Parameters**

- \( \text{overwrite\_dl} \) : input int, optional
  - Default: 0
- \( \text{overwrite\_d} \) : input int, optional
  - Default: 0
- \( \text{overwrite\_du} \) : input int, optional
  - Default: 0
- \( \text{overwrite\_b} \) : input int, optional
  - Default: 0

```python
scipy.linalg.lapack.dgtsv(dl, d, du, b[, overwrite_dl, overwrite_d, overwrite_du, overwrite_b]) =
<fortran object>
```

Wrapper for \texttt{dgtsv}.

**Parameters**

- \( \text{dl} \) : input rank-1 array('d') with bounds (n - 1)
- \( \text{d} \) : input rank-1 array('d') with bounds (*)
- \( \text{du} \) : input rank-1 array('d') with bounds (n - 1)
- \( \text{b} \) : input rank-2 array('d') with bounds (n)

**Returns**

- \( \text{du2} \) : rank-1 array('d') with bounds (n - 1) and dl storage
- \( \text{d} \) : rank-1 array('d') with bounds (*)
- \( \text{du} \) : rank-1 array('d') with bounds (n - 1)
- \( \text{x} \) : rank-2 array('d') with bounds (n) and b storage
- \( \text{info} \) : int

**Other Parameters**

- \( \text{overwrite\_dl} \) : input int, optional
  - Default: 0
- \( \text{overwrite\_d} \) : input int, optional
  - Default: 0
- \( \text{overwrite\_du} \) : input int, optional
  - Default: 0
- \( \text{overwrite\_b} \) : input int, optional
  - Default: 0

```python
scipy.linalg.lapack.cgtsv(dl, d, du, b[, overwrite_dl, overwrite_d, overwrite_du, overwrite_b]) =
<fortran object>
```

Wrapper for \texttt{cgtsv}.

**Parameters**

- \( \text{dl} \) : input rank-1 array('F') with bounds (n - 1)
- \( \text{d} \) : input rank-1 array('F') with bounds (*)
- \( \text{du} \) : input rank-1 array('F') with bounds (n - 1)
- \( \text{b} \) : input rank-2 array('F') with bounds (n)

**Returns**

- \( \text{du2} \) : rank-1 array('F') with bounds (n - 1) and dl storage
- \( \text{d} \) : rank-1 array('F') with bounds (*)
- \( \text{du} \) : rank-1 array('F') with bounds (n - 1)
- \( \text{x} \) : rank-2 array('F') with bounds (n) and b storage
- \( \text{info} \) : int

**Other Parameters**

- \( \text{overwrite\_dl} \) : input int, optional
  - Default: 0
- \( \text{overwrite\_d} \) : input int, optional
  - Default: 0
overwrite_du : input int, optional
    Default: 0
overwrite_b : input int, optional
    Default: 0

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 (*)
    du : input rank-1 array('D') with bounds (n - 1)
    b : input rank-2 array('D') with bounds ()

Returns
    du2 : rank-1 array('D') with bounds (n - 1) and dl storage
    d : rank-1 array('D') with bounds (*)
    du : rank-1 array('D') with bounds (n - 1)
    x : rank-2 array('D') with bounds (,) and b storage
    info : int

Other Parameters
    overwrite_du : 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.sptsv(d, e, b[, overwrite_d, overwrite_e, overwrite_b]) = <fortran object>

Wrapper for sptsv.

Parameters
    d : input rank-1 array('f') with bounds (*)
    e : input rank-1 array('f') with bounds (n - 1)
    b : input rank-2 array('f') with bounds ()

Returns
    d : rank-1 array('f') with bounds (*)
    du : rank-1 array('f') with bounds (n - 1) and e storage
    x : rank-2 array('f') with bounds (,) 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.dptsv(d, e, b[, overwrite_d, overwrite_e, overwrite_b]) = <fortran object>

Wrapper for dptsv.

Parameters
    d : input rank-1 array('d') with bounds (*)
    e : input rank-1 array('d') with bounds (n - 1)
    b : input rank-2 array('d') with bounds ()

Returns
    d : rank-1 array('d') with bounds (*)
    du : rank-1 array('d') with bounds (n - 1) and e storage
    x : rank-2 array('d') with bounds (,) and b storage
    info : int

5.17. All functions 581
SciPy Reference Guide, Release 0.16.0

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(d, e, b[, overwrite_d, overwrite_e, overwrite_b]) = <fortran object>
Wrapper for cptsv.

Parameters

    d : input rank-1 array('f') with bounds (*)
    e : input rank-1 array('F') with bounds (n - 1)
    b : input rank-2 array('F') with bounds (,)  

Returns

    d : rank-1 array('f') with bounds (*)
    du : rank-1 array('F') with bounds (n - 1) and e storage
    x : rank-2 array('F') with bounds (,) 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(d, e, b[, overwrite_d, overwrite_e, overwrite_b]) = <fortran object>
Wrapper for zptsv.

Parameters

    d : input rank-1 array('d') with bounds (*)
    e : input rank-1 array('D') with bounds (n - 1)
    b : input rank-2 array('D') with bounds (,)  

Returns

    d : rank-1 array('d') with bounds (*)
    du : rank-1 array('D') with bounds (n - 1) and e storage
    x : rank-2 array('D') with bounds (,) 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(cmach) = <fortran slamch>
Wrapper for slamch.

Parameters

    cmach : input string(len=1)

Returns

    slamch : float

scipy.linalg.lapack.dlamch(cmach) = <fortran dlamch>
Wrapper for dlamch.

Parameters

    cmach : input string(len=1)

Returns

    dlamch : float

scipy.linalg.lapack.sorghr(a, tau[, lo, hi, lwork, overwrite_a]) = <fortran object>
Wrapper for sorghr.
SciPy Reference Guide, Release 0.16.0

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: hi-lo

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: hi-lo

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: 3*n

scipy.linalg.lapack.dorgqr(a, tau[], lwork, 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: 3*n

5.17. All functions 583
Default: $3n$

```python
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: $3m$

```python
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: $3m$

```python
scipy.linalg.lapack.sormqr(side, trans, a, tau[, 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

```python
scipy.linalg.lapack.dormqr(side, trans, a, tau[, 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.ssbev(ab[, compute_v, lower, ldab, overwrite_ab]) = <fortran object>

Wrapper for ssbev.

Parameters

ab : input rank-2 array('f') with bounds (ldab,*)

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(ab[, compute_v, lower, ldab, overwrite_ab]) = <fortran object>

Wrapper for dsbev.

Parameters

ab : input rank-2 array('d') with bounds (ldab,*)

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)

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,*)

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(ab[, compute_v, lower, ldab, liwork, overwrite_ab]) = <fortran object>

Wrapper for dsbevd.

Parameters
- ab : input rank-2 array('d') with bounds (ldab,*)
- 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)

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)
- liwork : input int, optional
  Default: (compute_v?3+5*n:1)

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,*)
- vl : input float
- vu : input float
- il : input int
- iu : input int
- 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)

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: 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.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,*)
- 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.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: 3*n-1

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: 3*n-1
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: (compute_v?1+6*n+2*n*n:2*n+1)

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: (compute_v?1+6*n+2*n*n:2*n+1)

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: 26*n
scipy.linalg.lapack.\texttt{dsyevr}(a[, jobz, range, uplo, il, iu, lwork, overwrite_a]) = <fortran object>

Wrapper for \texttt{dsyevr}.

Parameters
\begin{itemize}
\item \texttt{a} : input rank-2 array(‘d’) with bounds (n,n)
\item \texttt{jobz} : input string(len=1), optional
  Default: ‘V’
\item \texttt{range} : input string(len=1), optional
  Default: ‘A’
\item \texttt{uplo} : input string(len=1), optional
  Default: ‘L’
\item \texttt{overwrite_a} : input int, optional
  Default: 0
\item \texttt{il} : input int, optional
  Default: 1
\item \texttt{iu} : input int, optional
  Default: n
\item \texttt{lwork} : input int, optional
  Default: 26*n
\end{itemize}

Returns
\begin{itemize}
\item \texttt{w} : rank-1 array(‘d’) with bounds (n)
\item \texttt{z} : rank-2 array(‘d’) with bounds (n,m)
\item \texttt{info} : int
\end{itemize}

\texttt{scipy.linalg.lapack.\texttt{ssygv}}(a, b[, itype, jobz, uplo, overwrite_a, overwrite_b]) = <fortran object>

Wrapper for \texttt{ssygv}.

Parameters
\begin{itemize}
\item \texttt{a} : input rank-2 array(‘f’) with bounds (n,n)
\item \texttt{b} : input rank-2 array(‘f’) with bounds (n,n)
\item \texttt{itype} : input int, optional
  Default: 1
\item \texttt{jobz} : input string(len=1), optional
  Default: ‘V’
\item \texttt{uplo} : input string(len=1), optional
  Default: ‘L’
\item \texttt{overwrite_a} : input int, optional
  Default: 0
\item \texttt{overwrite_b} : input int, optional
  Default: 0
\end{itemize}

Returns
\begin{itemize}
\item \texttt{a} : rank-2 array(‘f’) with bounds (n,n)
\item \texttt{w} : rank-1 array(‘f’) with bounds (n)
\item \texttt{info} : int
\end{itemize}

\texttt{scipy.linalg.lapack.\texttt{dsygv}}(a, b[, itype, jobz, uplo, overwrite_a, overwrite_b]) = <fortran object>

Wrapper for \texttt{dsygv}.

Parameters
\begin{itemize}
\item \texttt{a} : input rank-2 array(‘d’) with bounds (n,n)
\item \texttt{b} : input rank-2 array(‘d’) with bounds (n,n)
\item \texttt{itype} : input int, optional
  Default: 1
\item \texttt{jobz} : input string(len=1), optional
  Default: ‘V’
\end{itemize}

Returns
\begin{itemize}
\item \texttt{a} : rank-2 array(‘d’) with bounds (n,n)
\item \texttt{w} : rank-1 array(‘d’) with bounds (n)
\item \texttt{info} : int
\end{itemize}

\textbf{5.17. All functions} 589
**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: 1+6*n+2*n*n

**scipy.linalg.lapack.dsygvd**

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: 1+6*n+2*n*n

**scipy.linalg.lapack.ssygvd**

Wrapper for ssygvd.

**Parameters**

- `a`: 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**

Wrapper for ssygvd.

**Parameters**

- `a`: input string(len=1), optional
  Default: ‘L’
- `overwrite_a`: input int, optional
  Default: 0
- `overwrite_b`: input int, optional
  Default: 0

**scipy.linalg.lapack.dsygvd**

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: 1+6*n+2*n*n

**scipy.linalg.lapack.dsygvd**

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: 1+6*n+2*n*n

**scipy.linalg.lapack.ssygvd**

Wrapper for ssygvd.

**Parameters**

- `a`: 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**

Wrapper for ssygvd.

**Parameters**

- `a`: 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**

Wrapper for ssygvd.

**Parameters**

- `a`: 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**

Wrapper for ssygvd.

**Parameters**

- `a`: 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**

Wrapper for ssygvd.

**Parameters**

- `a`: 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**

Wrapper for ssygvd.

**Parameters**

- `a`: 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**

Wrapper for ssygvd.
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: 8*n

```
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: 8*n

```
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

5.17. All functions
scipy.linalg.lapack.dlange \( (\text{norm}, a) = \langle \text{fortran \ dlange} \rangle \)
Wrapper for \text{dlange}.

\textbf{Parameters} \hspace{1cm} \textbf{Returns}
\begin{align*}
\text{norm} & : \text{input string(len=1)} \\
\text{a} & : \text{input rank-2 array(‘d’) with bounds (m,n)} \\
\text{n2} & : \text{float}
\end{align*}

scipy.linalg.lapack.clange \( (\text{norm}, a) = \langle \text{fortran \ clange} \rangle \)
Wrapper for \text{clange}.

\textbf{Parameters} \hspace{1cm} \textbf{Returns}
\begin{align*}
\text{norm} & : \text{input string(len=1)} \\
\text{a} & : \text{input rank-2 array(‘F’) with bounds (m,n)} \\
\text{n2} & : \text{float}
\end{align*}

scipy.linalg.lapack.zlange \( (\text{norm}, a) = \langle \text{fortran \ zlange} \rangle \)
Wrapper for \text{zlange}.

\textbf{Parameters} \hspace{1cm} \textbf{Returns}
\begin{align*}
\text{norm} & : \text{input string(len=1)} \\
\text{a} & : \text{input rank-2 array(‘D’) with bounds (m,n)} \\
\text{n2} & : \text{float}
\end{align*}

5.18 BLAS Functions for Cython

Usable from Cython via:

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
• cscale
• csrot
• csscale
• cswap
• csymm
• csyr2k
• csyrk
• ctbmv
• ctbsv
• ctmmv
• ctmsv
• ctrmm
• ctrmv
• ctrsm
• ctrsv
• dasum
• daxpy
• dcabs1
• dcopy
• ddot
• dgbmv
• dgemm
• dgemv
• dger
• dnrm2
• drot
• drogt
• 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
• sscal
• sspmv
• sspr
• sspr2
• sswap
• ssymm
• ssymv
• ssyr
• ssyr2
• ssyr2k
• ssyrk
• stbmv
• stbsv
• stpmv
• stpsv
• strmm
• strmv
• strsm
• strsv
• zaxpy
• zcopy
• zdotc
• zdotu
• zdrot
• zdscal
• zgbmv
• zgemm
• zgemv
• zgerc
• zgeru
5.19 LAPACK functions for Cython

Usable from Cython via:

cimport scipy.linalg.cython_lapack

This module provides Cython-level wrappers for all primary routines included in LAPACK 3.1.0 except for \texttt{zgesv} since its interface is not consistent from LAPACK 3.1.0 to 3.5.0. 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):

- \texttt{cbdsqr}
- \texttt{cgbbrd}
• cgbcon
• cgbequ
• cgbrfs
• cgbsv
• cgbsvx
• cgbtf2
• cgbtrf
• cgbtrs
• cgebak
• cgebal
• cgebd2
• cgebrd
• cgecon
• cgeequ
• cgees
• cgeesx
• cgeev
• cgeevx
• cgegs
• cgegv
• cgehfd2
• cgehrd
• cgelq2
• cgelqf
• cgels
• cgelsd
• cgelss
• cgelsx
• cgelso
• cgeql2
• cgeqlf
• cgeqp3
• cgeqpf
• cgeqr2
• cgeqrf
• cgerfs
• cgerq2
• cgerqf
• cgesc2
• cgesdd
• cgesv
• cgesvd
• cgesvx
• cgetc2
• cgetf2
• cgetrf
• cgetri
• cgetrs
• cggbak
• cggbal
• cgges
• cggesx
• cggev
• cggevx
• cggglm
• cgghrd
• cgglse
• cggqrf
• cggrqf
• cggsvd
• cggsvp
• cgtrcon
• cgtrfs
• cgts
• cgtsv
• cgtsvx
• cgtrfs
• cgtrfs
• cgtts2
• chbev
• chbevd
• chbevx
• chbgst
5.19. LAPACK functions for Cython

- chbgv
- chbgvd
- chbgvx
- chbtrd
- checon
- cheev
- cheeved
- cheevr
- cheevx
- chegs2
- chegst
- chegv
- chegyd
- chegyx
- cherfs
- chesv
- chesvx
- chetd2
-chetf2
- chetrd
- chetrf
- chetri
- chetrs
- chgeqz
- chpcon
- chpev
- chpevd
- chpevx
- chpgst
- chpgv
- chpgvd
- chpgvx
- chprfs
- chpsv
- chpsvx
- chptrd
• chptrf
• chptri
• chptrs
• chptrs
• chsein
• chseqr
• clabrd
• clacgv
• clacn2
• clacon
• clacp2
• clacpy
• clacrm
• clacrt
• cladiv
• claed0
• claed7
• claed8
• claein
• claesy
• claev2
• clag2z
• clags2
• clagtm
• clahef
• clahqr
• clahr2
• clahrd
• claic1
• clals0
• clalsa
• clalsd
• clangb
• clange
• clangt
• clanhb
• clanhe
• clanhp
• clanhs
• clanht
• clansb
• clansp
• clansy
• clantb
• clantp
• clantr
• clapll
• clapmt
• claqgb
• claqge
• claqhb
• claqhe
• claqhp
• claqp2
• claqps
• claqr0
• claqr1
• claqr2
• claqr3
• claqr4
• claqr5
• claqsb
• claqsp
• claqsy
• clar1v
• clar2v
• clarcn
• clarf
• clarfb
• clarfg
• clarft
• clarfx
• clargv
• clarnv
• clarrv
• clartg
• clartv
• clarz
• clarzb
• clarzt
• clascl
• clasct
• clasr
• classq
• claswp
• clasyc
• clatbs
• clatdf
• clatps
• clatrd
• clatrs
• clatrz
• clatzm
• clauu2
• clauum
• cpbcon
• cpbequ
• cplrsfs
• cpbtrfs
• cpbsv
• cpbsvx
• cpbtf2
• cpbrfs
• cpbtrs
• cpocon
• cpoequ
• cporsf
• cporsv
• cporsvx
• cpotf2
• cpotrf
• cpotri
• cpotrs
• cppcon
• cppequ
• cpprfs
• cppsv
• cppsvx
• cpptrf
• cpptri
• cpptrs
• cptrcon
• cpteqr
• cptrfs
• cptsv
• cptsvx
• cptrtrf
• cptrtrs
• cptrts2
• crot
• cspcon
• cspmv
• cspr
• csprfs
• cspsv
• cspsvx
• csptrf
• csptri
• csptrs
• csrscl
• cstedc
• csteigr
• cstein
• cstemr
• csteqr

5.19. LAPACK functions for Cython
5.19. LAPACK functions for Cython

- ctzrzf
- cung2l
- cung2r
- cungbr
- cunghr
- cungl2
- cunglq
- cungql
- cungqr
- cungr2
- cungrq
- cungrq
- cungtr
- cunn2l
- cunn2r
- cunmbr
- cunnhr
- cunnml2
- cunnmlq
- cunnmlq
- cunmqr
- cunmr2
- cunmr3
- cunmrq
- cunmrz
- cunmtr
- cupgtr
- cupmtr
- dbdsdc
- dbdsqr
- ddisna
- dgbbrd
- dgbccon
- dgbequ
- dgbrfs
- dgbsv
- dgbsvx
• dgbtf2
• dgbtrf
• dgbtrs
• dgebak
• dgebal
• dgebd2
• dgebrd
• dgecon
• dgeequ
• dgees
• dgeesx
• dgeev
• dgeevo
• dgegs
• dgegv
• dgehd2
• dgehrd
• dgel2q
• dgelqf
• dgels
• dgelsd
• dgelss
• dgelsx
• dgelsy
• dgeql2
• dgeqlf
• dgeqpsp
• dgeqpf
• dgeqrs
• dgeqrf
• dgerfs
• dgerq2
• dgerqf
• dgesc2
• dgesdd
• dgesv
- dgesvd
- dgesvx
- dgetc2
- dgetf2
- dgetrf
- dgetri
- dgetrs
- dggbak
- dggbal
- dggges
- dgggesx
- dggev
- dggevx
- dggglm
- dgghrd
- dgglse
- dggqr
- dggqrf
- dggsvd
- dggsvp
- dgtcon
- dgtfs
- dgtv
- dgtsv
- dgtsvx
- dgttrf
- dgttrs
- dgtts2
- dhgeqz
- dhsein
- dhseqr
- disnan
- dlabad
- dlabrd
- dlabrd
- dlacn2
- dlacon
- dlacpy

5.19. LAPACK functions for Cython
• dladiv
• dlae2
• dlaebz
• dlaed0
• dlaed1
• dlaed2
• dlaed3
• dlaed4
• dlaed5
• dlaed6
• dlaed7
• dlaed8
• dlaed9
• dlaeda
• dlaein
• dlaev2
• dlaexc
• dlag2
• dlag2s
• dlags2
• dlagtf
• dlagtm
• dлагts
• dlagv2
• dlahqr
• dlahr2
• dlahrd
• dlaic1
• dlaqn2
• dlals0
• dlalsa
• dlalsd
• dlamch
• dlamrg
• dlaneg
• dlangb
• dlange
• dlangt
• dlanhs
• dlansb
• dlansp
• dlanst
• dlansy
• dlantb
• dlantp
• dlantr
• dlav2
• dlapl1
• dlapmt
• dlapy2
• dlapy3
• dlagb
• dlagge
• dlaqp2
• dlaqps
• dlaur0
• dlaur1
• dlaur2
• dlaur3
• dlaur4
• dlaur5
• dlaurb
• dlaurp
• dlaury
• dlaur
• dlar1v
• dlar2v
• dlarf
• dlarfb
• dlarfg
• dlarf
• dlarfx
• dlargv
• dlarnv
• dlarr
• dlarrb
• dlarrc
• dlarrd
• dlarr
• dlarr
• dlarr
• dlarr
• dlarr
• dlarr
• dlarrv
• dlartg
• dlartv
• dlaruv
• dlarz
• dlarzb
• dlarzt
• dlas2
• dlascl
• dlasd0
• dlasd1
• dlasd2
• dlasd3
• dlasd4
• dlasd5
• dlasd6
• dlasd7
• dlasd8
• dlasda
• dlasdq
• dlasdt
• dlaset
• dlasq1
• dlasq2
• dlasq6
- dlasr
- dlasrt
- dlassq
- dlasv2
- dlaswp
- dlasy2
- dlasyc
- dlatbs
- dlatdf
- dlatps
- dlatrd
- dlatrs
- dlatrz
- dlatzm
- dlauu2
- dlauum
- dopgtr
- dopmtr
- dorg2l
- dorg2r
- dorgbr
- dorghr
- dorgl2
- dorglq
- dorglq
- dorgqr
- dorgqr2
- dorgq2
- dorgq2
- dorgtr
- dorm2l
- dorm2r
- dormbr
- dormhr
- dorml2
- dormlq
- dormql
dormqr
• dormr2
• dormr3
• dormrq
• dormrz
• dormtr
• dpbcon
• dpbequ
• dpbrfs
• dpbstf
• dpbsv
• dpbsvx
• dpbtf2
• dpbtrf
• dpbtrs
• dpocon
• dpoequ
• dpors
• dposv
• dposvx
• dpotf2
• dpotrf
• dpotri
• dpotrs
• dppcon
• dppequ
• dpprfs
• dpssv
• dpssvx
• dpptf
• dpptrf
• dpptri
• dpptrs
• dptcon
• dpteqr
• dptrfs
• dptsv
5.19. LAPACK functions for Cython
• dstev
• dstevd
• dstevr
• dstevx
• dsycon
• dsyev
• dsyevd
• dsyevr
• dsyevx
• dsygs2
• dsygst
• dsygv
• dsygvd
• dsygvx
• dsyrfs
• dsysv
• dsyevx
• dsytd2
• dsytf2
• dsytrd
• dsytrf
• dsytri
• dsytrs
• dtbcon
• dtbfrs
• dtbtrs
• dtgevc
• dtgex2
• dtgexc
• dtgsen
• dtgsja
• dtgsna
• dtgsy2
• dtgsyl
• dtpcon
• dtprfs
• dptri
• dptrs
• dtrcon
• dtrevc
• dtrexc
• dtrrfs
• dtrsen
• dtrsna
• dtrsy1
• dtrti2
• dtrtri
• dtrtrs
• dtzrqf
• dtzrzf
• dzsum1
• icmax1
• ieeeck
• ilaver
• izmax1
• sbdsdc
• sbdsqr
• scsum1
• sdisna
• sgbbrd
• sgbcon
• sbgequ
• sgbrfs
• sgbv
• sgbsv
• sgbsvx
• sgbrtf2
• sgbtrf
• sgbtrs
• sgebak
• sgebal
• sgebd2
• sgebrd
• sgecon
• sgeequ
• sgees
• sgeesx
• sgeev
• sgeevx
• sgegs
• sgegv
• sgehd2
• sgehrd
• sgelq2
• sgelqf
• sgels
• sgelsd
• sgelss
• sgelsx
• sgelsy
• sgeql2
• sgeqlf
• sgeqps3
• sgeqpfs
• sgeqrf
• sgerfs
• sgerf2
• sgerq2
• sgerqf
• sgesc2
• sgesdd
• sgesv
• sgesvd
• sgesvvx
• sgetc2
• sgetrf2
• sgetrf
• sgetri
• sgetrs
5.19. LAPACK functions for Cython

- sggbak
- sggbal
- sgges
- sggesx
- sggev
- sggevx
- sggglm
- sgghrd
- sgglse
- sgglse
- sgqr
- sggqr
- sggsvd
- sggsvp
- sgtcon
- sgtrfs
- sgtsv
- sgtsvx
- sgtrf
- sgtrfs
- sgtts2
- shgeqz
- shsein
- shseqr
- slabad
- slabrd
- slacn2
- slacon
- slacpy
- sladiv
- slae2
- slaebz
- slaed0
- slaed1
- slaed2
- slaed3
- slaed4
- slaed5
- slaed6
- slaed7
- slaed8
- slaed9
- slaeda
- slacn
- slaev2
- slaexc
- slag2
- slag2d
- slags2
- slagt
- slagt
- slagt
- slagts
- slavg2
- slahqr
- slahr2
- slahrd
- slaic1
- slain2
- slals0
- slalsal
- slalsd
- slasal
- slamsal
- slamsalg
- slamsalg
- slangb
- slange
- slangt
- slanhs
- slansb
- slansp
- slanst
- slansy
- slantb
- slantp
• slantr
• slanv2
• slapll
• slapmt
• slapy2
• slapy3
• slaqgb
• slaqge
• slaqp2
• slaqps
• slaqr0
• slaqr1
• slaqr2
• slaqr3
• slaqr4
• slaqr5
• slaqsb
• slaqsp
• slaqsy
• slaqrt
• slar1v
• slar2v
• slarf
• slarfb
• slarfge
• slarfbg
• slarf
• slarfx
• slargv
• slarnv
• slarra
• slarvb
• slarvc
• slarvd
• slarre
• slarrr
• slarrrj
• slarrk
• slarr
• slarrv
• slartg
• slartv
• slaruv
• slarz
• slarzb
• slarzt
• slas2
• slascl
• slasd0
• slasd1
• slasd2
• slasd3
• slasd4
• slasd5
• slasd6
• slasd7
• slasd8
• slasda
• slasdq
• slasdt
• slaset
• slasq1
• slasq2
• slasq6
• slasr
• slasrt
• slassq
• slasv2
• slaswp
• slasy2
• slasyf
• slatbs
• slatdf
• slatps
• slatrd
• slatrs
• slatrz
• slatzm
• slauu2
• slauum
• sopgtr
• sopmtr
• sorg2l
• sorg2r
• sorghr
• sorgl2
• sorglq
• sorgql
• sorgqr
• sorg2l
• sorg2r
• sorgl2
• sorglq
• sorgql
• sorgqr
• sormbr
• sormhr
• sorml2
• sormlq
• sormql
• sormqr
• sorm2l
• sorm2r
• sormbr
• sormhr
• sorml2
• sormlq
• sormql
• sormqr
• sorm2l
• sorm2r
• sormbr
• sormhr
• sorml2
• sormlq
• sormql
• sormqr
• spbcon
• spbequ
• spbrfs
• spbstf
• spbsv
• spbsvx
• spbtf2
• spbtrf
• spbtrs
• spocon
• spoequ
• sporfs
• sposv
• sposvx
• spotf2
• spotrf
• spotri
• spotrs
• sppcon
• sppequ
• spprfs
• spps
• sppspx
• spptrf
• spptri
• spptrrs
• sptcon
• spteqr
• spttrfs
• sptsv
• sptsvx
• spttrf
• spttrs
• sptts2
• srsc1
• ssbev
• ssbevd
• ssbevx
• ssbgst
• ssbgv
• ssbgvd
• ssbgvx
• ssbtrd
• sspcon
• sspev
• sspevd
• sspevx
• sspgst
• sspgv
• sspgvd
• sspgvx
• ssprfs
• sspsv
• sspsvx
• ssptrd
• ssptrf
• ssptri
• ssptrs
• sstebz
• sstedc
• sstegr
• sstein
• sstemr
• ssteqr
• ssterf
• sstev
• sstevd
• sstevr
• sstevx
• ssycon
• ssyev
• ssyevd
• ssyevr
• ssyevx
• ssygs2
• ssygst
• ssygv
• ssygd
• ssygvx
• ssytrfs
• ssysv
• ssysvx
• ssytd2
• ssytf2
• ssytrd
• ssytrfs
• ssytri
• ssytrs
• stbcon
• stbrfs
• stbtrs
• stgevc
• stgex2
• stgexc
• stgsen
• stgsja
• stgsna
• stgsy2
• stgsyl
• stpcn
• stprfs
• stptri
• stptrs
• strcon
• strevc
• strexc
• strtrfs
• strsen
• strsna
• strsna
• strsy2l
• strti2
• strtri
• strtrs
• stzrqf
• stzrzf
• zbdsqr
• zdrscl
• zgbbzd
• zgbcon
• zgbequ
• zgbrfs
• zgbsv
• zgbsvx
• zgbtf2
• zgbtrf
• zgbtrs
• zgebak
• zgebal
• zgebd2
• zgebrd
• zgecon
• zgeequ
• zgees
• zgeesx
• zgeev
• zgeevx
• zgegs
• zgegy
• zgehd2
• zgehrd
• zgelq2
• zgelqf
• zgels
• zgelsd
• zgelsf
• zgelsx
• zgelsy
• zgeql2
• zgeqlf
• zgeqp3
• zgeqpf
• zgeqr2
• zgeqrf
• zgerfs
• zgerq2
• zgerqf
• zgesc2
• zgesdd
• zgesv
• zgesvd
• zgesvx
• zgetc2
• zgetf2
• zgetrf
• zgetri
• zgetrs
• zggbak
• zggbal
• zgges
• zggesx
• zggev
• zggevx
• zgglm
• zgghrd
• zgglse
• zgglr
• zggrqf
• zggrqf
• zggsvd
• zggsvd
• zggsyv
• zgtcon
• zgtcon
• zgtsv
• zgtsvx
- zgttrf
- zgttrs
- zgtts2
- zhbev
- zhbevd
- zhbevx
- zhbgst
- zhbgv
- zhbgvd
- zhbgvx
- zhbtrd
- zhecon
- zheev
- zheevd
- zheevr
- zheevx
- zhegs2
- zhegst
- zhegv
- zhegvd
- zhegvx
- zherfs
- zhesv
- zhesvx
- zhetd2
- zhetf2
- zhetrd
- zhetrf
- zhetri
- zhetrs
- zhgeqz
- zhpccon
- zhpev
- zhpevd
- zhpevx
- zhpgst
• zhpgv
• zhpgvd
• zhpgvx
• zhprfs
• zhpsv
• zhpsvx
• zhptrd
• zhptrf
• zhptri
• zhptrs
• zhsein
• zhseqr
• zlabrd
• zlacgv
• zlacn2
• zlacon
• zlap2
• zlacpy
• zlacrm
• zlacrt
• zladiv
• zlaed0
• zlaed7
• zlaed8
• zlaein
• zlaesy
• zlaev2
• zlag2c
• zlags2
• zlagtm
• zlahf
• zlahqr
• zlahr2
• zlahrd
• zlaic1
• zlals0
• zlalsa
• zlalzd
• zlangb
• zlange
• zlangt
• zlanhb
• zlanhe
• zlanhp
• zlanhs
• zlanht
• zlansb
• zlansp
• zlansy
• zlanb
• zlanp
• zlantr
• zlapll
• zlapmt
• zlaqgb
• zlaqge
• zlaqhb
• zlaqhe
• zlaqhp
• zlaqp2
• zlaqps
• zlaqr0
• zlaqr1
• zlaqr2
• zlaqr3
• zlaqr4
• zlaqr5
• zlaqsb
• zlaqsp
• zlaqsy
• zlar1v
• zlar2v
• zlarcm
• zlarf
• zlarfb
• zlarfg
• zlarft
• zlarfx
• zlargv
• zlarnv
• zlarrv
• zlartg
• zlartv
• zlarz
• zlarzb
• zlarzt
• zlascl
• zlaset
• zlasr
• zlassq
• zlaswp
• zlasyf
• zlatbs
• zlatdf
• zlatps
• zlatrd
• zlatrs
• zlatrz
• zlatzm
• zlaau2
• zlaauum
• zpbcon
• zpbcon
• zpbequ
• zpbequ
• zpbfs
• zpbfs
• zpbstf
• zpbstf
• zpbsv
• zpbsv
• zpbsvx
• zpbsvx
• zpbtf2
• zpbtf2
• zpbtrf
• zpbtrs
• zpocon
• zpoequ
• zporfs
• zposv
• zposvx
• zpotf2
• zpotrf
• zpotri
• zpotrs
• zppcon
• zppequ
• zpprfs
• zppsv
• zppsvx
• zppptrf
• zppptri
• zppptrs
• zptcon
• zpteqr
• zptrfs
• zptsv
• zptsvx
• zpttrf
• zpttrs
• zptts2
• zrot
• zspcon
• zspmv
• zspr
• zsprfs
• zspsv
• zspsvx
• zsptrfs
• zsptri
• zsptrs
• zstedc
• zstegr
• zstein
• zstemr
• zsteqr
• zsycon
• zsynv
• zsy
• zsyrf
• zsysv
• zsysvx
• zsytf2
• zsytrf
• zsytri
• zsytrs
• ztbcn
• ztbrfs
• ztbrts
• ztgevc
• ztgex2
• ztgexc
• ztgcn
• ztgja
• ztgna
• ztg2
• ztgsyl
• ztpcon
• ztrfs
• ztptri
• ztptrs
• ztrcon
• ztrevc
• ztrexc
• ztrfrs
• ztrsen
• ztrsen
• ztrsn
• ztrsy1
• ztrti2
• ztrtri
• ztrtrs
• ztzrqf
• ztzrzf
• zung2l
• zung2r
• zungbr
• zunghr
• zungl2
• zunglq
• zungql
• zungqr
• zungr2
• zungrq
• zungtr
• zunm2l
• zunm2r
• zunmbr
• zunmhr
• zunml2
• zunmlq
• zunmql
• zunmqr
• zunmr2
• zunmr3
• zunmrq
• zunmrx
• zunmxr
• zupgtr
• zupmtr
• zupmtr
• zupmtr

5.19. LAPACK functions for Cython
5.20 Interpolative matrix decomposition (\texttt{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

\[
A \Pi = \begin{bmatrix} A \Pi_1 & A \Pi_2 \end{bmatrix} = A \Pi_1 [I \ T],
\]

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) \( A \approx USV^* \), 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 \( P \).

5.20.1 Routines

Main functionality:

\begin{verbatim}
interp_decomp(A, eps_or_k[, rand]) Compute ID of a matrix.
reconstruct_matrix_from_id(B, idx, proj) Reconstruct matrix from its ID.
reconstruct_interp_matrix(idx, proj) Reconstruct interpolation matrix from ID.
reconstruct_skel_matrix(A, k, idx) Reconstruct skeleton matrix from ID.
id_to_svd(B, idx, proj) Convert ID to SVD.
svd(A, eps_or_k[, rand]) Compute SVD of a matrix via an ID.
estimate_spectral_norm(A[, its]) Estimate spectral norm of a matrix by the randomized power method.
estimate_spectral_norm_diff(A, B[, its]) Estimate spectral norm of the difference of two matrices by the randomized power method.
estimate_rank(A, eps) Estimate matrix rank to a specified relative precision using randomized methods.
\end{verbatim}

\texttt{scipy.linalg.interpolative \texttt{interp_decomp} (A, \textit{eps_or_k}, \textit{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:

\[
\text{numpy.dot}(A[:,idx[:k]], proj) = A[:,idx[k:]]
\]

The original matrix can then be reconstructed as:

\[
\text{numpy.hstack}([A[:,idx[:k]],
    
    \text{numpy.dot}(A[:,idx[:k]], proj)])
\][:,\text{numpy.argsort(idx)}]

or via the routine \texttt{reconstruct_matrix_from_id}. This can equivalently be written as:

\[
\text{numpy.dot}(A[:,idx[:k]],
    
    \text{numpy.hstack}([\text{numpy.eye}(k), proj]))
\][:,\text{np.argsort(idx)}]
in terms of the skeleton and interpolation matrices:

\[ B = A[:, \text{idx}[:k]] \]

and:

\[ P = \text{numpy.hstack([\text{numpy.eye(k), proj}][:, \text{np.argsort(idx)}])} \]

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 \((\text{eps}_or_k < 1)\), then this function has the output signature:

\[ k, \text{idx}, \text{proj} = \text{interp_decomp}(A, \text{eps}_or_k) \]

Otherwise, if a rank is specified \((\text{eps}_or_k \geq 1)\), then the output signature is:

\[ \text{idx}, \text{proj} = \text{interp_decomp}(A, \text{eps}_or_k) \]

**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 \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**

- **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(B, idx, proj)**

Reconstruct matrix from its ID.

A matrix \( A \) with skeleton matrix \( B \) and ID indices and coefficients \( \text{idx} \) and \( \text{proj} \), respectively, can be reconstructed as:

\[ \text{numpy.hstack}([B, \text{numpy.dot}(B, \text{proj})][:, \text{numpy.argsort(idx)}]) \]

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**

- **numpy.ndarray**: Reconstructed 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 \( \text{idx} \) and \( \text{proj} \), respectively, as:
\[
P = \text{numpy.hstack([numpy.eye(proj.shape[0]), proj]][:, \text{numpy.argsort(idx)}])
\]

The original matrix can then be reconstructed from its skeleton matrix \( B \) via:
\[
\text{numpy.dot}(B, P)
\]

See also \texttt{reconstruct\_matrix\_from\_id} and \texttt{reconstruct\_skel\_matrix}.

\begin{tabular}{ll}
\textbf{Parameters} & \textbf{idx} : \text{numpy.ndarray} \\
& Column index array. \\
\textbf{proj} : \text{numpy.ndarray} \\
& Interpolation coefficients. \\
\end{tabular}

Returns \text{numpy.ndarray} Interpolation matrix.

\texttt{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:
\[
B = A[:, \text{idx}[:k]]
\]

The original matrix can then be reconstructed via:
\[
\text{numpy.hstack([B, \text{numpy.dot}(B, proj)])[:, \text{numpy.argsort(idx)}]}
\]

See also \texttt{reconstruct\_matrix\_from\_id} and \texttt{reconstruct\_interp\_matrix}.

\begin{tabular}{ll}
\textbf{Parameters} & \textbf{A} : \text{numpy.ndarray} \\
& Original matrix. \\
\textbf{k} : \text{int} \\
& Rank of ID. \\
\textbf{idx} : \text{numpy.ndarray} \\
& Column index array. \\
\end{tabular}

Returns \text{numpy.ndarray} Skeleton matrix.

\texttt{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:
\[
U, S, V = \text{id\_to\_svd}(B, idx, proj) \\
A = \text{numpy.dot}(U, \text{numpy.dot}(\text{numpy.diag}(S), V.\text{conj}.T))
\]

See also \texttt{svd}.

\begin{tabular}{ll}
\textbf{Parameters} & \textbf{B} : \text{numpy.ndarray} \\
& Skeleton matrix. \\
\textbf{idx} : \text{numpy.ndarray} \\
& Column index array. \\
\textbf{proj} : \text{numpy.ndarray} \\
& Interpolation coefficients. \\
\end{tabular}

Returns \text{numpy.ndarray} \\
\begin{tabular}{l}
Left singular vectors. \\
Singular values. \\
\end{tabular}

\begin{tabular}{l}
\textbf{U} : \text{numpy.ndarray} \\
\textbf{S} : \text{numpy.ndarray} \\
\textbf{V} : \text{numpy.ndarray} \\
\end{tabular}
Right singular vectors.

\texttt{scipy.linalg.interpolative.svd}(A, \textit{eps_or_k}, \textit{rand}=True)

Compute SVD of a matrix via an ID.

An SVD of a matrix \( A \) is a factorization:

\[
A = \text{numpy.dot}(U, \text{numpy.dot}(\text{numpy.diag}(S), V.conj().T))
\]

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 \( \textit{eps_or_k} \)).

See also \texttt{interp_decomp} and \texttt{id_to_svd}.

\textbf{Parameters}
\begin{itemize}
  \item \texttt{A}: \texttt{numpy.ndarray} or \texttt{scipy.sparse.linalg.LinearOperator}
    Matrix to be factored, given as either a \texttt{numpy.ndarray} or a \texttt{scipy.sparse.linalg.LinearOperator} with the \texttt{matvec} and \texttt{rmatvec} methods (to apply the matrix and its adjoint).
  \item \texttt{eps_or_k} : float or int
    Relative error (if \( \textit{eps_or_k} < 1 \)) or rank (if \( \textit{eps_or_k} \geq 1 \)) of approximation.
  \item \texttt{rand} : bool, optional
    Whether to use random sampling if \( A \) is of type \texttt{numpy.ndarray}
    (randomized algorithms are always used if \( A \) is of type \texttt{scipy.sparse.linalg.LinearOperator}).
\end{itemize}

\textbf{Returns}
\begin{itemize}
  \item \texttt{U}: \texttt{numpy.ndarray}
    Left singular vectors.
  \item \texttt{S}: \texttt{numpy.ndarray}
    Singular values.
  \item \texttt{V}: \texttt{numpy.ndarray}
    Right singular vectors.
\end{itemize}

\texttt{scipy.linalg.interpolative.estimate_spectral_norm}(A, \textit{its}=20)

Estimate spectral norm of a matrix by the randomized power method.

\textbf{Parameters}
\begin{itemize}
  \item \texttt{A}: \texttt{scipy.sparse.linalg.LinearOperator}
    Matrix given as a \texttt{scipy.sparse.linalg.LinearOperator} with the \texttt{matvec} and \texttt{rmatvec} methods (to apply the matrix and its adjoint).
  \item \texttt{its} : int, optional
    Number of power method iterations.
\end{itemize}

\textbf{Returns}
\begin{itemize}
  \item \texttt{float}
    Spectral norm estimate.
\end{itemize}

\texttt{scipy.linalg.interpolative.estimate_spectral_norm_diff}(A, B, \textit{its}=20)

Estimate spectral norm of the difference of two matrices by the randomized power method.

\textbf{Parameters}
\begin{itemize}
  \item \texttt{A}: \texttt{scipy.sparse.linalg.LinearOperator}
    First matrix given as a \texttt{scipy.sparse.linalg.LinearOperator} with the \texttt{matvec} and \texttt{rmatvec} methods (to apply the matrix and its adjoint).
  \item \texttt{B}: \texttt{scipy.sparse.linalg.LinearOperator}
    Second matrix given as a \texttt{scipy.sparse.linalg.LinearOperator} with the \texttt{matvec} and \texttt{rmatvec} methods (to apply the matrix and its adjoint).
  \item \texttt{its} : int, optional
    Number of power method iterations.
\end{itemize}

\textbf{Returns}
\begin{itemize}
  \item \texttt{float}
    Spectral norm estimate of matrix difference.
\end{itemize}

\texttt{scipy.linalg.interpolative.estimate_rank}(A, \textit{eps})

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:

```python
seed([seed])  
Seed the internal random number generator used in this ID package.

rand(*shape)  
Generate standard uniform pseudorandom numbers via a very efficient lagged Fibonacci method.
```

scipy.linalg.interpolative.seed(seed=None)

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(*shape)

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

### 5.20.2 References

This module uses the ID software package [R439] by Martinsson, Rokhlin, Shkolnisky, and Tygert, which is a Fortran library for computing IDs using various algorithms, including the rank-revealing QR approach of [R440] and the more recent randomized methods described in [R441], [R442], and [R443]. 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.

### 5.20.3 Tutorial

**Initializing**

The first step is to import `scipy.linalg.interpolative` by issuing the command:
>>> import scipy.linalg.interpolative as sli

Now let's build a matrix. For this, we consider a Hilbert matrix, which is well know to have low rank:

```python
>>> from scipy.linalg import hilbert
```
```
>>> import numpy as np
```
```
>>> 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 idx; and
3. interpolation coefficients proj.

The ID is specified by the relation `np.dot(A[:,idx[:k]], proj) == A[:,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:

\[
>>> \text{idx, proj} = \text{sli.interp_decomp}(A, k)
\]

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:

\[
>>> k, \text{idx, proj} = \text{sli.interp_decomp}(A, \text{eps, rand=False})
\]

and:

\[
>>> \text{idx, proj} = \text{sli.interp_decomp}(A, k, \text{rand=False})
\]

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:

\[
>>> k, \text{idx, proj} = \text{sli.interp_decomp}(L, \text{eps})
\]

To compute an ID to a fixed rank, use:

\[
>>> \text{idx, proj} = \text{sli.interp_decomp}(L, k)
\]

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:

\[
>>> B = \text{sli.reconstruct_skel_matrix}(A, k, \text{idx})
\]

for the skeleton matrix and:

\[
>>> P = \text{sli.reconstruct_interp_matrix}(\text{idx, proj})
\]

for the interpolation matrix. The ID approximation can then be computed as:

\[
>>> C = \text{np.dot}(B, P)
\]

This can also be constructed directly using:

\[
>>> C = \text{sli.reconstruct_matrix_from_id}(B, \text{idx, proj})
\]
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.
5.21 Miscellaneous routines (scipy.misc)

Various utilities that don’t have another home.

Note that the Python Imaging Library (PIL) is not a dependency of SciPy and therefore the pilutil module is not available on systems that don’t have PIL installed.

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ascent()</td>
<td>Get an 8-bit grayscale bit-depth, 512 x 512 derived image for easy use in demos</td>
</tr>
<tr>
<td>bytescale()</td>
<td>Byte scales an array (image).</td>
</tr>
<tr>
<td>central_diff_weights()</td>
<td>Return weights for an Np-point central derivative.</td>
</tr>
<tr>
<td>comb(N, k[, exact, repetition])</td>
<td>The number of combinations of N things taken k at a time.</td>
</tr>
<tr>
<td>derivative()</td>
<td>Find the n-th derivative of a function at a point.</td>
</tr>
<tr>
<td>face()</td>
<td>Get a 1024 x 768, color image of a raccoon face.</td>
</tr>
<tr>
<td>factorial()</td>
<td>The factorial function, n! = special.gamma(n+1).</td>
</tr>
<tr>
<td>factorial2()</td>
<td>Double factorial.</td>
</tr>
<tr>
<td>factorialk()</td>
<td>n(!(!!...!)) = multifactorial of order k</td>
</tr>
<tr>
<td>fromimage()</td>
<td>Return a copy of a PIL image as a numpy array.</td>
</tr>
<tr>
<td>imfilter()</td>
<td>Simple filtering of an image.</td>
</tr>
<tr>
<td>imread()</td>
<td>Read an image from a file as an array.</td>
</tr>
<tr>
<td>imresize()</td>
<td>Resize an image.</td>
</tr>
<tr>
<td>imrotate()</td>
<td>Rotate an image counter-clockwise by angle degrees.</td>
</tr>
<tr>
<td>imsave()</td>
<td>Save an array as an image.</td>
</tr>
<tr>
<td>info()</td>
<td>Simple showing of an image through an external viewer.</td>
</tr>
<tr>
<td>lena()</td>
<td>Get classic image processing example image, Lena, at 8-bit grayscale bit-depth, 512 x 512 size.</td>
</tr>
<tr>
<td>logsumexp()</td>
<td>Compute the log of the sum of exponentials of input elements.</td>
</tr>
<tr>
<td>pade()</td>
<td>Return Padé approximation to a polynomial as the ratio of two polynomials.</td>
</tr>
<tr>
<td>toimage()</td>
<td>Takes a numpy array and returns a PIL image.</td>
</tr>
<tr>
<td>who()</td>
<td>Print the Numpy arrays in the given dictionary.</td>
</tr>
</tbody>
</table>

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 accent-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()
```
scipy.misc.bytescale(data, cmin=None, cmax=None, high=255, low=0)

Byte scales an array (image).

Byte scaling means converting the input image to uint8 dtype and scaling the range to (low, high) (default 0-255). If the input image already has dtype uint8, no scaling is done.

**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
>>> img = array([[ 91.06794177,  3.39058326,  84.4221549 ],
                [ 73.88003259,  80.91433048,  4.88878881],
                [ 51.53875334,  34.45808177,  27.5873488 ]])

>>> bytescale(img)
dtype=uint8)
array([[255,  0, 236],
       [205, 225,  4],
       [140,  90,  70]],

>>> bytescale(img, high=200, low=100)
dtype=uint8)
array([[200, 100, 192],
       [180, 188, 102],
       [155, 135, 128]],

>>> bytescale(img, cmin=0, cmax=255)
dtype=uint8)
array([[91,  3, 84],
       [74,  81,  5],
       [52,  34,  28]],
```
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] * f(x-h0*dx) + ... + w[-1] * f(x+h0*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.

scipy.misc.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, ndarray
   The total number of combinations.

Notes

• Array arguments accepted only for exact=False case.

• If k > N, N < 0, or k < 0, then a 0 is returned.

Examples

>>> from scipy.special import comb
>>> k = np.array([3, 4])
>>> n = np.array([10, 10])
>>> comb(n, k, exact=False)
array([[ 120.,  210.],
       [220L, 270L]])

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 : int, optional

5.21. Miscellaneous routines (scipy.misc)
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
def f(x):
    return x**3 + x**2
```
```python
derivative(f, 1.0, dx=1e-6)
4.999999999217337
```

`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 then return color image, otherwise return an 8-bit gray-scale

**Returns**

**face**: ndarray
image of a raccoon face

**Examples**
```python
import scipy.misc
face = scipy.misc.face()
face.shape
(768, 1024, 3)
face.max()
230
face.dtype
dtype('uint8')
```
```python
import matplotlib.pyplot as plt
plt.gray()
plt.imshow(face)
plt.show()
```
scipy.misc.factorial\((n, exact=False)\)

The factorial function, \(n! = \text{special.gamma}(n+1)\).

If `exact` is 0, then floating point precision is used, otherwise exact long integer is computed.

- Array argument accepted only for `exact=False` case.
- If \(n<0\), the return value is 0.

**Parameters**

- `n` : int or array_like of ints
  
  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. If `exact` is set to True, calculate the answer exactly using integer arithmetic. Default is False.

**Returns**

- `nf` : float or int
  
  Factorial of \(n\), as an integer or a float depending on `exact`.

**Examples**

```python
>>> from scipy.special import factorial
>>> arr = np.array([3, 4, 5])
>>> factorial(arr, exact=False)
array([  6.,  24., 120.])
>>> factorial(5, exact=True)
120L
```

scipy.misc.factorial2\((n, exact=False)\)

Double factorial.

This is the factorial with every second value skipped, i.e., \(7!! = 7 \times 5 \times 3 \times 1\). It can be approximated numerically as:

\[
\begin{align*}
n!! &= \text{special.gamma}(n/2+1) \times 2^{\frac{n}{2}} \gamma\left(\frac{m+1}{2}\right) / \sqrt{\pi} & n \text{ odd} \\
&= 2^{\frac{n}{2}} (n/2)! & n \text{ even}
\end{align*}
\]

**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)
array(105.00000000000001)
>>> factorial2(7, exact=True)
105L

scipy.misc.factorialk \((n, k, exact=True)\)
\(n(!!...) = \) multifactorial of order \( k \) \( k \) times

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 val : int
    Multi factorial of \( n \).

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.misc.fromimage \((im, flatten=0)\)
Return a copy of a PIL image as a numpy array.

Parameters
im : PIL image
    Input image.
flatten : bool
    If true, convert the output to grey-scale.

Returns fromimage : ndarray
    The different colour bands/channels are stored in the third dimension, such that a
grey-image is \( M \times N \), an RGB-image \( M \times N \times 3 \) and an RGBA-image \( M \times N \times 4 \).

scipy.misc.imfilter \((arr, ftype)\)
Simple filtering of an image.

Parameters
arr : ndarray
    The array of Image in which the filter is to be applied.
ftype : str

Returns imfilter : ndarray
    The array with filter applied.
**Raises**  
*ValueError*  
*Unknown filter type.* If the filter you are trying to apply is unsupported.

```python
scipy.misc.imread(name, flatten=0)
```

Read an image from a file as an array.

**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.

**Returns**  
- **imread**: ndarray  
  The array obtained by reading image from file `infile`.

**Notes**

The image is flattened by calling convert('F') on the resulting image object.

```python
scipy.misc.imresize(arr, size, interp='bilinear', mode=None)
```

Resize an image.

**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.  
- **interp**: str, optional  
  Interpolation to use for re-sizing (‘nearest’, ‘bilinear’, ‘bicubic’ or ‘cubic’).  
- **mode**: str, optional  
  The PIL image mode (‘P’, ‘L’, etc.) to convert `arr` before resizing.

**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.

```python
scipy.misc.imrotate(arr, angle, interp='bilinear')
```

Rotate an image counter-clockwise by angle degrees.

**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  
  - ‘cubic’ : cubic  
  - ‘bicubic’ : for bicubic

**Returns**  
- **imrotate**: ndarray  
  The rotated array of image.

```python
scipy.misc.imsave(name, arr, format=None)
```

Save an array as an image.
**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
gradient = np.zeros((255, 255))
gradient = np.zeros((255, 255), dtype=np.uint8)
gradient[:,] = np.arange(255)
imsave('/tmp/gradient.png', gradient)
```

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)
rgb[...], 1] = 55
rgb[...], 2] = 1 - np.arange(255)
imsave('/tmp/rgb_gradient.png', rgb)
```

**scipy.misc.imshow(arr)**

Simple showing of an image through an external viewer.

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.

**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.pilutil.imshow(a)
```

**scipy.misc.info(object=None, maxwidth=76, output=<open file '<stdout>', mode 'w' at 0x7fa42a301150>, toplevel='scipy')**

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
>>> 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.

>>> 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. ***

scipy.misc.lena()
Get classic image processing example image, Lena, at 8-bit grayscale bit-depth, 512 x 512 size.

Parameters

Returns
lena : ndarray
   Lena image

Notes
Though safe for work in most places, this sexualized image is drawn from Playboy and makes some viewers uncomfortable. It has been very widely used as an example in image processing and is therefore made available for compatibility. For new code that needs an example image we recommend face or ascent.

Examples
>>> import scipy.misc
>>> lena = scipy.misc.lena()
>>> lena.shape
(512, 512)
>>> lena.max()
245
>>> lena.dtype
dtype('int32')

>>> import matplotlib.pyplot as plt
>>> plt.gray()
>>> plt.imshow(lena)
>>> plt.show()
scipy.misc.logsumexp(a, axis=None, b=None, keepdims=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. Tuple of ints is not accepted if NumPy version is lower than 1.7.0.
  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 \( a \).
  New in version 0.12.0.

Returns

- **res**: ndarray
  The result, \( \log(\sum(\exp(a))) \) calculated in a numerically more stable way. If \( b \) is given then \( \log(\sum(b \times \exp(a))) \) 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.misc 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
```

`scipy.misc.pade(an, m)`

Return Pade approximation to a polynomial as the ratio of two polynomials.

**Parameters**

- `an`: (N,) array_like
  - Taylor series coefficients.
- `m`: int
  - The order of the returned approximating polynomials.

**Returns**

- `p, q`: Polynomial class
  - The pade approximation of the polynomial defined by `an` is `p(x)/q(x)`.

**Examples**

```python
>>> from scipy import misc
>>> e_exp = [1.0, 1.0, 1.0/2.0, 1.0/6.0, 1.0/24.0, 1.0/120.0]
>>> p, q = misc.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)`

```python
>>> e_poly(1)
2.7166666666666668
>>> p(1)/q(1)
2.7179487179487181
```

`scipy.misc.toimage(arr, high=255, low=0, cmin=None, cmax=None, pal=None, mode=None, channel_axis=None)`

Takes a numpy array and returns a PIL image.

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.

**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.

`scipy.misc.who(vardict=None)`

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

>>> 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
```

5.22 Multi-dimensional image processing (scipy.ndimage)

This package contains various functions for multi-dimensional image processing.

5.22.1 Filters scipy.ndimage.filters

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>convolve</td>
<td>Multidimensional convolution.</td>
</tr>
<tr>
<td>convolve1d</td>
<td>Calculate a one-dimensional convolution along the given axis.</td>
</tr>
<tr>
<td>correlate</td>
<td>Multidimensional correlation.</td>
</tr>
<tr>
<td>correlate1d</td>
<td>Calculate a one-dimensional correlation along the given axis.</td>
</tr>
<tr>
<td>gaussian_filter</td>
<td>Multidimensional Gaussian filter.</td>
</tr>
<tr>
<td>gaussian_filter1d</td>
<td>One-dimensional Gaussian filter.</td>
</tr>
<tr>
<td>gaussian_gradient_magnitude</td>
<td>Multidimensional gradient magnitude using Gaussian derivatives.</td>
</tr>
<tr>
<td>gaussian_laplace</td>
<td>Multidimensional Laplace filter using gaussian second derivatives.</td>
</tr>
<tr>
<td>generic_filter</td>
<td>Calculates a multi-dimensional filter using the given function.</td>
</tr>
<tr>
<td>generic_filter1d</td>
<td>Calculate a one-dimensional filter along the given axis.</td>
</tr>
<tr>
<td>generic_gradient_magnitude</td>
<td>Gradient magnitude using a provided gradient function.</td>
</tr>
<tr>
<td>generic_laplace</td>
<td>N-dimensional Laplace filter using a provided second derivative function.</td>
</tr>
<tr>
<td>laplace</td>
<td>N-dimensional Laplace filter based on approximate second derivatives.</td>
</tr>
<tr>
<td>maximum_filter</td>
<td>Calculates a multi-dimensional maximum filter.</td>
</tr>
<tr>
<td>maximum_filter1d</td>
<td>Calculate a one-dimensional maximum filter along the given axis.</td>
</tr>
<tr>
<td>median_filter</td>
<td>Calculates a multidimensional median filter.</td>
</tr>
<tr>
<td>minimum_filter</td>
<td>Calculates a multi-dimensional minimum filter.</td>
</tr>
<tr>
<td>minimum_filter1d</td>
<td>Calculate a one-dimensional minimum filter along the given axis.</td>
</tr>
<tr>
<td>percentile_filter</td>
<td>Calculates a multi-dimensional percentile filter.</td>
</tr>
</tbody>
</table>
scipy.ndimage.filters.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
  Input array to filter.
- **weights**: array_like
  Array of weights, same number of dimensions as input
- **output**: ndarray, optional
  The output parameter passes an array in which to store the filter output.
- **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**: array_like, optional
  The origin parameter controls the placement of the filter. Default is 0.

**Returns**

- **result**: ndarray
  The result of convolution of input with weights.

**See also**:

corrulate  Correlate an image with a kernel.

**Notes**

Each value in result is $C_i = \sum_j I_{i+j-k} W_j$, 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.

```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],
                .... [1,1,0],
                .... [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],
       [15, 12, 14, 7],
       [12, 3, 7, 0]])
```

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).
>>> 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]])

With mode='reflect' (the default), outer values are reflected at the edge of input to fill in missing values.

>>> 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, 0],
       [3, 0, 0],
       [1, 0, 0]])

This includes diagonally at the corners.

>>> 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]])

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.

>>> 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],
                [0, 1, 0]])
>>> ndimage.convolve(c, k, mode='nearest')
array([[7, 0, 3],
       [5, 0, 2],
       [3, 0, 1]])

**scipy.ndimage.filters.convolve1d**

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
  Input array to filter.
- **weights**: ndarray
  One-dimensional sequence of numbers.
- **axis**: int, optional
  The axis of input along which to calculate. Default is -1.
- **output**: array, optional
  The output parameter passes an array in which to store the filter output.
- **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 0.0.

**Returns**

`convolve1d`: ndarray

Convolved array with same shape as input.

```python
scipy.ndimage.filters.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
  - Input array to filter.
- `weights`: ndarray
  - Array of weights, same number of dimensions as input.
- `output`: array, optional
  - The `output` parameter passes an array in which to store the filter output.
- `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 0.0.

See also:

- `convolve`: Convolve an image with a kernel.

```python
scipy.ndimage.filters.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
  - Input array to filter.
- `weights`: array
  - One-dimensional sequence of numbers.
- `axis`: int, optional
  - The axis of `input` along which to calculate. Default is -1.
- `output`: array, optional
  - The `output` parameter passes an array in which to store the filter output.
- `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 0.0.

```python
scipy.ndimage.filters.gaussian_filter(input, sigma, order=0, output=None, mode='reflect', cval=0.0, truncate=4.0)
```

Multidimensional Gaussian filter.

**Parameters**

- `input`: array_like
  - Input array to filter.
**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** : {0, 1, 2, 3} or sequence from same set, 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. 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.

**output** : array, optional
The `output` parameter passes an array in which to store the filter output.

**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

**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.

**scipy.ndimage.filters.gaussian_filter1d**

One-dimensional Gaussian filter.

**Parameters**

**input** : array_like
Input array to filter.

**sigma** : scalar
Standard deviation for Gaussian kernel

**axis** : int, optional
The axis of `input` along which to calculate. Default is -1.

**order** : {0, 1, 2, 3}, optional
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.

**output** : array, optional
The `output` parameter passes an array in which to store the filter output.

**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

**truncate** : float, optional
Truncate the filter at this many standard deviations. Default is 4.0.

### Returns

**gaussian_filter1d** : ndarray

**scipy.ndimage.filters.gaussian_gradient_magnitude**

Multidimensional gradient magnitude using Gaussian derivatives.

**Parameters**

**input** : array_like
Input array to filter.

**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** : {0, 1, 2, 3} or sequence from same set, 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. 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.

**output** : array, optional
The `output` parameter passes an array in which to store the filter output.

**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

**truncate** : float, optional
Truncate the filter at this many standard deviations. Default is 4.0.

### Returns

**gaussian_gradient_magnitude** : ndarray

Multidimensional gradient magnitude using Gaussian derivatives.
Parameters

input : array_like
Input array to filter.
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, optional
The output parameter passes an array in which to store the filter output.
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

Extra keyword arguments will be passed to gaussian_filter().

scipy.ndimage.filters.gaussian_laplace(input, sigma, output=None, mode='reflect', cval=0.0, **kwargs)
Multidimensional Laplace filter using gaussian second derivatives.

Parameters

input : array_like
Input array to filter.
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, optional
The output parameter passes an array in which to store the filter output.
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

Extra keyword arguments will be passed to gaussian_filter().

scipy.ndimage.filters.generic_filter(input, function, size=None, footprint=None, output=None, mode='reflect', cval=0.0, origin=0, extra_arguments=(), extra_keywords=None)
Calculates 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
Input array to filter.
function : callable
Function to apply at each element.
size : scalar or tuple, optional
See footprint, below
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).
output : array, optional
The output parameter passes an array in which to store the filter output.
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 0.0.

**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

```python
calculator.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.

`calculator.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
  - Input array to filter.

- **function**: callable
  - 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, optional
  - The *output* parameter passes an array in which to store the filter output.

- **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 0.0.

- **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

```python
calculator.ndimage.filters.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
  - Input array to filter.

- **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, optional

The `output` parameter passes an array in which to store the filter output.

**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

**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

```python
scipy.ndimage.filters.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
  Input array to filter.

- **derivative2**: callable
  Callable with the following signature:

    ```python
derivative2(input, axis, output, mode, cval, *extra_arguments, **extra_keywords)
```

  See `extra_arguments`, `extra_keywords` below.

- **output**: array, optional
  The `output` parameter passes an array in which to store the filter output.

- **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

- **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

```python
scipy.ndimage.filters.laplace(input, output=None, mode='reflect', cval=0.0)
```

N-dimensional Laplace filter based on approximate second derivatives.

### Parameters

- **input**: array_like
  Input array to filter.

- **output**: array, optional
  The `output` parameter passes an array in which to store the filter output.

- **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

```python
scipy.ndimage.filters.maximum_filter(input, size=None, footprint=None, output=None, mode='reflect', cval=0.0, origin=0)
```

Calculates a multi-dimensional maximum filter.
**Parameters**  

- **input**: array_like  
  Input array to filter.
- **size**: scalar or tuple, optional
  See footprint, below
- **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).
- **output**: array, optional
  The *output* parameter passes an array in which to store the filter output.
- **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 0.0.

**scipy.ndimage.filters.maximum_filter1d**

```python
maximum_filter1d(input, size, axis=-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  
  Input array to filter.
- **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, optional
  The *output* parameter passes an array in which to store the filter output.
- **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 0.0.

**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 [R102], as described by Richard Harter [R103], and has a guaranteed O(n) performance, *n* being the input length, regardless of filter size.

**References**

[R102], [R103]
Calculates a multidimensional median filter.

**Parameters**

- **input**: array_like
  Input array to filter.
- **size**: scalar or tuple, optional
  See footprint, below
- **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)`.
- **output**: array, optional
  The `output` parameter passes an array in which to store the filter output.
- **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 `0.0`.

**Returns**

- **median_filter**: ndarray
  Return of same shape as `input`.

Calculates a multi-dimensional minimum filter.

**Parameters**

- **input**: array_like
  Input array to filter.
- **size**: scalar or tuple, optional
  See footprint, below
- **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)`.
- **output**: array, optional
  The `output` parameter passes an array in which to store the filter output.
- **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 `0.0`. 

5.22. Multi-dimensional image processing (scipy.ndimage)
scipy.ndimage.filters.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
  Input array to filter.
- **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, optional
  The output parameter passes an array in which to store the filter output.
- **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 0.0.

**Notes**

This function implements the MINLIST algorithm [R104], as described by Richard Harter [R105], and has a guaranteed O(n) performance, n being the input length, regardless of filter size.

**References**

[R104], [R105]

scipy.ndimage.filters.percentile_filter(input, percentile, size=None, footprint=None, output=None, mode='reflect', cval=0.0, origin=0)

Calculates a multi-dimensional percentile filter.

**Parameters**

- **input**: array_like
  Input array to filter.
- **percentile**: scalar
  The percentile parameter may be less then zero, i.e., percentile = -20 equals percentile = 80
- **size**: scalar or tuple, optional
  See footprint, below
- **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).
- **output**: array, optional
  The output parameter passes an array in which to store the filter output.
- **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 0.0.

scipy.ndimage.filters.prewitt (input, axis=-1, output=None, mode='reflect', cval=0.0)
Calculate a Prewitt filter.

Parameters
input : array_like
Input array to filter.
axis : int, optional
The axis of input along which to calculate. Default is -1.
output : array, optional
The output parameter passes an array in which to store the filter output.
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

scipy.ndimage.filters.rank_filter (input, rank, size=None, footprint=None, output=None, mode='reflect', cval=0.0, origin=0)
Calculates a multi-dimensional rank filter.

Parameters
input : array_like
Input array to filter.
rank : int
The rank parameter may be less then zero, i.e., rank = -1 indicates the largest element.
size : scalar or tuple, optional
See footprint, below
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).
output : array, optional
The output parameter passes an array in which to store the filter output.
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 0.0.

scipy.ndimage.filters.sobel (input, axis=-1, output=None, mode='reflect', cval=0.0)
Calculate a Sobel filter.

Parameters
input : array_like
Input array to filter.
axis : int, optional
The axis of input along which to calculate. Default is -1.
output : array, optional
The output parameter passes an array in which to store the filter output.
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’

```python
cval : scalar, optional
Value to fill past edges of input if `mode` is ‘constant’. Default is 0.0
```

**scipy.ndimage.filters.uniform_filter** *(input, size=3, output=None, mode='reflect', cval=0.0, origin=0)*

Multi-dimensional uniform filter.

**Parameters**

- **input**: array_like
  Input array to filter.
- **size**: int or sequence of ints, optional
  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.
- **output**: array, optional
  The `output` parameter passes an array in which to store the filter output.
- **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 0.0.

**Notes**

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.

**scipy.ndimage.filters.uniform_filter1d** *(input, size=-1, output=None, mode='reflect', cval=0.0, origin=0)*

Calculate a one-dimensional uniform filter along the given axis.

The lines of the array along the given axis are filtered with a uniform filter of given size.

**Parameters**

- **input**: array_like
  Input array to filter.
- **size**: int
  length of uniform filter
- **axis**: int, optional
  The axis of `input` along which to calculate. Default is -1.
- **output**: array, optional
  The `output` parameter passes an array in which to store the filter output.
- **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 0.0.

### 5.22.2 Fourier filters **scipy.ndimage.fourier**

**fourier_ellipsoid** *(input, size[, n, axis, output])*

Multi-dimensional ellipsoid fourier filter.

Continued on next page
scipy.ndimage.fourier.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 or None
  - The filtered input. If `output` is given as a parameter, None is returned.

**Notes**

This function is implemented for arrays of rank 1, 2, or 3.

scipy.ndimage.fourier.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 or None
  - The filtered input. If `output` is given as a parameter, None is returned.

scipy.ndimage.fourier.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.

**shift**: float or sequence
The size of the box used for filtering. If a float, `shift` is the same for all axes. If a sequence, `shift` 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 shifting the input is placed in this array. None is returned in this case.

Returns

**fourier_shift**: ndarray or None
The shifted input. If `output` is given as a parameter, None is returned.

### scipy.ndimage.fourier.fourier_uniform

Multi-dimensional uniform fourier filter.

The array is multiplied with the fourier transform of a box of given size.

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 or None
The filtered input. If `output` is given as a parameter, None is returned.

## 5.22.3 Interpolation

### scipy.ndimage.interpolation

- **affine_transform** *(input, matrix[, offset, ...])*
  Apply an affine transformation.

- **geometric_transform** *(input, mapping[, ...])*
  Apply an arbitrary geometric transform.

- **map_coordinates** *(input, coordinates[, ...])*
  Map the input array to new coordinates by interpolation.

- **rotate** *(input, angle[, axes, reshape, ...])*
  Rotate an array.

- **shift** *(input, shift[, output, order, mode, ...])*
  Shift an array.

- **spline_filter** *(input[, order, output])*
  Multi-dimensional spline filter.

- **spline_filter1d** *(input[, order, axis, output])*
  Calculates a one-dimensional spline filter along the given axis.

- **zoom** *(input, zoom[, output, order, mode, ...])*
  Zoom an array.
Apply an affine transformation.

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.

**Parameters**
- **input**: ndarray
  The input array.
- **matrix**: ndarray
  The 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 algorithms is then applied that exploits the separability of the problem.
- **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**: ndarray or dtype, optional
  The array in which to place the output, or the dtype of the returned array.
- **order**: int, optional
  The order of the spline interpolation, default is 3. The order has to be in the range 0-5.
- **mode**: str, optional
  Points outside the boundaries of the input are filled according to the given mode (‘constant’, ‘nearest’, ‘reflect’ or ‘wrap’). Default is ‘constant’.
- **cval**: scalar, optional
  Value used for points outside the boundaries of the input if mode='constant'. Default is 0.0
- **prefilter**: bool, optional
  The parameter prefilter determines if the input is pre-filtered with spline_filter before interpolation (necessary for spline interpolation of order > 1). If False, it is assumed that the input is already filtered. Default is True.

**Returns**
- **affine_transform**: ndarray or None
  The transformed input. If output is given as a parameter, None is returned.

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
  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**: ndarray or dtype, optional
  The transformed input. If output is given as a parameter, None is returned.

Scipy Reference Guide, Release 0.16.0
The array in which to place the output, or the dtype of the returned array.

**order**: int, optional

The order of the spline interpolation, default is 3. The order has to be in the range 0-5.

**mode**: str, optional

Points outside the boundaries of the input are filled according to the given mode (‘constant’, ‘nearest’, ‘reflect’ or ‘wrap’). Default is ‘constant’.

**cval**: scalar, optional

Value used for points outside the boundaries of the input if `mode='constant'`. Default is 0.0

**prefilter**: bool, optional

The parameter prefilter determines if the input is pre-filtered with `spline_filter` before interpolation (necessary for spline interpolation of order > 1). If False, it is assumed that the input is already filtered. Default is True.

**extra_arguments**: tuple, optional

Extra arguments passed to `mapping`.

**extra_keywords**: dict, optional

Extra keywords passed to `mapping`.

**Returns**

**return_value**: ndarray or None

The filtered input. If `output` is given as a parameter, None is returned.

See also:

`map_coordinates`, `affine_transform`, `spline_filter1d`

Examples

```python
>>> from scipy import ndimage
>>> a = np.arange(12.).reshape((4, 3))
>>> def shift_func(output_coords):
...     return (output_coords[0] - 0.5, output_coords[1] - 0.5)
... 
>>> ndimage.geometric_transform(a, shift_func)
array([[ 0. , 0. , 0. ],
       [ 4.812, 6.187],
       [ 8.263, 9.637]])
```

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**: ndarray
  
The input array.

- **coordinates**: array_like
  
The coordinates at which `input` is evaluated.

- **output**: ndarray or dtype, optional
  
The array in which to place the output, or the dtype of the returned array.

- **order**: int, optional
  
The order of the spline interpolation, default is 3. The order has to be in the range 0-5.

- **mode**: str, optional
  
Points outside the boundaries of the input are filled according to the given mode (‘constant’, ‘nearest’, ‘reflect’ or ‘wrap’). Default is ‘constant’.
**cval** : scalar, optional
Value used for points outside the boundaries of the input if `mode='constant'`. Default is 0.0

**prefilter** : bool, optional
The parameter prefilter determines if the input is pre-filtered with `spline_filter` before interpolation (necessary for spline interpolation of order > 1). If False, it is assumed that the input is already filtered. Default is True.

**Returns**

`map_coordinates` : ndarray
The result of transforming the input. The shape of the output is derived from that of `coordinates` by dropping the first axis.

**See also:**
`spline_filter, geometric_transform, scipy.interpolate`

**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)
```

**scipy.ndimage.interpolation.rotate**

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.

**Parameters**

- `input` : ndarray
  The input array.
- `angle` : float
  The rotation angle in degrees.
- `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` : ndarray or dtype, optional
  The array in which to place the output, or the dtype of the returned array.
- `order` : int, optional
  The order of the spline interpolation, default is 3. The order has to be in the range 0-5.
- `mode` : str, optional
Points outside the boundaries of the input are filled according to the given mode (‘constant’, ‘nearest’, ‘reflect’ or ‘wrap’). Default is ‘constant’.

cval : scalar, optional
Value used for points outside the boundaries of the input if mode=’constant’. Default is 0.0

prefilter : bool, optional
The parameter prefilter determines if the input is pre-filtered with spline_filter before interpolation (necessary for spline interpolation of order > 1). If False, it is assumed that the input is already filtered. Default is True.

Returns
rotate : ndarray or None
The rotated input. If output is given as a parameter, None is returned.

scipy.ndimage.interpolation.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 : ndarray
The input array.

shift : float or sequence, optional
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 : ndarray or dtype, optional
The array in which to place the output, or the dtype of the returned array.

order : int, optional
The order of the spline interpolation, default is 3. The order has to be in the range 0-5.

mode : str, optional
Points outside the boundaries of the input are filled according to the given mode (‘constant’, ‘nearest’, ‘reflect’ or ‘wrap’). Default is ‘constant’.

cval : scalar, optional
Value used for points outside the boundaries of the input if mode=’constant’. Default is 0.0

prefilter : bool, optional
The parameter prefilter determines if the input is pre-filtered with spline_filter before interpolation (necessary for spline interpolation of order > 1). If False, it is assumed that the input is already filtered. Default is True.

Returns
shift : ndarray or None
The shifted input. If output is given as a parameter, None is returned.

scipy.ndimage.interpolation.spline_filter (input, order=3, output=None)
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.interpolation.spline_filter1d(input, order=3, axis=-1, output=<type 'numpy.float64'>)

Calculates 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.

**Returns**
- **spline_filter1d**: ndarray or None
  - The filtered input. If output is given as a parameter, None is returned.

scipy.ndimage.interpolation.zoom(input, zoom, output=None, order=3, mode='constant', cval=0.0, prefilter=True)

Zoom an array.

The array is zoomed using spline interpolation of the requested order.

**Parameters**
- **input**: ndarray
  - The input array.
- **zoom**: float or sequence, optional
  - 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**: ndarray or dtype, optional
  - The array in which to place the output, or the dtype of the returned array.
- **order**: int, optional
  - The order of the spline interpolation, default is 3. The order has to be in the range 0-5.
- **mode**: str, optional
  - Points outside the boundaries of the input are filled according to the given mode ('constant', 'nearest', 'reflect' or 'wrap'). Default is 'constant'.
- **cval**: scalar, optional
  - Value used for points outside the boundaries of the input if mode='constant'. Default is 0.0
- **prefilter**: bool, optional
  - The parameter prefilter determines if the input is pre-filtered with spline_filter before interpolation (necessary for spline interpolation of order > 1). If False, it is assumed that the input is already filtered. Default is True.

**Returns**
- **zoom**: ndarray or None
  - The zoomed input. If output is given as a parameter, None is returned.

### 5.22.4 Measurements scipy.ndimage.measurements

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>center_of_mass(input[, labels, index])</td>
<td>Calculate the center of mass of the values of an array at labels.</td>
</tr>
<tr>
<td>extrema(input[, labels, index])</td>
<td>Calculate the minimums and maximums of the values of an array at labels.</td>
</tr>
<tr>
<td>find_objects(input[, max_label])</td>
<td>Find objects in a labeled array.</td>
</tr>
<tr>
<td>histogram(input, min, max, bins[, labels, index])</td>
<td>Calculate the histogram of the values of an array, optionally at labels.</td>
</tr>
<tr>
<td>label(input[, structure, output])</td>
<td>Label features in an array.</td>
</tr>
</tbody>
</table>
Table 5.86 – continued from previous page

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.
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 an 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.measurements.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.
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 centers-of-mass.

Examples

>>> a = np.array(((0,0,0,0),
    [0,1,1,0],
    [0,1,1,0],
    [0,1,1,0]))
>>> from scipy import ndimage
>>> ndimage.measurements.center_of_mass(a)
(2.0, 1.5)

Calculation of multiple objects in an image

>>> 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])
[(0.3333333333333333, 1.0), (1.6666666666666666, 2.0)]

scipy.ndimage.measurements.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, nlbl = ndimage.label(a)
>>> ndimage.extrema(a, lbl, index=np.arange(1, nlbl+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.measurements.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
>>> a = np.zeros((6,6), dtype=np.int)
>>> a[2:4, 2:4] = 1
>>> a[4, 4] = 1
>>> a[:, 2] = 1
>>> 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]])
>>> 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))]
>>> ndimage.find_objects(a, max_label=2)
[(slice(2, 5, None), slice(2, 5, None)), (slice(0, 2, None), slice(0, 3, None))]
>>> ndimage.find_objects(a == 1, max_label=2)
[(slice(2, 5, None), slice(2, 5, None)), None]

>>> loc = ndimage.find_objects(a)[0]
>>> a[loc]
array([[1, 1, 0],
       [1, 1, 0],
       [0, 0, 1]])

scipy.ndimage.measurements.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

>>> 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]])

>>> from scipy import ndimage
>>> ndimage.measurements.histogram(a, 0, 1, 10)
array([13, 0, 2, 1, 0, 1, 1, 2, 0, 0])

With labels and no indices, non-zero elements are counted:

>>> 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])
```

```python
scipy.ndimage.measurements.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
>>> a = np.array(
... [ [0, 0, 1, 1, 0, 0],
...  [0, 0, 0, 1, 0, 0],
...  [1, 1, 0, 0, 1, 0],
...  [0, 0, 0, 1, 0, 0]]
... )
```
```python
>>> labeled_array, num_features = label(a)
```
Each of the 4 features are labeled with a different integer:

```python
>>> print(num_features)
4
```
```python
>>> print(labeled_array)
array([[0, 0, 1, 1, 0, 0],
       [0, 0, 0, 1, 0, 0],
       [0, 0, 0, 1, 0, 0],
       [0, 0, 0, 1, 0, 0]],
      ...]
```
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, 1, 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
>>> print(num_features)
2
>>> print(labeled_array)
array([[0, 0, 1, 1, 0, 0],
       [0, 0, 0, 1, 0, 0],
       [2, 2, 0, 0, 1, 0],
       [0, 0, 0, 1, 0, 0]])
```

```python
scipy.ndimage.measurements.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` : 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],
```
>>> from scipy import ndimage
>>> lbl, nlbl = ndimage.label(a)
>>> lbls = np.arange(1, nlbl+1)
array([ 1, 2, 3, 4])

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())
...>
>>> 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.])

scipy.ndimage.measurements.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:

```
lable, 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([[0, 0, 0, 0],
        [0, 0, 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, 2, 0],
        [3, 3, 0, 0]])

scipy.ndimage.measurements.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 maximums. 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:
`scipy.ndimage.measurements.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**

```python
>>> a = np.arange(25).reshape((5,5))
>>> labels = np.zeros_like(a)
>>> labels[3:5,3:5] = 1
>>> index = np.unique(labels)
>>> labels
array([[0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1],
       [0, 0, 1, 1, 1]])
>>> index
array([0, 1])
>>> ndimage.mean(a, labels=labels, index=index)
[10.285714285714286, 21.0]
```

`scipy.ndimage.measurements.minimum(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**: 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
given a = np.array([[1, 2, 0, 0],
                    [5, 3, 0, 4],
                    [0, 0, 0, 7],
                    [9, 3, 0, 0]])
```
```python
labels, labels_nb = ndimage.label(a)
```
```python
print(labels)
```
```python
[[1, 1, 0, 0],
 [1, 1, 0, 2],
 [0, 0, 0, 2],
 [3, 3, 0, 0]]
```
```python
print(ndimage.minimum(a, labels=labels, index=np.arange(1, labels_nb + 1)))
```
```python
[1.0, 4.0, 3.0]
```
```python
print(ndimage.minimum(a))
```
```python
0.0
```
```python
print(ndimage.minimum(a, labels=labels))
```
```python
1.0
```

scipy.ndimage.measurements.minimum_position(input=None, 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. 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 minima. If index is None, the first minimum 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
  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

scipy.ndimage.measurements.standard_deviation(input=None, 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.

labels : 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**

```python
define the input array:
>>> a = np.array([[1, 2, 0, 0],
                [5, 3, 0, 4],
                [0, 0, 0, 7],
                [9, 3, 0, 0]])
```

```python
from scipy import ndimage
```

```python
>>> ndimage.standard_deviation(a)
2.7585095613392387
```

Features to process can be specified using labels and index:

```python
>>> 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:

```python
>>> ndimage.standard_deviation(a, lbl)
2.4874685927665499
```

**scipy.ndimage.measurements.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
>>> input = [0,1,2,3]
>>> labels = [1,1,2,2]
>>> sum(input, labels, index=[1,2])
[1.0, 5.0]
>>> sum(input, labels, index=1)
1
```
```python
>>> sum(input, labels)
6
```

```python
scipy.ndimage.measurements.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, 0]])
>>> 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
```

```python
scipy.ndimage.measurements.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`.
5.22.5 Morphology scipy.ndimage.morphology

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>binary_closing(input[, structure, ...])</td>
<td>Multi-dimensional binary closing with the given structuring element.</td>
</tr>
<tr>
<td>binary_dilation(input[, structure, ...])</td>
<td>Multi-dimensional binary dilation with the given structuring element.</td>
</tr>
<tr>
<td>binary_erosion(input[, structure, ...])</td>
<td>Multi-dimensional binary erosion with a given structuring element.</td>
</tr>
<tr>
<td>binary_fill_holes(input[, structure, ...])</td>
<td>Fill the holes in binary objects.</td>
</tr>
<tr>
<td>binary_hit_or_miss(input[, structure1, ...])</td>
<td>Multi-dimensional binary hit-or-miss transform.</td>
</tr>
<tr>
<td>binary_opening(input[, structure, ...])</td>
<td>Multi-dimensional binary opening with the given structuring element.</td>
</tr>
<tr>
<td>binary_propagation(input[, structure, mask, ...])</td>
<td>Multi-dimensional binary propagation with the given structuring element.</td>
</tr>
<tr>
<td>black_tophat(input[, size, footprint, ...])</td>
<td>Multi-dimensional black tophat filter.</td>
</tr>
<tr>
<td>distance_transform_bf(input[, metric, ...])</td>
<td>Distance transform function by a brute force algorithm.</td>
</tr>
<tr>
<td>distance_transform_cdt(input[, metric, ...])</td>
<td>Distance transform for chamfer type of transforms.</td>
</tr>
<tr>
<td>distance_transform_edt(input[, sampling, ...])</td>
<td>Exact euclidean distance transform.</td>
</tr>
<tr>
<td>generate_binary_structure(rank, connectivity)</td>
<td>Generate a binary structure for binary morphological operations.</td>
</tr>
<tr>
<td>grey_closing(input[, size, footprint, ...])</td>
<td>Multi-dimensional greyscale closing.</td>
</tr>
<tr>
<td>grey_dilation(input[, size, footprint, ...])</td>
<td>Calculate a greyscale dilation, using either a structuring element, or a footprint.</td>
</tr>
<tr>
<td>grey_erosion(input[, size, footprint, ...])</td>
<td>Calculate a greyscale erosion, using either a structuring element, or a footprint.</td>
</tr>
<tr>
<td>grey_opening(input[, size, footprint, ...])</td>
<td>Multi-dimensional greyscale opening.</td>
</tr>
<tr>
<td>iterate_structure(structure, iterations[, ...])</td>
<td>Iterate a structure by dilating it with itself.</td>
</tr>
<tr>
<td>morphological_gradient(input[, size, ...])</td>
<td>Multi-dimensional morphological gradient.</td>
</tr>
<tr>
<td>morphological_laplace(input[, size, ...])</td>
<td>Multi-dimensional morphological laplace.</td>
</tr>
<tr>
<td>white_tophat(input[, size, footprint, ...])</td>
<td>Multi-dimensional white tophat filter.</td>
</tr>
</tbody>
</table>

scipy.ndimage.morphology.binary_closing (input, structure=None, iterations=1, output=None, origin=0)

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 operations 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.

**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 [R107] is a mathematical morphology operation [R108] 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

[R107], [R108]

Examples

```python
>>> a = np.zeros((5,5), dtype=np.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(np.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]]))
>>> # Closing is the erosion of the dilation of the input
>>> ndimage.binary_dilation(a).astype(np.int)
array([[0, 1, 1, 1, 0],
       [1, 1, 1, 1, 1],
       [1, 1, 1, 1, 1],
       [1, 1, 1, 1, 1],
       [0, 1, 1, 1, 0]]))
>>> ndimage.binary_erosion(ndimage.binary_dilation(a)).astype(np.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=np.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, 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]]))
>>> # In addition to removing holes, closing can also
>>> # coarsen boundaries with fine hollows.
```
>>> ndimage.binary_closing(a).astype(np.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]])

>>> ndimage.binary_closing(a, structure=np.ones((2,2))).astype(np.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.morphology.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.

- **origin**: int or tuple of ints, optional
  Placement of the filter, by default 0.

- **border_value**: int (cast to 0 or 1), optional
  Value at the border in the output array.

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 [R109] is a mathematical morphology operation [R110] 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

[R109], [R110]

Examples

```python
>>> 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

```python
>>> 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

```python
>>> struct2 = ndimage.generate_binary_structure(2, 2)
>>> struct2
array([[True, True, True],
       [True, True, True],
       [True, True, True]], dtype=bool)
```

```python
>>> ndimage.binary_dilation(a, structure=struct1).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.]])
```
scipy.ndimage.morphology.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.
- `origin`: int or tuple of ints, optional
  Placement of the filter, by default 0.
- `border_value`: int (cast to 0 or 1), optional
  Value at the border in the output array.

**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 [R111] is a mathematical morphology operation [R112] 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**

[R111], [R112]

**Examples**

```python
>>> a = np.zeros((7,7), dtype=np.int)
>>> a[1:6, 2:5] = 1
>>> a
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 1, 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]])
>>> 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, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]], dtype=int64)
```
Erosion removes objects smaller than the structure.

```python
>>> 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.morphology.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 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

[R113]

Examples

```python
>>> 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, 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.morphology.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 : array_like (cast to booleans), optional
    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

[R114]

Examples

>>> a = np.zeros((7,7), dtype=np.int)
>>> a
array([[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, 1, 1, 0, 0, 0],
[0, 0, 1, 1, 0, 0, 0],
[0, 0, 0, 0, 1, 1, 0],
[0, 0, 0, 0, 0, 0, 0])}

```python
>> structure1 = np.array([[1, 0, 0], [0, 1, 1], [0, 1, 1]])
>> structure1
array([[1, 0, 0],
       [0, 1, 1],
       [0, 1, 1]])
>>> # Find the matches of structure1 in the array a
>>> ndimage.binary_hit_or_miss(a, structure1=structure1).astype(np.int)
array([[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, 1, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> # Change the origin of the filter
>>> ndimage.binary_hit_or_miss(a, structure1=structure1, origin1=1).astype(np.int)
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, 1, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 1],
       [0, 0, 0, 0, 0, 0, 0]])
```

scipy.ndimage.morphology.binary_opening(input, structure=None, iterations=1, output=None, origin=0)

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.

**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 [R115] is a mathematical morphology operation [R116] 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

[R115], [R116]

Examples

```python
>>> a = np.zeros((5,5), dtype=np.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, 1, 1, 1, 0],
       [0, 0, 0, 0, 1]])
>>> # Opening removes small objects
>>> ndimage.binary_opening(a, structure=np.ones((3,3))).astype(np.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]])
>>> # Opening can also smooth corners
>>> ndimage.binary_opening(a).astype(np.int)
array([[0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 1, 1, 0],
       [0, 0, 0, 0, 0]])
>>> # Opening is the dilation of the erosion of the input
>>> ndimage.binary_erosion(a).astype(np.int)
array([[0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0],
       [0, 0, 1, 1, 0],
       [0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0]])
>>> ndimage.binary_dilation(ndimage.binary_erosion(a)).astype(np.int)
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 1, 1, 0],
       [0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0]])
```

```
scipy.ndimage.morphology.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**

**binary_propagation**: ndarray
- Binary propagation of *input* inside *mask*.

**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**

[R117], [R118]

**Examples**

```python
>>> input = np.zeros((8, 8), dtype=np.int)
>>> input[2, 2] = 1
>>> mask = np.zeros((8, 8), dtype=np.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(np.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, 0, 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, 
... structure=np.ones((3,3))).astype(np.int)
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, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0]])

>>> # Comparison between opening and erosion+propagation
>>> a = np.zeros((6,6), dtype=np.int)
>>> a[2:5, 2:5] = 1; a[0, 0] = 1; a[5, 5] = 1
>>> a
array([[1, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0, 1]])

>>> ndimage.binary_opening(a).astype(np.int)
array([[0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 0, 1, 0, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 0, 1, 0, 0],
       [0, 0, 0, 0, 0, 0]])

>>> b = ndimage.binary_erosion(a)
>>> b.astype(int)
array([[0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 0, 1, 0, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0, 0]])

>>> ndimage.binary_propagation(b, mask=a).astype(np.int)
array([[0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0, 0]])

scipy.ndimage.morphology.black_tophat (input, size=None, footprint=None, structure=None, output=None, mode='reflect', cval=0.0, origin=0)

Multi-dimensional black tophat filter.

**Parameters**

<table>
<thead>
<tr>
<th>input: array_like</th>
<th>Input.</th>
</tr>
</thead>
<tbody>
<tr>
<td>size: tuple of ints, optional</td>
<td>Shape of a flat and full structuring element used for the filter. Optional if footprint or structure is provided.</td>
</tr>
</tbody>
</table>
**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

---

```python
scipy.ndimage.morphology.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 background element (zero values), with its shortest distance to the foreground (any element non-zero).

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.

```python
scipy.ndimage.morphology.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`.

```python
scipy.ndimage.morphology.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 dimension. 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 `return_distances/return_indices` must be True. Default is True.

- `return_indices` : bool, optional
  Whether to return indices matrix. Default is False.

- `distances, indices` : ndarrays, optional
  Used for output of distance array, must be of type float64.

- `indices` : ndarrays, 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 \textit{return}\_x flags and \textit{distance} and \textit{indices} input parameters.

\textbf{Notes}

The euclidean distance transform gives values of the euclidean distance:

\[ y_i = \sqrt{\sum (x[i]-b[i])**2} \]

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.

\textbf{Examples}

```python
>>> a = np.array([[0,1,1,1,1],
                [0,0,1,1,1],
                [0,1,1,1,0],
                [0,1,1,0,0]])
```

```python
>>> from scipy import ndimage
```

```python
>>> 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. , 2.2361, 2. ],
       [ 0. , 1. , 2. , 1. , 0. ],
       [ 0. , 1. , 1. , 0. , 0. ]])
```

Asking for indices as well:

```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, 4],
        [0, 0, 1, 4],
        [0, 0, 3, 4],
        [0, 0, 3, 4]]])
```

With arrays provided for inplace outputs:

```python
>>> indices = np.zeros(((np.ndim(a),) + a.shape), dtype=np.int32)
```

```python
>>> 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. ]])
```
scipy.ndimage.morphology.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
>>> 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.,  0.,  1.,  0.,  0.],
        [ 0.,  0.,  0.,  0.,  0.],
        [ 0.,  0.,  0.,  0.,  0.]])
>>> 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.,  1.,  0.,  0.],
        [ 0.,  0.,  0.,  0.,  0.]])
```
scipy.ndimage.morphology.grey_closing(input, size=None, footprint=None, structure=None, output=None, mode='reflect', cval=0.0, origin=0)

Multi-dimensional greyscale closing.

A greyscale closing consists in the succession of a greyscale dilation, and a greyscale erosion.

**Parameters**

- **input**: array_like
  
  Array over which the greyscale closing is to be computed.

- **size**: tuple of ints
  
  Shape of a flat and full structuring element used for the greyscale 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 greyscale closing.

- **structure**: array of ints, optional
  
  Structuring element used for the greyscale 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 0

**Returns**

- **grey_closing**: ndarray
  
  Result of the greyscale 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
[119]

Examples
>>> 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],
       [19, 19, 20,  0, 22, 23],
       [25, 25, 26, 27, 28, 29],
       [31, 31, 32, 33, 34, 35]])
>>> # Note that the local minimum a[3,3] has disappeared

scipy.ndimage.morphology.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.
    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:

$$ (\text{input} + s)(x) = \max \{ \text{input}(y) + s(x-y), \text{for } y \in E \} $$

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 [R120] is a mathematical morphology operation [R121].

References

[R120], [R121]

Examples

```python
>>> a = np.zeros((7,7), dtype=np.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, 1, 2, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```

```python
>>> 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, 3, 3, 3, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```

```python
>>> 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, 3, 3, 3, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```

```python
>>> s = ndimage.generate_binary_structure(2,1)
>>> s
array([[False, True, False],
       [True, True, True],
       [False, True, False]], dtype=bool)
```

```python
>>> 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, 3, 3, 3, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```
```python
>>> ndimage.grey_dilation(a, size=(3,3), structure=np.ones((3,3)))
array([[1, 1, 1, 1, 1, 1, 1],
       [1, 2, 4, 4, 4, 2, 1],
       [1, 2, 4, 4, 4, 2, 1],
       [1, 2, 4, 4, 3, 1],
       [1, 2, 2, 3, 3, 1],
       [1, 2, 2, 3, 3, 1],
       [1, 1, 1, 1, 1, 1]])
```

calculated by

```
scipy.ndimage.morphology.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 element 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. `$structure$` may be a non-flat structuring element.
- **output**: array, optional
  - An array used for storing the output of the erosion 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**

- **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 $E$.

5.22. Multi-dimensional image processing (scipy.ndimage)
Grayscale erosion [R122] is a mathematical morphology operation [R123].

References

[R122], [R123]

Examples

```python
>>> a = np.zeros((7,7), dtype=np.int)
>>> a[1:6, 1:6] = 3
>>> a[4,4] = 2; a[2,3] = 1
>>> a
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]])
```

```python
>>> footprint = ndimage.generate_binary_structure(2, 1)
>>> footprint
array([[False, True, False],
        [True, True, True],
        [False, True, False]], dtype=bool)
```

```python
>>> # 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, 2, 2, 0, 0],
        [0, 0, 0, 0, 0, 0, 0],
        [0, 0, 0, 0, 0, 0, 0]])
```

scipy.ndimage.morphology.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
[R124]

Examples
>>> 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, 15, 16, 17],
       [18, 19, 20, 50, 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 maxima a[3,3] has disappeared

scipy.ndimage.morphology.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 : ndarray of bools
A new structuring element obtained by dilating structure (iterations - 1) times with
itself.
See also:

*generate_binary_structure*

**Examples**

```python
>>> struct = ndimage.generate_binary_structure(2, 1)
>>> struct.astype(int)
array([[0, 1, 0],
       [1, 1, 1],
       [0, 1, 0]])
```

```python
>>> 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]])
```

```python
>>> 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]])
```

```
scipy.ndimage.morphology.morphological_gradient

```

The morphological gradient is calculated as the difference between a dilation and an erosion of the input with a given structuring element.

**Parameters**

- **input**: array_like
  Array over which to compute the morphological gradient.

- **size**: tuple of ints
  Shape of a flat and full structuring element used for the mathematical morphology operations. Optional if footprint or structure is provided. A larger size yields a more blurred gradient.

- **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.

- **structure**: array of ints, optional
  Structuring element used for the morphology operations. structure may be a non-flat structuring element.

- **output**: array, optional
  An array used for storing the output of the morphological gradient may be provided.

  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**

- **morphological_gradient**: ndarray
  Morphological gradient of input.
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
[R125]

Examples
```python
grey_dilationGrey_erosion
```

```python
>>> a = np.zeros((7,7), dtype=np.int)
>>> a[2:5, 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, 0, 0, 0, 0, 0, 0]])
```

```python
>>> # 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, 3, 3, 3, 1, 0],
       [0, 1, 3, 3, 3, 1, 0],
       [0, 1, 3, 2, 3, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```

```python
>>> a = np.zeros((7,7), dtype=np.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, 1, 2, 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, 2, 3, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```

```python
scipy.ndimage.morphology.morphological_laplace(input, size=None, footprint=None, structure=None, output=None, mode='reflect', cval=0.0, origin=0)
```

5.22. Multi-dimensional image processing (scipy.ndimage) 707
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

```python
scipy.ndimage.morphology.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`

5.22.6 Utility

```python
imread(fname[, flatten, mode])
```  
Read an image from a file as an array.
scipy.ndimage.imread(fname, flatten=False, mode=None)

Read an image from a file as an array.

Parameters:
- fname : str
  Image file name, e.g. test.jpg, or a file object.
- flatten : bool, optional
  If true, convert the output to grey-scale. Default is False.
- mode : str, optional
  mode to convert image to, e.g. RGB.

Returns:
- img_array : 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.

Raises:
- ImportError
  If the Python Imaging Library (PIL) can not be imported.

5.23 Orthogonal distance regression (scipy.odr)

5.23.1 Package Content

- Data(x[, y, we, wd, fix, meta])
  The data to fit.

- RealData(x[, y, sx, sy, covx, covy, fix, meta])
  The data, with weightings as actual standard deviations and/or covariances.

- Model(fcn[, fjacb, fjacd, extra_args, ...])
  The Model class stores information about the function you wish to fit.

- ODR(data, model[, beta0, delta0, ifixb, ...])
  The ODR class gathers all information and coordinates the running of the main fitting routine.

- Output(output)
  The Output class stores the output of an ODR run.

- odr(fcn, beta0, y, x[, we, wd, fjacb, ...])
  Low-level function for ODR.

- odr_error
  Exception indicating an error in fitting.

- odr_stop
  Exception stopping fitting.

class scipy.odr.Data (x=y=None, we=None, wd=None, fix=None, meta={})

The data to fit.

Parameters:
- x : array_like
  Input data for regression.
- y : array_like, optional
  Input data for regression.
- 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 \((m, m)\), 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** : dict, optional
Free-form dictionary for metadata.

**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.
```

```
Data.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")
```

**class** `scipy.odr.RealData` *(x, y=\(\text{None}\), sx=\(\text{None}\), sy=\(\text{None}\), covx=\(\text{None}\), covy=\(\text{None}\), fix=\(\text{None}\), meta=\(\varnothing\))*

The data, with weightings as actual standard deviations and/or covariances.

**Parameters**

- `x` : array_like
- `y` : array_like, optional
- `sx`, `sy` : 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.
  - 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 covariance matrix.

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 : dict, optional
   Free-form dictionary for metadata.

Notes
The weights wd and we are computed from provided values as follows:

sx and sy are converted to weights by dividing 1.0 by their squares. For example, wd = 1./numpy.power('sx', 2).

covx and covy are arrays of covariance matrices and are converted to weights by performing a matrix inversion on each observation’s covariance matrix. For example, we[i] = numpy.linalg.inv(covy[i]).

These arguments follow the same structured argument conventions as wd and we only restricted by their natures: sx and sy can’t be rank-3, but covx and covy can be.

Only set either sx or covx (not both). Setting both will raise an exception. Same with sy and covy.

Methods

set_meta(**kwds) Update the metadata dictionary with the keywords and data provided by keywords.

RealData.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")

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) -> y

fjacb : function
   Jacobian of fcn wrt the fit parameters beta.
   fjacb(beta, x) -> @f_i(x,B)/@B_j

fjacd : function
   Jacobian of fcn wrt the (possibly multidimensional) input variable.
   fjacd(beta, x) -> @f_i(x,B)/@x_j

extra_args : tuple, optional
If specified, \texttt{extra_args} should be a tuple of extra arguments to pass to \texttt{fcn}, \texttt{fjacb}, and \texttt{fjacd}. Each will be called by \texttt{apply(fcn, (beta, x) + extra_args)}

\textbf{estimate} : array\_like of rank-1
  Provides estimates of the fit parameters from the data
  \texttt{estimate(data) \rightarrow estbeta}

\textbf{implicit} : boolean
  If \texttt{TRUE}, specifies that the model is implicit; i.e \texttt{fcn(beta, x) \sim 0} and there is no \texttt{y} data to fit against

\textbf{meta} : dict, optional
  freeform dictionary of metadata for the model

Notes
Note that the \texttt{fcn}, \texttt{fjacb}, and \texttt{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 \texttt{x} is rank-1 array; i.e. \texttt{x = array([1, 2, 3, ...,])}; \texttt{x.shape = (n,)}. If the input data is multi-dimensional, then \texttt{x} is a rank-2 array; i.e., \texttt{x = array([[1, 2, ...], [2, 4, ...]])}; \texttt{x.shape = (m, n)}. In all cases, it has the same shape as the input data array passed to \texttt{odr}. \texttt{m} is the dimensionality of the input data, \texttt{n} is the number of observations.

\textbf{y}
if the response variable is single-dimensional, then \texttt{y} is a rank-1 array, i.e., \texttt{y = array([2, 4, ...])}; \texttt{y.shape = (n,)}. If the response variable is multi-dimensional, then \texttt{y} is a rank-2 array, i.e., \texttt{y = array([[2, 4, ...], [3, 6, ...]])}; \texttt{y.shape = (q, n)} where \texttt{q} is the dimensionality of the response variable.

\textbf{beta}
rank-1 array of length \texttt{p} where \texttt{p} is the number of parameters; i.e. \texttt{beta = array([B_1, B_2, ..., B_p])}

\textbf{fjacb}
if the response variable is multi-dimensional, then the return array’s shape is \((q, p, n)\) such that \texttt{fjacb(x,beta)[l,k,i] = d f_l(X,B)/d B_k} evaluated at the \texttt{i}’th data point. If \texttt{q == 1}, then the return array is only rank-2 and with shape \((p, n)\).

\textbf{fjacd}
as with \texttt{fjacb}, only the return array’s shape is \((q, m, n)\) such that \texttt{fjacd(x,beta)[l,j,i] = d f_l(X,B)/d X_j} at the \texttt{i}’th data point. If \texttt{q == 1}, then the return array’s shape is \((m, n)\). If \texttt{m == 1}, the shape is \((q, n)\). If \texttt{m == q == 1}, the shape is \((n,)\).

Methods

\texttt{set_meta(**kwds)}  Update the metadata dictionary with the keywords and data provided here.

Model.\texttt{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")

\textbf{class scipy.odr.ODR (data, model, beta0=None, delta0=None, ifxb=None, ifx0=None, job=None, imprint=None, errfile=None, rptfile=None, ndigit=None, tautfac=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

- **data**: Data class instance
  - instance of the Data class
- **model**: Model class instance
  - instance of the Model class

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.

`scld` : array_like, optional
array (scld.shape == data.x.shape or scld.shape == (m,)) of scaling factors for the errors in the input variables. Again, these factors are automatically computed if you do not provide them. If scld.shape == (m,), then the scaling factors are broadcast to all observations.

`work` : ndarray, optional
array to hold the double-valued working data for ODRPACK. When restarting, takes the value of self.output.work.

`iwork` : ndarray, optional
array to hold the integer-valued working data for ODRPACK. When restarting, takes the value of self.output.iwork.

**Attributes**

<table>
<thead>
<tr>
<th>data</th>
<th>(Data) The data for this fit</th>
</tr>
</thead>
<tbody>
<tr>
<td>model</td>
<td>(Model) The model used in fit</td>
</tr>
<tr>
<td>output</td>
<td>(Output) An instance if the Output class containing all of the returned data from an invocation of ODR.run() or ODR.restart()</td>
</tr>
</tbody>
</table>

**Methods**

<table>
<thead>
<tr>
<th>restart([iter])</th>
<th>Restarts the run with iter more iterations.</th>
</tr>
</thead>
<tbody>
<tr>
<td>run()</td>
<td>Run the fitting routine with all of the information given.</td>
</tr>
<tr>
<td><code>set_iprint</code>([init, so_init, iter, so_iter, ...])</td>
<td>Set the iprint parameter for the printing of computation reports.</td>
</tr>
<tr>
<td><code>set_job</code>([fit_type, deriv, var_calc, ...])</td>
<td>Sets the “job” parameter is a hopefully comprehensible way.</td>
</tr>
</tbody>
</table>

**ODR.restart** (iter=None)
Restarts the run with iter more iterations.

**Parameters**

<table>
<thead>
<tr>
<th>iter</th>
<th>int, optional</th>
</tr>
</thead>
<tbody>
<tr>
<td>ODRPACK’s default for the number of new iterations is 10.</td>
<td></td>
</tr>
</tbody>
</table>

**Returns**

<table>
<thead>
<tr>
<th>output</th>
<th>Output instance</th>
</tr>
</thead>
<tbody>
<tr>
<td>This object is also assigned to the attribute .output .</td>
<td></td>
</tr>
</tbody>
</table>

**ODR.run()**
Run the fitting routine with all of the information given.

**Returns**

<table>
<thead>
<tr>
<th>output</th>
<th>Output instance</th>
</tr>
</thead>
<tbody>
<tr>
<td>This object is also assigned to the attribute .output .</td>
<td></td>
</tr>
</tbody>
</table>

**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
ODR.set_job(fit_type=None, deriv=None, var_calc=None, del_init=None, restart=None)
```

Sets the “job” parameter is 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
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**

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>beta</td>
<td>(ndarray) Estimated parameter values, of shape (q,).</td>
</tr>
<tr>
<td>sd_beta</td>
<td>(ndarray) Standard errors of the estimated parameters, of shape (p,).</td>
</tr>
<tr>
<td>cov_beta</td>
<td>(ndarray) Covariance matrix of the estimated parameters, of shape (p,p).</td>
</tr>
<tr>
<td>delta</td>
<td>(ndarray, optional) Array of estimated errors in input variables, of same shape as x.</td>
</tr>
<tr>
<td>eps</td>
<td>(ndarray, optional) Array of estimated errors in response variables, of same shape as y.</td>
</tr>
<tr>
<td>xplus</td>
<td>(ndarray, optional) Array of x + delta.</td>
</tr>
<tr>
<td>y</td>
<td>(ndarray, optional) Array y = fcn(x + delta).</td>
</tr>
<tr>
<td>res_var</td>
<td>(float, optional) Residual variance.</td>
</tr>
<tr>
<td>sum_square</td>
<td>(float, optional) Sum of squares error.</td>
</tr>
<tr>
<td>sum_square_delta</td>
<td>(float, optional) Sum of squares of delta error.</td>
</tr>
<tr>
<td>sum_square_eps</td>
<td>(float, optional) Sum of squares of eps error.</td>
</tr>
<tr>
<td>inv_condnum</td>
<td>(float, optional) Inverse condition number (cf. ODRPACK UG p. 77).</td>
</tr>
<tr>
<td>rel_error</td>
<td>(float, optional) Relative error in function values computed within fcn.</td>
</tr>
<tr>
<td>work</td>
<td>(ndarray, optional) Final work array.</td>
</tr>
<tr>
<td>work_ind</td>
<td>(dict, optional) Indices into work for drawing out values (cf. ODRPACK UG p. 83).</td>
</tr>
<tr>
<td>info</td>
<td>(int, optional) Reason for returning, as output by ODRPACK (cf. ODRPACK UG p. 38).</td>
</tr>
<tr>
<td>stopreason</td>
<td>(list of str, optional) info interpreted into English.</td>
</tr>
</tbody>
</table>

**Methods**

**pprint()**  Pretty-print important results.

```python
scipy.odr.pprint()  Pretty-print important results.
```

```python
scipy.odr.odr(fcn, beta0, y, x, we=None, wd=None, fjacb=None, fjacd=None, extra_args=None, ifixx=None, ifixb=None, job=0, iprint=0, errfile=None, rptfile=None, ndigit=0, taufac=0.0, sstol=-1.0, partol=-1.0, maxit=-1, stpb=None, stdp=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.

**exception scipy.odr.odr_error**  Exception indicating an error in fitting.

This is raised by scipy.odr if an error occurs during fitting.

**exception scipy.odr.odr_stop**  Exception stopping fitting.

You can raise this exception in your objective function to tell scipy.odr to stop fitting.
5.23.2 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 [R468] 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:
   
   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()
   ``

myoutput.pprint()

References

5.24 Optimization and root finding (scipy.optimize)

5.24.1 Optimization

Local Optimization

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>minimize</td>
<td>Minimization of scalar function of one or more variables.</td>
</tr>
<tr>
<td>minimize_scalar</td>
<td>Minimization of scalar function of one variable.</td>
</tr>
<tr>
<td>OptimizeResult</td>
<td>Represents the optimization result.</td>
</tr>
</tbody>
</table>

`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.

In general, the optimization problems are of the form:

minimize f(x)

subject to:

\[ g_i(x) \geq 0, i = 1, \ldots, m \]

\[ h_j(x) = 0, j = 1, \ldots, p \]

Where \( x \) is a vector of one or more variables. \( g_i(x) \) are the inequality constraints. \( h_j(x) \) are the equality constraints.

Optionally, the lower and upper bounds for each element in \( x \) can also be specified using the `bounds` argument.

**Parameters**

- **fun** : callable
  - Objective function.
- **x0** : ndarray
  - Initial guess.
- **args** : tuple, optional
  - Extra arguments passed to the objective function and its derivatives (Jacobian, Hessian).
- **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](#))
    - ‘dogleg’ ([see here](#))
    - ‘trust-ncg’ ([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 : 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.

hess, hessp : callable, optional
   Hessian (matrix of second-order derivatives) of objective function or Hessian of ob-
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 ap-
proximated using finite differences on jac. hessp must compute the Hessian times an
arbitrary vector.

bounds : sequence, optional
   Bounds for variables (only for L-BFGS-B, TNC and SLSQP). (min, max) pairs
for each element in x, defining the bounds on that parameter. Use None for one of
min or max when there is no bound in that direction.

constraints : dict or sequence of dict, optional
   Constraints definition (only for COBYLA and SLSQP). 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.

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, as callback(xk), where xk is the current parameter
vector.

Returns
   res : OptimizeResult
      The optimization result represented as a OptimizeResult object. Important at-
ttributes 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_scalar
   Interface to minimization algorithms for scalar univariate 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 \textit{BFGS}.

Unconstrained minimization

Method \textit{Nelder-Mead} uses the Simplex algorithm \cite{R142}, \cite{R143}. This algorithm has been successful in many applications but other algorithms using the first and/or second derivatives information might be preferred for their better performances and robustness in general.

Method \textit{Powell} is a modification of Powell’s method \cite{R144}, \cite{R145} which is a conjugate direction method. It performs sequential one-dimensional minimizations along each vector of the directions set \textit{(direct field in options and info)}, which is updated at each iteration of the main minimization loop. The function need not be differentiable, and no derivatives are taken.

Method \textit{CG} uses a nonlinear conjugate gradient algorithm by Polak and Ribiere, a variant of the Fletcher-Reeves method described in \cite{R146} pp. 120-122. Only the first derivatives are used.

Method \textit{BFGS} uses the quasi-Newton method of Broyden, Fletcher, Goldfarb, and Shanno (BFGS) \cite{R146} 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 \textit{hess_inv} in the \texttt{OptimizeResult} object.

Method \textit{Newton-CG} uses a Newton-CG algorithm \cite{R146} pp. 168 (also known as the truncated Newton method). It uses a CG method to the compute the search direction. See also \textit{TNC} method for a box-constrained minimization with a similar algorithm.

Method \textit{dogleg} uses the dog-leg trust-region algorithm \cite{R146} for unconstrained minimization. This algorithm requires the gradient and Hessian; furthermore the Hessian is required to be positive definite.

Method \textit{trust-ncg} uses the Newton conjugate gradient trust-region algorithm \cite{R146} 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.

Constrained minimization

Method \textit{L-BFGS-B} uses the L-BFGS-B algorithm \cite{R147}, \cite{R148} for bound constrained minimization.

Method \textit{TNC} uses a truncated Newton algorithm \cite{R146}, \cite{R149} 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 \textit{Newton-CG} method described above as it wraps a C implementation and allows each variable to be given upper and lower bounds.

Method \textit{COBYLA} uses the Constrained Optimization BY Linear Approximation (COBYLA) method \cite{R150}, \cite{R151}. 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 \textit{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 \cite{R152}. Note that the wrapper handles infinite values in bounds by converting them into large floating values.

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, **kwargs, **options)` where `kwargs` 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

[R142], [R143], [R144], [R145], [R146], [R147], [R148], [R149], [R150], 10, 11, 12

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')
>>> 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: 52
  Function evaluations: 64
  Gradient evaluations: 64
>>> 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 [R146]). The objective function is:

```python
>>> fun = lambda x: (x[0] - 1)**2 + (x[1] - 2.5)**2
```

There are three constraints defined as:
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).

**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)*

  - custom - a callable object (added in version 0.14.0), see below

- **tol** : float, optional
  
  Tolerance for termination. For detailed control, use solver-specific options.

- **options** : dict, optional
  
  A dictionary of solver 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 an 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, **kwargs, **options) where kwargs 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:

```python
>>> res = minimize_scalar(f, bounds=(-3, -1), method='bounded')
>>> res.x
-2.0000002026
```

class scipy.optimize.OptimizeResult

Represents the optimization result.

Notes

There may be additional attributes not listed above depending of 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

<table>
<thead>
<tr>
<th>x</th>
<th>(ndarray) The solution of the optimization.</th>
</tr>
</thead>
<tbody>
<tr>
<td>success</td>
<td>(bool) Whether or not the optimizer exited successfully.</td>
</tr>
<tr>
<td>status</td>
<td>(int) Termination status of the optimizer. Its value depends on the underlying solver. Refer to <code>message</code> for details.</td>
</tr>
<tr>
<td>message</td>
<td>(str) Description of the cause of the termination.</td>
</tr>
<tr>
<td>fun, jac, hess, hess_inv</td>
<td>(ndarray) Values of objective function, Jacobian, Hessian or its inverse (if available). The Hessians may be approximations, see the documentation of the function in question.</td>
</tr>
<tr>
<td>nev, njev, nhev</td>
<td>(int) Number of evaluations of the objective functions and of its Jacobian and Hessian.</td>
</tr>
<tr>
<td>nit</td>
<td>(int) Number of iterations performed by the optimizer.</td>
</tr>
<tr>
<td>maxcv</td>
<td>(float) The maximum constraint violation.</td>
</tr>
</tbody>
</table>

Methods

```
clear() -> None. Remove all items from D.
copy() -> a shallow copy of D
fromkeys(...) v defaults to None.
get(k[,d]) -> D[k] if k in D, ... has_key(k) -> True if D has a key k, else False
items() -> list of D’s (key, value) pairs, ...
iteritems() -> an iterator over the (key, ...)
iterkeys() -> an iterator over the keys of D
itervalues() ...
keys() -> list of D’s keys
pop(k[,d]) -> v, ... If key is not found, d is returned if given, otherwise KeyError is raised
popitem() -> (k, v), ... 2-tuple; but raise KeyError if D is empty.
setdefault((k[,d]) -> D.get(k,d), ...)
update(([,E, ...]) If E present and has a .keys() method, does: for k in E: D[k] = E[k]
values() -> list of D’s values
viewItems(...)
viewkeys(...)
viewvalues(...)```

```
OptimizeResult.clear() -> None. Remove all items from D.
OptimizeResult.copy() -> a shallow copy of D

static OptimizeResult.fromkeys(S[, v]) -> New dict with keys from S and values equal to v. v defaults to None.
OptimizeResult.get(k[, d]) -> D[k] if k in D, else d. d defaults to None.
OptimizeResult.has_key(k) -> True if D has a key k, else False
OptimizeResult.items() -> list of D’s (key, value) pairs, as 2-tuples
OptimizeResult.iteritems() -> an iterator over the (key, value) items of D```
OptimizeResult.iterkeys() → an iterator over the keys of D

OptimizeResult.itervalues() → an iterator over the values of D

OptimizeResult.keys() → list of D’s keys

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

OptimizeResult.popitem() → (k, v), remove and return some (key, value) pair as a 2-tuple; but raise KeyError if D is empty.

OptimizeResult.setdefault(k[, d]) → D.get(k,d), also set D[k]=d if k not in D

OptimizeResult.update([E, **F]) → None. Update D from dict/iterable E and F.
If E present and has a .keys() method, does: for k in E: D[k] = E[k] If E present and lacks .keys() method, does: for (k, v) in E: D[k] = v In either case, this is followed by: for k in F: D[k] = F[k]

OptimizeResult.values() → list of D’s values

OptimizeResult.viewitems() → a set-like object providing a view on D’s items

OptimizeResult.viewkeys() → a set-like object providing a view on D’s keys

OptimizeResult.viewvalues() → an object providing a view on D’s values

The minimize function supports the following methods:

**minimize(method=’Nelder-Mead’)**

scipy.optimize.minimize(fun, x0, args=(), method=’Nelder-Mead’, tol=None, callback=None, options={'disp': False, 'maxiter': None, 'return_all': False, 'func': None, 'maxfev': None, 'xtol': 0.0001, 'ftol': 0.0001})

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.

xtol : float
  Relative error in solution xopt acceptable for convergence.

ftol : float
  Relative error in fun(xopt) acceptable for convergence.

maxiter : int
  Maximum number of iterations to perform.

maxfev : int
  Maximum number of function evaluations to make.
minimize(method='Powell')

```python
scipy.optimize.minimize(fun, x0, args=(), method='Powell', tol=None, callback=None, options={‘disp’: False, ‘return_all’: False, ‘maxiter’: None, ‘direc’: None, ‘func’: None, ‘maxfev’: None, ‘xtol’: 0.0001, ‘ftol’: 0.0001})
```

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 $x_{opt}$ acceptable for convergence.
- **ftol** : float
  - Relative error in $f(x_{opt})$ acceptable for convergence.
- **maxiter** : int
  - Maximum number of iterations to perform.
- **maxfev** : int
  - Maximum number of function evaluations to make.
- **direc** : ndarray
  - Initial set of direction vectors for the Powell method.

minimize(method='CG')

```python
scipy.optimize.minimize(fun, x0, args=(), method='CG', jac=None, tol=None, callback=None, options={‘disp’: False, ‘gtol’: 1e-05, ‘eps’: 1.4901161193847656e-08, ‘return_all’: False, ‘maxiter’: None, ‘norm’: inf})
```

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 $g_{tol}$ 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
scipy.optimize.minimize(fun, x0, args=(), method='BFGS', jac=None, tol=None, callback=None, options={‘disp’: False, ‘gtol’: 1e-05, ‘eps’: 1.4901161193847656e-08, ‘return_all’: False, ‘maxiter’: None, ‘norm’: inf})
```

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
scipy.optimize.minimize(fun, x0, args=(), method='Newton-CG', jac=None, hess=None,
hessp=None, tol=None, callback=None, options={'disp': False, 'xtol': 1e-05, 'eps': 1.4901161193847656e-08, 'return_all': False, 'maxiter': None})
```

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')`

```python
scipy.optimize.minimize(fun, x0, args=(), method='L-BFGS-B', jac=None, bounds=None,
tol=None, callback=None, options={'disp': None, 'iprint': -1, 'gtol': 1e-05, 'eps': 1e-08, 'maxiter': 15000, 'ftol': 2.220446049250313e-09, 'maxcor': 10, 'maxfun': 15000})
```

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 : bool
  Set to True to print convergence messages.
- 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.)
- factr : float
  The iteration stops when \((f^k - f^{k+1})/\max\{|f^k|,|f^{k+1}|,1\} <= \text{factr} \times \text{eps}\), 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.
- 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 \( \max(\|\text{proj } g_i \| \mid i = 1, \ldots, n) \leq gtol \)
where \( pg_i \) is the i-th component of the projected gradient.

eps : float
Step size used for numerical approximation of the jacobian.

disp : int
Set to True to print convergence messages.

maxfun : int
Maximum number of function evaluations.

maxiter : int
Maximum number of iterations.

\textbf{minimize}(method='TNC')

\texttt{scipy.optimize.minimize}(fun, x0, args=(), method='TNC', jac=None, bounds=None, tol=None, callback=None, options={})

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 \texttt{scipy.optimize.minimize}

\textbf{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| to 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*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 <= machine_precision, set to sqrt(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(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(accuracy). Setting it to 0.0 is not recommended. Defaults to -1.

rescale : float
    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.

**minimize(method='COBYLA')**

```python
scipy.optimize.minimize(fun, x0, args=(), method='COBYLA', constraints=(), tol=None, callback=None, options={'iprint': 1, 'disp': True, 'maxiter': 1000, 'catol': 0.0002, 'rhobeg': 1.0})
```

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 and set to 0.
- **maxiter** : int
  - Maximum number of function evaluations.
- **catol** : float
  - Tolerance (absolute) for constraint violations

**minimize(method='SLSQP')**

```python
scipy.optimize.minimize(fun, x0, args=(), method='SLSQP', jac=None, bounds=None, constraints=(), tol=None, callback=None, options={'disp': False, 'iprint': 1, 'eps': 1.4901161193847656e-08, 'func': None, 'maxiter': 100, 'ftol': 1e-06})
```

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.
- **disp** : bool
  - Set to True to print convergence messages. If False, verbosity is ignored and set to 0.
- **maxiter** : int
  - Maximum number of iterations.
minimize(method='dogleg')

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')

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.

The minimize_scalar function supports the following methods:

minimize_scalar(method='brent')

scipy.optimize.minimize_scalar(fun, args=(), method='brent', tol=None, options={'xtol': 1.48e-08, 'brack': None, 'func': None, '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.
Notes

Uses inverse parabolic interpolation when possible to speed up convergence of golden section method.

`minimize_scalar('bounded')`

```python
scipy.optimize.minimize_scalar(fun, bounds=None, args=(), method='bounded', tol=None, options={
    'disp': 0, 'maxiter': 500, 'func': None, 'xatol': 1e-05})
```

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**: bool
  - Set to True to print convergence messages.
- **xatol**: float
  - Absolute error in solution `xopt` acceptable for convergence.

`minimize_scalar('golden')`

```python
scipy.optimize.minimize_scalar(fun, args=(), method='golden', tol=None, options={
    'xtol': 1.4901161193847656e-08, 'brack': None, 'func': None})
```

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.

The specific optimization method interfaces below in this subsection are not recommended for use in new scripts; all of these methods are accessible via a newer, more consistent interface provided by the functions above.

General-purpose multivariate methods:

- `fmin(func, x0[, args, xtol, ftol, maxiter, ...])`: Minimize a function using the downhill simplex algorithm.
- `fmin_powell(func, x0[, args, xtol, ftol, ...])`: Minimize a function using modified Powell’s method.
- `fmin_cg(f, x0[, fprime, args, gtol, norm, ...])`: Minimize a function using a nonlinear conjugate gradient algorithm.
- `fmin_bfgs(f, x0[, fprime, args, gtol, norm, ...])`: Minimize a function using the BFGS algorithm.
- `fmin_ncg(f, x0[, fprime[, fhess_p, fhess, ...]])`: Unconstrained minimization of a function using the Newton-CG method.

```python
scipy.optimize.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.

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).
- **callback**: callable, optional

5.24. Optimization and root finding (`scipy.optimize`) 731
Called after each iteration, as callback(xk), where xk is the current parameter vector.

**xtol** : float, optional
Relative error in xopt acceptable for convergence.

**ftol** : number, optional
Relative error in func(xopt) 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.

**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.

**References**

[R136], [R137]

scipy.optimize.fmin_powell (func, x0, args=(), xtol=0.0001, ftol=0.0001, maxiter=None, maxfun=None, full_output=0, disp=1, retall=0, callback=None, direc=None)

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).
direc : ndarray
   Current direction set.
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


```python
scipy.optimize.fmin_cg(f, x0, fprime=None, args=(), gtol=1e-05, norm=inf, epsilon=1.4901161193847656e-08, maxiter=None, full_output=0, disp=1, retall=0, callback=None)
```

Minimize a function using a nonlinear conjugate gradient algorithm.

**Parameters**

- `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 (`-np.inf` is min, `np.inf` 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(eps)`, with `eps` the floating point machine precision. Usually `sqrt(eps)` is about 1.5e-8.

- `maxiter`: int, optional
  - Maximum number of iterations to perform. Default is `200 * len(x0)`.

- `full_output`: bool, optional
  - If True, return `fopt`, `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.

- `callback`: callable, optional
  - An optional user-supplied function, called after each iteration. Called as `callback(xk)`, where `xk` is the current value of `x0`.

**Returns**

- `xopt`: ndarray
  - Parameters which minimize `f`, i.e. `f(xopt) == 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 `restr` is True.

See also:

`minimize` 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'`.

**Notes**
This conjugate gradient algorithm is based on that of Polak and Ribiere [R138].

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. $fprime$ 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**

[R138]

**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 $(u, v) = (0, 0)$.

```
>>> 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)
>>> print('res1 = ', res1)
Optimization terminated successfully.
Current function value: 1.617021
Iterations: 2
Function evaluations: 5
```
Gradient evaluations: 5
res1 = [-1.80851064 -0.25531915]

Example 2: solve the same problem using the `minimize` function. (This `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: 2
Function evaluations: 5
Gradient evaluations: 5
```

```python
>>> res2.x  # minimum found
array([-1.80851064 -0.25531915])
```

```
scipy.optimize.fmin_bfgs(f, x0, fprime=None, args=(), gtol=1e-05, norm=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.
- `fopt`: float
  - Minimum value.
SciPy Reference Guide, Release 0.16.0

\[ \text{gopt} : \text{ndarray} \]
Value of gradient at minimum, \( f'(\text{xopt}) \), which should be near 0.

\[ \text{Bopt} : \text{ndarray} \]
Value of \( 1/f''(\text{xopt}) \), i.e. the inverse hessian matrix.

\[ \text{func_calls} : \text{int} \]
Number of function calls made.

\[ \text{grad_calls} : \text{int} \]
Number of gradient calls made.

\[ \text{warnflag} : \text{integer} \]
1 : Maximum number of iterations exceeded. 2 : Gradient and/or function calls not changing.

\[ \text{allvecs} : \text{list} \]
OptimizeResult 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**

```
scipy.optimize.fmin_ncg(f, x0, fprime, fhess_p=None, fhess=None, args=(), avextol=1e-05, epsilon=1.4901161193847656e-08, maxiter=None, full_output=0, disp=1, retall=0, callback=None)
```

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

5.24. Optimization and root finding (scipy.optimize) 737
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. \( f(x_{\text{opt}}) = f_{\text{opt}} \).

fopt : float
  Value of the function at xopt, i.e. \( f_{\text{opt}} = f(x_{\text{opt}}) \).

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 \( f_{\text{hess\_p}} \) or \( f_{\text{hess}} \) need to be given. If \( f_{\text{hess}} \) is provided, then \( f_{\text{hess\_p}} \) will be ignored. If neither \( f_{\text{hess}} \) nor \( f_{\text{hess\_p}} \) is provided, then the hessian product will be approximated using finite differences on \( f_{\text{prime}} \). \( f_{\text{hess\_p}} \) must compute the hessian times an arbitrary vector. If it is not given, finite-differences on \( f_{\text{prime}} \) are used to compute it.

Newton-CG methods are also called truncated Newton methods. This function differs from scipy.optimize.fmin_tnc because

1. \texttt{scipy.optimize.fmin\_ncg} is written purely in python using numpy
   and scipy while scipy.optimize.fmin_tnc calls a C function.

2. \texttt{scipy.optimize.fmin\_neq} 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:

\begin{verbatim}
minimize(func, x0[, fprime, args, ...]) Minimize a function func using the L-BFGS-B algorithm.
minimize(func, x0[, fprime, args, ...]) Minimize a function with variables subject to bounds, using gradient information in a truncated Newton algorithm.
minimize(func, x0[, args, ...]) Minimize a function using the Constrained Optimization BY Linear Approximation (COBYLA) method.
minimize(func, x0[, args, ...]) Minimize a function using Sequential Least SQares Programming


differential\_evolution(func, bounds[, args, ...]) Finds the global minimum of a multivariate function.
\end{verbatim}

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)
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.
- `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` means write messages to stdout; `iprint > 1` in addition means write logging information to a file named `iterate.dat` in the current working directory.
- `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.

**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.

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(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`.

If the function returns None, the minimization is aborted.

`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 facor (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

---

5.24. Optimization and root finding (**scipy.optimize**) 741
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 unconstrained 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’

scipy.optimize.fmin_cobyla (func, x0, cons=(), args=(), consargs=None, rhobeg=1.0, rhoend=0.0001, iprint=1, maxfun=1000, disp=None, catol=0.0002)

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.

**iprint**: {0, 1, 2, 3}, optional
Controls the frequency of output; 0 implies no output. Deprecated.

**disp**: {0, 1, 2, 3}, optional
Over-rides the iprint interface. Preferred.

**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_i 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:
>>> 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)

Normal return from subroutine COBYLA

NFVALS = 64  F = -5.000000E-01  MAXCV = 1.998401E-14
X = -7.071069E-01  7.071067E-01
array([-0.70710685, 0.70710671])

The exact solution is (-sqrt(2)/2, sqrt(2)/2).

scipy.optimize.fmin_slsqp(func, x0, eqcons=(), f_eqcons=None, ieqcons=(), f_ieqcons=None, bounds=(), fprime=None, fprime_eqcons=None, fprime_ieqcons=None, args=(), iter=100, acc=1e-06, iprint=1, disp=None, full_output=0, epsilon=1.4901161193847656e-08, callback=None)

Minimize a function using Sequential Least SQquares Programming

Parameters

- **func**: callable f(x,*args)
  Objective function.
- **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
  [(xl0, xu0),(xl1, 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 of the form f(x, *args) that returns the m by n array of equality constraint normals. If not provided, the normals will be approximated. The array returned by fprime_eqcons should be sized as (len(eqcons), len(x0) ).
- **fprime_ieqcons**: 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_ieqcons should be sized as (len(ieqcons), 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.
imiento : int, optional
   The verbosity of fmin_slsqp :
   • iprint <= 0 : Silent operation
   • iprint == 1 : Print summary upon completion (default)
   • iprint >= 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 callback(x), where x is the current parameter vec-

tor.

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.

```python
scipy.optimize.differential_evolution(func, bounds, args=(), strategy='best1bin', maxiter=None, popsize=15, tol=0.01, mutation=(0.5, 1), recombination=0.7, seed=None, callback=None, disp=False, polish=True, init='latinhypercube')
```

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 [R133].

**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`.

- `args` : tuple, optional
  Any additional fixed parameters needed to completely specify the objective function.

- `strategy` : str, optional
  The differential evolution strategy to use. Should be one of:
  - `'best1bin'`
  - `'best1exp'`
  - `'rand1exp'`
  - `'randtobest1exp'`
  - `'best2exp'`
  - `'rand2exp'`
  - `'randtobest1bin'`
  - `'best2bin'`
  - `'rand2bin'`
  - `'rand1bin'`
  The default is `'best1bin'`.

- `maxiter` : int, optional
  The maximum number of times the entire population is evolved. The maximum number of function evaluations is: `maxiter * popsize * len(x)`

- `popsize` : int, optional
  A multiplier for setting the total population size. The population has `popsize * len(x)` individuals.

- `tol` : float, optional
  When the mean of the population energies, multiplied by `tol`, divided by the standard deviation of the population energies is greater than 1 the solving process terminates:
  ```
  convergence = mean(pop) * tol / stdev(pop) > 1
  ```

- `mutation` : float or tuple(float, float), optional
  The mutation constant. If specified as a float it should be in the range [0, 2]. If specified as a tuple `(min, 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[min, 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]. 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 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, 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**: string, optional
Specify how the population initialization is performed. Should be one of:
- ‘latinhypercube’
- ‘random’

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.

**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, 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 [R134] 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), b0, so far:

\[ b' = b_0 + \text{mutation} \times (\text{population}[\text{rand0}] - \text{population}[\text{rand1}]) \]

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.

New in version 0.15.0.
References
[R133], [R134], [R135]

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)
```

Next find the minimum of the Ackley function (http://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)
```

Univariate (scalar) minimization methods:

- **fminbound**
  - `func(x1, x2[, args, xtol, ...])` 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.

- **brent**
  - `func(args, brack, tol, full_output, ...)`: Given a function of one-variable and a possible bracketing interval, return the minimum value.

- **golden**
  - `func(args, brack, tol, full_output)`: Return the minimum of a function of one variable.
SciPy Reference Guide, Release 0.16.0

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).

**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 bracketing interval, return the 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
  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 the obtained solution will satisfy a<=x<=c.
- `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.

**scipy.optimize.golden** (`func`, `args=()`, `brack=None`, `tol=1.4901161193847656e-08`, `full_output=0`)

Return the minimum of a function of one variable.
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
  - 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.

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.

### Equation (Local) Minimizers

- `leastsq(func, x0[, args, Dfun, full_output, ...])`
  - Minimize the sum of squares of a set of equations.
  
  - `nnls(A, b)`
    - Solve argmin_x || Ax - b ||^2 for x>=0.

```python
cipy.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, epsfcn=None, factor=100, diag=None)
```

Minimize the sum of squares of a set of equations.

```python
x = arg min(sum(func(y)**2,axis=0))
```

**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:

- **nfev**: The number of function calls
- **fvec**: The function evaluated at the output
- **fjac**: A permutation of the R matrix of a QR factorization of the final ap-
approximate Jacobian matrix, stored column wise. Together with ipvt,
the covariance of the estimate can be approximated.
- **ipvt**: An integer array of length N which defines a permutation matrix, p,
such that fjac*p = q*r, where r is upper triangular with diagonal ele-
ments of nonincreasing magnitude. Column j of p is column ipvt(j) of
the identity matrix.
- **qtf**: The vector (transpose(q) * fvec).
- **mesg**: str
A string message giving information about the cause of failure.
- **ier**: int
An integer flag. If it is equal to 1, 2, 3 or 4, the solution was found. Otherwise, the
solution was not found. In either case, the optional output variable ‘mesg’ gives more
information.

**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)
func(params) = ydata - f(xdata, params)

so that the objective function is

\[
\min \sum (ydata - f(xdata, params))^2, \text{axis}=0
\]

params

scipy.optimize.nnls(A, b)

Solve \( \argmin_x \| Ax - b \|_2 \) for \( x \geq 0 \). This is a wrapper for a FORTAN non-negative least squares solver.

**Parameters**

- **A**: ndarray
  - Matrix \( A \) as shown above.
- **b**: ndarray
  - Right-hand side vector.

**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**


**Global Optimization**

scipy.optimize.basinhopping(func, x0[, niter, T, stepsize, ...])

Find the global minimum of a function using the basin-hopping algorithm

**Parameters**

- **func**: callable \( f(x, *args) \)
  - Function to be optimized. \( args \) can be passed as an optional item in the dict \( \text{minimizer_kwargs} \)
- **x0**: ndarray
  - 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**: float, optional
  - initial step size for use in the random displacement.
- **minimizer_kwargs**: 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. "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 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 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.

**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. 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 [R127] [R128] [R129] [R130]. The algorithm in its current form was described by David Wales and Jonathan Doye [R128] 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 [R129].

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. Ideally it should be comparable to the typical separation 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 value for stepsize.

Choosing T: The parameter T is the temperature used in the metropolis criterion. Basinhopping steps are accepted with probability 1 if \( \text{func}(x_{\text{new}}) < \text{func}(x_{\text{old}}) \), or otherwise with probability:

\[
\exp\left(\frac{- (\text{func}(x_{\text{new}}) - \text{func}(x_{\text{old}}))}{T} \right)
\]

So, for best results, T should to be comparable to the typical difference in function values between local minima.

New in version 0.12.0.

References
[R127], [R128], [R129], [R130]

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_kwars 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_kwars = {"method": "BFGS"}
    >>> ret = basinhopping(func, x0, minimizer_kwars=minimizer_kwars, niter=200)
```  

Next consider a two-dimensional minimization problem. Also, this time we will use gradient information to significantly speed up the search.
SciPy Reference Guide, Release 0.16.0

>>> 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)
>>> 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
then the rest of the coordinates. This can be implemented like so:
>>> 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
>>> 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
>>> 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.
>>> 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

5.24. Optimization and root finding (scipy.optimize)

755


at minimum -0.1021 accepted 1
at minimum -1.0109 accepted 1
at minimum -1.0109 accepted 1

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(func, ranges, args=(), Ns=20, full_output=0, finish=<function fmin at 0x7f9a41234d9b0>, 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).

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.)
SciPy Reference Guide, Release 0.16.0

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. (Returned 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 gobal 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.

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 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.

>>> 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)

>>> 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))

5.24. Optimization and root finding (scipy.optimize) 757
>>> 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 fmin to polish its gridpoint result, we may then continue as follows:

>>> 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)

Note that if finish had been set to None, we would have gotten the gridpoint [-1.0 1.75] where the rounded function value is -2.892.

scipy.optimize.differential_evolution(func, bounds, args=(), strategy='best1bin', maxiter=None, popsize=15, tol=0.01, mutation=(0.5, 1), recombination=0.7, seed=None, callback=None, disp=False, polish=True, init='latinhypercube')

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 [R133].

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.

args : tuple, optional
Any additional fixed parameters needed to completely specify the objective function.

strategy : str, optional
The differential evolution strategy to use. Should be one of:

- 'best1bin'
- 'best1exp'
- 'rand1exp'
- 'randtobest1exp'
- 'best2exp'
- 'rand2exp'
- 'randtobest1bin'
- 'best2bin'
- 'rand2bin'
- 'rand1bin'

The default is ‘best1bin’.
maxiter : int, optional
    The maximum number of times the entire population is evolved. The maximum number of function evaluations is: maxiter * popsize * len(x)

popsize : int, optional
    A multiplier for setting the total population size. The population has popsize * len(x) individuals.

tol : float, optional
    When the mean of the population energies, multiplied by tol, divided by the standard deviation of the population energies is greater than 1 the solving process terminates:
    convergence = mean(pop) * tol / stdev(pop) > 1

mutation : float or tuple(float, float), optional
    The mutation constant. If specified as a float it should be in the range [0, 2]. If specified as a tuple (min, 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[min, 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]. 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 np.random.RandomState, optional
    If seed is not specified the np.random.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, 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 : string, optional
    Specify how the population initialization is performed. Should be one of:
    • ‘latinhypercube’
    • ‘random’
    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.

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, 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 [R134] 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:

$$b' = b_0 + \text{mutation} \times (\text{population}[\text{rand0}] - \text{population}[\text{rand1}])$$

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.

New in version 0.15.0.

References
[R133], [R134], [R135]

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)
```

Next find the minimum of the Ackley function (http://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)
```

Rosenbrock function

<table>
<thead>
<tr>
<th>rosen(x)</th>
<th>The Rosenbrock function.</th>
</tr>
</thead>
<tbody>
<tr>
<td>rosen_der(x)</td>
<td>The derivative (i.e.</td>
</tr>
<tr>
<td>rosen_hess(x)</td>
<td>The Hessian matrix of the Rosenbrock function.</td>
</tr>
<tr>
<td>rosen_hess_prod(x, p)</td>
<td>Product of the Hessian matrix of the Rosenbrock function with a vector.</td>
</tr>
</tbody>
</table>
scipy.optimize.rosen(x)
The Rosenbrock function.

The function computed is:
\[
\text{sum}(100.0 \times (x[1:] - x[:-1]**2.0)**2.0 + (1 - x[:-1])**2.0)
\]

**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, rosen_nest, rosen_hess, rosen_hess_prod

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_nest, rosen_hess, rosen_hess_prod

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_nest, rosen_hess_nest, 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**
- **rosen_hess_prod**: ndarray
  - The Hessian matrix of the Rosenbrock function at \( x \) multiplied by the vector \( p \).

See also:
- rosen, rosen_nest, rosen_nest, rosen_hess

### 5.24.2 Fitting

```
curve_fit(f, xdata, ydata[, p0, sigma, ...])
```
Use non-linear least squares to fit a function, \( f \), to data.
scipy.optimize.curve_fit(f, xdata, ydata, p0=None, sigma=None, absolute_sigma=False, check_finite=True, **kw)

Use non-linear least squares to fit a function, f, to data.

Assumes \( ydata = f(xdata, \ast \text{params}) + \epsilon \)

**Parameters**

- \( f \): callable
  
The model function, \( f(x, \ldots) \). 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 \( f(xdata, \ldots) \)

- \( p0 \): 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 Value Error is raised).

- \( sigma \): None or M-length sequence, optional
  
  If not None, the uncertainties in the ydata array. These are used as weights in the least-squares problem i.e. \( \text{minimising } \sum \frac{(f(xdata, \ast popt) - ydata)}{sigma}^2 \) If None, the uncertainties are assumed to be 1.

- \( \text{absolute}_\text{sigma} \): bool, optional
  
  If False, \( sigma \) denotes relative weights of the data points. The returned covariance matrix \( pcov \) is based on estimated errors in the data, and is not affected by the overall magnitude of the values in \( sigma \). Only the relative magnitudes of the \( sigma \) values matter.

  If True, \( sigma \) describes one standard deviation errors of the input data points. The estimated covariance in \( pcov \) is based on these values.

- \( \text{check}_\text{finite} \): bool, optional
  
  If True, check that the input arrays do not contain nans or infs, and raise a Value Error if they do. Setting this parameter to False may silently produce nonsensical results if the input arrays do contain nans. Default is True.

**Returns**

- \( popt \): array
  
  Optimal values for the parameters so that the sum of the squared error of \( f(xdata, \ast popt) - ydata \) is minimized

- \( pcov \): 2d array
  
  The estimated covariance of \( popt \). The diagonals provide the variance of the parameter estimate. To compute one standard deviation errors on the parameters use \( perr = \text{np.sqrt(np.diag(pcov))} \).

  How the \( sigma \) parameter affects the estimated covariance depends on \( \text{absolute}_\text{sigma} \) argument, as described above.

**Raises**

- OptimizeWarning
  
  if covariance of the parameters can not be estimated.

- ValueError
  
  if ydata and xdata contain NaNs.

**See also:**

- leastsq

**Notes**

The algorithm uses the Levenberg-Marquardt algorithm through leastsq. Additional keyword arguments are passed directly to that algorithm.
Examples

```python
>>> import numpy as np
>>> from scipy.optimize import curve_fit
>>> def func(x, a, b, c):
...     return a * np.exp(-b * x) + c

>>> xdata = np.linspace(0, 4, 50)
>>> y = func(xdata, 2.5, 1.3, 0.5)
>>> ydata = y + 0.2 * np.random.normal(size=len(xdata))

>>> popt, pcov = curve_fit(func, xdata, ydata)
```

5.24.3 Root finding

Scalar functions

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
<th>Parameters</th>
</tr>
</thead>
<tbody>
<tr>
<td>brentq</td>
<td>Find a root of a function in given interval.</td>
<td>f, a, b, xtol, rtol, maxiter, full_output, disp</td>
</tr>
<tr>
<td>brent</td>
<td>Find root of f in [a,b].</td>
<td>f, a, b, xtol, rtol, maxiter, full_output, disp</td>
</tr>
<tr>
<td>ridder</td>
<td>Find a root of a function in an interval.</td>
<td>f, a, b, xtol, rtol, maxiter, full_output, disp</td>
</tr>
<tr>
<td>bisect</td>
<td>Find root of a function within an interval.</td>
<td>f, a, b, xtol, rtol, maxiter, full_output, disp</td>
</tr>
<tr>
<td>newton</td>
<td>Find a zero using the Newton-Raphson or secant method.</td>
<td>func, x0, fprime, args, tol, full_output, disp</td>
</tr>
</tbody>
</table>

SciPy.optimize.brentq(f, a, b, xtol=1e-12, rtol=4.4408920985006262e-16, maxiter=100, full_output=False, disp=True)

Find a root of a function in given interval.

Return float, a zero of f between a and b. f must be a continuous function, and [a,b] must be a sign changing interval.

Description: Uses the classic Brent (1973) 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. f must be continuous, and f(a) and f(b) must have opposite signs.

- **a** : number
  - One end of the bracketing interval [a,b].

- **b** : number
  - The other end of the bracketing interval [a,b].

- **xtol** : number, optional
  - The routine converges when a root is known to lie within xtol of the value return. Should be >= 0. The routine modifies this to take into account the relative precision of doubles.

- **rtol** : number, optional
The routine converges when a root is known to lie within $rtol$ times the value returned of the value returned. Should be $\geq 0$. Defaults to $\text{np.finfo(float).eps} \times 2$.

**maxiter**: number, 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.

**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:**

- multivariate
  - $\text{fmin}, \text{fmin_powell}, \text{fmin_cg}, \text{fmin_bfgs}, \text{fmin_ncg}$
- nonlinear $\text{leastsq}$
- constrained
  - $\text{fmin_l_bfgs_b}, \text{fmin_tnc}, \text{fmin_cobyla}$
- global $\text{basinhopping, brute, differential_evolution}$
- local $\text{fminbound, brent, golden, bracket}$
- n-dimensional $\text{fsolve}$
- one-dimensional
  - $\text{brentq, brenth, ridder, bisect, newton}$
- scalar $\text{fixed_point}$

**Notes**

$f$ must be continuous. $f(a)$ and $f(b)$ must have opposite signs.

**References**

[Brent1973], [PressEtal1992]

```
scipy.optimize.brent(f, a, b, args=(), xtol=1e-12, rtol=4.440892098500626e-16, maxiter=100, full_output=False, disp=True)
```

Find root of $f$ in $[a,b]$.

A variation on the classic Brent routine to find a zero of the function $f$ between the arguments $a$ and $b$ that uses hyperbolic extrapolation instead of inverse quadratic extrapolation. There was a paper back in the 1980’s ... $f(a)$ and $f(b)$ cannot have the same signs. Generally on a par with the brent routine, but not as heavily tested. It is a safe version of the secant method that uses hyperbolic extrapolation. The version here is by Chuck Harris.

**Parameters**

- **f**: function
  - Python function returning a number. $f$ must be continuous, and $f(a)$ and $f(b)$ must have opposite signs.
- **a**: number
One end of the bracketing interval \([a,b]\).

\(b\) : number

The other end of the bracketing interval \([a,b]\).

\(xtol\) : number, optional

The routine converges when a root is known to lie within \(xtol\) of the value return. Should be \(\geq 0\). The routine modifies this to take into account the relative precision of doubles.

\(rtol\) : number, optional

The routine converges when a root is known to lie within \(rtol\) times the value returned of the value returned. Should be \(\geq 0\). Defaults to \(\text{np.finfo(float).eps} \times 2\).

\(maxiter\) : number, 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 \(\text{apply}(f,(x)+args)\).

\(full\_output\) : 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 \(\text{RootResults}\) object.

\(disp\) : bool, optional

If True, raise \(\text{RuntimeError}\) if the algorithm didn’t converge.

Returns

\(x0\) : float

Zero of \(f\) between \(a\) and \(b\).

\(r\) : \(\text{RootResults}\) (present if \(full\_output = \text{True}\))

Object containing information about the convergence. In particular, \(r.converged\) is True if the routine converged.

See also:

\(\text{fmin, fmin_powell, fmin_cg}\)

\(\text{leastsq}\)  nonlinear least squares minimizer

\(\text{fmin_l_bfgs_b, fmin_tnc, fmin_cobyla, basinhopping, differential_evolution, brute, fminbound, brent, golden, bracket}\)

\(\text{fsolve}\)  \(n\)-dimensional root-finding

\(\text{brentq, brent, ridder, bisect, newton}\)

\(\text{fixed_point}\)  scalar fixed-point finder

\(\text{scipy.optimize.ridder}(f, a, b, args=(), xtol=1e-12, rtol=4.4408920985006262e-16, maxiter=100, full_output=False, disp=True)\)

Find a root of a function in an interval.

Parameters

\(f\) : function

Python function returning a number. \(f\) must be continuous, and \(f(a)\) and \(f(b)\) must have opposite signs.

\(a\) : number

One end of the bracketing interval \([a,b]\).

\(b\) : number

The other end of the bracketing interval \([a,b]\).

\(xtol\) : number, optional

The routine converges when a root is known to lie within \(xtol\) of the value return. Should be \(\geq 0\). The routine modifies this to take into account the relative precision of doubles.

\(rtol\) : number, optional
The routine converges when a root is known to lie within \( rtol \) times the value returned of the value returned. Should be >= 0. Defaults to \( \text{np.finfo(float).eps * 2} \).

\[ \text{maxiter} : \text{number, optional} \]
if convergence is not achieved in maxiter iterations, an error is raised. Must be >= 0.

\[ \text{args} : \text{tuple, optional} \]
containing extra arguments for the function \( f \). \( f \) is called by \( \text{apply}(f, (x)+\text{args}) \).

\[ \text{full_output} : \text{bool, optional} \]
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.

\[ \text{disp} : \text{bool, optional} \]
If True, raise RuntimeError if the algorithm didn’t converge.

Returns

\[ x0 : \text{float} \]
Zero of \( f \) between \( a \) and \( b \).

\[ r : \text{RootResults (present if full_output = True)} \]
Object containing information about the convergence. In particular, \( r\text{.converged} \) is True if the routine converged.

See also:

\[ \text{brentq, brent, bisect, newton} \]

\[ \text{fixed_point} \]
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]

\[ \text{scipy.optimize.bisect} (f, a, b, args=(), xtol=1e-12, rtol=4.4408920985006262e-16, \text{maxiter}=100, \text{full_output}=False, \text{disp}=True) \]

Find root of a function within an interval.

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

\[ f : \text{function} \]
Python function returning a number. \( f \) must be continuous, and \( f(a) \) and \( f(b) \) must have opposite signs.

\[ a : \text{number} \]
One end of the bracketing interval \([a,b]\).

\[ b : \text{number} \]
The other end of the bracketing interval \([a,b]\).

\[ xtol : \text{number, optional} \]
The routine converges when a root is known to lie within \( xtol \) of the value return. Should be >= 0. The routine modifies this to take into account the relative precision of doubles.

\[ rtol : \text{number, optional} \]
The routine converges when a root is known to lie within \( rtol \) times the value returned of the value returned. Should be >= 0. Defaults to \( \text{np.finfo(float).eps * 2} \).
maxiter : number, 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 \( \text{apply}(f, (x) + \text{args}) \).

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.

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, \( r.converged \) is True if the routine converged.

See also:

brentq, brent, bisect, newton

fixed_point
    scalar fixed-point finder

fsolve
    n-dimensional root-finding

scipy.optimize.newton \( (\text{func}, x_0, fprime=\text{None}, \text{args}=(), \text{tol}=1.48e-08, \text{maxiter}=50, fprime2=\text{None}) \)
Find a zero using the Newton-Raphson or secant method.

Find a zero of the function \( \text{func} \) given a nearby starting point \( x_0 \). The Newton-Raphson method is used if the derivative \( fprime \) of \( \text{func} \) is provided, otherwise the secant method is used. If the second order derivate \( fprime2 \) of \( \text{func} \) is provided, parabolic Halley’s method is used.

Parameters

\( \text{func} \) : function
    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 \( \text{args} \) parameter.

\( x_0 \) : float
    An initial estimate of the zero that should be somewhere near the actual zero.

\( fprime \) : function, optional
    The derivative of the function when available and convenient. If it is None (default),
    then the secant method is used.

\( \text{args} \) : tuple, optional
    Extra arguments to be used in the function call.

\( \text{tol} \) : float, optional
    The allowable error of the zero value.

\( \text{maxiter} \) : int, optional
    Maximum number of iterations.

\( fprime2 \) : function, 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 given, parabolic Halley’s method is used.

Returns

\( \text{zero} \) : float
    Estimated location where function is zero.

See also:

brentq, brent, ridder, bisect

fsolve
    find zeroes 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 is approximately the square (cube for Halley) of the requested tolerance up to roundoff error. 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.

Fixed point finding:

```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.])
result = optimize.fixed_point(func, [1.2, 1.3], args=(c1, c2))
```

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

General nonlinear solvers:

```python
from scipy.optimize import root, fsolve, broyden1, broyden2
```
scipy.optimize.root (fun, x0, args=(), method='hybr', jac=None, tol=None, callback=None, options=None)

Find a root of a vector function.

**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)
  - ‘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 an `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 [R153].

Method `lm` solves the system of nonlinear equations in a least squares sense using a modification of the Levenberg-Marquardt algorithm as implemented in MINPACK [R153].
Method \texttt{df-sane} is a derivative-free spectral method. [R155]

Methods \texttt{broyden1}, \texttt{broyden2}, \texttt{anderson}, \texttt{linearmixing}, \texttt{diagbroyden}, \texttt{excitingmixing}, \texttt{krylov} are inexact Newton methods, with backtracking or full line searches [R154]. Each method corresponds to a particular Jacobian approximations. See \texttt{nonlin} for details.

- Method \texttt{broyden1} uses Broyden’s first Jacobian approximation, it is known as Broyden’s good method.
- Method \texttt{broyden2} uses Broyden’s second Jacobian approximation, it is known as Broyden’s bad method.
- Method \texttt{anderson} uses (extended) Anderson mixing.
- Method \texttt{Krylov} uses Krylov approximation for inverse Jacobian. It is suitable for large-scale problem.
- Method \texttt{diagbroyden} uses diagonal Broyden Jacobian approximation.
- Method \texttt{linearmixing} uses a scalar Jacobian approximation.
- Method \texttt{excitingmixing} uses a tuned diagonal Jacobian approximation.

\textbf{Warning:} The algorithms implemented for methods \texttt{diagbroyden}, \texttt{linearmixing} and \texttt{excitingmixing} may be useful for specific problems, but whether they will work may depend strongly on the problem.

New in version 0.11.0.

\textbf{Examples}

The following functions define a system of nonlinear equations and its jacobian.

\begin{verbatim}
>>> def fun(x):
...     return [x[0] + 0.5 * (x[0] - x[1])**3 - 1.0,
...             0.5 * (x[1] - x[0])**3 + x[1]]

>>> 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.

>>> from scipy import optimize
>>> sol = optimize.root(fun, [0, 0], jac=jac, method='hybr')
>>> sol.x
array([ 0.8411639, 0.1588361])
\end{verbatim}

\texttt{scipy.optimize.fsolve} (func, x0, args=(), fprime=None, full_output=0, col_deriv=0, xtol=1.49012e-08, maxfev=0, band=None, epsfcn=None, factor=100, diag=None)

Find the roots of a function.

Return the roots of the (non-linear) equations defined by \texttt{func(x) = 0} given a starting estimate.

\textbf{Parameters}

- \texttt{func}: callable \texttt{f(x, \*args)}
  
  A function that takes at least one (possibly vector) argument.

- \texttt{x0} : \texttt{ndarray}
  
  The starting estimate for the roots of \texttt{func(x) = 0}.

- \texttt{args} : tuple, optional
  
  Any extra arguments to \texttt{func}.
fprime : callable(x), optional
A function to compute the Jacobian of 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
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*(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 (factor * || diag * 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 ma-
trix
qtf the vector (transpose(q) * 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

fsolve is a wrapper around MINPACK’s hybrd and hybrj algorithms.
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 \((-1/alpha)\).
- **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 \((method, param1, param2, \ldots)\) 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 \(\text{max_rank} - 2\).
- **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 **xin**) containing the final solution.
NoConvergence

When a solution was not found.

Notes

This algorithm implements the inverse Jacobian Quasi-Newton update

\[ H_+ = H + (dx - Hdf)dx^\dagger H/(dx^\dagger Hdf) \]

which corresponds to Broyden’s first Jacobian update

\[ J_+ = J + (df - Jdx)dx^\dagger /dx^\dagger dx \]

References

[R131]

`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.
- **x0**: 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.
  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

\[
H_+ = H + (dx - H df)df^\dagger/(df^\dagger df)
\]

corresponding to Broyden’s second method.

**References**

[R132]
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={'full_output': 0, 'col_deriv': 0, 'diag': None, 'factor': 100, 'eps': None, 'band': None, 'func': None, 'maxfev': 0, 'xtol': 1.49012e-08})

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`
A suitable step length for the forward-difference approximation of the Jacobian (for
\( fprime=None \)). If \( eps \) is less than the machine precision, it is assumed that the
relative errors in the functions are of the order of the machine precision.

\textbf{factor} : float

A parameter determining the initial step bound \((factor \times ||diag \times x||)\).
Should be in the interval \((0.1, 100)\).

\textbf{diag} : sequence

N positive entries that serve as a scale factors for the variables.

\textbf{root(method='lm')}

\texttt{scipy.optimize.root} \((fun, x0, args=(), method='lm', jac=None, tol=None, callback=None, options={})\)

Solve for least squares with Levenberg-Marquardt

\textbf{See also:}

For documentation for the rest of the parameters, see \texttt{scipy.optimize.root}

\textbf{Options}

\textbf{col_deriv} : bool

\texttt{non-zero to specify that the Jacobian function computes derivatives down the columns}
\texttt{(faster, because there is no transpose operation).}

\textbf{ftol} : float

Relative error desired in the sum of squares.

\textbf{xtol} : float

Relative error desired in the approximate solution.

\textbf{gtol} : float

Orthogonality desired between the function vector and the columns of the Jacobian.

\textbf{maxiter} : int

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 \(x0\).

\textbf{epsfcn} : float

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.

\textbf{factor} : float

A parameter determining the initial step bound \((factor \times ||diag \times x||)\).
Should be in interval \((0.1, 100)\).

\textbf{diag} : sequence

N positive entries that serve as a scale factors for the variables.

\textbf{root(method='broyden1')}

\texttt{scipy.optimize.root} \((fun, x0, args=(), method='broyden1', tol=None, callback=None, options={})\)

\textbf{See also:}

For documentation for the rest of the parameters, see \texttt{scipy.optimize.root}

\textbf{Options}

\textbf{nit} : int, optional

Number of iterations to make. If omitted (default), make as many as required to meet
tolerances.

\textbf{disp} : bool, optional

Print status to stdout on every iteration.

\textbf{maxiter} : int, optional
Maximum number of iterations to make. If more are needed to meet convergence, 
\texttt{NoConvergence} is raised.

\texttt{ftol} : float, optional
   Relative tolerance for the residual. If omitted, not used.

\texttt{fatol} : float, optional
   Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

\texttt{xtol} : float, optional
   Relative minimum step size. If omitted, not used.

\texttt{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.

\texttt{tol\_norm} : function(vector) -> scalar, optional
   Norm to use in convergence check. Default is the maximum norm.

\texttt{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’.

\texttt{jac\_options} : dict, optional
   Options for the respective Jacobian approximation.

   \texttt{alpha} [float, optional] Initial guess for the Jacobian is (-1/alpha).

   \texttt{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 addi- 
   tional parameters.

   Methods available:

   \texttt{restart: drop all matrix columns. Has no} 
   extra parameters.

   \texttt{simple: drop oldest matrix column. Has no} 
   extra parameters.

   \texttt{svd: keep only the most significant SVD} 
   components.

   Extra parameters:

   \texttt{to\_retain: number of SVD components} 
   retain when 
   rank re- 
   duc- 
   tion is 
   done. De- 
   fault
is
\[ \text{max\_rank} = \text{max\_rank} - 2. \]

**max_rank**  
[int, optional] Maximum rank for the Broyden matrix. Default is infinity (ie., no rank reduction).

### scipy.optimize.root

```python
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`

<table>
<thead>
<tr>
<th>Options</th>
<th>Description</th>
</tr>
</thead>
</table>
| **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_reduction_method

[Float, optional] Initial guess for the Jacobian is (-1/alpha).

Methods available:

- **restart**: drop all matrix columns. Has no extra parameters.
- **simple**: drop oldest matrix column. Has no extra parameters.

---

5.24. Optimization and root finding (**scipy.optimize**) 777
• **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 (ie., no rank reduction).

    ```python
cipy.optimize.root(fun, x0, args=(), method='anderson', tol=None, callback=None, options={})
```

See also:

For documentation for the rest of the parameters, see `cipy.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) -&gt; 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’.
root(method='linearmixing')

\texttt{scipy.optimize.root}\,(\textit{fun}, \textit{x0}, \textit{args}=(), \textit{method}= 'linearmixing', \textit{tol}=None, \textit{callback}=None, \textit{options}=\{})

\textbf{See also:}

For documentation for the rest of the parameters, see \texttt{scipy.optimize.root}

\textbf{Options}

\begin{itemize}
  \item \texttt{nit} : int, optional
    Number of iterations to make. If omitted (default), make as many as required to meet tolerances.
  \item \texttt{disp} : bool, optional
    Print status to stdout on every iteration.
  \item \texttt{maxiter} : int, optional
    Maximum number of iterations to make. If more are needed to meet convergence, \texttt{NoConvergence} is raised.
  \item \texttt{ftol} : float, optional
    Relative tolerance for the residual. If omitted, not used.
  \item \texttt{fatol} : float, optional
    Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.
  \item \texttt{xtol} : float, optional
    Relative minimum step size. If omitted, not used.
  \item \texttt{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.
  \item \texttt{tol_norm} : function(vector) \rightarrow scalar, optional
    Norm to use in convergence check. Default is the maximum norm.
  \item \texttt{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’.
  \item \texttt{jac_options} : dict, optional
    Options for the respective Jacobian approximation.
    \begin{itemize}
      \item \texttt{alpha} : [float, optional] Initial guess for the Jacobian is (-1/alpha).
      \item \texttt{M} : [float, optional] Number of previous vectors to retain. Defaults to 5.
      \item \texttt{w0} : [float, optional] Regularization parameter for numerical stability. Compared to unity, good values of the order of 0.01.
    \end{itemize}
\end{itemize}

root(method='diagbroyden')

\texttt{scipy.optimize.root}\,(\textit{fun}, \textit{x0}, \textit{args}=(), \textit{method}= 'diagbroyden', \textit{tol}=None, \textit{callback}=None, \textit{options}=\{})

\textbf{See also:}

For documentation for the rest of the parameters, see \texttt{scipy.optimize.root}

\textbf{Options}

\begin{itemize}
  \item \texttt{nit} : int, optional
    Number of iterations to make. If omitted (default), make as many as required to meet tolerances.
  \item \texttt{disp} : bool, optional
\end{itemize}
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).

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’.

```
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 re-
    quired 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 con-
    vergence, 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 approxima-
    tion. If the step size is smaller than this, optimization is terminated as suc-
    cessful. 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.
artist
    Initial Jacobian approximation is (-1/artist).
alphamax
    The entries of the diagonal Jacobian are kept
in the range [artist, alphamax].
```

```
5.24. Optimization and root finding (scipy.optimize) 781
```
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')


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

[R509], [R510], [R511]

Large-scale nonlinear solvers:
newton_krylov(F, xin[, iter, rdiff, method,...])  Find a root of a function, using Krylov approximation for inverse Jacobian.

anderson(F, xin[, iter, alpha, w0, M,...])  Find a root of a function, using (extended) Anderson mixing.

scipy.optimize.newton_krylov(F, xin[, iter, rdiff, method,...])
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.

- **x0** : 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,

  >>> 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 
  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.

- **iter** : int, optional  
  Number of iterations to make. If omitted (default), make as many as re- 
  quired 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 con- 
  vergence, 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.
SciPy Reference Guide, Release 0.16.0

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:

\[ Jv \approx \frac{(f(x + \omega \cdot v/|v|) - f(x))/\omega}{v} \]

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 [R151], and for the LGMRES sparse inverse method, see [R152].

References
[R151], [R152]

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 MxM matrix inversions and MxN multiplications are required. [Ey]

Parameters
F : function(x) -> f
    Function whose root to find; should take and return an array-like object.

x0 : array_like
    Initial guess for the solution

alpha : float, optional
    Initial guess for the Jacobian is (-1/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 re-
   quired 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 con-
   vergence, *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 approxima-
   tion. If the step size is smaller than this, optimization is terminated as suc-
   cessful. 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 correspond-
   ing 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

[Ey]

Simple iterations:

```python
scipy.optimize.excitingmixing(F, xin[, iter, alpha, ...])
```
Find a root of a function, using a tuned diagonal Jacobian approximation.

```python
scipy.optimize.linearmixing(F, xin[, iter, alpha, verbose, ...])
```
Find a root of a function, using a scalar Jacobian approximation.

```python
scipy.optimize.diagbroyden(F, xin[, iter, alpha, verbose, ...])
```
Find a root of a function, using diagonal Broyden Jacobian approximation.

The Jacobian matrix is diagonal and is tuned on each iteration.
### Parameters

- **F**: function(x) -> f
  
  Function whose root to find; should take and return an array-like object.

- **x0**: 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.

### Example

```python
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.
SciPy Reference Guide, Release 0.16.0

x0 : 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 re-
    quired 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 con-
    vergence, 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 approxima-
    tion. If the step size is smaller than this, optimization is terminated as suc-
    cessful. 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 correspond-

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(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.

x0 : array_like
    Initial guess for the solution

alpha : float, optional
    Initial guess for the Jacobian is (-1/alpha).

iter : int, optional

5.24. Optimization and root finding (scipy.optimize)  787
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.

---

## 5.24.4 Linear Programming

Simplex Algorithm:

```python
linprog(c[, A_ub, b_ub, A_eq, b_eq, bounds, ...])
```
Minimize a linear objective function subject to linear equality and inequality constraints.

```python
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:** $c^T \cdot x$

**Subject to:** $A_{ub} \cdot x \leq b_{ub}$

$A_{eq} \cdot x = b_{eq}$

**Parameters**

- **c** : array_like
  Coefficients of the linear objective function to be minimized.

- **A_ub** : array_like, optional
  2-D array which, when matrix-multiplied by `x`, gives the values of the upper-bound inequality constraints at `x`. 
b_ub : array_like, optional
1-D array of values representing the upper-bound of each inequality constraint (row) in A_ub.

A_eq : array_like, optional
2-D array which, when matrix-multiplied by x, gives the values of the equality constraints at x.

b_eq : array_like, optional
1-D array of values representing the RHS of each equality constraint (row) in A_eq.

bounds : sequence, optional
(min, max) pairs for each element in x, defining the bounds on that parameter. Use None for one of min or max when there is no bound in that direction. By default bounds are (0, None) (non-negative) If a sequence containing a single tuple is provided, then min and max will be applied to all variables in the problem.

method : str, optional
Type of solver. At this time only ‘simplex’ is supported (see here).

callback : callable, optional
If a callback function is provide, it will be called within each iteration of the simplex algorithm. The callback must have the signature callback(xk, **kwargs) where xk is the current solution vector and kwargs is a dictionary containing the following:

"tableau" : The current Simplex algorithm tableau
"nit" : The current iteration.
"pivot" : The pivot (row, column) used for the next iteration.
"phase" : Whether the algorithm is in Phase 1 or Phase 2.
"basis" : The indices of the columns of the basic variables.

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
A scipy.optimize.OptimizeResult consisting of the following fields:

x : [ndarray] The independent variable vector which optimizes the linear programming problem.
slack : [ndarray] 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.
success : [bool] Returns True if the algorithm succeeded in finding an optimal solution.
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

nit : [int] The number of iterations performed.
message : [str] A string descriptor of the exit status of the optimization.

See also:

show_options
Additional options accepted by the solvers

5.24. Optimization and root finding (scipy.optimize)
SciPy Reference Guide, Release 0.16.0

Notes
This section describes the available solvers that can be selected by the ‘method’ parameter. The default method
is Simplex.
Method Simplex uses the Simplex algorithm (as it relates to Linear Programming, NOT the Nelder-Mead Simplex) [R139], [R140]. This algorithm should be reasonably reliable and fast.
New in version 0.15.0.
References
[R139], [R140], [R141]
Examples
Consider the following problem:
Minimize: f = -1*x[0] + 4*x[1]
Subject to: -3*x[0] + 1*x[1] <= 6
1*x[0] + 2*x[1] <= 4
x[1] >= -3
where: -inf <= x[0] <= inf
This problem deviates from the standard linear programming problem. In standard form, linear programming
problems assume the variables x are non-negative. Since the variables don’t have standard bounds where 0 <=
x <= inf, the bounds of the variables must be explicitly set.
There are two upper-bound constraints, which can be expressed as
dot(A_ub, x) <= b_ub
The input for this problem is as follows:
>>> c = [-1, 4]
>>> A = [[-3, 1], [1, 2]]
>>> b = [6, 4]
>>> x0_bounds = (None, None)
>>> x1_bounds = (-3, None)
>>> from scipy.optimize import linprog
>>> res = linprog(c, A_ub=A, b_ub=b, bounds=(x0_bounds, x1_bounds),
...
options={"disp": True})
>>> print(res)
Optimization terminated successfully.
Current function value: -11.428571
Iterations: 2
status: 0
success: True
fun: -11.428571428571429
x: array([-1.14285714, 2.57142857])
message: 'Optimization terminated successfully.'
nit: 2

Note the actual objective value is 11.428571. In this case we minimized the negative of the objective function.
The linprog function supports the following methods:

790

Chapter 5. Reference


linprog(method='Simplex')

scipy.optimize.linprog(c, A_ub=None, b_ub=None, A_eq=None, b_eq=None, bounds=None, method='simplex', callback=None, options={'disp': False, 'bland': False, 'tol': 1e-12, 'maxiter': 1000})

Solve the following linear programming problem via a two-phase simplex algorithm.

maximize: \( c^T \cdot x \)

subject to: \( A_{ub} \cdot x \leq b_{ub} \)

\( A_{eq} \cdot x = b_{eq} \)

Parameters

\( c \) : array_like  
Coefficients of the linear objective function to be maximized.

\( A_{ub} \) : array_like  
2-D array which, when matrix-multiplied by \( x \), gives the values of the upper-bound inequality constraints at \( x \).

\( b_{ub} \) : array_like  
1-D array of values representing the upper-bound of each inequality constraint (row) in \( A_{ub} \).

\( A_{eq} \) : array_like  
2-D array which, when matrix-multiplied by \( x \), gives the values of the equality constraints at \( x \).

\( b_{eq} \) : array_like  
1-D array of values representing the RHS of each equality constraint (row) in \( A_{eq} \).

\( \text{bounds} \) : array_like  
The bounds for each independent variable in the solution, which can take one of three forms:: None : The default bounds, all variables are non-negative. (lb, ub) : If a 2-element sequence is provided, the same lower bound (lb) and upper bound (ub) will be applied to all variables. 

\([\text{lb}_0, \text{ub}_0], \text{(lb}_1, \text{ub}_1), ...\)  
[If an \( n \times 2 \) sequence is provided.] each variable \( x_i \) will be bounded by \( \text{lb}[i] \) and \( \text{ub}[i] \).

Infinite bounds are specified using -np.inf (negative) or np.inf (positive).

\( \text{callback} \) : callable  
If a callback function is provided, it will be called within each iteration of the simplex algorithm. The callback must have the signature \( \text{callback}(xk, **\text{kwargs}) \) where \( xk \) is the current solution vector and \( \text{kwargs} \) is a dictionary containing the following:: "tableau" : The current Simplex algorithm tableau “nit” : The current iteration. “pivot” : The pivot (row, column) used for the next iteration. “phase” : Whether the algorithm is in Phase 1 or Phase 2. “bv” : A structured array containing a string representation of each basic variable and its current value.

Returns

A scipy.optimize.OptimizeResult consisting of the following fields:

\( x \) : ndarray  
The independent variable vector which optimizes the linear programming problem.

\( \text{slack} \) : ndarray  
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.

\( \text{success} \) : bool

5.24. Optimization and root finding (scipy.optimize) 791
Returns True if the algorithm succeeded in finding an optimal solution.

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

nit : int
The number of iterations performed.

message : str
A string descriptor of the exit status of the optimization.

See also:
For documentation for the rest of the parameters, see scipy.optimize.linprog

Options

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 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.

References
[R502], [R503], [R504]

Examples
Consider the following problem:
Minimize: \( f = -x[0] + 4x[1] \)
Subject to: 
\[ -3x[0] + 1x[1] \leq 6 \]
\[ 1x[0] + 2x[1] \leq 4 \]
\[ x[1] \geq -3 \]
where: \(-\infty \leq x[0] \leq \infty\)

This problem deviates from the standard linear programming problem. In standard form, linear programming problems assume the variables \( x \) are non-negative. Since the variables don’t have standard bounds where \( 0 \leq x \leq \infty \), the bounds of the variables must be explicitly set.

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
>>> from scipy.optimize import linprog
>>> c = [-1, 4]
>>> A = [[-3, 1], [1, 2]]
>>> b = [6, 4]
>>> x0_bnds = (None, None)
>>> x1_bnds = (-3, None)
>>> res = linprog(c, A, b, bounds=(x0_bnds, x1_bnds))
>>> print(res)
Optimization terminated successfully.
  Current function value: -22.000000
  Iterations: 1
  status: 0
  x: array([ 10., -3.])
  slack: array([ 39.,  0.])
  nit: 1
  message: 'Optimization terminated successfully.'
  fun: -22.0
  success: True
```

## 5.24.5 Utilities

- `approx_fprime(xk, f, epsilon, *args)`: Finite-difference approximation of the gradient of a scalar function.
- `bracket(func[, xa, xb, args, grow_limit, ...])`: Bracket the minimum of the function.
- `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.
- `line_search(f, myfprime, xk, pk[, gfk, ...])`: Find alpha that satisfies strong Wolfe conditions.
- `show_options([solver, method, disp])`: Show documentation for additional options of optimization solvers.
- `LbfgsInvHessProduct(sk, yk)`: Linear operator for the L-BFGS approximate inverse Hessian.

`scipy.optimize.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

**Returns**

- `grad`: ndarray
  Any other arguments that are to be passed to `f`. The partial derivatives of `f` to `xk`.

**See also:**

- `check_grad`: Check correctness of gradient function against `approx_fprime`.

**Notes**

The function gradient is determined by the forward finite difference formula:
\[
f'(i) = \frac{f(x_k[i] + \epsilon[i]) - f(x_k[i])}{\epsilon[i]}
\]

The main use of `approx_fprime` is in scalar function optimizers like `fmin_bfgs`, to determine numerically the Jacobian of a function.

**Examples**

```python
generate code
```
```python
generate code
```
```python
generate code
```
```python
generate code
```
```python
generate code
```
Extra arguments passed to `func` and `grad`.

**epsilon**: float, optional
Step size used for the finite difference approximation. It defaults to \(\sqrt{\text{numpy.finfo(float).eps}}\), 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
```

`scipy.optimize.line_search(f, myfprime, xk, pk, gfk=None, old_fval=None, old_old_fval=None, args=(), c1=0.0001, c2=0.9, amax=50)`

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

**Returns**

- `alpha`: float or None
  Alpha for which `x_new = x0 + alpha * pk`, or None if the line search algorithm did not converge.
- `fc`: int
  Number of function evaluations made.
- `gc`: int

5.24. Optimization and root finding (`scipy.optimize`) 795
Number of gradient evaluations made.

**new_fval**: float or None

New function value \( f(x_{\text{new}}) = f(x_0 + \alpha \cdot pk) \), 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 \(<\text{myfprime}(x_{\text{new}}), pk>\), 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 [...].

```
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**

- **solver**: str
  
  Type of optimization solver. One of ‘minimize’, ‘minimize_scalar’, ‘root’, or ‘linprog’.

- **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**: str
  
  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
```
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.

**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**

[R126]

**Attributes**

- `H`: Hermitian adjoint.
- `T`: Transpose this linear operator.

**Methods**

- `__call__`(x)
- `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.

Continued on next page
Table 5.112 – continued from previous page

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>todense()</td>
<td>Return a dense array representation of this operator.</td>
</tr>
<tr>
<td>transpose()</td>
<td>Transpose this linear operator.</td>
</tr>
</tbody>
</table>

LbfgsInvHessProduct.__call__(x)

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

\[ A^H \]

: LinearOperator

Hermitian adjoint of self.

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 \( x \).

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.

LbfgsInvHessProduct.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.

LbfgsInvHessProduct.rmatvec(x)

Adjoint matrix-vector multiplication.
Perform the operation $y = A^H \cdot x$ where $A$ is an $M \times N$ 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.

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.

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().

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.

### 5.25 Routines

#### Large-scale nonlinear solvers:

- **newton_krylov**($F$, $xin$, [iter, rdiff, method, ...]) Find a root of a function, using Krylov approximation for inverse Jacobian.
- **anderson**($F$, $xin$, [iter, alpha, w0, M, ...]) Find a root of a function, using (extended) Anderson mixing.

#### General nonlinear solvers:

- **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.

#### Simple iterations:

- **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.
5.26 Examples

5.26.1 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.])
```

5.26.2 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
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])/hy/hy
    d2y[:,0] = (P[:,1] - 2*P[:,0] + P_bottom)/hy/hy
    d2y[:,-1] = (P_top - 2*P[:,-1] + P[:,-2])/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()

5.27 Signal processing (scipy.signal)

5.27.1 Convolution

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>convolve(in1, in2[, mode])</td>
<td>Conolve two N-dimensional arrays.</td>
</tr>
<tr>
<td>correlate(in1, in2[, mode])</td>
<td>Cross-correlate two N-dimensional arrays.</td>
</tr>
<tr>
<td>fftconvolve(in1, in2[, mode])</td>
<td>Conolve two N-dimensional arrays using FFT.</td>
</tr>
<tr>
<td>convolve2d(in1, in2[, mode, boundary, fillvalue])</td>
<td>Conolve two 2-dimensional arrays.</td>
</tr>
<tr>
<td>correlate2d(in1, in2[, mode, boundary, ...])</td>
<td>Cross-correlate two 2-dimensional arrays.</td>
</tr>
<tr>
<td>sepfir2d((input, hrow, hcol) -&gt; output)</td>
<td>Description:</td>
</tr>
</tbody>
</table>

scipy.signal.convolve(in1, in2, mode='full')
Conolve two N-dimensional arrays.

Conolve 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; if sizes of in1 and in2 are not equal then in1 has to be the larger array.
- 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.
The output is the same size as \( in1 \), centered with respect to the ‘full’ output.

**Returns**

\( convolve : \text{array} \)

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)

**Examples**

Smooth a square pulse using a Hann window:

```python
>>> from scipy import signal
>>> sig = np.repeat([0., 1., 0.], 100)
>>> win = signal.hann(50)
>>> filtered = signal.convolve(sig, win, mode='same') / sum(win)
```

```python
>>> import matplotlib.pyplot as plt
>>> fig, (ax_orig, ax_win, ax_filt) = plt.subplots(3, 1, sharex=True)
>>> ax_orig.plot(sig)
>>> ax_orig.set_title('Original pulse')
>>> ax_orig.margins(0, 0.1)
>>> ax_win.plot(win)
>>> ax_win.set_title('Filter impulse response')
>>> ax_win.margins(0, 0.1)
>>> ax_filt.plot(filtered)
>>> ax_filt.set_title('Filtered signal')
>>> ax_filt.margins(0, 0.1)
>>> fig.tight_layout()
>>> fig.show()
```

![Graphs of Original pulse, Filter impulse response, and Filtered signal](image)

 scipy.signal.correlate \((in1, in2, mode='full')\)

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`; if sizes of `in1` and `in2` are not equal then `in1` has to be the larger array.
- `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.
  - `same`: The output is the same size as `in1`, centered with respect to the ‘full’ output.

**Returns**

- `correlate`: array
  An N-dimensional array containing a subset of the discrete linear cross-correlation of `in1` with `in2`.

**Notes**

The correlation $z$ of two d-dimensional arrays $x$ and $y$ is defined as:

$$z[\ldots,k,\ldots] = \sum[\ldots,i_1,\ldots] x[\ldots,i_1,\ldots] \cdot \text{conj}(y[\ldots,i_1+k,\ldots])$$

**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

>>> import matplotlib.pyplot as plt
>>> clock = np.arange(64, len(sig), 128)
>>> fig, (ax_orig, ax_noise, ax_corr) = plt.subplots(3, 1, sharex=True)
>>> ax_orig.plot(sig)
>>> ax_orig.plot(clock, sig[clock], 'ro')
>>> ax_orig.set_title('Original signal')
>>> ax_noise.plot(sig_noise)
>>> ax_noise.set_title('Signal with noise')
>>> ax_corr.plot(corr)
>>> ax_corr.plot(clock, corr[clock], 'ro')
>>> ax_corr.axhline(0.5, ls=':)
>>> ax_corr.set_title('Cross-correlated with rectangular pulse')
>>> ax_orig.margins(0, 0.1)
>>> fig.tight_layout()
>>> fig.show()
```
scipy.signal.fftconvolve(in1, in2, mode='full')

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).

**Parameters**

- in1 : array_like
  First input.
- in2 : array_like
  Second input. Should have the same number of dimensions as in1; if sizes of in1 and in2 are not equal then in1 has to be the larger array.
- 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.
  - **same** The output is the same size as in1, centered with respect to the 'full' output.

**Returns**

- out : array
  An N-dimensional array containing a subset of the discrete linear convolution of in1 with in2.

**Examples**

Autocorrelation of white noise is an impulse. (This is at least 100 times as fast as convolve.)

```python
>>> from scipy import signal
>>> sig = np.random.randn(1000)
>>> autocorr = signal.fftconvolve(sig, sig[::-1], mode='full')
```

```python
>>> import matplotlib.pyplot as plt
>>> fig, (ax_orig, ax_mag) = plt.subplots(2, 1)
>>> ax_orig.plot(sig)
>>> ax_orig.set_title('White noise')
>>> ax_mag.plot(np.arange(-len(sig)+1, len(sig)), autocorr)
```
Gaussian blur implemented using FFT convolution. Notice the dark borders around the image, due to the zero-padding beyond its boundaries. The \texttt{convolve2d} function allows for other types of image boundaries, but is far slower.

```python
>>> from scipy import misc

>>> lena = misc.lena()
>>> kernel = np.outer(signal.gaussian(70, 8), signal.gaussian(70, 8))
>>> blurred = signal.fftconvolve(lena, kernel, mode='same')
```

```python
>>> fig, (ax_orig, ax_kernel, ax_blurred) = plt.subplots(1, 3)
>>> ax_orig.imshow(lena, 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**(*in1, in2, mode='full', boundary='fill', fillvalue=0*)

Convolves two 2-dimensional arrays.

Convolves `in1` and `in2` with output size determined by `mode`, and boundary conditions determined by `boundary` and `fillvalue`.

**Parameters**

- **in1, in2**: array_like
  Two-dimensional input arrays to be convolved.
- **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.
  - **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.

```python
>>> from scipy import signal
>>> from scipy import misc
>>> lena = misc.lena()
>>> scharr = np.array([[ -3-3j, 0-10j, +3 -3j],
... [-10+0j, 0+ 0j, +10 +0j],
... [-3+3j, 0+10j, +3 +3j]])  # Gx + j*Gy
>>> grad = signal.convolve2d(lena, scharr, boundary='symm', mode='same')
```
```python
>>> import matplotlib.pyplot as plt
>>> fig, (ax_orig, ax_mag, ax_ang) = plt.subplots(1, 3)
>>> ax_orig.imshow(lena, cmap='gray')
>>> ax_orig.set_title('Original')
>>> ax_orig.set_axis_off()
>>> ax_mag.imshow(np.abs(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(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, in2`: array_like
  Two-dimensional input arrays to be convolved.
- `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
  - `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`.

5.27. Signal processing (scipy.signal) 807
**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

>>> lena = misc.lena() - misc.lena().mean()  # right eye
>>> template = np.copy(lena[235:295, 310:370])
>>> template -= template.mean()
>>> lena = lena + np.random.randn(*lena.shape) * 50  # add noise
>>> corr = signal.correlate2d(lena, template, boundary='symm', mode='same')
>>> y, x = np.unravel_index(np.argmax(corr), corr.shape)  # find the match

>>> import matplotlib.pyplot as plt

>>> fig, (ax_orig, ax_template, ax_corr) = plt.subplots(1, 3)
>>> ax_orig.imshow(lena, 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()
```

**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.

### 5.27.2 B-splines
bspline(x, n)  B-spline basis function of order n.
cubic(x)  A cubic B-spline.
quadratic(x)  A quadratic B-spline.
 gauss_spline(x, n)  Gaussian approximation to B-spline basis function of order n.
cspline1d(signal[, lamb])  Compute cubic spline coefficients for rank-1 array.
qspline1d(signal[, lamb])  Compute quadratic spline coefficients for rank-1 array.
cspline2d(input {, lambda, precision}) -> ck  Description:
qspline2d((input {, lambda, precision}) -> qk)  Description:
cspline1d_eval(cj, newx[, dx, x0])  Evaluate a spline at the new set of points.
qspline1d_eval(cj, newx[, dx, x0])  Evaluate a quadratic spline at the new set of points.
spline_filter(Iin[, lmbda])  Smoothing spline (cubic) filtering of a rank-2 array.

scipy.signal.bspline(x, n)
B-spline basis function of order n.

Notes
Uses numpy.piecewise and automatic function-generator.

scipy.signal.cubic(x)
A cubic B-spline.

This is a special case of bspline, and equivalent to bspline(x, 3).

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(x, n)
Gaussian approximation to B-spline basis function of order n.

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
signal : ndarray
A rank-1 array representing samples of a signal.
lamb : float, optional
Smoothing coefficient, default is 0.0.

Returns
c : ndarray
Cubic spline coefficients.

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(input, lambda, precision) → 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(input, lambda, precision) → 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/csplineld_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:

\[
\text{oldx} = x0 + j \times \text{dx} \quad j=0\ldots N-1, \text{ with } N=\text{len}(cj)
\]

Edges are handled using mirror-symmetric boundary conditions.

scipy.signal/qsplineld_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:

\[
\text{oldx} = x0 + j \times \text{dx} \quad j=0\ldots N-1, \text{ with } N=\text{len}(cj)
\]

Edges are handled using mirror-symmetric boundary conditions.

scipy.signal/spline_filter(in, lambda=5.0)

Smoothing spline (cubic) filtering of a rank-2 array.
Filter an input data set, **in**, using a (cubic) smoothing spline of fall-off **lambda**.

### 5.27.3 Filtering

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>order_filter(a, domain, rank)</td>
<td>Perform an order filter on an N-dimensional array.</td>
</tr>
<tr>
<td>medfilt(volume[, kernel_size])</td>
<td>Perform a median filter on an N-dimensional array.</td>
</tr>
<tr>
<td>medfilt2d(input[, kernel_size])</td>
<td>Median filter a 2-dimensional array.</td>
</tr>
<tr>
<td>wiener(im[, mysize, noise])</td>
<td>Perform a Wiener filter on an N-dimensional array.</td>
</tr>
<tr>
<td>symiirorder1((input, c0, z1 {, ...)</td>
<td>Implement a smoothing IIR filter with mirror-symmetric boundary conditions.</td>
</tr>
<tr>
<td>symiirorder2((input, r, omega {, ...)</td>
<td>Implement a smoothing IIR filter with mirror-symmetric boundary conditions.</td>
</tr>
<tr>
<td>lfilter(b, a, x[, axis, zi])</td>
<td>Filter data along one-dimension with an IIR or FIR filter.</td>
</tr>
<tr>
<td>lfilteric(b, a, y[, x])</td>
<td>Construct initial conditions for lfilter.</td>
</tr>
<tr>
<td>lfilter_zi(b, a)</td>
<td>Compute an initial state zi for the lfilter function that corresponds to the steady state in the system.</td>
</tr>
<tr>
<td>filtfilt(b, a[, axis, padtype, padlen, ...])</td>
<td>A forward-backward filter.</td>
</tr>
<tr>
<td>savgol_filter(x, window_length, polyorder[, ...])</td>
<td>Apply a Savitzky-Golay filter to an array.</td>
</tr>
<tr>
<td>deconvolve(signal, divisor)</td>
<td>Deconvolves divisor out of signal.</td>
</tr>
<tr>
<td>sosfilt(sos, x[, axis, zi])</td>
<td>Filter data along one dimension using cascaded second-order sections</td>
</tr>
</tbody>
</table>
**Table 5.118 – continued from previous page**

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>sosfilt_zi</code></td>
<td>Compute an initial state ( z_i ) for the sosfilt function that corresponds to the steady state of the step response.</td>
</tr>
<tr>
<td><code>hilbert</code></td>
<td>Compute the analytic signal, using the Hilbert transform.</td>
</tr>
<tr>
<td><code>hilbert2</code></td>
<td>Compute the ‘2-D’ analytic signal of ( x ).</td>
</tr>
<tr>
<td><code>decimate</code></td>
<td>Downsample the signal by using a filter.</td>
</tr>
<tr>
<td><code>detrend</code></td>
<td>Remove linear trend along axis from data.</td>
</tr>
<tr>
<td><code>resample</code></td>
<td>Resample ( x ) to ( num ) samples using Fourier method along the given axis.</td>
</tr>
</tbody>
</table>

**scipy.signal.order_filter** \((a, \text{domain}, \text{rank})\)

Perform an order filter on an N-dimensional array.

Perform an order filter on the array \( a \). 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.
- \( \text{domain} \): array_like  
  - A mask array with the same number of dimensions as \( in \). Each dimension should have an odd number of elements.
- \( \text{rank} \): 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**  
- \( \text{out} \): ndarray  
  - The results of the order filter in an array with the same shape as \( in \).

**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** \((\text{volume}, \text{kernel_size}=\text{None})\)

Perform a median filter on an N-dimensional array.

Apply a median filter to the input array using a local window-size given by \( \text{kernel_size} \).

**Parameters**  
- \( \text{volume} \): array_like  
  - An N-dimensional input array.
- \( \text{kernel_size} \): 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(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(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**

- **im** : ndarray
  An N-dimensional array.
- **mysize** : int or arraylike, 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(input, c0, z1 [, precision]) → output
```

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:

\[
H(z) = \frac{c0}{(1-z1/z) (1 - \frac{z1}{z})}
\]

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(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:

- \( a2 = (2 r \cos \omega) \)
- \( a3 = -r^2 \)
- \( cs = 1 - 2 r \cos \omega + r^2 \)

**Parameters**
- **input**: ndarray
  The input signal.
- **r**, **omega**: scalar
  Parameters in the transfer function.
- **precision**: scalar
  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(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 \texttt{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.

**Notes**
The filter function is implemented as a direct II transposed structure. This means that the filter implements:
\[a[0]\cdot y[n] = b[0]\cdot x[n] + b[1]\cdot x[n-1] + \ldots + b[nb]\cdot x[n-nb] - a[1]\cdot y[n-1] - \ldots - a[na]\cdot y[n-na]\]

using the following difference equations:

\[y[m] = b[0]\cdot x[m] + z[0,m-1]\]
\[z[0,m] = b[1]\cdot x[m] + z[1,m-1] - a[1]\cdot y[m]\]
\[
\vdots
\]
\[z[n-3,m] = b[n-2]\cdot x[m] + z[n-2,m-1] - a[n-2]\cdot y[m]\]
\[z[n-2,m] = b[n-1]\cdot x[m] - a[n-1]\cdot y[m]\]

where \(m\) is the output sample number and \(n=\max(\text{len}(a),\text{len}(b))\) is the model order.

The rational transfer function describing this filter in the z-transform domain is:

\[
Y(z) = \frac{-1 - nb}{a[0] + a[1]z + \ldots + a[na]z} X(z)
\]

**scipy.signal.lfiltic** *(b, a, y=None)*

Construct initial conditions for lfilter.

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 \(N=\text{len}(a)-1\), then \(y = \{y[-1], y[-2], \ldots, y[-N]\}\).
    - If \(y\) is too short, it is padded with zeros.
- **x**: array_like, optional
  - Initial conditions.
    - If \(M=\text{len}(b)-1\), then \(x = \{x[-1], x[-2], \ldots, x[-M]\}\).
    - If \(x\) is not given, its initial conditions are assumed zero.

**Returns**
- **zi**: ndarray
  - The state vector \(zi\). \(zi = \{z_0[-1], z_1[-1], \ldots, z_{K-1}[-1]\}\), where \(K = \max(M,N)\).

**See also:**
- **lfilter**
- **lfilter_zi** *(b, a)*

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)

**Returns**
- **zi**: 1-D ndarray
  - The IIR filter coefficients. See lfilter for more information.
  - The initial state for the filter.
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). lfilter_zi solves:

\[
zi = A \cdot zi + B
\]

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:

\[
A = \text{scipy.linalg.companion}(a).T \\
B = b[1:] - a[1:] \cdot b[0]
\]

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 zi argument of 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 zi argument to lfilter was computed using 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 (b, a, x, axis=-1, padtype='odd', padlen=None, method='pad', irlen=None)

A forward-backward filter.

This function applies a linear filter twice, once forward and once backwards. The combined filter has linear phase.

The function provides options for handling the edges of the signal.

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 [R173] 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.

**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 \( 3 \times \max(\text{len}(a), \text{len}(b)) \).
- **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 `irlen` is ignored. When `method` is “gust”, Gustafsson’s method is used, and `padtype` and `padlen` are ignored.
- **irlen**: int or None, optional
  - When `method` is “gust”, `irlen` specifies the length of the impulse response of the filter. If `irlen` is None, no part of the impulse response is ignored. For a long signal, specifying `irlen` can significantly improve the performance of the filter.

**Returns**

- **y**: ndarray
  - The filtered output, an array of type numpy.float64 with the same shape as \( x \).

See also:

- `lfilter_zi`, `lfilter`

Notes

The option to use Gustafsson’s method was added in scipy version 0.16.0.

References

[R173]

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 rate, or 125 Hz, and apply it to \(x\) with `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 `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 `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()
```
The \textit{irlen} argument can be used to improve the performance of Gustafsson’s method.

Estimate the impulse response length of the filter.

\begin{verbatim}
>>> 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
\end{verbatim}

Apply the filter to a longer signal, with and without the \textit{irlen} argument. The difference between \texttt{y1} and \texttt{y2} is small. For long signals, using \textit{irlen} gives a significant performance improvement.

\begin{verbatim}
>>> 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
\end{verbatim}

\texttt{scipy.signal.savgol_filter} (\texttt{x}, \texttt{window_length}, \texttt{polyorder}, \texttt{deriv=0}, \texttt{delta=1.0}, \texttt{axis=-1}, \texttt{mode='interp'}, \texttt{cval=0.0})

Apply a Savitzky-Golay filter to an array.

This is a 1-d filter. If \texttt{x} has dimension greater than 1, \texttt{axis} determines the axis along which the filter is applied.

\textbf{Parameters}

\begin{itemize}
  \item \texttt{x} : array_like
    The data to be filtered. If \texttt{x} is not a single or double precision floating point array, it will be converted to type \texttt{numpy.float64} before filtering.
  \item \texttt{window_length} : int
    The length of the filter window (i.e. the number of coefficients). \texttt{window_length} must be a positive odd integer.
  \item \texttt{polyorder} : int
    The order of the polynomial used to fit the samples. \texttt{polyorder} must be less than \texttt{window_length}.
  \item \texttt{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.
\end{itemize}
**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>7 6 5</td>
</tr>
<tr>
<td>'nearest'</td>
<td>1 1 1</td>
<td>1 2 3 4 5 6 7 8</td>
<td>8 8 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</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</td>
</tr>
</tbody>
</table>

New in version 0.14.0.

**Examples**

```python
>>> 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.

```py
>>> y = savgol_filter(x, 5, 2)
array([ 1.66, 3.17, 3.54, 2.86, 0.66, 0.17, 1. , 4. , 9. ])
```

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
5.27. Signal processing (scipy.signal) 819
```
```python
>>> savgol_filter(x, 5, 2, mode='nearest')
array([ 1.74,  3.03,  3.54,  2.86,  0.66,  0.17,  1.  ,  4.6 ,  7.97])
```

**scipy.signal.deconvolve (signal, divisor)**

Deconvolves divisor out of signal.
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 (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 `lfilteric` 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`

**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 `lfilter` and `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 = np.zeros(700)
>>> x[0] = 1.
>>> 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()
```

`scipy.signal.sosfilt_zi(sos)`

Compute an initial state `zi` for the 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**

- `sos`: array_like
  Array of second-order filter coefficients, must have shape `(n_sections, 6)`. See `sosfilt` for the SOS filter format specification.

**Returns**

- `zi`: ndarray
  Initial conditions suitable for use with `sosfilt`, shape `(n_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()
```

![Graph](https://via.placeholder.com/150)
scipy.signal.hilbert($x$, $N=None, axis=-1$)
Compute the analytic signal, using the Hilbert transform.

The transformation is done along the last axis by default.

**Parameters**

- $x$: array_like
  Signal data. Must be real.
- $N$: int, optional
  Number of Fourier components. Default: $x.shape[axis]$.
- $axis$: int, optional
  Axis along which to do the transformation. Default: -1.

**Returns**

- $xa$: ndarray
  Analytic signal of $x$, of each 1-D array along $axis$.

**Notes**

The analytic signal $x_a(t)$ of signal $x(t)$ is:

$$x_a = F^{-1}(F(x)2U) = x + iy$$

where $F$ is the Fourier transform, $U$ the unit step function, and $y$ the Hilbert transform of $x$. [R186]

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 `np.imag(hilbert(x))`, and the original signal from `np.real(hilbert(x))`.

**References**

[R186]

scipy.signal.hilbert2($x$, $N=None$)
Compute the ‘2-D’ analytic signal of $x$

**Parameters**

- $x$: array_like
  2-D signal data.
- $N$: 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**

[R187]

scipy.signal.decimate($x$, $q$, $n=None, ftype='iir', axis=-1$)
Downsample the signal by using a 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**

- $x$: ndarray
  The signal to be downsampled, as an N-dimensional array.
- $q$: int
  The downsampling factor.
- $n$: int, optional
  The order of the filter (1 less than the length for ‘fir’).
- $ftype$: str {‘iir’, ‘fir’}, optional
  The type of the lowpass filter.
- $axis$: int, optional
  The axis along which to decimate.

**Returns**

- $y$: ndarray
  The down-sampled signal.
See also:

resample

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 = 1e3
>>> noise = randgen.randn(npoints)
>>> x = 3 + 2*np.linspace(0, 1, npoints) + noise
>>> (signal.detrend(x) - noise).max() < 0.01
True
```

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 len(x) / 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.
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 samples is large and prime, see scipy.fftpack.fft.

5.27.4 Filter design

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>scipy.signal.bilinear(b, a[, fs])</td>
<td>Return a digital filter from an analog one using a bilinear transform.</td>
</tr>
<tr>
<td>scipy.signal.findfreqs(num, den, N)</td>
<td>Find an array of frequencies for computing the response of a filter.</td>
</tr>
<tr>
<td>scipy.signal.firwin(numtaps, cutoff[, width, window, ...])</td>
<td>FIR filter design using the window method.</td>
</tr>
<tr>
<td>scipy.signal.firwin2(numtaps, freq, gain[, nfreqs, ...])</td>
<td>FIR filter design using the window method.</td>
</tr>
<tr>
<td>scipy.signal.freqs(b, a[, worN, plot])</td>
<td>Compute frequency response of analog filter.</td>
</tr>
<tr>
<td>scipy.signal.freqz(b[, a, worN, whole, plot])</td>
<td>Compute the frequency response of a digital filter.</td>
</tr>
<tr>
<td>scipy.signal.group_delay(system[, w, whole])</td>
<td>Compute the group delay of a digital filter.</td>
</tr>
<tr>
<td>scipy.signal.iirfilter(N, Wn[, rp, rs, btype, analog, ...])</td>
<td>Complete IIR digital and analog filter design.</td>
</tr>
<tr>
<td>scipy.signal.iirfilter(N, Wn[, rp, rs, btype, analog, ...])</td>
<td>IIR digital and analog filter design given order and critical points.</td>
</tr>
<tr>
<td>scipy.signal.kaiser_atten(numtaps, width)</td>
<td>Compute the attenuation of a Kaiser FIR filter.</td>
</tr>
<tr>
<td>scipy.signal.kaiser_beta(a)</td>
<td>Compute the Kaiser parameter beta, given the attenuation a.</td>
</tr>
<tr>
<td>scipy.signal.kaiserord(ripple, width)</td>
<td>Design a Kaiser window to limit ripple and width of transition region.</td>
</tr>
<tr>
<td>scipy.signal.savgol_coeffs(window_length, polyorder[, ...])</td>
<td>Compute the coefficients for a 1-d Savitzky-Golay FIR filter.</td>
</tr>
<tr>
<td>scipy.signal.remez(numtaps, bands, desired[, weight, Hz, ...])</td>
<td>Calculate the minimax optimal filter using the Remez exchange algorithm.</td>
</tr>
</tbody>
</table>

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.

scipy.signal.findfreqs(num, den, N)

Find an array of frequencies for computing the response of a 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. The coefficients are ordered from...
SciPy Reference Guide, Release 0.16.0

highest to lowest degree.

Returns

w : (N,) ndarray

A 1-D array of frequencies, logarithmically spaced.

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
>>> 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.firwin

FIR filter design using the window method.

This function 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 rate, so a ValueError exception is raised if firwin is
called with `numtaps` even and having a passband whose right end is at the Nyquist rate.

Parameters

- `numtaps` : int
  Length of the filter (number of coefficients, i.e. the filter order + 1). `numtaps` must be even if a passband includes the Nyquist frequency.
- `cutoff` : float or 1D array_like
  Cutoff frequency of filter (expressed in the same units as `nyq`) 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 `nyq`. The values 0 and `nyq` 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 `nyq`) 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)
  - `nyq` (the Nyquist rate) if the first passband ends at `nyq` (i.e. the filter is a single band highpass filter); center of first passband otherwise
- `nyq` : float, optional
  Nyquist frequency. Each frequency in `cutoff` must be between 0 and `nyq`.

Returns

- `h` : (numtaps,) ndarray
  Coefficients of length `numtaps` FIR filter.

Raises

- ValueError
  Raised if `numtaps` is even and having a passband whose right end is at the Nyquist rate.
If any value in `cutoff` is less than or equal to 0 or greater than or equal to `nyq`, if the values in `cutoff` are not strictly monotonically increasing, or if `numtaps` is even but a passband includes the Nyquist frequency.

See also:

`scipy.signal.firwin2`

**Examples**

Low-pass from 0 to f:

```python
>>> from scipy import signal
>>> signal.firwin(numtaps, f)
```

Use a specific window function:

```python
>>> signal.firwin(numtaps, f, window='nuttall')
```

High-pass (‘stop’ from 0 to f):

```python
>>> signal.firwin(numtaps, f, pass_zero=False)
```

Band-pass:

```python
>>> signal.firwin(numtaps, [f1, f2], pass_zero=False)
```

Band-stop:

```python
>>> signal.firwin(numtaps, [f1, f2])
```

Multi-band (passbands are [0, f1], [f2, f3] and [f4, 1]):

```python
>>> signal.firwin(numtaps, [f1, f2, f3, f4])
```

Multi-band (passbands are [f1, f2] and [f3,f4]):

```python
>>> signal.firwin(numtaps, [f1, f2, f3, f4], pass_zero=False)
```

`scipy.signal.firwin2(numtaps, freq, gain, nfreqs=None, window='hamming', nyq=1.0, antisymmetric=False)`

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 can be redefined with the argument `nyq`. 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 `nyq`.

- `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

Nyquist frequency. Each frequency in `freq` must be between 0 and `nyq`
(inclusive).

**antisymmetric**: bool, optional

Whether resulting impulse response is symmetric/antisymmetric. See Notes
for more details.

**Returns**

**taps**: ndarray

The filter coefficients of the FIR filter, as a 1-D array of length `numtaps`.

See also:

`scipy.signal.firwin`

**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`
tag. 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**

[R175], [R176]

**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:

```python
>>> 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(b, a, worN=None, plot=None)`

Compute frequency response of analog filter.

Given the numerator `b` and denominator `a` of a filter, compute its frequency response:
\[ H(w) = \frac{b[0] \times (jw) \times (nb-1) + b[1] \times (jw) \times (nb-2) + \ldots + b[nb-1]}{a[0] \times (jw) \times (na-1) + a[1] \times (jw) \times (na-2) + \ldots + a[na-1]} \]

**Parameters**
- **b**: ndarray
  - Numerator of a linear filter.
- **a**: ndarray
  - Denominator of a linear filter.
- **worN**: {None, int}, 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.freqz(b, a=1, worN=None, whole=0, plot=None)

Compute the frequency response of a digital filter.

Given the numerator $b$ and denominator $a$ of a digital filter, compute its frequency response:

$$
H(e^{j\omega}) = \frac{b[0] + b[1]e^{-j\omega} + \ldots + b[m]e^{-jm\omega}}{a[0] + a[1]e^{-j\omega} + \ldots + a[n]e^{-jn\omega}}
$$

**Parameters**

- **b**: ndarray
  - numerator of a linear filter
- **a**: ndarray
  - denominator of a linear filter
- **worN**: {None, int, array_like}, optional
  - If None (default), then compute at 512 frequencies equally spaced around the unit circle. If a single integer, then compute at that many frequencies. If an array_like, compute the response at the frequencies given (in radians/sample).
- **whole**: bool, optional
  - Normally, 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.
- **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 freqz.

**Returns**

- **w**: ndarray
  - The normalized frequencies at which $h$ was computed, in radians/sample.
- **h**: ndarray
  - The frequency response.

**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 import signal
>>> b = signal.firwin(80, 0.5, window=('kaiser', 8))
>>> w, h = signal.freqz(b)

>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.title('Digital filter frequency response')
>>> ax1 = fig.add_subplot(111)

>>> plt.plot(w, 20 * np.log10(abs(h)), 'b')
>>> plt.ylabel('Amplitude [dB]', color='b')
>>> plt.xlabel('Frequency [rad/sample]')

>>> ax2 = ax1.twinx()
>>> angles = np.unwrap(np.angle(h))
>>> plt.plot(w, angles, 'g')
>>> plt.ylabel('Angle (radians)', color='g')
>>> plt.grid()
>>> plt.axis('tight')
>>> plt.show()
```

scipy.signal.group_delay(system, w=None, whole=False)
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:

\[
D(w) = -\frac{d}{dw} \arg H(e^{jw})
\]

Parameters:
- `system`: tuple of array_like (b, a)
  Numerator and denominator coefficients of a filter transfer function.
- `w`: [None, int, array-like], optional
If None (default), then compute at 512 frequencies equally spaced around
the unit circle. If a single integer, then compute at that many frequencies. If
array, compute the delay at the frequencies given (in radians/sample).

whole : bool, optional

Normally, frequencies are computed from 0 to the Nyquist frequency, pi
radians/sample (upper-half of unit-circle). If whole is True, compute fre-
quencies from 0 to 2*pi radians/sample.

Returns w : ndarray

The normalized frequencies at which the group delay was computed, in
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 [R177].

References

[R177]

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))

>>> 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(wp, ws, gpass, gstop, analog=False, ftype='ellip', output='ba')

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 normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. (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.

-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'.

**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

5.27. Signal processing (scipy.signal) 833
Second-order sections representation of the IIR filter. Only returned if `output==‘sos’`.

**See also:**

- **butter**: Filter design using order and critical points
- **cheby1, cheby2, ellip, bessel**: Filter design using order and critical frequencies
- **buttord**: Find order and critical points from passband and stopband spec
- **cheb1ord, cheb2ord, ellipord**: Filter design using order and critical frequencies
- **iirfilter**: General filter design using order and critical frequencies

**Notes**

The ‘sos’ output parameter was added in 0.16.0.

```python
scipy.signal.iirfilter(N, Wn, rp=None, rs=None, btype='band', analog=False, ftype='butter', output='ba')
```

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` is normalized from 0 to 1, where 1 is the Nyquist frequency, π radians/sample. (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)
- btype : {'bandpass', 'lowpass', 'highpass', 'bandstop'}, optional
  The type of filter. Default 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’.

**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

cheb1, cheb2, ellip, bessel

**buttord**  Find order and critical points from passband and stopband spec

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 bandpass filter and plot the frequency response:

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

>>> b, a = signal.iirfilter(17, [50, 200], rs=60, btype='band', analog=True, ftype='cheby2')
>>> w, h = signal.freqs(b, a, 1000)
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.semilogx(w, 20 * np.log10(abs(h)) )
>>> ax.set_title('Chebyshev Type II bandpass frequency response')
>>> ax.set_xlabel('Frequency [radians / second]')
>>> ax.set_ylabel('Amplitude [dB]')
>>> ax.axis((10, 1000, -100, 10))
>>> ax.grid(which='both', axis='both')
>>> plt.show()
```

**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.

Returns

- **a**: float
  - The attenuation of the ripple, in dB.

See also:

- `kaiserord`, `kaiser_beta`

```python
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


```python
scipy.signal.kaiserord(ripple, width)
```

Design a Kaiser window to limit ripple and width of transition region.

Parameters

- **ripple**: float
  - Positive number specifying maximum ripple in passband (dB) and minimum ripple in stopband.

- **width**: float
  - Width of transition region (normalized so that 1 corresponds to pi radians / sample).

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=0)`
- `signal.get_window(beta, numtaps)`
- `signal.get_window(('kaiser', beta), numtaps)`

The empirical equations discovered by Kaiser are used.

References


```python
scipy.signal.savgol_coeffs(window_length, polyorder, deriv=0, delta=1.0, pos=None, use='conv')
```

Compute the coefficients for a 1-d Savitzky-Golay FIR filter.

Parameters

- **window_length**: int
  - The length of the filter window (i.e. the number of coefficients). `window_length` must be an odd positive integer.
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.

pos : int or None, optional
   If pos is not None, it specifies evaluation position within the window. The
   default is the middle of the window.

use : str, optional
   Either ‘conv’ or ‘dot’. This argument chooses the order of the coefficients.
   The default is ‘conv’, which means that the coefficients are ordered to be
   used in a convolution. With use=’dot’, the order is reversed, so the filter is
   applied by dotting the coefficients with the data set.

Returns

   coeffs : 1-d ndarray
      The filter coefficients.

See also:

savgol_filter

Notes

New in version 0.14.0.

References

A. Savitzky, M. J. E. Golay, Smoothing and Differentiation of Data by Simplified Least Squares Procedures.

Examples

>>> from scipy.signal import savgol_coeffs
>>> savgol_coeffs(5, 2)
aarray([-0.08571429, 0.34285714, 0.48571429, 0.34285714, -0.08571429])
>>> savgol_coeffs(5, 2, deriv=1)
aarray([ 2.00000000e-01, 1.00000000e-01, 2.00607895e-16, 
       -1.00000000e-01, -2.00000000e-01])

Note that use=’dot’ simply reverses the coefficients.

>>> savgol_coeffs(5, 2, pos=3)
aarray([ 0.25714286, 0.37142857, 0.34285714, 0.17142857, -0.14285714])
>>> savgol_coeffs(5, 2, pos=3, use=’dot’)
aarray([-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.

>>> x = np.array([1, 0, 1, 4, 9])
>>> c = savgol_coeffs(5, 2, pos=4, deriv=1, use=’dot’)
>>> c.dot(x)
6.000000000000018
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 in Hz. All elements must be non-negative and less than half the sampling frequency as given by `Hz`.

- `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
  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.

**Returns**

- `out` : ndarray
  A rank-1 array containing the coefficients of the optimal (in a minimax sense) filter.

**See also:**

- `freqz` : Compute the frequency response of a digital filter.

**References**

[R196], [R197]

**Examples**

We want to construct a filter with a passband at 0.2-0.4 Hz, and stop bands at 0-0.1 Hz and 0.45-0.5 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
>>> bpass = signal.remez(72, [0, 0.1, 0.2, 0.4, 0.45, 0.5], [0, 1, 0])
>>> freq, response = signal.freqz(bpass)
>>> ampl = np.abs(response)
```
```python
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(111)
>>> ax1.semilogy(freq/(2*np.pi), ampl, 'b-')  # freq in Hz
>>> plt.show()

scipy.signal.unique_roots(p, tol=0.001, rtype='min')
Determine unique roots and their multiplicities from a list of roots.

Parameters
- **p**: array_like
  The list of roots.
- **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
- **pout**: ndarray
  The list of unique roots, sorted from low to high.
- **mult**: 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 numpy.unique.

Examples
```python
>>> from scipy import signal
>>> vals = [0, 1.3, 1.31, 2.8, 1.25, 2.2, 10.3]
>>> uniq, mult = signal.unique_roots(vals, tol=2e-2, rtype='avg')
```

Check which roots have multiplicity larger than 1:
scipy.signal.residue(b, a, tol=0.001, rtype='avg')
Compute partial-fraction expansion of b(s) / a(s).

If M = len(b) and N = len(a), then the partial-fraction expansion H(s) is defined as:

\[
H(s) = \frac{b(s)}{a(s)} = \frac{b[0] s^{(M-1)} + \ldots + b[M-1]}{a[0] s^{(N-1)} + \ldots + a[N-1]}
\]

\[
r[0] \quad r[1] \quad r[-1] = \frac{r[0]}{(s-p[0])} + \frac{r[1]}{(s-p[1])} + \frac{r[-1]}{(s-p[-1])}
\]

If there are any repeated roots (closer together than tol), then H(s) has terms like:

\[
\frac{r[i]}{(s-p[i])} + \frac{r[i+1]}{(s-p[i])^2} + \ldots + \frac{r[i+n-1]}{(s-p[i])^n}
\]

**Returns**

- **r**: ndarray
  Residues.
- **p**: ndarray
  Poles.
- **k**: ndarray
  Coefficients of the direct polynomial term.

See also:

- scipy.signal.invres
- numpy.poly
- unique_roots

scipy.signal.residuez(b, a, tol=0.001, rtype='avg')
Compute partial-fraction expansion of b(z) / a(z).

If M = len(b) and N = len(a):

\[
H(z) = \frac{b(z)}{a(z)} = \frac{b[0] + b[1] z^(-1) + \ldots + b[M-1] z^(-M+1)}{a[0] + a[1] z^(-1) + \ldots + a[N-1] z^(-N+1)}
\]

\[
r[0] \quad r[-1] = \frac{r[0]}{(1-p[0] z^(-1))} + \frac{r[-1]}{(1-p[-1] z^(-1))}
\]

If there are any repeated roots (closer than tol), then the partial fraction expansion has terms like:

\[
\frac{r[i]}{(1-p[i] z^(-1))} + \frac{r[i+1]}{(1-p[i] z^(-1))^2} + \ldots + \frac{r[i+n-1]}{(1-p[i] z^(-1))^n}
\]

See also:

- scipy.signal.invresz
- unique_roots
scipy.signal.invres\( r, p, k, \text{tol}=0.001, \text{rtype}='\text{avg}' \)
Compute \( b(s) \) and \( a(s) \) from partial fraction expansion.

If \( M = \text{len}(b) \) and \( N = \text{len}(a) \):

\[
\begin{align*}
H(s) &= \frac{b(s)}{a(s)} = \frac{b[0] x^{(M-1)} + b[1] x^{(M-2)} + \ldots + b[M-1]}{a[0] x^{(N-1)} + a[1] x^{(N-2)} + \ldots + a[N-1]} \\
&= \frac{r[0]}{s-p[0]} + \frac{r[1]}{s-p[1]} + \ldots + \frac{r[-1]}{s-p[-1]} + k(s)
\end{align*}
\]

If there are any repeated roots (closer than \( \text{tol} \)), then the partial fraction expansion has terms like:

\[
\frac{r[i]}{1-p[i]z^{-1}} + \frac{r[i+1]}{(1-p[i]z^{-1})^2} + \ldots + \frac{r[i+n-1]}{(1-p[i]z^{-1})^n}
\]

**Parameters**

- \( r \): ndarray
  Residues.
- \( p \): ndarray
  Poles.
- \( k \): ndarray
  Coefficients of the direct polynomial term.
- \( \text{tol} \): float, optional
  The tolerance for two roots to be considered equal. Default is \( 1\text{e-3} \).
- \( \text{rtype} \): \{'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.

See also:

residue, unique_roots

scipy.signal.invresz\( r, p, k, \text{tol}=0.001, \text{rtype}='\text{avg}' \)
Compute \( b(z) \) and \( a(z) \) from partial fraction expansion.

If \( M = \text{len}(b) \) and \( N = \text{len}(a) \):

\[
\begin{align*}
H(z) &= \frac{b(z)}{a(z)} = \frac{b[0] + b[1] z^{-1} + \ldots + b[M-1] z^{-(M-1)}}{a[0] + a[1] z^{-1} + \ldots + a[N-1] z^{-(N-1)}} \\
&= \frac{r[0]}{1-p[0]z^{-1}} + \frac{r[-1]}{1-p[-1]z^{-1}} + \ldots + k[0] + k[1]z^{-1} + \ldots + k[-1]z^{-(N-1)}
\end{align*}
\]

If there are any repeated roots (closer than \( \text{tol} \)), then the partial fraction expansion has terms like:

\[
\frac{r[i]}{1-p[i]z^{-1}} + \frac{r[i+1]}{(1-p[i]z^{-1})^2} + \ldots + \frac{r[i+n-1]}{(1-p[i]z^{-1})^n}
\]
See also:

residuez, unique_roots, invres

Lower-level filter design functions:

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>abcd_normalize</code></td>
<td>Check state-space matrices and ensure they are two-dimensional.</td>
</tr>
<tr>
<td><code>band_stop_obj</code></td>
<td>Band Stop Objective Function for order minimization.</td>
</tr>
<tr>
<td><code>besselap</code></td>
<td>Return (z,p,k) for analog prototype of an Nth order Bessel filter.</td>
</tr>
<tr>
<td><code>butterap</code></td>
<td>Return (z,p,k) for analog prototype of Nth order Butterworth filter.</td>
</tr>
<tr>
<td><code>cheb1ap</code></td>
<td>Return (z,p,k) for Nth order Chebyshev type I analog lowpass filter.</td>
</tr>
<tr>
<td><code>cheb2ap</code></td>
<td>Return (z,p,k) for Nth order Chebyshev type I analog lowpass filter.</td>
</tr>
<tr>
<td><code>cmplx_sort</code></td>
<td>Sort roots based on magnitude.</td>
</tr>
<tr>
<td><code>ellipap</code></td>
<td>Return (z,p,k) of Nth order elliptic analog lowpass filter.</td>
</tr>
<tr>
<td><code>lp2bp</code></td>
<td>Transform a lowpass filter prototype to a bandpass filter.</td>
</tr>
<tr>
<td><code>lp2bs</code></td>
<td>Transform a lowpass filter prototype to a bandstop filter.</td>
</tr>
<tr>
<td><code>lp2hp</code></td>
<td>Transform a lowpass filter prototype to a highpass filter.</td>
</tr>
<tr>
<td><code>lp2lp</code></td>
<td>Transform a lowpass filter prototype to a different frequency.</td>
</tr>
<tr>
<td><code>normalize</code></td>
<td>Normalize polynomial representation of a transfer function.</td>
</tr>
</tbody>
</table>

**scipy.signal.abcd_normalize**

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.

**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**

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**

Return (z,p,k) for analog prototype of an Nth order Bessel filter.
The filter is normalized such that the filter asymptotes are the same as a Butterworth filter of the same order with an angular (e.g. rad/s) cutoff frequency of 1.

**Parameters**

- **N**: int
  - The order of the Bessel filter to return zeros, poles and gain for. Values in the range 0-25 are supported.

**Returns**

- **z**: ndarray
  - Zeros. Is always an empty array.
- **p**: ndarray
  - Poles.
- **k**: scalar
  - Gain. Always 1.

**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.

**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 $-rp$.

**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 $-rs$.

**scipy.signal.cmplx_sort(p)**

Sort roots based on magnitude.

**Parameters**

- **p**: array_like
  - The roots to sort, as a 1-D array.

**Returns**

- **p_sorted**: ndarray
  - Sorted roots.
- **indx**: ndarray
  - Array of indices needed to sort the input $p$.

**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 $rp$ decibels of ripple in the passband and a stopband $rs$ 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 $-rp$.

**References**

Lutova, Tocis, and Evans, “Filter Design for Signal Processing”, Chapters 5 and 12.

**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.
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.

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.

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.

scipy.signal.normalize(b, a)
Normalize polynomial representation of a transfer function.
If values of b are too close to 0, they are removed. In that case, a BadCoefficients warning is emitted.

5.27.5 Matlab-style IIR filter design

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>butter</td>
<td>Butterworth digital and analog filter design.</td>
</tr>
<tr>
<td>buttord</td>
<td>Butterworth filter order selection.</td>
</tr>
<tr>
<td>cheby1</td>
<td>Chebyshev type I digital and analog filter design.</td>
</tr>
<tr>
<td>cheb1ord</td>
<td>Chebyshev type I filter order selection.</td>
</tr>
<tr>
<td>cheby2</td>
<td>Chebyshev type II digital and analog filter design.</td>
</tr>
<tr>
<td>cheb2ord</td>
<td>Chebyshev type II filter order selection.</td>
</tr>
<tr>
<td>ellip</td>
<td>Elliptic (Cauer) digital and analog filter design.</td>
</tr>
<tr>
<td>ellipord</td>
<td>Elliptic (Cauer) filter order selection.</td>
</tr>
<tr>
<td>bessel</td>
<td>Bessel/Thomson digital and analog filter design.</td>
</tr>
</tbody>
</table>

scipy.signal.butter(N, Wn, btype='low', analog=False, output='ba')
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 is normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. (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`

**Notes**

The Butterworth filter has maximally flat frequency response in the passband.

The `‘sos’` output parameter was added in 0.16.0.

**Examples**

Plot the filter’s 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](image-url)
scipy.signal.buttord(wp, ws, gpass, gstop, analog=False)

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 normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. ($wp$ and $ws$ are thus in half-cycles / sample.) For example:
  - Lowpass: $wp = 0.2$, $ws = 0.3$
  - Highpass: $wp = 0.7$, $ws = 0.2$
  - Bandpass: $wp = [0.2, 0.5]$, $ws = [0.1, 0.6]$
  - Bandstop: $wp = [0.1, 0.6]$, $ws = [0.2, 0.3]$
  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.

**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.

See also:
- butter  Filter design using order and critical points
- cheby1ord  Find order and critical points from passband and stopband spec
- cheby2ord, 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*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()
```
Design an Nth order digital or analog Chebyshev type I 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.
- **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 is normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. (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:

- cheb1ord

### scipy.signal.cheby1

`scipy.signal.cheby1(N, rp, Wn, btype='low', analog=False, output='ba')`

Chebyshev type I digital and analog filter design.

Design an Nth order digital or analog Chebyshev type I filter and return the filter coefficients.
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

Plot the filter’s 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

plt.axhline(-5, color='green') # rp

plt.show()
```

Scipy’s `signal.cheby1` function creates a Chebyshev type I filter.

```python
scipy.signal.cheb1ord(wp, ws, gpass, gstop, analog=False)
```

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**

- `wp`, `ws` : float
Passband and stopband edge frequencies. For digital filters, these are normalized from 0 to 1, where 1 is the Nyquist frequency, \( \pi \) radians/sample. (\( wp \) 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).

**Parameters**

- \( gpass \) : 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.

**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.

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.cheb1ord(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([.01, 0.2, 0.2, .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 \((N, rs, Wn, btype='low', analog=False, output='ba')\)

Chebyshev type II digital and analog filter design.

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.
- \(Wn\) : 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, \(Wn\) is normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. (\(Wn\) 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:**

cheb2ord
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

Plot the filter’s 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()
```

```python
scipy.signal.cheb2ord(wp, ws, gpass, gstop, analog=False)
```

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 normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. (wp and ws are thus in half-cycles / sample.) For example:
  - Lowpass: wp = 0.2, ws = 0.3
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.

**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.

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(N, rp, rs, Wn, btype='low', analog=False, output='ba')

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.
- **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 is normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. (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:
ellipord

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

Plot the filter's 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.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.axvline(100, color='green') # cutoff frequency
>>> plt.axhline(-40, color='green') # rs
>>> plt.axhline(-5, color='green') # rp
>>> plt.show()
```

![Elliptic filter frequency response](image)

```
scipy.signal.ellipord(wp, ws, gpass, gstop, analog=False)
Elliptic (Cauer) filter order selection.
```
Return the order of the lowest order digital or analog elliptic filter that loses no more than $g_{\text{pass}}$ dB in the passband and has at least $g_{\text{stop}}$ dB attenuation in the stopband.

**Parameters**

- **wp, ws** : float
  Passband and stopband edge frequencies. For digital filters, these are normalized from 0 to 1, where 1 is the Nyquist frequency, $\pi$ radians/sample. (wp and ws are thus in half-cycles / sample.) For example:
  - Lowpass: wp = 0.2, ws = 0.3
  - Highpass: wp = 0.7, ws = 0.5
  - Bandpass: 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.

**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.

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\((N, Wn, btype='low', analog=False, output='ba')\)

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. For a Bessel filter, this is defined as the point at which the asymptotes of the response are the same as a Butterworth filter of the same order. For digital filters, \(Wn\) is normalized from 0 to 1, where 1 is the Nyquist frequency, pi radians/sample. (\(Wn\) 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'.

**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.

As order increases, the Bessel filter approaches a Gaussian filter.
The digital Bessel filter is generated 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.

For a given \( W_n \), the lowpass and highpass filter have the same phase vs frequency curves; they are “phase-matched”.

The ‘sos’ output parameter was added in 0.16.0.

**Examples**

Plot the filter’s frequency response, showing the flat group delay and the relationship to the Butterworth’s cutoff frequency:

```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.plot(w, 20 * np.log10(np.abs(h)), color='silver', ls='dashed')
>>> b, a = signal.bessel(4, 100, 'low', analog=True)
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(np.abs(h)))
>>> plt.title('Bessel filter frequency 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()

>>> plt.figure()
>>> plt.semilogx(w[:-1], -np.diff(np.unwrap(np.angle(h)))/np.diff(w))
>>> plt.title('Bessel filter group delay')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Group delay [seconds]')
```

**5.27. Signal processing (scipy.signal)**
5.27.6 Continuous-Time Linear Systems

`freqresp(system[, w, n])` Calculate the frequency response of a continuous-time system.

`lti(*system)` Linear Time Invariant system base class.

`StateSpace(*system)` Linear Time Invariant system class in state-space form.

`TransferFunction(*system)` Linear Time Invariant system class in transfer function form.

`ZerosPolesGain(*system)` Linear Time Invariant system class in zeros, poles, gain form.

`lsim(system, U[, T, X0, interp])` Simulate output of a continuous-time linear system.

`lsim2(system[, U, T, X0])` Simulate output of a continuous-time linear system, by using the ODE solver `scipy.integrate.odeint`.

`impulse(system[, X0, T, N])` Impulse response of a single-input, continuous-time linear system.

`step(system[, X0, T, N])` Step response of continuous-time system.

`bode(system[, w, n])` Calculate Bode magnitude and phase data of a continuous-time system.

`scipy.signal.freqresp(system, w=0, n=0)` 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:
  
  - 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
**Returns**  

- **w**: 1D ndarray  
  Frequency array [rad/s]
- **H**: 1D ndarray  
  Array of complex magnitude values

**Examples**

# Generating the Nyquist plot of a transfer function

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

>>> s1 = signal.lti([], [1, 1, 1], [5])  
# transfer function: H(s) = 5 / (s-1)^3

>>> w, H = signal.freqresp(s1)

>>> plt.figure()
>>> plt.plot(H.real, H.imag, "b")
>>> plt.plot(H.real, -H.imag, "r")
>>> plt.show()
```

**class `scipy.signal.lti(*system)`**

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 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.
Notes

$lti$ instances do not exist directly. Instead, $lti$ 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.

Attributes

<table>
<thead>
<tr>
<th>Property</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>A matrix of the $StateSpace$ system.</td>
</tr>
<tr>
<td>B</td>
<td>B matrix of the $StateSpace$ system.</td>
</tr>
<tr>
<td>C</td>
<td>C matrix of the $StateSpace$ system.</td>
</tr>
<tr>
<td>D</td>
<td>D matrix of the $StateSpace$ system.</td>
</tr>
<tr>
<td>den</td>
<td>Denominator of the $TransferFunction$ system.</td>
</tr>
<tr>
<td>gain</td>
<td>Gain of the $ZerosPolesGain$ system.</td>
</tr>
<tr>
<td>num</td>
<td>Numerator of the $TransferFunction$ system.</td>
</tr>
<tr>
<td>poles</td>
<td>Poles of the $ZerosPolesGain$ system.</td>
</tr>
<tr>
<td>zeros</td>
<td>Zeros of the $ZerosPolesGain$ system.</td>
</tr>
</tbody>
</table>

Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>$bode([w, n])$</td>
<td>Calculate Bode magnitude and phase data of a continuous-time system.</td>
</tr>
<tr>
<td>$freqresp([w, n])$</td>
<td>Calculate the frequency response of a continuous-time system.</td>
</tr>
<tr>
<td>$impulse([X0, T, N])$</td>
<td>Return the impulse response of a continuous-time system.</td>
</tr>
<tr>
<td>$output(U, T[, X0])$</td>
<td>Return the response of a continuous-time system to input $U$.</td>
</tr>
<tr>
<td>$step([X0, T, N])$</td>
<td>Return the step response of a continuous-time system.</td>
</tr>
</tbody>
</table>

$lti.bode$ ($w=None, n=100$)
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 `scipy.signal.bode` for details.

**Notes**

New in version 0.11.0.

**Examples**

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

>>> s1 = signal.lti([1], [1, 1])
>>> w, mag, phase = s1.bode()

>>> plt.figure()
>>> plt.semilogx(w, mag)  # Bode magnitude plot
>>> plt.figure()
>>> plt.semilogx(w, phase)  # Bode phase plot
>>> plt.show()
```
lti\texttt{.freqresp}(w=\texttt{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 \texttt{scipy.signal.freqresp} for details.

lti\texttt{.impulse}(X0=\texttt{None}, T=\texttt{None}, N=\texttt{None})
\> Return the impulse response of a continuous-time system. See \texttt{scipy.signal.impulse} for details.

lti\texttt{.output}(U, T, X0=\texttt{None})
\> Return the response of a continuous-time system to input \(U\). See \texttt{scipy.signal.lsim} for details.

lti\texttt{.step}(X0=\texttt{None}, T=\texttt{None}, N=\texttt{None})
\> Return the step response of a continuous-time system. See \texttt{scipy.signal.step} for details.

class \texttt{scipy.signal.StateSpace}(*system)
\> Linear Time Invariant system class in state-space form.
\> Represents the system as the first order differential equation \(\dot{x} = Ax + Bu\).

\> **Parameters**
\>
\> \*system : arguments
\>
\> The \texttt{StateSpace} class can be instantiated with 1 or 4 arguments. The following gives the number of input arguments and their interpretation:
\>
\> • 1: \texttt{lti} system: (\texttt{StateSpace}, \texttt{TransferFunction} or \texttt{ZerosPolesGain}),
\>
\> • 4: \texttt{array\_like}: (A, B, C, D)

\> **Notes**
\>
\> Changing the value of properties that are not part of the \texttt{StateSpace} system representation (such as \texttt{zeros} or \texttt{poles}) is very inefficient and may lead to numerical inaccuracies.

\> **Attributes**

\begin{verbatim}
A
B
C
D
\end{verbatim}

Continued on next page
Table 5.125 – continued from previous page

| Denominator of the **TransferFunction** system. |
| **den** |
| Gain of the **ZerosPolesGain** system. |
| **gain** |
| Numerator of the **TransferFunction** system. |
| **num** |
| Poles of the **ZerosPolesGain** system. |
| **poles** |
| Zeros of the **ZerosPolesGain** system. |
| **zeros** |

**StateSpace.**

**A**

**B**

**C**

**D**

**StateSpace.**

**den**

Denominator of the **TransferFunction** system.

**gain**

Gain of the **ZerosPolesGain** system.

**num**

Numerator of the **TransferFunction** system.

**poles**

Poles of the **ZerosPolesGain** system.

**zeros**

Zeros of the **ZerosPolesGain** 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_ss**()

Return a copy of the current StateSpace system.

**to_tf**(**kwargs)

Convert system representation to TransferFunction.

**to_zpk**(**kwargs)

Convert system representation to ZerosPolesGain.

**StateSpace.**

**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 scipy.signal.bode for details.

**Notes**

New in version 0.11.0.
Examples

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

>>> s1 = signal.lti([1], [1, 1])
>>> w, mag, phase = s1.bode()

>>> plt.figure()
>>> plt.semilogx(w, mag)  # Bode magnitude plot
>>> plt.figure()
>>> plt.semilogx(w, phase)  # Bode phase plot
>>> plt.show()
```

**StateSpace.freqresp** \(w=\text{None}, n=10000\)

Calculate the frequency response of a continuous-time system.
Returns a 2-tuple containing arrays of frequencies [rad/s] and complex magnitude. See scipy.signal.freqresp for details.

StateSpace.impulse(X0=None, T=None, N=None)
Return the impulse response of a continuous-time system. See scipy.signal.impulse for details.

StateSpace.output(U, T, X0=None)
Return the response of a continuous-time system to input U. See scipy.signal.lsim for details.

StateSpace.step(X0=None, T=None, N=None)
Return the step response of a continuous-time system. See scipy.signal.step for details.

StateSpace.to_ss()
Return a copy of the current StateSpace system.

   Returns sys : instance of StateSpace
                 The current system (copy)

StateSpace.to_tf(**kwargs)
Convert system representation to TransferFunction.

   Parameters kwags : dict, optional
   Returns sys : instance of TransferFunction
                 Transfer function of the current system

StateSpace.to_zpk(**kwargs)
Convert system representation to ZerosPolesGain.

   Parameters kwags : dict, optional
   Returns sys : instance of ZerosPolesGain
                 Zeros, poles, gain representation of the current system

class scipy.signal.TransferFunction(*system)
Linear Time Invariant system class in transfer function form.

   Represents the system as the transfer function \( H(s) = \sum_i b[i]s^i / \sum_j a[j]s^j \), where \( a \) are elements of the numerator num and \( b \) are the elements of the denominator den.

   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 system: (StateSpace, TransferFunction or ZerosPolesGain)
   •2: array_like: (numerator, denominator)

   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.

Attributes

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>A matrix of the StateSpace system.</td>
</tr>
<tr>
<td>B</td>
<td>B matrix of the StateSpace system.</td>
</tr>
<tr>
<td>C</td>
<td>C matrix of the StateSpace system.</td>
</tr>
<tr>
<td>D</td>
<td>D matrix of the StateSpace system.</td>
</tr>
<tr>
<td>den</td>
<td></td>
</tr>
<tr>
<td>gain</td>
<td>Gain of the ZerosPolesGain system.</td>
</tr>
<tr>
<td>num</td>
<td></td>
</tr>
</tbody>
</table>

Continued on next page
Table 5.127 – continued from previous page

<table>
<thead>
<tr>
<th>poles</th>
<th>Poles of the ZerosPolesGain system.</th>
</tr>
</thead>
<tbody>
<tr>
<td>zeros</td>
<td>Zeros of the ZerosPolesGain system.</td>
</tr>
</tbody>
</table>

TransferFunction.A
A matrix of the StateSpace system.

TransferFunction.B
B matrix of the StateSpace system.

TransferFunction.C
C matrix of the StateSpace system.

TransferFunction.D
D matrix of the StateSpace system.

TransferFunction.den

TransferFunction.gain
Gain of the ZerosPolesGain system.

TransferFunction.num

TransferFunction.poles
Poles of the ZerosPolesGain system.

TransferFunction.zeros
Zeros of the ZerosPolesGain system.

Methods

- bode([w, n]) Calculates Bode magnitude and phase data of a continuous-time system.
- freqresp([w, n]) Calculates the frequency response of a continuous-time system.
- impulse([X0, T, N]) Returns the impulse response of a continuous-time system.
- output(U, T[, X0]) Returns the response of a continuous-time system to input U.
- step([X0, T, N]) Returns the step response of a continuous-time system.
- to_ss() Converts system representation to StateSpace.
- to_tf() Returns a copy of the current TransferFunction system.
- to_zpk() Converts system representation to ZerosPolesGain.

TransferFunction.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 scipy.signal.bode for details.

Notes

New in version 0.11.0.

Examples

>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```python
>>> s1 = signal.lti([1], [1, 1])
>>> w, mag, phase = s1.bode()

>>> plt.figure()
>>> plt.semilogx(w, mag)  # Bode magnitude plot
>>> plt.figure()
>>> plt.semilogx(w, phase)  # Bode phase plot
>>> plt.show()
```

5.27. Signal processing (`scipy.signal`)

**`TransferFunction.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 `scipy.signal.freqresp` for details.

**`TransferFunction.impulse(X0=None, T=None, N=None)`**

Return the impulse response of a continuous-time system. See `scipy.signal.impulse` for details.
TransferFunction.output \((U, T, X0=None)\)
Return the response of a continuous-time system to input \(U\). See scipy.signal.lsim for details.

TransferFunction.step \((X0=None, T=None, N=None)\)
Return the step response of a continuous-time system. See scipy.signal.step for details.

TransferFunction.to_ss()
Convert system representation to StateSpace.

Returns
sys : instance of StateSpace
State space model of the current system

TransferFunction.to_tf()
Return a copy of the current TransferFunction system.

Returns
sys : instance of TransferFunction
The current system (copy)

TransferFunction.to_zpk()
Convert system representation to ZerosPolesGain.

Returns
sys : instance of ZerosPolesGain
Zeros, poles, gain representation of the current system

class scipy.signal.ZerosPolesGain(*system)
Linear Time Invariant system class in zeros, poles, gain form.

Represents the system as the 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.

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 system: (StateSpace, TransferFunction or ZerosPolesGain)
*3: array_like: (zeros, poles, gain)

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.

Attributes

<table>
<thead>
<tr>
<th>Attribute</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>A matrix of the StateSpace system.</td>
</tr>
<tr>
<td>B</td>
<td>B matrix of the StateSpace system.</td>
</tr>
<tr>
<td>C</td>
<td>C matrix of the StateSpace system.</td>
</tr>
<tr>
<td>D</td>
<td>D matrix of the StateSpace system.</td>
</tr>
<tr>
<td>den</td>
<td>Denominator of the TransferFunction system.</td>
</tr>
<tr>
<td>gain</td>
<td></td>
</tr>
<tr>
<td>num</td>
<td>Numerator of the TransferFunction system.</td>
</tr>
<tr>
<td>poles</td>
<td></td>
</tr>
<tr>
<td>zeros</td>
<td></td>
</tr>
</tbody>
</table>

ZerosPolesGain.A
A matrix of the StateSpace system.

ZerosPolesGain.B
B matrix of the StateSpace system.
ZerosPolesGain.C
C matrix of the StateSpace system.

ZerosPolesGain.D
D matrix of the StateSpace system.

ZerosPolesGain.den
Denominator of the TransferFunction system.

ZerosPolesGain.gain

ZerosPolesGain.num
Numerator of the TransferFunction system.

ZerosPolesGain.poles

ZerosPolesGain.zeros

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_ss() Convert system representation to StateSpace.
to_tf() Convert system representation to TransferFunction.
to_zpk() Return a copy of the current ‘ZerosPolesGain’ system.

ZerosPolesGain.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 scipy.signal.bode for details.

Notes
New in version 0.11.0.

Examples

>>> from scipy import signal
>>> import matplotlib.pyplot as plt

>>> s1 = signal.lti([1], [1, 1])
>>> w, mag, phase = s1.bode()

>>> plt.figure()
>>> plt.semilogx(w, mag) # Bode magnitude plot
>>> plt.figure()
>>> plt.semilogx(w, phase) # Bode phase plot
>>> plt.show()
ZerosPolesGain.\texttt{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 \texttt{scipy.signal.freqresp} for details.

ZerosPolesGain.\texttt{impulse}(X0=None, T=None, N=None)
Return the impulse response of a continuous-time system. See \texttt{scipy.signal.impulse} for details.

ZerosPolesGain.\texttt{output}(U, T, X0=None)
Return the response of a continuous-time system to input \texttt{U}. See \texttt{scipy.signal.lsim} for details.

ZerosPolesGain.\texttt{step}(X0=None, T=None, N=None)
Return the step response of a continuous-time system. See \texttt{scipy.signal.step} for details.

ZerosPolesGain.\texttt{to_ss}()
Convert system representation to \texttt{StateSpace}.

\textbf{Returns} \hspace{1cm} \texttt{sys} : instance of \texttt{StateSpace}
State space model of the current system

ZerosPolesGain.to_tf()
Convert system representation to TransferFunction.

Returns
sys : instance of TransferFunction
Transfer function of the current system

ZerosPolesGain.to_zpk()
Return a copy of the current 'ZerosPolesGain' system.

Returns
sys : instance of ZerosPolesGain
The current system (copy)

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:
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) interpo-
lation for the input array.

Returns
T : 1D ndarray
Time values for the output.
yout : 1D ndarray
System response.
xout : ndarray
Time evolution of the state vector.

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(system, U=None, T=None, X0=None, **kwargs)

Simulate output of a continuous-time linear system, by using the ODE solver \texttt{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:
  - \(2\): (num, den)
  - \(3\): (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 \texttt{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.

- **xout**: ndarray
  The time-evolution of the state-vector.

**Notes**

This function uses \texttt{scipy.integrate.odeint} to solve the system’s differential equations. Additional keyword arguments given to \texttt{lsim2} are passed on to \texttt{odeint}. See the documentation for \texttt{scipy.integrate.odeint} for the full list of arguments.

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:

- `2` (num, den)
- `3` (zeros, poles, gain)
- `4` (A, B, C, D)

**X0** : array_like, optional

Initial state-vector. Defaults to zero.

**T** : array_like, optional

Time points. Computed if not given.

**N** : int, optional

The number of time points to compute (if T is not given).

Returns

**T** : ndarray

A 1-D array of time points.

**yout** : ndarray

A 1-D array containing the impulse response of the system (except for singularities at zero).

**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:

- `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

**T** : ndarray

The time values for the output.

**yout** : ndarray

The output response of the system.

See also:

- **impulse.lsim2**, **integrate.odeint**

Notes

The solution is generated by calling **scipy.signal.lsim2**, which uses the differential equation solver **scipy.integrate.odeint**.

New in version 0.8.0.

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)
```

```
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:
  - 2 (num, den)
  - 3 (zeros, poles, gain)

- **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`

```
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:
```
**SciPy Reference Guide, Release 0.16.0**

- (num, den)
- (zeros, poles, gain)

**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**
- New in version 0.8.0.

**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:
  - (num, den)
  - (zeros, poles, gain)

- **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**
- New in version 0.11.0.

**Examples**
- ```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```
```python
>>> s1 = signal.lti([1], [1, 1])
>>> w, mag, phase = signal.bode(s1)

>>> plt.figure()
>>> plt.semilogx(w, mag)  # Bode magnitude plot
>>> plt.figure()
>>> plt.semilogx(w, phase)  # Bode phase plot
>>> plt.show()
```

5.27.7 Discrete-Time Linear Systems

**dlsim**

```
dlsim(system, u[, t, x0]) Simulate output of a discrete-time linear system.
```

**dimpulse**

```
dimpulse(system[, x0, t, n]) Impulse response of discrete-time system.
```
scipy.signal.dlsim(system, u, t=None, x0=None)
Simulate output of a discrete-time linear 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:
  - 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 state-space systems.

**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
array([ 0., 0., 0., 1.])
```

scipy.signal.dimpulse(system, x0=None, t=None, n=None)
Impulse 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:
  - 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.
- **t**: array_like, optional
  Time points. Defaults to zero.

**See also:**
- lsim, dstep, dimpulse, cont2discrete

5.27. Signal processing (scipy.signal)
SciPy Reference Guide, Release 0.16.0

```

n : int, optional

Returns

tout : ndarray
    Time values for the output, as a 1-D array.
yout : 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(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:
    • 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.
t : array_like, optional
    Time points. Computed if not given.
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 : 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

5.27.8 LTI Representations

tf2zpk(b, a)
Return zero, pole, gain (z, p, k) representation from a numerator, denominator representation of a linear filter.

Parameters

b : array_like
    Numerator polynomial coefficients.

878 Chapter 5. Reference
```
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** (*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(num, den)
   Transfer function to state-space representation.

   Parameters
   ----------
   num, den : array_like
      Sequences representing the numerator and denominator polynomials. 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.

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(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. Although they can operate on analog
filters, the results may be sub-optimal.

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.

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
>>> z, p, k = 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]])
```

This conditional can only be met for specific odd-order inputs with the `pairing == 'keep_odd'` method.
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 {-0.5-0.05j, -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. , 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.

```python
scipy.signal.zpk2ss(z, p, k)
Zero-pole-gain representation to state-space representation

Parameters
  - `z, p`: sequence
    Zeros and poles.
  - `k`: float

Returns
  - `A, B, C, D`: ndarray
    State space representation of the system, in controller canonical form.

scipy.signal.ss2tf(A, B, C, D, input=0)
State-space to transfer function.

Parameters
  - `A, B, C, D`: ndarray
    State-space representation of linear system.
  - `input`: int, optional
    For multiple-input systems, 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.

scipy.signal.ss2zpk(A, B, C, D, input=0)
State-space representation to zero-pole-gain representation.

Parameters
  - `A, B, C, D`: ndarray
    State-space representation of linear system.
  - `input`: int, optional

Returns
  - `z, p`: sequence
    Zeros and poles.
  - `k`: float
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_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(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_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(sys, dt, method='zoh', alpha=None)

Transform a continuous to a discrete state-space system.

Parameters
sys : a tuple describing the system.
The following gives the number of elements in the tuple and the interpretation:
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

5.27. Signal processing (scipy.signal)
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 [R168], the generalized bilinear approximation is based on
[R169] and [R170].

References

[R168], [R169], [R170]

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 [2D ndarray] The transfer matrix such as
X * diag(poles) = (A - B*K)*X
(see Notes)

rtol [float] The relative tolerance achieved on
det(X) (see Notes). rtol will be NaN if
the optimisation algorithms can not run, i.e
When \( B.shape[1] == 1 \), or 0 when the solution is unique.

\[ nb_iter \] The number of iterations performed before converging. \( nb_iter \) will be NaN if the optimisation algorithms cannot run, i.e., when \( B.shape[1] == 1 \), or 0 when the solution is unique.

Notes

The Tits and Yang (YT), [R195] paper is an update of the original Kautsky et al. (KNV) paper [R194]. KNV relies on rank-1 updates to find the transfer matrix \( X \) such that \( X * \text{diag}(\text{poles}) = (A - B*K)*X \), whereas YT uses rank-2 updates. This yields an average more robust solutions (see [R195] 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 \( \text{abs(det}(X)) \) is used as a robustness indicator.

[R195] is available as a technical report on the following URL: `http://drum.lib.umd.edu/handle/1903/5598`

References

[R194], [R195]

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 ([R194]):

```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.
>>> 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]])

>>> fsf2 = signal.place_poles(A, B, P)  # uses YT method
>>> fsf2.computed_poles
array([-8.6659, -5.0566, -0.5 , -0.2 ])

>>> 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:

>>> 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:

>>> 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:

>>> 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)
5.27.9 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.
- `sweep_poly(t, poly[, phi])` Frequency-swept cosine generator, with a time-dependent frequency.

**scipy.signal.chirp**

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 $t1$.
- `method` : {'linear', 'quadratic', 'logarithmic', 'hyperbolic'}, optional
  Kind of frequency sweep. If not given, linear is assumed. See Notes below for more details.
- `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
  Array of values of the waveform at the given times.
A numpy array containing the signal evaluated at $t$ with the requested time-varying frequency. More precisely, the function returns $\cos(\text{phase} + (\pi/180) \cdot \phi)$ where $\text{phase}$ 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:

$$f(t) = f_0 + (f_1 - f_0) \cdot t / t_1$$

quadratic, quad, q:

The graph of the frequency $f(t)$ is a parabola through $(0, f_0)$ and $(t_1, f_1)$. By default, the vertex of the parabola is at $(0, f_0)$. If `vertex_zero` is False, then the vertex is at $(t_1, f_1)$. The formula is:

if `vertex_zero` is True:

$$f(t) = f_0 + (f_1 - f_0) \cdot t^2 / t_1^2$$

else:

$$f(t) = f_1 - (f_1 - f_0) \cdot (t_1 - t)^2 / t_1^2$$

To use a more general quadratic function, or an arbitrary polynomial, use the function `scipy.signal.waveforms.sweep_poly`.

logarithmic, log, lo:

$$f(t) = f_0 \cdot (f_1/f_0)^{(t/t_1)}$$

$f_0$ and $f_1$ must be nonzero and have the same sign.

This signal is also known as a geometric or exponential chirp.

hyperbolic, hyp:

$$f(t) = f_0 \cdot f_1 \cdot t_1 / ((f_0 - f_1) \cdot t + f_1 \cdot t_1)$$

$f_0$ and $f_1$ must be nonzero.

`scipy.signal.gausspulse(t, fc=1000, bw=0.5, bwr=-6, tpr=-60, retquad=False, retenv=False)`

Return a Gaussian modulated sinusoid:

$$\exp(-a \cdot t^2) \cdot \exp(1j \cdot 2 \pi f_c \cdot t).$$

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
  - Reference level at which fractional bandwidth is calculated (dB). Default is -60.
SciPy Reference Guide, Release 0.16.0

returns quad : bool, optional
    If True, return the quadrature (imaginary) as well as the real part of the
    signal. Default is False.
returns env : bool, optional
    If True, return the envelope of the signal. Default is False.

Returns

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:

```python
>>> 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(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 | None, 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:
http://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:
http://www.newwaveinstruments.com/resources/articles/
m_sequence_linear_feedback_shift_register_lfsr.htm

New in version 0.15.0.

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 \(width*2\pi\), then drops
    from 1 to -1 on the interval \(width*2\pi\) 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. \(t = 0.5\) 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
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> t = np.linspace(0, 1, 500)
>>> plt.plot(t, signal.sawtooth(2 * np.pi * 5 * t))
```
scipy.signal.square(t, duty=0.5)

Return a periodic square-wave waveform.

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.

**Parameters**

- `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.

**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.plot(t, sig)
>>> plt.plot(t, pwm)
>>> plt.ylim(-1.5, 1.5)
```
scipy.signal.

```
sweep_poly(t, 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 \( poly \).

**Parameters**
- \( t \): ndarray
  Times at which to evaluate the waveform.
- \( poly \): 1-D array_like or instance of numpy.poly1d
  The desired frequency expressed as a polynomial. If \( poly \) is a list or ndarray of length \( n \), then the elements of \( poly \) are the coefficients of the polynomial, and the instantaneous frequency is
  \[
  f(t) = poly[0] \cdot t^{(n-1)} + poly[1] \cdot t^{(n-2)} + \ldots + poly[n-1]
  \]
  If \( poly \) is an instance of numpy.poly1d, then the instantaneous frequency is
  \[
  f(t) = poly(t)
  \]
- \( phi \): 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 \( \cos(\text{phase} + (\pi/180)\times\phi) \), where `phase` is the integral (from 0 to `t`) of \( 2 \times \pi \times f(t) \); `f(t)` is defined above.

See also:

chirp

Notes

New in version 0.8.0.

If `poly` is a list or ndarray of length `n`, then the elements of `poly` are the coefficients of the polynomial, and the instantaneous frequency is:

\[
f(t) = poly[0]*t^{(n-1)} + poly[1]*t^{(n-2)} + \ldots + poly[n-1]
\]

If `poly` is an instance of `numpy.poly1d`, then the instantaneous frequency is:

\[
f(t) = poly(t)
\]

Finally, the output `s` is:

\[
\cos(\text{phase} + (\pi/180)\times\phi)
\]

where `phase` is the integral from 0 to `t` of \( 2 \times \pi \times f(t) \); `f(t)` as defined above.

5.27.10 Window functions

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>get_window(window, Nx[, fftbins])</code></td>
<td>Return a window.</td>
</tr>
<tr>
<td><code>barthann(M[, sym])</code></td>
<td>Return a modified Bartlett-Hann window.</td>
</tr>
<tr>
<td><code>bartlett(M[, sym])</code></td>
<td>Return a Bartlett window.</td>
</tr>
<tr>
<td><code>blackman(M[, sym])</code></td>
<td>Return a Blackman window.</td>
</tr>
<tr>
<td><code>blackmanharris(M[, sym])</code></td>
<td>Return a minimum 4-term Blackman-Harris window.</td>
</tr>
<tr>
<td><code>bohman(M[, sym])</code></td>
<td>Return a Bohman window.</td>
</tr>
<tr>
<td><code>boxcar(M[, sym])</code></td>
<td>Return a boxcar or rectangular window.</td>
</tr>
<tr>
<td><code>chebwin(M, at[, sym])</code></td>
<td>Return a Dolph-Chebyshev window.</td>
</tr>
<tr>
<td><code>cosine(M[, sym])</code></td>
<td>Return a window with a simple cosine shape.</td>
</tr>
<tr>
<td><code>exponential(M[, center, tau, sym])</code></td>
<td>Return an exponential (or Poisson) window.</td>
</tr>
<tr>
<td><code>flattop(M[, sym])</code></td>
<td>Return a flat top window.</td>
</tr>
<tr>
<td><code>gaussian(M, std[, sym])</code></td>
<td>Return a Gaussian window.</td>
</tr>
<tr>
<td><code>general_gaussian(M, p, sig[, sym])</code></td>
<td>Return a window with a generalized Gaussian shape.</td>
</tr>
<tr>
<td><code>hamming(M[, sym])</code></td>
<td>Return a Hamming window.</td>
</tr>
<tr>
<td><code>hann(M[, sym])</code></td>
<td>Return a Hann window.</td>
</tr>
<tr>
<td><code>kaiser(M, beta[, sym])</code></td>
<td>Return a Kaiser window.</td>
</tr>
<tr>
<td><code>nuttall(M[, sym])</code></td>
<td>Return a minimum 4-term Blackman-Harris window according to Nuttall.</td>
</tr>
<tr>
<td><code>parzen(M[, sym])</code></td>
<td>Return a Parzen window.</td>
</tr>
<tr>
<td><code>slepian(M, width[, sym])</code></td>
<td>Return a digital Slepian (DPSS) window.</td>
</tr>
<tr>
<td><code>triang(M[, sym])</code></td>
<td>Return a triangular window.</td>
</tr>
<tr>
<td><code>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(window, Nx, fftbins=True)`

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, create a “periodic” window ready to use with ifftshift and be multiplied by the result of an fft (SEE ALSO fftfreq).

Returns

get_window : ndarray
  Returns a window of length $Nx$ and type $window$.

Notes

Window types:

- boxcar, triang, blackman, hamming, hann, bartlett, flattop, parzen, bohman, blackmanharris, nuttall, barthann, kaiser (needs beta), gaussian (needs std), general_gaussian (needs power, width), sleipan (needs width), 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([ 0.25, 0.5 , 0.75, 1. , 0.75, 0.5 , 0.25])
>>> signal.get_window(('kaiser', 4.0), 9)
array([ 0.08848053, 0.32578323, 0.63343178, 0.89640418, 1. , 0.89640418, 0.63343178, 0.32578323, 0.08848053])
>>> signal.get_window(4.0, 9)
array([ 0.08848053, 0.32578323, 0.63343178, 0.89640418, 1. , 0.89640418, 0.63343178, 0.32578323, 0.08848053])
```

scipy.signal.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
```
```python
>>> window = signal.barthann(51)
>>> plt.plot(window)
>>> plt.title("Bartlett-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(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]")
```

**scipy.signal.bartlett** (*M*, *sym=True*)

### 5.27. Signal processing (scipy.signal)
Return a Bartlett window.

The Bartlett window is very similar to a triangular window, except that the end points are at zero. 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 `sym` is True).

**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.

**References**

[R156], [R157], [R158], [R159], [R160]

**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")

>>> 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 Bartlett window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```
scipy.signal.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

\[ w(n) = 0.42 - 0.5 \cos(2\pi n/M) + 0.08 \cos(4\pi n/M) \]

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**

[R161], [R162]

**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]"
```

![Blackman window](image_url)
scipy.signal.blackmanharris(M, sym=True)

Return a minimum 4-term Blackman-Harris 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.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]")
```
Return a Bohman window.

Parameters

- `M` : int
  The 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])
>>> plt.title("Frequency response of the Bohman window")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]"
```

![Bohman window](image)
scipy.signal.boxcar(M, sym=True)

Return a boxcar or rectangular window.

Included for completeness, 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.chebwin** *(M, at, sym=True)*

Return a Dolph-Chebyshev window.

**Parameters**

- **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 \(at\), using Chebyshev polynomials. It was originally developed by Dolph to optimize the directionality of radio...
Unlike most windows, the Dolph-Chebyshev is defined in terms of its frequency response:

\[
W(k) = \frac{\cos(M \cos^{-1}(\beta \cos(\frac{\pi k}{M})))}{\cosh[M \cosh^{-1}(\beta)]}
\]

where

\[
\beta = \cosh \left[ \frac{1}{M} \cosh^{-1}(10^{\frac{20}{A}}) \right]
\]

and 0 <= abs(k) <= M-1. A is the attenuation in decibels (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

[R163], [R164], [R165]

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.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

- **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

New in version 0.13.0.
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.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()
```

![Cosine window](image-url)
scipy.signal.exponential(M, center=None, tau=1.0, sym=True)

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.fft 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))
>>> response = 20 * np.log10(np.abs(fftshift(A / abs(A).max())))
>>> plt.plot(freq, response)
>>> plt.axis([-0.5, 0.5, -35, 0])
>>> plt.title("Frequency response of the Exponential window (tau=3.0)"")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]"")

This function can also generate non-symmetric windows:

>>> 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.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).

**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
```
scipy.signal.gaussian($M$, $std$, $sym=\text{True}$)

Return a Gaussian window.

**Parameters**

- $M$: 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

$$w(n) = e^{-\frac{1}{2} \left( \frac{n}{\sigma} \right)^2}$$

**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")
```

![Frequency response of the flat top window](image)
```python
>>> 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 Gaussian window ($\sigma$=7)")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```

scipy.signal.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.

- **p**: float
  - Gaussian power parameter.
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

$$w(n) = e^{-\frac{1}{2}\left|\frac{n}{\sigma}\right|^{2p}}$$

the half-power point is at

$$\left(2 \log(2)\right)^{1/(2p)}\sigma$$

**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")

>>> 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"Freq. resp. of the gen. Gaussian window (p=1.5, \sigma=7)"
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]"
```

5.27. Signal processing (`scipy.signal`) 913
scipy.signal.hamming(M, sym=True)

Return a Hamming window.

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

[R178], [R179], [R180], [R181]

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.hann**(*M*, *sym=True*)

Return a Hann window.

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 van 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

[R182], [R183], [R184], [R185]

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.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).
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 many other windows by varying the beta parameter.

<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 get 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

[R188], [R189], [R190]

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])
```
```python
>>> plt.title(r"Frequency response of the Kaiser window ($\beta=14$)"
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]"

scipy.signal.nuttall(M, sym=True)
Return a minimum 4-term Blackman-Harris window according to Nuttall.

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
g = signal.nuttall(51)
plt.plot(g)
plt.title('Nuttall window')
plt.ylabel('Amplitude')
plt.xlabel('Sample')
```

```python
A = fft(g, 2048) / (len(g)/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 Nuttall window')
plt.ylabel('Normalized magnitude [dB]')
plt.xlabel('Normalized frequency [cycles per sample]')
```
scipy.signal.parzen(M, sym=True)

Return a Parzen 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.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]")
```
scipy.signal.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).

**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
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.slepian(51, width=0.3)
>>> plt.plot(window)
>>> plt.title("Slepian (DPSS) window (BW=0.3)")
>>> 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 Slepian window (BW=0.3)")
>>> plt.ylabel("Normalized magnitude [dB]")
>>> plt.xlabel("Normalized frequency [cycles per sample]")
```
scipy.signal.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).

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 Reference Guide, Release 0.16.0

```python
scipy.signal.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.

- `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).
References

[R198], [R199]

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]")
```

![Tukey window](image.png)
5.27.11 Wavelets

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>cascade(hk[, J])</code></td>
<td>Return (x, phi, psi) at dyadic points $K/2^*J$ from filter coefficients.</td>
</tr>
<tr>
<td><code>daub(p)</code></td>
<td>The coefficients for the FIR low-pass filter producing Daubechies wavelets.</td>
</tr>
<tr>
<td><code>morlet([M[, w, s, complete]])</code></td>
<td>Complex Morlet wavelet.</td>
</tr>
<tr>
<td><code>qmf(hk)</code></td>
<td>Return high-pass qmf filter from low-pass</td>
</tr>
<tr>
<td><code>ricker(points, a)</code></td>
<td>Return a Ricker wavelet, also known as the “Mexican hat wavelet”.</td>
</tr>
<tr>
<td><code>cwt(data, wavelet, widths)</code></td>
<td>Continuous wavelet transform.</td>
</tr>
</tbody>
</table>

```python
scipy.signal.cascade(hk, J=7)
```

Return (x, phi, psi) at dyadic points $K/2^*J$ from filter coefficients.

**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 \( x \):
  \[ \phi(x) = \sum(hk \ast \phi(2x-k)), \text{where } k \text{ is from } 0 \text{ to } N. \]
- `psi` : ndarray, optional
  The wavelet function \( \psi(x) \) at \( x \):
  \[ \psi(x) = \sum(gk \ast \psi(2x-k)), \text{where } k \text{ is from } 0 \text{ to } N. \psi \text{ is only returned if } gk \text{ is not None.} \]

**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(p)
The coefficients for the FIR low-pass filter producing Daubechies wavelets.

\( p \geq 1 \) gives the order of the zero at \( f=1/2 \). There are \( 2p \) filter coefficients.

**Parameters**  
- **p**: int

**Returns**  
- **daub**: ndarray

scipy.signal.morlet(M, w=5.0, s=1.0, complete=True)
Complex Morlet wavelet.

**Parameters**  
- **M**: int
- **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

**Returns**  
- **morlet**: (M,) ndarray

See also: scipy.signal.gausspulse

**Notes**
The standard version:

\[
\pi^{-0.25} \ast \exp(\text{i} \ast w \ast x) \ast \exp(-0.5 \ast (x \ast 2))
\]

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:

\[
\pi^{-0.25} \ast (\exp(\text{i} \ast w \ast x) - \exp(-0.5 \ast (w \ast 2))) \ast \exp(-0.5 \ast (x \ast 2))
\]

The complete version of the Morlet wavelet, with 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 \( f = 2 \ast s \ast w \ast r / M \) where \( r \) is the sampling rate.

scipy.signal.qmf(hk)
Return high-pass qmf filter from low-pass

**Parameters**  
- **hk**: array_like

scipy.signal.ricker(points, a)
Return a Ricker wavelet, also known as the “Mexican hat wavelet”.

It models the function:

\[
A \ast (1 - x^2/a^2) \ast \exp(-x^2/2 \ast a^2),
\]

where \( A = 2/\sqrt{3a} \pi^{1/4} \).

**Parameters**  
- **points**: int

Number of points in vector. Will be centered around 0.
a : scalar

Returns

vector : (N,) ndarray

Array of length points in shape of ricker curve.

Examples

```python
>>> 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()
```

---

scipy.signal.cwt(data, wavelet, widths)

Continuous wavelet transform.

Performs a continuous wavelet transform on data, using the wavelet function. A CWT performs a convolution with data using the 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(width,length)) == 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

Returns

cwt : (M, N) ndarray

Will have shape of (len(widths), len(data)).
Notes

```python
>>> length = min(10 * width[ii], len(data))
>>> cwt[ii,:] = scipy.signal.convolve(data, wavelet(length, ...

Examples

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

```python
>>> t = np.linspace(-1, 1, 200, endpoint=False)
>>> sig = np.cos(2 * np.pi * 7 * t) + signal.gausspulse(t - 0.4, fc=2)
```
```python
>>> widths = np.arange(1, 31)
>>> cwtmatr = signal.cwt(sig, signal.ricker, widths)
>>> plt.imshow(cwtmatr, extent=[-1, 1, 1, 31], cmap='PRGn', aspect='auto', ...
```python
```python
>>> plt.show()
```

5.27.12 Peak finding

```python
find_peaks_cwt(vector, widths[, wavelet, ...]) Attempt to find the peaks in a 1-D array.
argrelmin(data[, axis, order, mode]) Calculate the relative minima of data.
argrelmax(data[, axis, order, mode]) Calculate the relative maxima of data.
argrelextrema(data, comparator[, axis, ...]) Calculate the relative extrema of data.
```

```python
scipy.signal.find_peaks_cwt(vector, widths, wavelet=None, max_distances=None, gap_thresh=None, min_length=None, min_snr=1, noise_perc=10)
```

Attempt to find the peaks in a 1-D array.

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 a single variable and return a 1-D array to convolve with vector. Should be normalized to unit area. 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 2.

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 : list
Indices of the locations in the vector where peaks were found. The list is sorted.

See also:
cwt

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
[R174]

Examples
>>> 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))
```python
>>> peakind, xs[peakind], data[peakind]
([32], array([ 1.6]), array([ 0.9995736]))
```

`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`

**Notes**
This function uses `argrelextrema` with `np.less` as comparator.

New in version 0.11.0.

**Examples**
```python
>>> 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, 2]), array([2, 1]))
```

`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`.

**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.
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`

Notes

This function uses `argrelextrema` with np.greater as comparator.

New in version 0.11.0.

Examples

```python
>>> 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(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 2 numbers 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’.

**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
>>> x = np.array([2, 1, 2, 3, 2, 0, 1, 0])
>>> argrelextrema(x, np.greater)
(array([3, 6]),)
>>> y = np.array([[1, 2, 1, 2],
    ... [2, 2, 0, 0],
    ... [5, 3, 4, 4]])
>>> argrelextrema(y, np.less, axis=1)
(array([0, 2]), array([2, 1]))
```

### 5.27.13 Spectral Analysis

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
<th>Parameters</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>periodogram(x[, fs, window, nfft, detrend, return_onesided, scaling, axis])</code></td>
<td>Estimate power spectral density using a periodogram.</td>
<td>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. see get_window for a list of windows and required parameters. If window is an array it will be used directly as the window. Defaults to None; equivalent 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 x prior to computing the spectrum. If detrend is a string, it is passed as the type argument to detrend. If it is a function, it should return a detrended array. 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<strong>2/Hz and computing the power spectrum ('spectrum') where $Pxx$ has units of V</strong>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).</td>
</tr>
<tr>
<td><code>welch(x[, fs, window, nperseg, noverlap])</code></td>
<td>Estimate power spectral density using Welch’s method.</td>
<td>x: array_like, Time series of measurement values. fs: float, optional, Sampling frequency of the x time series. window: str or tuple or array_like, optional, Desired window to use. see get_window for a list of windows and required parameters. If window is an array it will be used directly as the window. nperseg: int, optional, Number of points per segment. noverlap: int, optional, Number of points to overlap between segments.</td>
</tr>
<tr>
<td><code>csd(x, y[, fs, window, nperseg, noverlap])</code></td>
<td>Estimate the cross power spectral density, $P_{xy}$, using Welch’s method.</td>
<td>x, y: array_like, Time series of measurement values. fs: float, optional, Sampling frequency of the x time series. window: str or tuple or array_like, optional, Desired window to use. see get_window for a list of windows and required parameters. If window is an array it will be used directly as the window. nperseg: int, optional, Number of points per segment. noverlap: int, optional, Number of points to overlap between segments.</td>
</tr>
<tr>
<td><code>coherence(x, y[, fs, window, nperseg, noverlap])</code></td>
<td>Estimate the magnitude squared coherence estimate, $C_{xy}$, of discrete-time signals X and Y using Welch’s method.</td>
<td>x, y: array_like, Time series of measurement values. fs: float, optional, Sampling frequency of the x time series. window: str or tuple or array_like, optional, Desired window to use. see get_window for a list of windows and required parameters. If window is an array it will be used directly as the window. nperseg: int, optional, Number of points per segment. noverlap: int, optional, Number of points to overlap between segments.</td>
</tr>
<tr>
<td><code>spectrogram(x[, fs, window, nperseg])</code></td>
<td>Compute a spectrogram with consecutive Fourier transforms.</td>
<td>x: array_like, Time series of measurement values. fs: float, optional, Sampling frequency of the x time series. window: str or tuple or array_like, optional, Desired window to use. see get_window for a list of windows and required parameters. If window is an array it will be used directly as the window. nperseg: int, optional, Number of points per segment.</td>
</tr>
<tr>
<td><code>lombscargle(x, y, freqs)</code></td>
<td>Computes the Lomb-Scargle periodogram.</td>
<td>x, y: array_like, Time series of measurement values. freqs: array_like, Frequency array.</td>
</tr>
<tr>
<td><code>vectorstrength(events, period)</code></td>
<td>Determine the vector strength of the events corresponding to the given period.</td>
<td>events: array_like, Time series of measurement values. period: float, Period.</td>
</tr>
</tbody>
</table>

**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. See `get_window` for a list of windows and required parameters. If window is an array it will be used directly as the window. Defaults to None; equivalent 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 x prior to computing the spectrum. If detrend is a string, it is passed as the type argument to detrend. If it is a function, it should return a detrended array. 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

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
code
>>> np.mean(Pxx_den[256:])
0.0009924865443739191
```

Now compute and plot the power spectrum.

```python
code
>>> f, Pxx_spec = signal.periodogram(x, fs, 'flattop', scaling='spectrum')
>>> plt.figure()
>>> plt.semilogy(f, np.sqrt(Pxx_spec))
>>> plt.ylim([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
code
>>> np.sqrt(Pxx_spec.max())
2.0077340678640727
```

scipy.signal.welch(x, fs=1.0, window='hanning', nperseg=256, noverlap=None, nfft=None, detrend='constant', return_onesided=True, scaling='density', axis=-1)

Estimate power spectral density using Welch’s method.

Welch’s method [R200] 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. 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 will be used for nperseg. Defaults to ‘hanning’.
- **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.

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 detrend. 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 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:

periodogram
    Simple, optionally modified periodogram

lombscargle
    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 ‘hanning’ 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 [R201].

New in version 0.12.0.

References

[R200], [R201]

Examples

>>> from scipy import signal
>>> import matplotlib.pyplot as plt

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.
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.

```python
>>> np.sqrt(Pxx_spec.max())
2.0077340678640727
```

`scipy.signal.csd(x, y, fs=1.0, window='hanning', nperseg=256, noverlap=None, nfft=None, detrend='constant', return_onesided=True, scaling='density', axis=-1)`

Estimate the cross power spectral density, Pxy, 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. 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 will be used for nperseg. Defaults to ‘hanning’.
- **nperseg**: int, optional
  Length of each segment. Defaults to 256.
- **noverlap**: int, optional
  Number of points to overlap between segments. If None, nooverlap = 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 detrend. 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 $P_{xy}$
has units of V**2/Hz and computing the cross spectrum (‘spectrum’) where
$P_{xy}$ has units of 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).

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, $P_{xy}$ 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 ‘hanning’ 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
[R171], [R172]

Examples

>>> from scipy import signal
>>> import matplotlib.pyplot as plt

Generate two test signals with some common features.

>>> 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()
```

```python
scipy.signal.coherence(x, y, fs=1.0, window='hanning', nperseg=256, noverlap=None, nfft=None, detrend='constant', axis=-1)
```

Estimate the magnitude squared coherence estimate, Cxy, of discrete-time signals X and Y using Welch’s method.

Cxy = abs(Pxy)**2 / (Pxx*Pyy), where Pxx and Pyy are power spectral density estimates of X and Y, and Pxy 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. 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 will be used for nperseg. Defaults to ‘hanning’.
- `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.
- `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 `detrend`. 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 ‘hanning’ 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**

[R166], [R167]

**Examples**

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

Generate two test signals with some common features.

```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 coherence.

```python
>>> 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(x, fs=1.0, window=('tukey', 0.25), nperseg=256, noverlap=None, nfft=None, detrend='constant', return_onesided=True, scaling='density', axis=-1)

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. 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 will be used for nperseg. Defaults to a Tukey window with shape parameter of 0.25.

- **nperseg**: int, optional
  Length of each segment. Defaults to 256.

- **noverlap**: int, optional
  Number of points to overlap between segments. If None, noverlap = 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 detrend. 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 fs is measured in Hz. Defaults to 'density'.

\[ \text{axis} : \text{int, optional} \]
Axis along which the spectrogram is computed; the default is over the last axis (i.e. \text{axis}=-1).

**Returns**

\[ f : \text{ndarray} \]
Array of sample frequencies.

\[ t : \text{ndarray} \]
Array of segment times.

\[ S_{xx} : \text{ndarray} \]
Spectrogram of \( x \). By default, the last axis of \( S_{xx} \) 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.

New in version 0.16.0.

**References**


**Examples**

```python
>>> from scipy import signal
>>> import matplotlib.pyplot as plt

Generate a test signal, a 2 Vrms sine wave whose frequency linearly changes with time from 1kHz to 2kHz, corrupted by 0.001 V**2/Hz of white noise sampled at 10 kHz.

```python
>>> fs = 10e3
>>> N = 1e5
>>> amp = 2 + np.sqrt(2)
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> freq = np.linspace(1e3, 2e3, N)
>>> 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 spectrogram.
```python
>>> t, f, Sxx = signal.spectrogram(x, fs)
>>> plt.pcolormesh(t, f, Sxx)
>>> plt.ylabel('Frequency [Hz]')
>>> plt.xlabel('Time [sec]')
>>> plt.show()
```

scipy.signal.lombscargle(x, y, freqs)
Computes the Lomb-Scargle periodogram.

The Lomb-Scargle periodogram was developed by Lomb [R191] and further extended by Scargle [R192] to find, and test the significance of weak periodic signals with uneven temporal sampling.

The computed periodogram is unnormalized, it takes the value \((A^2) \times N/4\) for a harmonic signal with amplitude \(A\) for sufficiently large \(N\).

**Parameters**

- `x`: array_like
  Sample times.
- `y`: array_like
  Measurement values.
- `freqs`: array_like
  Angular frequencies for output periodogram.

**Returns**

- `pgram`: array_like
  Lomb-Scargle periodogram.

**Raises**

- `ValueError`
  If the input arrays `x` and `y` do not have the same shape.

**Notes**

This subroutine calculates the periodogram using a slightly modified algorithm due to Townsend [R193] 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**

[R191], [R192], [R193]
Examples

```python
>>> import scipy.signal
>>> 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 = 100000
>>> 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]
>>> normval = x.shape[0] # For normalization of the periodogram
```

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)
```

Now make a plot of the input data:
```python
>>> plt.subplot(2, 1, 1)
<matplotlib.axes.AxesSubplot object at 0x102154f50>
>>> plt.plot(x, y, 'b+')[<matplotlib.lines.Line2D object at 0x102154a10>]
```

Then plot the normalized periodogram:
```python
>>> plt.subplot(2, 1, 2)
<matplotlib.axes.AxesSubplot object at 0x104b0a990>
>>> plt.plot(f, np.sqrt(4*(pgram/normval)))[<matplotlib.lines.Line2D object at 0x104b2f910>]
>>> plt.show()
```
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 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**


5.28 Sparse matrices (scipy.sparse)

SciPy 2-D sparse matrix package for numeric data.

5.28.1 Contents

Sparse matrix classes

<table>
<thead>
<tr>
<th>class</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>scipy.sparse.bsr_matrix</td>
<td>Block Sparse Row matrix</td>
</tr>
<tr>
<td>coo_matrix</td>
<td>A sparse matrix in COOrdinate format.</td>
</tr>
<tr>
<td>csc_matrix</td>
<td>Compressed Sparse Column matrix</td>
</tr>
<tr>
<td>csr_matrix</td>
<td>Compressed Sparse Row matrix</td>
</tr>
<tr>
<td>dia_matrix</td>
<td>Sparse matrix with DIAgonal storage</td>
</tr>
<tr>
<td>dok_matrix</td>
<td>Dictionary Of Keys based sparse matrix.</td>
</tr>
<tr>
<td>lil_matrix</td>
<td>Row-based linked list sparse matrix.</td>
</tr>
</tbody>
</table>

**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:

- \texttt{bsr\_matrix(D, \{blocksize=(R,C)\})}
  where D is a dense matrix or 2-D ndarray.
- \texttt{bsr\_matrix(S, \{blocksize=(R,C)\})}
  with another sparse matrix S (equivalent to S.tobsr())
- \texttt{bsr\_matrix((M, N), \{blocksize=(R,C), dtype\})}
  to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype='d'.
- \texttt{bsr\_matrix((data, ij), \{blocksize=(R,C), shape=(M, N)\})}
  where data and ij satisfy a[ij[0, k], ij[1, k]] = data[k]
- \texttt{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, 2])
>>> col = np.array([0, 2, 2, 0, 1, 2])
>>> data = np.array([1, 2, 3, 4, 5, 6])
>>> 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, 2])
>>> 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

```python
has_sorted_indices
Determine whether the matrix has sorted indices
```

```python
bsr_matrix.has_sorted_indices
Determine whether the matrix has sorted indices

Returns

- True: if the indices of the matrix are in sorted order
- False: otherwise
```

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dtype</td>
<td>(dtype) Data type of the matrix</td>
</tr>
<tr>
<td>shape</td>
<td>(2-tuple) Shape of the matrix</td>
</tr>
<tr>
<td>ndim</td>
<td>(int) Number of dimensions (this is always 2)</td>
</tr>
<tr>
<td>nnz</td>
<td>Number of nonzero elements</td>
</tr>
<tr>
<td>data</td>
<td>Data array of the matrix</td>
</tr>
<tr>
<td>indices</td>
<td>BSR format index array</td>
</tr>
<tr>
<td>indptr</td>
<td>BSR format index pointer array</td>
</tr>
<tr>
<td>blocksize</td>
<td>Block size of the matrix</td>
</tr>
</tbody>
</table>

Methods

```python
arcsin() Element-wise arcsin.
arcsinh() Element-wise arcsinh.
arctan() Element-wise arctan.
arctanh() Element-wise arctanh.
asformat(format) Return this matrix in a given sparse format
```
Table 5.140 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>asfptype()</code></td>
<td>Upcast matrix to a floating point format (if necessary)</td>
</tr>
<tr>
<td><code>astype(t)</code></td>
<td>Element-wise ceil.</td>
</tr>
<tr>
<td><code>check_format([full_check])</code></td>
<td>check whether the matrix format is valid</td>
</tr>
<tr>
<td><code>conj()</code></td>
<td>Element-wise deg2rad.</td>
</tr>
<tr>
<td><code>diagonal()</code></td>
<td>Returns the main diagonal of the matrix</td>
</tr>
<tr>
<td><code>dot(other)</code></td>
<td>Ordinary dot product</td>
</tr>
<tr>
<td><code>eliminate_zeros()</code></td>
<td></td>
</tr>
<tr>
<td><code>expm1()</code></td>
<td>Element-wise expm1.</td>
</tr>
<tr>
<td><code>floor()</code></td>
<td>Element-wise floor.</td>
</tr>
<tr>
<td><code>getdata(ind)</code></td>
<td>Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).</td>
</tr>
<tr>
<td><code>getformat()</code></td>
<td>Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).</td>
</tr>
<tr>
<td><code>getmaxprint()</code></td>
<td>Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).</td>
</tr>
<tr>
<td><code>getnnz()</code></td>
<td>Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).</td>
</tr>
<tr>
<td><code>log1p()</code></td>
<td>Element-wise log1p.</td>
</tr>
<tr>
<td><code>matmat(other)</code></td>
<td></td>
</tr>
<tr>
<td><code>matvec(other)</code></td>
<td></td>
</tr>
<tr>
<td><code>max([axis])</code></td>
<td>Maximum of the elements of this matrix</td>
</tr>
<tr>
<td><code>maximum(other)</code></td>
<td>Maximum of the elements of this matrix</td>
</tr>
<tr>
<td><code>mean([axis])</code></td>
<td>Average the matrix over the given axis.</td>
</tr>
<tr>
<td><code>min([axis])</code></td>
<td>Minimum of the elements of this matrix.</td>
</tr>
<tr>
<td><code>minimum(other)</code></td>
<td>Minimum of the elements of this 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>
<tr>
<td><code>power(n[, dtype])</code></td>
<td>This function performs element-wise power.</td>
</tr>
<tr>
<td><code>prune()</code></td>
<td>Remove empty space after all non-zero elements.</td>
</tr>
<tr>
<td><code>rad2deg()</code></td>
<td>Element-wise rad2deg.</td>
</tr>
<tr>
<td><code>reshape(shape)</code></td>
<td></td>
</tr>
<tr>
<td><code>rint()</code></td>
<td>Element-wise rint.</td>
</tr>
<tr>
<td><code>set_shape(shape)</code></td>
<td></td>
</tr>
<tr>
<td><code>setdiag(values[, k])</code></td>
<td>Set diagonal or off-diagonal elements of the array.</td>
</tr>
<tr>
<td><code>sign()</code></td>
<td>Element-wise sign.</td>
</tr>
<tr>
<td><code>sin()</code></td>
<td>Element-wise sin.</td>
</tr>
<tr>
<td><code>sinh()</code></td>
<td>Element-wise sinh.</td>
</tr>
<tr>
<td><code>sort_indices()</code></td>
<td>Sort the indices of this matrix in place</td>
</tr>
<tr>
<td><code>sorted_indices()</code></td>
<td>Return a copy of this matrix with sorted indices</td>
</tr>
<tr>
<td><code>sqrt()</code></td>
<td>Element-wise sqrt.</td>
</tr>
<tr>
<td><code>sum([axis])</code></td>
<td>Sum the matrix over the given axis.</td>
</tr>
<tr>
<td><code>sum_duplicates()</code></td>
<td></td>
</tr>
<tr>
<td><code>tan()</code></td>
<td>Element-wise tan.</td>
</tr>
<tr>
<td><code>tanh()</code></td>
<td>Element-wise tanh.</td>
</tr>
<tr>
<td><code>toarray([order, out])</code></td>
<td>See the docstring for spmatrix.toarray.</td>
</tr>
<tr>
<td><code>tobsr([blocksize, copy])</code></td>
<td>Continued on next page</td>
</tr>
</tbody>
</table>
Table 5.140 – continued from previous page

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>toco0()</code></td>
<td>Convert this matrix to COOrdinate format.</td>
</tr>
<tr>
<td><code>tocsc()</code></td>
<td></td>
</tr>
<tr>
<td><code>tocsr()</code></td>
<td></td>
</tr>
<tr>
<td><code>todense()</code></td>
<td>Return a dense matrix representation of this matrix.</td>
</tr>
<tr>
<td><code>todia()</code></td>
<td></td>
</tr>
<tr>
<td><code>todok()</code></td>
<td></td>
</tr>
<tr>
<td><code>tolil()</code></td>
<td></td>
</tr>
<tr>
<td><code>transpose()</code></td>
<td></td>
</tr>
<tr>
<td><code>trunc()</code></td>
<td>Element-wise trunc.</td>
</tr>
</tbody>
</table>

### bsr_matrix methods

**bsr_matrix.arcsin()**

Element-wise arcsin.

See numpy.arcsin for more information.

**bsr_matrix.arcsinh()**

Element-wise arcsinh.

See numpy.arcsinh for more information.

**bsr_matrix.arctan()**

Element-wise arctan.

See numpy.arctan for more information.

**bsr_matrix.arctanh()**

Element-wise arctanh.

See numpy.arctanh for more information.

**bsr_matrix.asformat(format)**

Return this matrix in a given sparse format

- Parameters: 
  - `format`: {string, None}

  **desired sparse matrix format**

  - None for no format conversion
  - "csr" for csr_matrix format
  - "csc" for csc_matrix format
  - "lil" for lil_matrix format
  - "dok" for dok_matrix format and so on

**bsr_matrix.asfptype()**

Upcast matrix to a floating point format (if necessary)

**bsr_matrix.astype(t)**

**bsr_matrix.ceil()**

Element-wise ceil.

See numpy.ceil for more information.

**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
bsr_matrix.

bsr_matrix.

bsr_matrix.

bsr_matrix.

bsr_matrix.

bsr_matrix.

bsr_matrix.

bsr_matrix.

bsr_matrix.

bsr_matrix.

bsr_matrix.

Example

```python
csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
```

```python
A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
```
bsr_matrix.getrow(i)

   Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

bsr_matrix.log1p()

   Element-wise log1p.

   See numpy.log1p for more information.

bsr_matrix.matmat(other)

bsr_matrix.matvec(other)

bsr_matrix.max(axis=None)

   Maximum of the elements of this matrix.

   This takes all elements into account, not just the non-zero ones.

   Returns
   anax : self.dtype
      Maximum element.

bsr_matrix.maximum(other)

bsr_matrix.mean(axis=None)

   Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning
   a scalar.

bsr_matrix.min(axis=None)

   Minimum of the elements of this matrix.

   This takes all elements into account, not just the non-zero ones.

   Returns
   amin : self.dtype
      Minimum element.

bsr_matrix.minimum(other)

bsr_matrix.multiply(other)

   Point-wise multiplication by another matrix, vector, or scalar.

bsr_matrix.nonzero()

   nonzero indices

   Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

>>> 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]))

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.

bsr_matrix.prune()

   Remove empty space after all non-zero elements.
bsr_matrix.rad2deg()
Element-wise rad2deg.
See numpy.rad2deg for more information.

bsr_matrix.reshape(shape)

bsr_matrix.rint()
Element-wise rint.
See numpy.rint for more information.

bsr_matrix.set_shape(shape)

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).

bsr_matrix.sign()
Element-wise sign.
See numpy.sign for more information.

bsr_matrix.sin()
Element-wise sin.
See numpy.sin for more information.

bsr_matrix.sinh()
Element-wise sinh.
See numpy.sinh for more information.

bsr_matrix.sort_indices()
Sort the indices of this matrix in place

bsr_matrix.sorted_indices()
Return a copy of this matrix with sorted indices

bsr_matrix.sqrt()
Element-wise sqrt.
See numpy.sqrt for more information.

bsr_matrix.sum(axis=None)
Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

bsr_matrix.sum_duplicates()
bsr_matrix.tan()
Element-wise tan.
See numpy.tan for more information.

bsr_matrix.tanh()
Element-wise tanh.
See numpy.tanh for more information.

bsr_matrix.toarray(order=None, out=None)
See the docstring for spmatrix.toarray.

bsr_matrix.tobsr(blocksize=None, copy=False)

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.

bsr_matrix.tocsc()

bsr_matrix.tocsr()

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.

bsr_matrix.todia()

bsr_matrix.todok()

bsr_matrix.tolil()

bsr_matrix.transpose()

bsr_matrix.trunc()
Element-wise trunc.
See numpy.trunc for more information.

```python
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**

```python
>>> from scipy.sparse import coo_matrix
>>> coo_matrix(((3, 4), dtype=np.int8).toarray()
```
>>> 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]])

>>> # example with duplicates
>>> row = np.array([0, 0, 1, 3, 1, 0, 0])
>>> col = np.array([0, 2, 1, 3, 1, 0, 0])
>>> data = np.array([1, 1, 1, 1, 1, 1, 1])
>>> coo_matrix((data, (row, col)), shape=(4, 4)).toarray()
array([[3, 0, 1, 0],
       [0, 2, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 1]])

Attributes

**nnz**  Get the count of explicitly-stored values (nonzeros)

coo_matrix.nnz
Get the count of explicitly-stored values (nonzeros)

**Parameters**  **axis** : None, 0, or 1

Select between the number of values across the whole matrix, in each column, or in each row.

| dtype (dtype) | Data type of the matrix |
| shape (2-tuple) | Shape of the matrix |
| ndim (int) | Number of dimensions (this is always 2) |
| 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.
asformat(format)  Return this matrix in a given sparse format
asfptype()  Upcast matrix to a floating point format (if necessary)
astype(t)  Element-wise ceil.

Continued on next page
Table 5.142 – continued from previous page

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dot(other)</td>
<td>Ordinary dot product</td>
</tr>
<tr>
<td>expm1()</td>
<td>Element-wise expm1.</td>
</tr>
<tr>
<td>floor()</td>
<td>Element-wise floor.</td>
</tr>
<tr>
<td>getH()</td>
<td></td>
</tr>
<tr>
<td>get_shape()</td>
<td></td>
</tr>
<tr>
<td>getcol(j)</td>
<td>Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).</td>
</tr>
<tr>
<td>getformat()</td>
<td></td>
</tr>
<tr>
<td>getnnz(axis)</td>
<td>Get the count of explicitly-stored values (nonzeros)</td>
</tr>
<tr>
<td>getrow(i)</td>
<td>Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).</td>
</tr>
<tr>
<td>log1p()</td>
<td>Element-wise log1p.</td>
</tr>
<tr>
<td>maxaxis)</td>
<td>Maximum of the elements of this matrix.</td>
</tr>
<tr>
<td>maximum(other)</td>
<td></td>
</tr>
<tr>
<td>mean(axis)</td>
<td>Average the matrix over the given axis.</td>
</tr>
<tr>
<td>min(axis)</td>
<td>Minimum of the elements of this matrix.</td>
</tr>
<tr>
<td>minimum(other)</td>
<td></td>
</tr>
<tr>
<td>multiply(other)</td>
<td>Point-wise multiplication by another matrix</td>
</tr>
<tr>
<td>nonzero()</td>
<td>nonzero indices</td>
</tr>
<tr>
<td>power(n, dtype)</td>
<td>This function performs element-wise power.</td>
</tr>
<tr>
<td>rad2deg()</td>
<td>Element-wise rad2deg.</td>
</tr>
<tr>
<td>reshape(shape)</td>
<td></td>
</tr>
<tr>
<td>rint()</td>
<td>Element-wise rint.</td>
</tr>
<tr>
<td>set_shape(shape)</td>
<td></td>
</tr>
<tr>
<td>setdiag(values[, k])</td>
<td>Set diagonal or off-diagonal elements of the array.</td>
</tr>
<tr>
<td>sign()</td>
<td>Element-wise sign.</td>
</tr>
<tr>
<td>sin()</td>
<td>Element-wise sin.</td>
</tr>
<tr>
<td>sinh()</td>
<td>Element-wise sinh.</td>
</tr>
<tr>
<td>sqrt()</td>
<td>Element-wise sqrt.</td>
</tr>
<tr>
<td>sum(axis)</td>
<td>Sum the matrix over the given axis.</td>
</tr>
<tr>
<td>sum_duplicates()</td>
<td>Eliminate duplicate matrix entries by adding them together</td>
</tr>
<tr>
<td>tan()</td>
<td>Element-wise tan.</td>
</tr>
<tr>
<td>tanh()</td>
<td>Element-wise tanh.</td>
</tr>
<tr>
<td>toarray(order, out)</td>
<td>See the docstring for spmatrix.toarray.</td>
</tr>
<tr>
<td>tobsr(blocksize)</td>
<td></td>
</tr>
<tr>
<td>tocoo(copy)</td>
<td></td>
</tr>
<tr>
<td>tocsr()</td>
<td>Return a copy of this matrix in Compressed Sparse Column format</td>
</tr>
<tr>
<td>todense(order, out)</td>
<td>Return a copy of this matrix in Compressed Sparse Row format</td>
</tr>
<tr>
<td>todia()</td>
<td></td>
</tr>
<tr>
<td>todok()</td>
<td></td>
</tr>
<tr>
<td>toil()</td>
<td></td>
</tr>
<tr>
<td>transpose(copy)</td>
<td>Element-wise trunc.</td>
</tr>
</tbody>
</table>

coo_matrix.arcsin()
Element-wise arcsin.

See numpy.arcsin for more information.

coo_matrix.arcsinh()
Element-wise arcsinh.

See numpy.arcsinh for more information.
coo_matrix.arctan()
    Element-wise arctan.
    See numpy.arctan for more information.

coo_matrix.arctanh()
    Element-wise arctanh.
    See numpy.arctanh for more information.

coo_matrix.asformat(format)
    Return this matrix in a given sparse format

    Parameters
    format : {string, None}
        desired sparse matrix format

        • None for no format conversion
        • “csr” for csr_matrix format
        • “csc” for csc_matrix format
        • “lil” for lil_matrix format
        • “dok” for dok_matrix format and so on

coo_matrix.asfptype()
    Upcast matrix to a floating point format (if necessary)

coo_matrix.astype(t)

coo_matrix.ceil()
    Element-wise ceil.
    See numpy.ceil for more information.

coo_matrix.conj()

coo_matrix.conjugate()

coo_matrix.copy()

coo_matrix.deg2rad()
    Element-wise deg2rad.
    See numpy.deg2rad for more information.

coo_matrix.diagonal()
    Returns the main diagonal of the matrix

coo_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)
coo_matrix.exp1()  
Element-wise exp1.  
See numpy.exp1 for more information.

coo_matrix.floor()  
Element-wise floor.  
See numpy.floor for more information.

coo_matrix.getH()  

coo_matrix.get_shape()  

coo_matrix.getcol(j)  
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

coo_matrix.getH()  

coo_matrix.getmaxprint()  

coo_matrix.getnnz(axis=None)  
Get the count of explicitly-stored values (nonzeros)  

Parameters  
axis : None, 0, or 1  
Select between the number of values across the whole matrix, in each column, or in each row.

coo_matrix.getrow(i)  
Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

coo_matrix.log1p()  
Element-wise log1p.  
See numpy.log1p for more information.

coo_matrix.max(axis=None)  
Maximum of the elements of this matrix.  
This takes all elements into account, not just the non-zero ones.  

Returns  
amax : self.dtype  
Maximum element.

coo_matrix.maximum(other)  

coo_matrix.mean(axis=None)  
Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning a scalar.

coo_matrix.min(axis=None)  
Minimum of the elements of this matrix.  
This takes all elements into account, not just the non-zero ones.  

Returns  
amin : self.dtype  
Minimum element.

coo_matrix.minimum(other)
coo_matrix.multiply(other)
Point-wise multiplication by another matrix

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]))
```

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.

coo_matrix.rad2deg()
Element-wise rad2deg.

See numpy.rad2deg for more information.

coo_matrix.reshape(shape)

coo_matrix.rint()
Element-wise rint.

See numpy.rint for more information.

coo_matrix.set_shape(shape)

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).

coo_matrix.sign()
Element-wise sign.

See numpy.sign for more information.

coo_matrix.sin()
Element-wise sin.

See numpy.sin for more information.

coo_matrix.sinh()
Element-wise sinh.
See numpy.sinh for more information.

coo_matrix.sqrt()

Element-wise sqrt.

See numpy.sqrt for more information.

coo_matrix.sum(axis=None)

Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

coo_matrix.sum_duplicates()

Eliminate duplicate matrix entries by adding them together.

This is an in place operation.

coo_matrix.tan()

Element-wise tan.

See numpy.tan for more information.

coo_matrix.tanh()

Element-wise tanh.

See numpy.tanh for more information.

coo_matrix.toarray(order=None, out=None)

See the docstring for spmatrix.toarray.

coo_matrix.tobsr(blocksize=None)

coo_matrix.tocoo(copy=False)

coo_matrix.tocsc()

Return a copy of this matrix in 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, 0])
>>> col = array([0, 2, 1, 3, 1, 0, 0])
>>> data = array([1, 1, 1, 1, 1, 1, 1])
>>> A = coo_matrix((data, (row, col)), shape=(4, 4)).tocsc()
>>> A.toarray()
array([[3, 0, 1, 0],
       [0, 2, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 1]])
```

coo_matrix.tocsr()

Return a copy of this matrix in 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, 0])
>>> col = array([0, 2, 1, 3, 1, 0, 0])
>>> data = array([1, 1, 1, 1, 1, 1, 1])

>>> A = coo_matrix((data, (row, col)), shape=(4, 4)).tocsr()

>>> A.toarray()
array([[3, 0, 1, 0],
       [0, 2, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 1]])
```

**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 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.

**Methods**

- `coo_matrix.todia()`
- `coo_matrix.todok()`
- `coo_matrix.tolil()`
- `coo_matrix.transpose(copy=False)`
- `coo_matrix.trunc()`

See `numpy.trunc` for more information.

**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'`.

```python
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]`.

---

**Chapter 5. Reference**
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

- **nnz**: Get the count of explicitly-stored values (nonzeros)
- **has_sorted_indices**: Determine whether the matrix has sorted indices

```python
csc_matrix.nnz
Get the count of explicitly-stored values (nonzeros)
```

Parameters

- **axis**: (None, 0, 1), optional
Select between the number of values across the whole matrix, in each column, or in each row.

csc_matrix.has_sorted_indices
Determine whether the matrix has sorted indices

Returns
• True: if the indices of the matrix are in sorted order
• False: otherwise

<table>
<thead>
<tr>
<th>dtype</th>
<th>(dtype) Data type of the matrix</th>
</tr>
</thead>
<tbody>
<tr>
<td>shape</td>
<td>(2-tuple) Shape of the matrix</td>
</tr>
<tr>
<td>ndim</td>
<td>(int) Number of dimensions (this is always 2)</td>
</tr>
<tr>
<td>data</td>
<td>Data array of the matrix</td>
</tr>
<tr>
<td>indices</td>
<td>CSC format index array</td>
</tr>
<tr>
<td>indptr</td>
<td>CSC format index pointer array</td>
</tr>
</tbody>
</table>

**Methods**

<table>
<thead>
<tr>
<th>arccos</th>
<th>Element-wise arccos.</th>
</tr>
</thead>
<tbody>
<tr>
<td>arcsinh</td>
<td>Element-wise arcsinh.</td>
</tr>
<tr>
<td>arctan</td>
<td>Element-wise arctan.</td>
</tr>
<tr>
<td>arctanh</td>
<td>Element-wise arctanh.</td>
</tr>
<tr>
<td>asformat(format)</td>
<td>Return this matrix in a given sparse format</td>
</tr>
<tr>
<td>asfptype()</td>
<td>Upcast matrix to a floating point format (if necessary)</td>
</tr>
<tr>
<td>astype(t)</td>
<td></td>
</tr>
<tr>
<td>ceil</td>
<td>Element-wise ceil.</td>
</tr>
<tr>
<td>check_format([full_check])</td>
<td>check whether the matrix format is valid</td>
</tr>
<tr>
<td>conj</td>
<td></td>
</tr>
<tr>
<td>conjugate</td>
<td></td>
</tr>
<tr>
<td>copy</td>
<td></td>
</tr>
<tr>
<td>deg2rad</td>
<td>Element-wise deg2rad.</td>
</tr>
<tr>
<td>diagonal</td>
<td>Returns the main diagonal of the matrix</td>
</tr>
<tr>
<td>dot(other)</td>
<td>Ordinary dot product</td>
</tr>
<tr>
<td>eliminate_zeros()</td>
<td>Remove zero entries from the matrix</td>
</tr>
<tr>
<td>expm1()</td>
<td>Element-wise expm1.</td>
</tr>
<tr>
<td>floor</td>
<td>Element-wise floor.</td>
</tr>
<tr>
<td>get()</td>
<td></td>
</tr>
<tr>
<td>get_shape()</td>
<td></td>
</tr>
<tr>
<td>getcol(i)</td>
<td>Returns a copy of column i of the matrix, as a (m x 1) CSC matrix (column vector).</td>
</tr>
<tr>
<td>getformat()</td>
<td></td>
</tr>
<tr>
<td>getmaxprint()</td>
<td></td>
</tr>
<tr>
<td>getnnz([axis])</td>
<td>Get the count of explicitly-stored values (nonzeros)</td>
</tr>
<tr>
<td>getrow(i)</td>
<td>Returns a copy of row i of the matrix, as a (1 x n) CSR matrix (row vector).</td>
</tr>
<tr>
<td>log1p</td>
<td>Element-wise log1p.</td>
</tr>
<tr>
<td>max([axis])</td>
<td>Maximum of the elements of this matrix.</td>
</tr>
<tr>
<td>maximum(other)</td>
<td></td>
</tr>
<tr>
<td>mean([axis])</td>
<td>Average the matrix over the given axis.</td>
</tr>
<tr>
<td>min([axis])</td>
<td>Minimum of the elements of this matrix.</td>
</tr>
<tr>
<td>minimum(other)</td>
<td></td>
</tr>
<tr>
<td>multiply(other)</td>
<td>Point-wise multiplication by another matrix, vector, or scalar.</td>
</tr>
<tr>
<td>nonzero</td>
<td>nonzero indices</td>
</tr>
<tr>
<td>power(n[, dtype])</td>
<td>This function performs element-wise power.</td>
</tr>
<tr>
<td>prune</td>
<td>Remove empty space after all non-zero elements.</td>
</tr>
</tbody>
</table>
Table 5.144 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rad2deg()</code></td>
<td>Element-wise <code>rad2deg</code>.</td>
</tr>
<tr>
<td><code>reshape(shape)</code></td>
<td></td>
</tr>
<tr>
<td><code>rint()</code></td>
<td>Element-wise <code>rint</code>.</td>
</tr>
<tr>
<td><code>set_shape(shape)</code></td>
<td></td>
</tr>
<tr>
<td><code>setdiag(values[, k])</code></td>
<td>Set diagonal or off-diagonal elements of the array.</td>
</tr>
<tr>
<td><code>sign()</code></td>
<td>Element-wise <code>sign</code>.</td>
</tr>
<tr>
<td><code>sin()</code></td>
<td>Element-wise <code>sin</code>.</td>
</tr>
<tr>
<td><code>sinh()</code></td>
<td>Element-wise <code>sinh</code>.</td>
</tr>
<tr>
<td><code>sort_indices()</code></td>
<td>Sort the indices of this matrix in place</td>
</tr>
<tr>
<td><code>sorted_indices()</code></td>
<td>Return a copy of this matrix with sorted indices</td>
</tr>
<tr>
<td><code>sqrt()</code></td>
<td>Element-wise <code>sqrt</code>.</td>
</tr>
<tr>
<td><code>sum([axis])</code></td>
<td>Sum the matrix over the given axis.</td>
</tr>
<tr>
<td><code>sum_duplicates()</code></td>
<td>Eliminate duplicate matrix entries by adding them together</td>
</tr>
<tr>
<td><code>tan()</code></td>
<td>Element-wise <code>tan</code>.</td>
</tr>
<tr>
<td><code>tanh()</code></td>
<td>Element-wise <code>tanh</code>.</td>
</tr>
<tr>
<td><code>toarray([order, out])</code></td>
<td>See the docstring for spmatrix.toarray.</td>
</tr>
<tr>
<td><code>tobsr([blocksize])</code></td>
<td></td>
</tr>
<tr>
<td><code>tocoo([copy])</code></td>
<td>Return a COOrdinate representation of this matrix</td>
</tr>
<tr>
<td><code>tocsc([copy])</code></td>
<td></td>
</tr>
<tr>
<td><code>tocsr()</code></td>
<td></td>
</tr>
<tr>
<td><code>todense([order, out])</code></td>
<td>Return a dense matrix representation of this matrix</td>
</tr>
<tr>
<td><code>todia()</code></td>
<td></td>
</tr>
<tr>
<td><code>todok()</code></td>
<td></td>
</tr>
<tr>
<td><code>tolil()</code></td>
<td></td>
</tr>
<tr>
<td><code>transpose([copy])</code></td>
<td></td>
</tr>
<tr>
<td><code>trunc()</code></td>
<td>Element-wise <code>trunc</code>.</td>
</tr>
</tbody>
</table>

**csc_matrix.arcsin()**
Element-wise `arcsin`.
See numpy.arcsin for more information.

**csc_matrix.arcsinh()**
Element-wise `arcsinh`.
See numpy.arcsinh for more information.

**csc_matrix.arctan()**
Element-wise `arctan`.
See numpy.arctan for more information.

**csc_matrix.arctanh()**
Element-wise `arctanh`.
See numpy.arctanh for more information.

**csc_matrix.asformat(format)**
Return this matrix in a given sparse format

- **Parameters**
  - format: {string, None}

  **desired sparse matrix format**
  - `None` for no format conversion
  - "csr" for csr_matrix format
  - "csc" for csc_matrix format

5.28. Sparse matrices (scipy.sparse)
•“lil” for lil_matrix format
•“dok” for dok_matrix format and so on

csc_matrix.asfptype()
    Upcast matrix to a floating point format (if necessary)

csc_matrix.astype(t)

csc_matrix.ceil()
    Element-wise ceil.
    See numpy.ceil for more information.

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).

csc_matrix.conj()

csc_matrix.conjugate()

csc_matrix.copy()

csc_matrix.deg2rad()
    Element-wise deg2rad.
    See numpy.deg2rad for more information.

csc_matrix.diagonal()
    Returns the main diagonal of the matrix

csc_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)

csc_matrix.eliminate_zeros()
    Remove zero entries from the matrix
    This is an in place operation

csc_matrix.expm1()
    Element-wise expm1.
    See numpy.expm1 for more information.

csc_matrix.floor()
    Element-wise floor.
    See numpy.floor for more information.
csc_matrix.getH()

csc_matrix.get_shape()

csc_matrix.getcol(i)
    Returns a copy of column i of the matrix, as a (m x 1) CSC matrix (column vector).

csc_matrix.getformat()

csc_matrix.getmaxprint()

csc_matrix.getnnz(axis=None)
    Get the count of explicitly-stored values (nonzeros)

    Parameters
    axis : {None, 0, 1}, optional
        Select between the number of values across the whole matrix, in each column, or in each row.

csc_matrix.getrow(i)
    Returns a copy of row i of the matrix, as a (1 x n) CSR matrix (row vector).

csc_matrix.log1p()
    Element-wise log1p.
    See numpy.log1p for more information.

csc_matrix.max(axis=None)
    Maximum of the elements of this matrix.
    This takes all elements into account, not just the non-zero ones.

    Returns
    amax : self.dtype
        Maximum element.

    csc_matrix.maximum(other)

csc_matrix.mean(axis=None)
    Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning a scalar.

csc_matrix.min(axis=None)
    Minimum of the elements of this matrix.
    This takes all elements into account, not just the non-zero ones.

    Returns
    amin : self.dtype
        Minimum element.

    csc_matrix.minimum(other)

csc_matrix.multiply(other)
    Point-wise multiplication by another matrix, vector, or scalar.

csc_matrix.nonzero()
    nonzero indices
    Returns a tuple of arrays (row, col) containing the indices of the non-zero elements of the matrix.

5.28. Sparse matrices (scipy.sparse)
**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]))
```

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.

csc_matrix.**prune**()
   Remove empty space after all non-zero elements.

csc_matrix.**rad2deg**()
   Element-wise rad2deg.
   
   See numpy.rad2deg for more information.

csc_matrix.**reshape**(shape)

csc_matrix.**rint**()
   Element-wise rint.
   
   See numpy.rint for more information.

csc_matrix.**set_shape**(shape)

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]. De-
      fault: 0 (the main diagonal).

csc_matrix.**sign**()
   Element-wise sign.
   
   See numpy.sign for more information.

csc_matrix.**sin**()
   Element-wise sin.
   
   See numpy.sin for more information.

csc_matrix.**sinh**()
   Element-wise sinh.
   
   See numpy.sinh for more information.

csc_matrix.**sort_indices**()
   Sort the indices of this matrix in place
csc_matrix.sorted_indices()  
Return a copy of this matrix with sorted indices

csc_matrix.sqrt()  
Element-wise sqrt.  
See numpy.sqrt for more information.

csc_matrix.sum(axis=None)  
Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

csc_matrix.sum_duplicates()  
Eliminate duplicate matrix entries by adding them together  
The is an in place operation

csc_matrix.tan()  
Element-wise tan.  
See numpy.tan for more information.

csc_matrix.tanh()  
Element-wise tanh.  
See numpy.tanh for more information.

csc_matrix.toarray(order=None, out=None)  
See the docstring for spmatrix.toarray.

csc_matrix.tobsr(blocksize=None)  

csc_matrix.toco() (copy=True)  
Return a COOrdinate representation of this matrix  
When copy=False the index and data arrays are not copied.

csc_matrix.tocsc(copy=False)  

csc_matrix.tocsr()  

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 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
csc_matrix.todia()

csc_matrix.todok()

csc_matrix.tolil()

csc_matrix.transpose(copy=False)

csc_matrix.trunc()
    Element-wise trunc.
    See numpy.trunc for more information.

class scipy.sparse.csc_matrix (arg1, shape=None, dtype=None, copy=False)
    Compressed Sparse Column 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

    >>> import numpy as np
    >>> from scipy.sparse import csr_matrix
    >>> csr_matrix((3, 4), dtype=np.int8).toarray()
    array([[0, 0, 0, 0],
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

- **nnz**: Get the count of explicitly-stored values (nonzeros)
- **has_sorted_indices**: Determine whether the matrix has sorted indices

`csr_matrix.nnz`  
Get the count of explicitly-stored values (nonzeros)

**Parameters**  
axis : {None, 0, 1}, optional  
Select between the number of values across the whole matrix, in each column, or in each row.

`csr_matrix.has_sorted_indices`  
Determine whether the matrix has sorted indices

**Returns**

- True: if the indices of the matrix are in sorted order
- False: otherwise
| **dtype** | (dtype) Data type of the matrix |
| **shape** | (2-tuple) Shape of the matrix |
| **ndim** | (int) Number of dimensions (this is always 2) |
| **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 |

**Methods**

- `arcsin()`  
  Element-wise arcsin.
- `arcsinh()`  
  Element-wise arcsinh.
- `arctan()`  
  Element-wise arctan.
- `arctanh()`  
  Element-wise arctanh.
- `asformat(format)`  
  Return this matrix in a given sparse format.
- `asfptype()`  
  Upcast matrix to a floating point format (if necessary).
- `astype(t)`
- `ceil()`  
  Element-wise ceil.
- `check_format([full_check])`  
  Check whether the matrix format is valid.
- `conj()`
- `conjugate()`
- `copy()`
- `deg2rad()`  
  Element-wise deg2rad.
- `diagonal()`  
  Returns the main diagonal of the matrix.
- `dot(other)`  
  Ordinary dot product.
- `eliminate_zeros()`  
  Remove zero entries from the matrix.
- `expm1()`  
  Element-wise expm1.
- `floor()`  
  Element-wise floor.
- `getH()`
- `get_shape()`  
  Returns a copy of column i of the matrix, as a (m x 1) CSR matrix (column vector).
- `getcol(i)`
- `getformat()`
- `getmaxprint()`
- `getnnz([axis])`  
  Get the count of explicitly-stored values (nonzeros).
- `getrow(i)`  
  Returns a copy of row i of the matrix, as a (1 x n) CSR matrix (row vector).
- `log1p()`  
  Element-wise log1p.
- `max([axis])`  
  Maximum of the elements of this matrix.
- `maximum(other)`
- `mean([axis])`  
  Average the matrix over the given axis.
- `min([axis])`  
  Minimum of the elements of this matrix.
- `minimum(other)`
- `multiply(other)`  
  Point-wise multiplication by another matrix, vector, or scalar.
- `nonzero()`  
  Nonzero indices.
- `power(n[, dtype])`  
  This function performs element-wise power.
- `prune()`  
  Remove empty space after all non-zero elements.
- `rad2deg()`  
  Element-wise rad2deg.
- `reshape(shape)`
- `rint()`  
  Element-wise rint.
- `set_shape(shape)`
- `setdiag(values[, k])`  
  Set diagonal or off-diagonal elements of the array.
- `sign()`  
  Element-wise sign.
- `sin()`  
  Element-wise sin.
Table 5.146 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>sinh()</td>
<td>Element-wise sinh</td>
</tr>
<tr>
<td>sort_indices()</td>
<td>Sort the indices of this matrix in place</td>
</tr>
<tr>
<td>sorted_indices()</td>
<td>Return a copy of this matrix with sorted indices</td>
</tr>
<tr>
<td>sqrt()</td>
<td>Element-wise sqrt</td>
</tr>
<tr>
<td>sum([axis])</td>
<td>Sum the matrix over the given axis.</td>
</tr>
<tr>
<td>sum_duplicates()</td>
<td>Eliminate duplicate matrix entries by adding them together</td>
</tr>
<tr>
<td>tan()</td>
<td>Element-wise tan</td>
</tr>
<tr>
<td>tanh()</td>
<td>Element-wise tanh</td>
</tr>
<tr>
<td>toarray([order, out])</td>
<td>See the docstring for spmatrix.toarray.</td>
</tr>
<tr>
<td>tobar([blocksize, copy])</td>
<td></td>
</tr>
<tr>
<td>tocsc([copy])</td>
<td>Return a COOrdinate representation of this matrix</td>
</tr>
<tr>
<td>tocsc()</td>
<td></td>
</tr>
<tr>
<td>todense([order, out])</td>
<td>Return a dense matrix representation of this matrix</td>
</tr>
<tr>
<td>todia()</td>
<td></td>
</tr>
<tr>
<td>todok()</td>
<td></td>
</tr>
<tr>
<td>tolil()</td>
<td></td>
</tr>
<tr>
<td>transpose([copy])</td>
<td></td>
</tr>
<tr>
<td>trunc()</td>
<td>Element-wise trunc</td>
</tr>
<tr>
<td>csr_matrix.arcsin()</td>
<td>Element-wise arcsin</td>
</tr>
<tr>
<td>csr_matrix.arcsinh()</td>
<td>Element-wise arcsinh</td>
</tr>
<tr>
<td>csr_matrix.arctan()</td>
<td>Element-wise arctan</td>
</tr>
<tr>
<td>csr_matrix.arctanh()</td>
<td>Element-wise arctanh</td>
</tr>
<tr>
<td>csr_matrix.asformat(format)</td>
<td>Return this matrix in a given sparse format</td>
</tr>
<tr>
<td>csr_matrix.asfptype()</td>
<td>Upcast matrix to a floating point format (if necessary)</td>
</tr>
<tr>
<td>csr_matrix.astype(t)</td>
<td></td>
</tr>
</tbody>
</table>

Parameters

format : {string, None}  

desired sparse matrix format

• None for no format conversion
• “csr” for csr_matrix format
• “csc” for csc_matrix format
• “lil” for lil_matrix format
• “dok” for dok_matrix format and so on

5.28. Sparse matrices (scipy.sparse)
csr_matrix.ceil()
Element-wise ceil.

See numpy.ceil for more information.

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).

csr_matrix.conj()

csr_matrix.conjugate()

csr_matrix.copy()

csr_matrix.deg2rad()
Element-wise deg2rad.

See numpy.deg2rad for more information.

csr_matrix.diagonal()
Returns the main diagonal of the matrix

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)

csr_matrix.eliminate_zeros()
Remove zero entries from the matrix

This is an in place operation

csr_matrix.expm1()
Element-wise expm1.

See numpy.expm1 for more information.

csr_matrix.floor()
Element-wise floor.

See numpy.floor for more information.

csr_matrix.getH()

csr_matrix.get_shape()

csr_matrix.getcol(i)
Returns a copy of column i of the matrix, as a (m x 1) CSR matrix (column vector).
csr_matrix.getformat()

csr_matrix.getmaxprint()

csr_matrix.getnnz(axis=None)
    Get the count of explicitly-stored values (nonzeros)

    Parameters
    axis : {None, 0, 1}, optional
        Select between the number of values across the whole matrix, in each
        column, or in each row.

csr_matrix.getrow(i)
    Returns a copy of row i of the matrix, as a (1 x n) CSR matrix (row vector).

csr_matrix.log1p()
    Element-wise log1p.
    See numpy.log1p for more information.

csr_matrix.max(axis=None)
    Maximum of the elements of this matrix.
    This takes all elements into account, not just the non-zero ones.

    Returns
    amax : self.dtype
        Maximum element.

csr_matrix.maximum(other)

csr_matrix.mean(axis=None)
    Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning
    a scalar.

csr_matrix.min(axis=None)
    Minimum of the elements of this matrix.
    This takes all elements into account, not just the non-zero ones.

    Returns
    amin : self.dtype
        Minimum element.

csr_matrix.minimum(other)

csr_matrix.multiply(other)
    Point-wise multiplication by another matrix, vector, or scalar.

csr_matrix.nonzero()
    nonzero indices
    Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

>>> 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]))
csr_matrix.power\( (n, \text{dtype}=\text{None}) \)
This function performs element-wise power.

**Parameters**
- **n**: n is a scalar
- **dtype**: If dtype is not specified, the current dtype will be preserved.

csr_matrix.prune()
Remove empty space after all non-zero elements.

csr_matrix.rad2deg()
Element-wise rad2deg.

See numpy.rad2deg for more information.

csr_matrix.reshape\( (shape) \)

csr_matrix.rint()
Element-wise rint.

See numpy.rint for more information.

csr_matrix.set_shape\( (shape) \)

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).

csr_matrix.sign()
Element-wise sign.

See numpy.sign for more information.

csr_matrix.sin()
Element-wise sin.

See numpy.sin for more information.

csr_matrix.sinh()
Element-wise sinh.

See numpy.sinh for more information.

csr_matrix.sort_indices()
Sort the indices of this matrix in place

csr_matrix.sorted_indices()
Return a copy of this matrix with sorted indices

csr_matrix.sqrt()
Element-wise sqrt.

See numpy.sqrt for more information.
csr_matrix.sum(axis=None)
    Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

csr_matrix.sum_duplicates()
    Eliminate duplicate matrix entries by adding them together
    The is an in place operation

csr_matrix.tan()
    Element-wise tan.
    See numpy.tan for more information.

csr_matrix.tanh()
    Element-wise tanh.
    See numpy.tanh for more information.

csr_matrix.toarray(order=None, out=None)
    See the docstring for spmatrix.toarray.

csr_matrix.tobsr(blocksize=None, copy=True)

csr_matrix.tocoo(copy=True)
    Return a COOrdinate representation of this matrix
    When copy=False the index and data arrays are not copied.

csr_matrix.tocsc()

csr_matrix.tocsr(copy=False)

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.

csr_matrix.todia()

csr_matrix.todok()
csr_matrix.tolil()

csr_matrix.transpose(copy=False)

csr_matrix.trunc()
   Element-wise trunc.
   See numpy.trunc for more information.

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

>>> 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

    nnz  number of nonzero values

    dia_matrix.nnz
       number of nonzero values
       explicit zero values are included in this number
dtype: (dtype) Data type of the matrix
shape: (2-tuple) Shape of the matrix
ndim: (int) Number of dimensions (this is always 2)
data: DIA format data array of the matrix
offsets: DIA format offset array of the matrix

Methods

arcsin(): Element-wise arcsin.
arcsinh(): Element-wise arcsinh.
arctan(): Element-wise arctan.
arctanh(): Element-wise arctanh.
asformat(format): Return this matrix in a given sparse format
asfptype(): Upcast matrix to a floating point format (if necessary)
astype(t):
ceil(): Element-wise ceil.
conj():
conjugate():
copy():
deg2rad(): Element-wise deg2rad.
diagonal(): Returns the main diagonal of the matrix
dot(other): Ordinary dot product
expm1(): Element-wise expm1.
floor(): Element-wise floor.
getH():
get_shape():
getcol(j): Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).
getformat():
getmaxprint():
getnnz(): number of nonzero values
getrow(i): Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).
log1p(): Element-wise log1p.
maximum(other): Average the matrix over the given axis.
minimum(other):
multiply(other): Point-wise multiplication by another matrix
nonzero(): nonzero indices
power(n, dtype): This function performs element-wise power.
radd2deg(): Element-wise radd2deg.
reshape(shape):
rint(): Element-wise rint.
set_shape(shape):
setdiag(values[, k]): Set diagonal or off-diagonal elements of the array.
sign(): Element-wise sign.
sin(): Element-wise sin.
sinh(): Element-wise sinh.
sqrt(): Element-wise sqrt.
sum(axis): Sum the matrix over the given axis.
tan(): Element-wise tan.
tanh(): Element-wise tanh.
toarray([order, out]): Return a dense ndarray representation of this matrix.
Table 5.148 – continued from previous page

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>tobsr([blocksize])</code></td>
<td>Return a dense matrix representation of this matrix.</td>
</tr>
<tr>
<td><code>tocoo()</code></td>
<td></td>
</tr>
<tr>
<td><code>tocsc()</code></td>
<td></td>
</tr>
<tr>
<td><code>tocsr()</code></td>
<td></td>
</tr>
<tr>
<td><code>todense([order, out])</code></td>
<td>Return a dense matrix representation of this matrix.</td>
</tr>
<tr>
<td><code>todia([copy])</code></td>
<td></td>
</tr>
<tr>
<td><code>todok()</code></td>
<td></td>
</tr>
<tr>
<td><code>tolil()</code></td>
<td></td>
</tr>
<tr>
<td><code>transpose()</code></td>
<td></td>
</tr>
<tr>
<td><code>trunc()</code></td>
<td>Element-wise trunc.</td>
</tr>
<tr>
<td><code>dia_matrix. arcsin()</code></td>
<td>Element-wise arcsin.</td>
</tr>
<tr>
<td></td>
<td>See numpy.arcsin for more information.</td>
</tr>
<tr>
<td><code>dia_matrix. arcsinh()</code></td>
<td>Element-wise arcsinh.</td>
</tr>
<tr>
<td></td>
<td>See numpy.arcsinh for more information.</td>
</tr>
<tr>
<td><code>dia_matrix. arctan()</code></td>
<td>Element-wise arctan.</td>
</tr>
<tr>
<td></td>
<td>See numpy.arctan for more information.</td>
</tr>
<tr>
<td><code>dia_matrix. arctanh()</code></td>
<td>Element-wise arctanh.</td>
</tr>
<tr>
<td></td>
<td>See numpy.arctanh for more information.</td>
</tr>
<tr>
<td><code>dia_matrix. asformat(format)</code></td>
<td>Return this matrix in a given sparse format</td>
</tr>
<tr>
<td></td>
<td><strong>Parameters</strong> format : {string, None}</td>
</tr>
<tr>
<td></td>
<td><strong>desired sparse matrix format</strong></td>
</tr>
<tr>
<td></td>
<td>• None for no format conversion</td>
</tr>
<tr>
<td></td>
<td>• “csr” for csr_matrix format</td>
</tr>
<tr>
<td></td>
<td>• “csc” for csc_matrix format</td>
</tr>
<tr>
<td></td>
<td>• “lil” for lil_matrix format</td>
</tr>
<tr>
<td></td>
<td>• “dok” for dok_matrix format and so on</td>
</tr>
<tr>
<td><code>dia_matrix. asfptype()</code></td>
<td>Upcast matrix to a floating point format (if necessary)</td>
</tr>
<tr>
<td><code>dia_matrix. astype(t)</code></td>
<td></td>
</tr>
<tr>
<td><code>dia_matrix.ceil()</code></td>
<td>Element-wise ceil.</td>
</tr>
<tr>
<td></td>
<td>See numpy.ceil for more information.</td>
</tr>
<tr>
<td><code>dia_matrix.conj()</code></td>
<td></td>
</tr>
<tr>
<td><code>dia_matrix.conjugate()</code></td>
<td></td>
</tr>
</tbody>
</table>
dia_matrix.copy()

dia_matrix.deg2rad()
   Element-wise deg2rad.
   See numpy.deg2rad for more information.

dia_matrix.diagonal()
   Returns the main diagonal of the matrix

dia_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)

dia_matrix.expml()
   Element-wise expml.
   See numpy.expml for more information.

dia_matrix.floor()
   Element-wise floor.
   See numpy.floor for more information.

dia_matrix.getH()

dia_matrix.get_shape()

dia_matrix.getcol(j)
   Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

dia_matrix.getformat()

dia_matrix.getmaxprint()

dia_matrix.getnnz()
   number of nonnnz values
   explicit zero values are included in this number

dia_matrix.getrow(i)
   Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

dia_matrix.log1p()
   Element-wise log1p.
   See numpy.log1p for more information.

5.28. Sparse matrices (scipy.sparse)
dia_matrix.mean(axis=None)
   Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning
   a scalar.

dia_matrix.minimum(other)

dia_matrix.multiply(other)
   Point-wise multiplication by another matrix

dia_matrix.nonzero()
   nonzero indices
   Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

   Examples

   >>> 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]))

   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.

dia_matrix.rad2deg()
   Element-wise rad2deg.
   See numpy.rad2deg for more information.

dia_matrix.reshape(shape)

dia_matrix.rint()
   Element-wise rint.
   See numpy.rint for more information.

dia_matrix.set_shape(shape)

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).

   dia_matrix.sign()
   Element-wise sign.
   See numpy.sign for more information.
dia_matrix.sin()
   Element-wise sin.
   See numpy.sin for more information.

dia_matrix.sinh()
   Element-wise sinh.
   See numpy.sinh for more information.

dia_matrix.sqrt()
   Element-wise sqrt.
   See numpy.sqrt for more information.

dia_matrix.sum(axis=None)
   Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a
   scalar.

dia_matrix.tan()
   Element-wise tan.
   See numpy.tan for more information.

dia_matrix.tanh()
   Element-wise tanh.
   See numpy.tanh for more information.

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 repre-
      sented 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.


dia_matrix.tobsr(blocksize=None)

dia_matrix.tocoo()

dia_matrix.tocsc()

dia_matrix.tocsr()

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.

dia_matrix.todia(copy=False)

dia_matrix.todok()

dia_matrix.tolil()

dia_matrix.transpose()

dia_matrix.trunc()
Element-wise trunc.
See numpy.trunc for more information.

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
globally
>>> 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

<table>
<thead>
<tr>
<th>ATTRIBUTE</th>
<th>DESCRIPTION</th>
</tr>
</thead>
<tbody>
<tr>
<td>dtype</td>
<td>(dtype) Data type of the matrix</td>
</tr>
<tr>
<td>shape</td>
<td>(2-tuple) Shape of the matrix</td>
</tr>
<tr>
<td>ndim</td>
<td>(int) Number of dimensions (this is always 2)</td>
</tr>
<tr>
<td>nnz</td>
<td>Number of nonzero elements</td>
</tr>
</tbody>
</table>

### Methods

<table>
<thead>
<tr>
<th>METHOD</th>
<th>DESCRIPTION</th>
</tr>
</thead>
<tbody>
<tr>
<td>asformat</td>
<td>Return this matrix in a given sparse format</td>
</tr>
<tr>
<td>asfptype</td>
<td>Upcast matrix to a floating point format (if necessary)</td>
</tr>
<tr>
<td>astype(t)</td>
<td></td>
</tr>
<tr>
<td>clear()</td>
<td>None. Remove all items from D.</td>
</tr>
<tr>
<td>conj()</td>
<td>Return the conjugate transpose</td>
</tr>
<tr>
<td>conjtransp()</td>
<td></td>
</tr>
<tr>
<td>conjugate()</td>
<td></td>
</tr>
<tr>
<td>copy()</td>
<td></td>
</tr>
<tr>
<td>diagonal()</td>
<td>Returns the main diagonal of the matrix</td>
</tr>
<tr>
<td>dot(other)</td>
<td>Ordinary dot product</td>
</tr>
<tr>
<td>fromkeys(...)</td>
<td>v defaults to None.</td>
</tr>
<tr>
<td>get(key[, default])</td>
<td>This overrides the dict.get method, providing type checking but otherwise equivalent.</td>
</tr>
<tr>
<td>geth()</td>
<td></td>
</tr>
<tr>
<td>get_shape()</td>
<td></td>
</tr>
<tr>
<td>getcol(j)</td>
<td>Returns a copy of column j of the matrix as a (m x 1) DOK matrix.</td>
</tr>
<tr>
<td>getformat()</td>
<td></td>
</tr>
<tr>
<td>getmaxprint()</td>
<td></td>
</tr>
<tr>
<td>getnnz()</td>
<td></td>
</tr>
<tr>
<td>getrow(i)</td>
<td>Returns a copy of row i of the matrix as a (1 x n) DOK matrix.</td>
</tr>
<tr>
<td>has_key(k) -&gt; True if D has a key k, else False</td>
<td></td>
</tr>
<tr>
<td>items() -&gt; list of D’s (key, value) pairs, ...</td>
<td></td>
</tr>
<tr>
<td>iteritems() -&gt; an iterator over the (key, ...)</td>
<td></td>
</tr>
<tr>
<td>iterkeys() -&gt; an iterator over the keys of D</td>
<td></td>
</tr>
<tr>
<td>itervalues(...)</td>
<td></td>
</tr>
<tr>
<td>keys() -&gt; list of D’s keys</td>
<td></td>
</tr>
<tr>
<td>maximum(other)</td>
<td></td>
</tr>
<tr>
<td>mean([axis])</td>
<td>Average the matrix over the given axis.</td>
</tr>
<tr>
<td>minimum(other)</td>
<td></td>
</tr>
<tr>
<td>multiply(other)</td>
<td>Point-wise multiplication by another matrix</td>
</tr>
<tr>
<td>nonzero()</td>
<td>nonzero indices</td>
</tr>
<tr>
<td>pop(k,d) -&gt; v, ...</td>
<td>If key is not found, d is returned if given, otherwise KeyError is raised</td>
</tr>
<tr>
<td>popitem() -&gt; (k, v), ...</td>
<td>2-tuple; but raise KeyError if D is empty.</td>
</tr>
<tr>
<td>power(n[, dtype])</td>
<td></td>
</tr>
<tr>
<td>reshape(shape)</td>
<td></td>
</tr>
<tr>
<td>resize(shape)</td>
<td>Resize the matrix in-place to dimensions given by ‘shape’.</td>
</tr>
<tr>
<td>set_shape(shape)</td>
<td></td>
</tr>
</tbody>
</table>

5.28. Sparse matrices (`scipy.sparse`)
Table 5.149 – continued from previous page

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>setdefault</td>
<td>((k[,d]) -&gt; D.get(k,d), ...)</td>
</tr>
<tr>
<td>setdiag</td>
<td>(values[, k]) Set diagonal or off-diagonal elements of the array.</td>
</tr>
<tr>
<td>sum</td>
<td>([axis]) Sum the matrix over the given axis.</td>
</tr>
<tr>
<td>toarray</td>
<td>([order, out]) Return a dense ndarray representation of this matrix.</td>
</tr>
<tr>
<td>tocsr</td>
<td>([blocksize])</td>
</tr>
<tr>
<td>tocoo</td>
<td>() Return a copy of this matrix in COOrdinate format</td>
</tr>
<tr>
<td>tocsc</td>
<td>() Return a copy of this matrix in Compressed Sparse Column format</td>
</tr>
<tr>
<td>todense</td>
<td>([order, out]) Return a dense matrix representation of this matrix.</td>
</tr>
<tr>
<td>todia</td>
<td>()</td>
</tr>
<tr>
<td>todok</td>
<td>([copy])</td>
</tr>
<tr>
<td>tolil</td>
<td>()</td>
</tr>
<tr>
<td>transpose</td>
<td>() Return the transpose</td>
</tr>
<tr>
<td>update</td>
<td>([[E, ...)] If E present and has a .keys() method, does: for k in E: D[k] = E[k]</td>
</tr>
<tr>
<td>values</td>
<td>() -&gt; list of D’s values</td>
</tr>
<tr>
<td>viewitems</td>
<td>(...)</td>
</tr>
<tr>
<td>viewkeys</td>
<td>(...)</td>
</tr>
<tr>
<td>viewvalues</td>
<td>(...)</td>
</tr>
</tbody>
</table>

**dok_matrix.asformat** *(format)*
Return this matrix in a given sparse format

**Parameters**

- **format**: {string, None}
  - desired sparse matrix format
    - None for no format conversion
    - “csr” for csr_matrix format
    - “csc” for csc_matrix format
    - “lil” for lil_matrix format
    - “dok” for dok_matrix format and so on

**dok_matrix.asfptype**
Upcast matrix to a floating point format (if necessary)

**dok_matrix.astype** *(t)*

**dok_matrix.clear** () -> None. Remove all items from D.

**dok_matrix.conj**

**dok_matrix.conjtransp**
Return the conjugate transpose

**dok_matrix.conjugate**

**dok_matrix.copy**

**dok_matrix.diagonal**
Return the main diagonal of the matrix

**dok_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)
aarray([ 1, -3, -1], dtype=int64)
```

```
static dok_matrix.fromkeys(S[, v]) → New dict with keys from S and values equal to v.
  v defaults to None.

dok_matrix.get(key, default=0.0)
  This overrides the dict.get method, providing type checking but otherwise equivalent functionality.


dok_matrix.getH()

dok_matrix.get_shape()


dok_matrix.getcol(j)
  Returns a copy of column j of the matrix as a (m x 1) DOK matrix.


dok_matrix.getformat()

dok_matrix.getmaxprint()


dok_matrix.getnnz()


dok_matrix.getrow(i)
  Returns a copy of row i of the matrix as a (1 x n) DOK matrix.


dok_matrix.has_key(k) → True if D has a key k, else False


dok_matrix.items() → list of D’s (key, value) pairs, as 2-tuples


dok_matrix.iteritems() → an iterator over the (key, value) items of D


dok_matrix.iterkeys() → an iterator over the keys of D


dok_matrix.itervalues() → an iterator over the values of D


dok_matrix.keys() → list of D’s keys


dok_matrix.maximum(other)


dok_matrix.mean(axis=0)
  Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning
  a scalar.


dok_matrix.minimum(other)
```
dok_matrix.multiply(other)
Point-wise multiplication by another matrix

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, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

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

dok_matrix.popitem() → (k, v), remove and return some (key, value) pair as a 2-tuple; but raise KeyError if D is empty.

dok_matrix.power(n, dtype=None)

dok_matrix.reshape(shape)

dok_matrix.resize(shape)
Resize the matrix in-place to dimensions given by ‘shape’.
Any non-zero elements that lie outside the new shape are removed.

dok_matrix.set_shape(shape)

dok_matrix.setdefault(k[, d]) → D.get(k,d), also set D[k]=d if k not in D

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).

dok_matrix.sum(axis=None)
Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

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.

dok_matrix.tobsr(blocksize=None)

dok_matrix.tocoo()
   Return a copy of this matrix in COOrdinate format

dok_matrix.tocsc()
   Return a copy of this matrix in Compressed Sparse Column format

dok_matrix.tocsr()
   Return a copy of this matrix in Compressed Sparse Row format

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.

dok_matrix.todia()

dok_matrix.todok(copy=False)

dok_matrix.tolil()

dok_matrix.transpose()
   Return the transpose

5.28. Sparse matrices (`scipy.sparse`)
dok_matrix.update([E], **F) → None. Update D from dict/iterable E and F.
If E present and has a .keys() method, does: for k in E: D[k] = E[k]
If E present and lacks .keys() method, does: for (k, v) in E: D[k] = v
In either case, this is followed by: for k in F: D[k] = F[k]

dok_matrix.values() → list of D’s values

dok_matrix.viewitems() → a set-like object providing a view on D’s items

dok_matrix.viewkeys() → a set-like object providing a view on D’s keys

dok_matrix.viewvalues() → an object providing a view on D’s values

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:

lil_matrix(D) with a dense matrix or rank-2 ndarray D
lil_matrix(S) with another sparse matrix S (equivalent to S.tolil())
lil_matrix((M, N), [dtype]) to construct an empty matrix with shape (M, N) dtypes 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
lil_matrix.nnz
Get the count of explicitly-stored values (nonzeros)

**Parameters**

- **axis**: None, 0, or 1
  Select between the number of values across the whole matrix, in each column, or in each row.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dtype</td>
<td>(dtype) Data type of the matrix</td>
</tr>
<tr>
<td>shape</td>
<td>(2-tuple) Shape of the matrix</td>
</tr>
<tr>
<td>ndim</td>
<td>(int) Number of dimensions (this is always 2)</td>
</tr>
<tr>
<td>data</td>
<td>LIL format data array of the matrix</td>
</tr>
<tr>
<td>rows</td>
<td>LIL format row index array of the matrix</td>
</tr>
</tbody>
</table>

**Methods**

- **asformat(format)** Return this matrix in a given sparse format
- **asfptype()** Upcast matrix to a floating point format (if necessary)
- **astype(t)**
- **conj()**
- **conjugate()**
- **copy()**
- **diagonal()** Returns the main diagonal of the matrix
- **dot(other)** Ordinary dot product
- **getH()**
- **get_shape()**
- **getcol(j)** Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).
- **getformat()**
- **getmaxprint()**
- **getnnz([axis])** Get the count of explicitly-stored values (nonzeros)
- **getrow(i)** Returns a copy of the ‘i’th row.
- **getrowview(i)** Returns a view of the ‘i’th row (without copying).
- **maximum(other)**
- **mean([axis])** Average the matrix over the given axis.
- **minimum(other)**
- **multiply(other)** Point-wise multiplication by another matrix
- **nonzero()** nonzero indices
- **power(n[, dtype])**
- **reshape(shape)**
- **set_shape(shape)**
- **setdiag(values[, k])** Set diagonal or off-diagonal elements of the array.
- **sum([axis])** Sum the matrix over the given axis.
- **toarray([order, out])** See the docstring for spmatrix.toarray.
- **tobsr([blocksize])**
- **tocoo()**
- **tocsc()** Return Compressed Sparse Column format arrays for this matrix.
- **tocsr()** Return Compressed Sparse Row format arrays for this matrix.
- **todense([order, out])** Return a dense matrix representation of this matrix.
- **todia()**
- **todok()**
Table 5.151 – continued from previous page

```python
tolil([copy])
transpose()
```

```
lil_matrix.asformat(format)
    Return this matrix in a given sparse format

    Parameters
        format : {string, None}
            desired sparse matrix format
            • None for no format conversion
            • “csr” for csr_matrix format
            • “csc” for csc_matrix format
            • “lil” for lil_matrix format
            • “dok” for dok_matrix format and so on

lil_matrix.asfptype()
    Upcast matrix to a floating point format (if necessary)

lil_matrix.astype(t)

lil_matrix.conj()

lil_matrix.conjugate()

lil_matrix.copy()

lil_matrix.diagonal()
    Returns the main diagonal of the matrix

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)
```

lil_matrix.getH()

lil_matrix.get_shape()

lil_matrix.getcol(j)
    Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

lil_matrix.getformat()

lil_matrix.getmaxprint()
lil_matrix.getnnz(axis=None)
   Get the count of explicitly-stored values (nonzeros)

   Parameters  axis : None, 0, or 1
               Select between the number of values across the whole matrix, in each
               column, or in each row.

lil_matrix.getrow(i)
   Returns a copy of the ‘i’th row.

lil_matrix.getrowview(i)
   Returns a view of the ‘i’th row (without copying).

lil_matrix.maximum(other)

lil_matrix.mean(axis=None)
   Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning
   a scalar.

lil_matrix.minimum(other)

lil_matrix.multiply(other)
   Point-wise multiplication by another matrix

lil_matrix.nonzero()
   nonzero indices
   Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

>>> 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]))

lil_matrix.power(n, dtype=None)

lil_matrix.reshape(shape)

lil_matrix.set_shape(shape)

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).
lil_matrix.sum(axis=None)
    Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

lil_matrix.toarray(order=None, out=None)
    See the docstring for spmatrix.toarray.

lil_matrix.tobsr(blocksize=None)

lil_matrix.tocoo()

lil_matrix.tocsc()
    Return Compressed Sparse Column format arrays for this matrix.

lil_matrix.tocsr()
    Return Compressed Sparse Row format arrays for this matrix.

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.

lil_matrix.todia()

lil_matrix.todok()

lil_matrix.tolil(copy=False)

lil_matrix.transpose()

Functions

Building sparse matrices:

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>eye(m[, n, k, dtype, format])</td>
<td>Sparse matrix with ones on diagonal</td>
</tr>
<tr>
<td>identity(n[, dtype, format])</td>
<td>Identity matrix in sparse format</td>
</tr>
</tbody>
</table>

Continued on next page
Table 5.152 – continued from previous page

- `kron(A, B[, format])`: kronecker product of sparse matrices A and B
- `kronsum(A, B[, format])`: kronecker sum of sparse matrices A and B
- `diags(diagonals, offsets[, shape, format, dtype])`: Construct a sparse matrix from diagonals.
- `spdiags(data, diags, m, n[, format])`: Return a sparse matrix from diagonals.
- `block_diag(mats[, format, dtype])`: Build a block diagonal sparse matrix from provided matrices.
- `tril(A[, k, format])`: Return the lower triangular portion of a matrix in sparse format
- `triu(A[, k, format])`: Return the upper triangular portion of a matrix in sparse format
- `bmat(blocks[, format, dtype])`: Build a sparse matrix from sparse sub-blocks
- `hstack(blocks[, format, dtype])`: Stack sparse matrices horizontally (column wise)
- `vstack(blocks[, format, dtype])`: Stack sparse matrices vertically (row wise)
- `rand(m, n[, density, format, dtype, ...])`: Generate a sparse matrix of the given shape and density with uniformly distributed values.

### scipy.sparse.eye

**Returns** a sparse (m x n) matrix where the k-th diagonal is all ones and everything else is zeros.

**Parameters**

- `n`: int
  - Number of rows in the matrix.
- `m`: int, optional
  - Number of columns. Default: n
- `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.]])
```

### scipy.sparse.identity

**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
>>> identity(3).toarray()
array([[ 1., 0., 0.],
       [ 0., 1., 0.],
       [ 0., 0., 1.]])
```

```python
>>> identity(3, dtype='int8', format='dia')
<3x3 sparse matrix of type '<type 'numpy.int8'>'
with 3 stored elements (1 diagonals) in DIAgonal format>
```

```python
scipy.sparse.kron(A, B, format=None)
kroncker 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

kroncker product in a sparse matrix format
```

```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]])

>>> 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]])
```

```python
scipy.sparse.kronsum(A, B, format=None)
kroncker 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

kroncker sum in a sparse matrix format
```

```python
scipy.sparse.diags(diagonals, offsets, shape=None, format=None, dtype=None)
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

Diagonals to set:

- k = 0 the main diagonal
- 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:

np.diag(diagonals[0], offsets[0])
+ ...
+ np.diag(diagonals[k], offsets[k])

Repeated diagonal offsets are disallowed.

New in version 0.11.

Examples

>>> 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):

>>> diags([1, -2, 1], [-1, 0, 1], shape=(4, 4)).toarray()
array([[1., 0., 0., 0.],
       [1., -2., 1., 0.],
       [0., 1., -2., 1.],
       [0., 0., 1., -2.]])

If only one diagonal is wanted (as in numpy.diag), the following works as well:

>>> diags([1, 2, 3], 1).toarray()
array([[0., 1., 0., 0.],
       [0., 0., 2., 0.],
       [0., 0., 0., 3.],
       [0., 0., 0., 0.]])

5.28. Sparse matrices (scipy.sparse)
scipy.sparse.spdiags(data, diags, m, n, format=None)
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
>>> 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(mats, format=None, dtype=None)
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
>>> 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, 0, 0]])
```
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
>>> 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, 8, 0, 0]])
>>> 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 '<type 'numpy.int32'>'
  with 4 stored elements in Compressed Sparse Column format>
```

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

5.28. Sparse matrices (scipy.sparse)
SciPy Reference Guide, Release 0.16.0

• 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

>>> 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([[1, 2, 0, 0, 3],
       [4, 5, 0, 6, 7],
       [0, 0, 8, 9, 0]])

>>> triu(A, format='csc')
<3x5 sparse matrix of type '<type 'numpy.int32'>'
with 8 stored elements in Compressed Sparse Column format>

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, 6],
       [0, 0, 7]])
```

```python
>>> bmat([[A, None], [None, C]]).toarray()
array([[1, 2, 0],
       [3, 4, 0],
       [0, 0, 7]])
```

cipy.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, 5],
       [3, 4, 6]])
```

cipy.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]])
```

`sparse.rand(m, n, density=0.01, format='coo', dtype=None, random_state=None)`

Generates 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.

Notes

Only float types are supported for now.

Sparse matrix tools:

```python
scipy.sparse.find(A)  # Return the indices and values of the nonzero elements of a matrix
```

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
>>> A = csr_matrix([[7.0, 8.0, 0], [0, 0, 9.0]])
>>> find(A)
(array([0, 0, 1], dtype=int32), array([0, 1, 2], dtype=int32), array([ 7., 8., 9.]))
```

Identifying sparse matrices:

- `issparse(x)`
- `isspmatrix(x)`
- `isspmatrix_csc(x)`
- `isspmatrix_csr(x)`

Continued on next page
Table 5.154 – continued from previous page

| isspmatrix_bsr(x) |
| isspmatrix_lil(x) |
| isspmatrix_dok(x) |
| isspmatrix_coo(x) |
| isspmatrix_dia(x) |

scipy.sparse.issparse(x)

scipy.sparse.isspmatrix(x)

scipy.sparse.isspmatrix_csc(x)

scipy.sparse.isspmatrix_csr(x)

scipy.sparse.isspmatrix_bsr(x)

scipy.sparse.isspmatrix_lil(x)

scipy.sparse.isspmatrix_dok(x)

scipy.sparse.isspmatrix_coo(x)

scipy.sparse.isspmatrix_dia(x)

Submodules

csgraph

linalg

Compressed Sparse Graph Routines (scipy.sparse.csgraph)  Fast graph algorithms based on sparse matrix representations.

| connected_components(csgraph[, directed, ...]) | Analyze the connected components of a sparse graph |
| laplacian(csgraph[, normed, return_diag, ...]) | Return the Laplacian matrix of a directed graph. |
| shortest_path(csgraph[, method, directed, ...]) | Perform a shortest-path graph search on a positive directed or undirected graph. |
| dijkstra(csgraph[, directed, indices, ...]) | Dijkstra algorithm using Fibonacci Heaps |
| floyd_warshall(csgraph[, directed, ...]) | Compute the shortest path lengths using the Floyd-Warshall algorithm |
| bellman_ford(csgraph[, directed, indices, ...]) | Compute the shortest path lengths using the Bellman-Ford algorithm. |
| 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 |

5.28. Sparse matrices (scipy.sparse)
### Table 5.156 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>depth_first_tree(csgraph, i_start[, directed])</td>
<td>Return a tree generated by a depth-first search.</td>
</tr>
<tr>
<td>minimum_spanning_tree(csgraph[,...])</td>
<td>Return a minimum spanning tree of an undirected graph</td>
</tr>
<tr>
<td>reverse_cuthill_mckee</td>
<td>Returns the permutation array that orders a sparse CSR or CSC matrix in Reverse-Cuthill McKee ordering.</td>
</tr>
<tr>
<td>maximum_bipartite_matching</td>
<td>Returns an array of row or column permutations that makes the diagonal of a nonsingular square sparse matrix zero free.</td>
</tr>
</tbody>
</table>

### Contents

**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**: str, 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**

[R13]

**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
  The N x N Laplacian matrix of graph.
- **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.newaxis] * np.arange(5)
>>> 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(csgraph, method='auto', directed=True, return_predecessors=False, unweighted=False, overwrite=False)`

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* $O[N(N \times k + N \times \log(N))]$, 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* $O[N(N^2 k)]$, 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.

**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.

**scipy.sparse.csgraph.dijkstra(csgraph, directed=True, indices=None, return_predecessors=False, unweighted=False)**
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]. 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.

**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). .. versionadded:: 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.

**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

5.28. Sparse matrices (**scipy.sparse**) 1009
path from point i to point j. If no path exists between point i and j, then \( \text{predecessors}[i, j] = -9999 \)

*Raises*  
**NegativeCycleError:**  
if there are negative cycles in the graph

```python
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.

```python
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.

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.
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].
- 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.

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)
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.

```python
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**

- `ctree` : 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:

```
incomplete graph     depth first tree from (0)
(0)                 (0)
/ \                  / \ \\
3 8 8 8
```

5.28. Sparse matrices (scipy.sparse)
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.

```python
scipy.sparse.csgraph.minimun_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:

```
input graph               minimum spanning tree
                    (0)                  (0)
   / \                /  \\
  3   8                3
```
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.tocoo().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()

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**


### scipy.sparse.csgraph.maximum_bipartite_matching()

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


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:
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]. 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. 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.

### Functions

- `bellman_ford(csgraph[, directed, indices, ...])` Compute the shortest path lengths using the Bellman-Ford algorithm.
- `breadth_first_order(csgraph, i_start[, ...])` Return a breadth-first ordering starting with specified node.
- `breadth_first_tree(csgraph, i_start[, directed])` Return the tree generated by a breadth-first search.
- `connected_components(csgraph[, directed, ...])` Analyze the connected components of a sparse graph.
- `construct_dist_matrix(graph, predecessors[, ...])` Construct distance matrix from a predecessor matrix.
- `cs_graph_components(*args, **kwds)` cs_graph_components is deprecated!
- `csgraph_from_dense(graph[, null_value, ...])` Construct a CSR-format sparse graph from a dense matrix.
- `csgraph_from_masked(graph)` Construct a CSR-format graph from a masked array.
- `csgraph_masked_from_dense(graph[, ...])` Construct a masked array graph representation from a dense matrix.
- `csgraph_to_dense(csgraph, null_value)` Convert a sparse graph representation to a dense representation.
- `depth_first_order(csgraph, i_start[, directed])` Return a depth-first ordering starting with specified node.
- `depth_first_tree(csgraph, i_start[, directed])` Return a tree generated by a depth-first search.
- `dijkstra(csgraph[, directed, indices, ...])` Dijkstra algorithm using Fibonacci Heaps.
- `floyd_warshall(csgraph[, directed, ...])` Compute the shortest path lengths using the Floyd-Warshall algorithm.
- `johnson(csgraph[, directed, indices, ...])` Compute the shortest path lengths using Johnson’s algorithm.
- `laplacian(csgraph[, normed, return_diag, ...])` Return the Laplacian matrix of a directed graph.
- `maximum_bipartite_matching` Returns an array of row or column permutations that makes the diagonal entries maximum.
- `minimum_spanning_tree(csgraph[, overwrite])` Return a minimum spanning tree of an undirected graph.
- `reconstruct_path(csgraph, predecessors[, ...])` Construct a tree from a graph and a predecessor list.
- `reverse_cuthill_mckee` Returns the permutation array that orders a sparse CSR or CSC matrix in Reverse-Cuthill McKee ordering.
- `shortest_path(csgraph[, method, directed, ...])` Perform a shortest-path graph search on a positive directed or undirected graph.

### Classes

- `Tester` alias of `NoseTester`

5.28. Sparse matrices (`scipy.sparse`) 1017
Exceptions

NegativeCycleError

Sparse linear algebra (scipy.sparse.linalg)

<table>
<thead>
<tr>
<th>LinearOperator</th>
<th>Common interface for performing matrix vector products</th>
</tr>
</thead>
<tbody>
<tr>
<td>aslinearoperator</td>
<td>Return A as a LinearOperator.</td>
</tr>
</tbody>
</table>

Abstract linear operators

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 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 * 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 LinearOperator with unspecified dtype>
>>> 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>
</tr>
</thead>
<tbody>
<tr>
<td><strong>call</strong>(x)</td>
<td>Transpose this linear operator.</td>
</tr>
<tr>
<td>adjoint()</td>
<td>Hermitian adjoint.</td>
</tr>
<tr>
<td>dot(x)</td>
<td>Matrix-matrix or matrix-vector multiplication.</td>
</tr>
<tr>
<td>matmat(X)</td>
<td>Matrix-matrix multiplication.</td>
</tr>
<tr>
<td>matvec(x)</td>
<td>Matrix-vector multiplication.</td>
</tr>
<tr>
<td>rmatvec(x)</td>
<td>Adjoint matrix-vector multiplication.</td>
</tr>
<tr>
<td>transpose()</td>
<td>Transpose this linear operator.</td>
</tr>
</tbody>
</table>

LinearOperator.__call__(x)

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

<table>
<thead>
<tr>
<th>A_H</th>
<th>LinearOperator</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Hermitian adjoint of self.</td>
</tr>
</tbody>
</table>

LinearOperator.dot(x)

Matrix-matrix or matrix-vector multiplication.

Parameters

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>x</td>
<td>array_like</td>
</tr>
</tbody>
</table>

Returns

<table>
<thead>
<tr>
<th>Ax</th>
<th>array</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1-d or 2-d array (depending on the shape of x) that represents the result of applying this linear operator on x.</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>X</th>
<th>(matrix, ndarray)</th>
</tr>
</thead>
</table>

5.28. Sparse matrices (scipy.sparse)
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.

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}

Returns

y : {matrix, ndarray}

An array with shape (N,) or (N,1).
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.

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}

Returns

y : {matrix, ndarray}

An array with shape (M,) or (M,1).
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.

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(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.
Examples

```python
>>> from scipy import matrix
>>> M = matrix( [[1,2,3],[4,5,6]], dtype='int32' )
>>> aslinearoperator( M )
<2x3 LinearOperator with dtype=int32>
```
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 $e^{t_k A} B$.

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

[R19], [R20]

onenormest(A[, t, itmax, compute_v, compute_w]) Compute a lower bound of the 1-norm of a sparse matrix.

Matrix norms

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 $\|Av\|_1 = est \times \|v\|_1$. 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

[R31], [R32]

Solving linear problems  
Direct methods for linear equation systems:

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>scipy.sparse.linalg.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>factorized(A)</code></td>
<td>Return a function for solving a sparse linear system, with $A$ pre-factorized.</td>
</tr>
</tbody>
</table>

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, $b$.size 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 $A^TA$.
  - ‘MMD_AT_PLUS_A’: minimum degree ordering on the structure of $A^TA$.
  - ‘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.

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
>>> 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])
>>> x1 = solve( rhs1 )  # Uses the LU factors.
array([ 1., -2., -2.])
```

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 ( A x = b )</td>
</tr>
<tr>
<td><code>bicgstab</code></td>
<td>Use BIConjugate Gradient STABilized iteration to solve ( A x = b )</td>
</tr>
<tr>
<td><code>cg</code></td>
<td>Use Conjugate Gradient iteration to solve ( A x = b )</td>
</tr>
<tr>
<td><code>cgs</code></td>
<td>Use Conjugate Gradient Squared iteration to solve ( A x = b )</td>
</tr>
<tr>
<td><code>gmres</code></td>
<td>Use Generalized Minimal RESidual iteration to solve ( A x = 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 ( A x = b )</td>
</tr>
</tbody>
</table>

**scipy.sparse.linalg.bicg**

Use BIConjugate Gradient iteration to solve \( A x = b \)

**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.
- \( tol \) : float
  Tolerance to achieve. The algorithm terminates when either the relative
  or the absolute 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 conver-
  gence, 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 call-
  back(xk), where xk is the current solution vector.
**bicgstab**

Use BIConjugate Gradient STABilized iteration to solve $A x = b$

**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).
- **x0**: {array, matrix}
  - Starting guess for the solution.
- **tol**: float
  - Tolerance to achieve. The algorithm terminates when either the relative or the absolute 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.
- **xtype**: {'f','d','F','D'}
  - This parameter is deprecated – avoid using it.
  - The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f','d','F', or 'D'. This parameter has been superseded by LinearOperator.

**cg**

Use Conjugate Gradient iteration to solve $A x = b$

**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.

\[ b : \{\text{array, matrix}\} \]

Right hand side of the linear system. Has shape (N,) or (N,1).

\[ x : \{\text{array, matrix}\} \]

The converged solution.

\[ \text{info} : \text{integer} \]

Provides convergence information:

\[
0 : \text{successful exit} >0 : \text{convergence to tolerance not achieved, number of iterations} <0 : \text{illegal input or breakdown}
\]

Other Parameters

\[ x0 : \{\text{array, matrix}\} \]

Starting guess for the solution.

\[ \text{tol} : \text{float} \]

Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below tol.

\[ \text{maxiter} : \text{integer} \]

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.

\[ \text{callback} : \text{function} \]

User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

\[ \text{xtype} : \{’f’, ’d’, ’F’, ’D’\} \]

This parameter is deprecated – avoid using it.

The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype=’F’,’D’,’f’,or ’d’. This parameter has been superseded by LinearOperator.

**scipy.sparse.linalg.cgs** (A, b, x0=None, tol=1e-05, maxiter=None, xtype=None, M=None, callback=None)

Use Conjugate Gradient Squared iteration to solve \( A \cdot x = b \)

Parameters

\[ A : \{\text{sparse matrix, dense matrix, LinearOperator}\} \]

The real-valued 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).

\[ x : \{\text{array, matrix}\} \]

The converged solution.

\[ \text{info} : \text{integer} \]

Provides convergence information:

\[
0 : \text{successful exit} >0 : \text{convergence to tolerance not achieved, number of iterations} <0 : \text{illegal input or breakdown}
\]

Other Parameters

\[ x0 : \{\text{array, matrix}\} \]

Starting guess for the solution.

\[ \text{tol} : \text{float} \]
SciPy Reference Guide, Release 0.16.0

Tolerance to achieve. The algorithm terminates when either the relative or the absolute 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.

**xtype** : {'f','d','F','D'}
This parameter is deprecated – avoid using it.

The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f','d','F',or 'D'. This parameter has been superseded by LinearOperator.

**scipy.sparse.linalg.gmres** (A, b, x0=None, tol=1e-05, restart=None, maxiter=None, xtype=None, M=None, callback=None)

Use Generalized Minimal RESidual iteration to solve \(A x = b\).

**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

**Provided 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** : float
Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below \(tol\).
- **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.
- **xtype** : {'f','d','F','D'}
This parameter is DEPRECATED — avoid using it.

The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A...
does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f', 'd', 'F', or 'D'. This parameter has been superseded by LinearOperator.

\[ M : \text{\{sparse matrix, dense matrix, LinearOperator\}} \]

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.

\[ \text{callback} : \text{function} \]

User-supplied function to call after each iteration. It is called as callback(rk), where rk is the current residual vector.

\[ \text{restrt} : \text{int, optional} \]

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:

\[ \text{# Construct a linear operator that computes } P^{-1} \times x. \]

\[ \text{import scipy.sparse.linalg as spla} \]
\[ \text{M}_x = \lambda x: \text{splaspsolve}(P, x) \]
\[ M = \text{spla.LinearOperator((n, n), M}_x) \]

scipy.sparse.linalg.lgmres \( (A, b, x0=None, tol=1e-05, maxiter=1000, M=None, callback=None, \]
\[ \text{inner_m=30, outer_k=3, outer_v=None, store_outer_Av=True}) \]

Solve a matrix equation using the LGMRES algorithm.

The LGMRES algorithm \[ \text{[R21]} \] \[ \text{[R22]} \] is designed to avoid some problems in the convergence in restarted GMRES, and often converges in fewer iterations.

\[ \text{Parameters} \]

\[ A : \text{\{sparse matrix, dense matrix, LinearOperator\}} \]

The real or complex 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).

\[ x0 : \text{\{array, matrix\}} \]

Starting guess for the solution.

\[ tol : \text{float, optional} \]

Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below tol.

\[ \text{maxiter} : \text{int, optional} \]

Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

\[ M : \text{\{sparse matrix, dense matrix, LinearOperator\}}, \text{optional} \]

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.

\[ \text{callback} : \text{function, optional} \]

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 [R21], 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 [R21] [R22] 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

[R21], [R22]

scipy.sparse.linalg.minres (A, b, x0=None, shift=0.0, tol=1e-05, maxiter=None, xtype=None, M=None, callback=None, show=False, check=False)

Use MINimum RESidual iteration to solve Ax=b

MINRES minimizes norm(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 : {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 either the relative or the absolute 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.
- **xtype** : {'f','d','F','D'}
  This parameter is deprecated – avoid using it.

  The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f','d','F',or ‘D’. This parameter has been superseded by LinearOperator.

**Notes**

THIS FUNCTION IS EXPERIMENTAL AND SUBJECT TO CHANGE!

**References**

Solution of sparse indefinite systems of linear equations,
http://www.stanford.edu/group/SOL/software/minres.html

This file is a translation of the following MATLAB implementation:
http://www.stanford.edu/group/SOL/software/minres/matlab/

**scipy.sparse.linalg.qmr** (A, b, x0=None, tol=1e-05, maxiter=None, xtype=None, M1=None, M2=None, callback=None)

Use Quasi-Minimal Residual iteration to solve A x = 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 : float
    Tolerance to achieve. The algorithm terminates when either the relative or
    the absolute 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.

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 call-
    back(xk), where xk is the current solution vector.

xtype : {'f','d','F','D'}
    This parameter is DEPRECATED – avoid using it.
    The type of the result. If None, then it will be determined from A.dtype.char
    and b. If A does not have a typecode method then it will compute
    A.matvec(x0) to get a typecode. To save the extra computation when A
    does not have a typecode attribute use xtype=0 for the same type as b or use
    xtype='f','d','F',or ‘D’. This parameter has been superseded by LinearOp-
    erator.

See also:

LinearOperator

Iterative methods for least-squares problems:

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>lsqr(A, b[, damp, atol, btol, conlim, ...])</td>
<td>Find the least-squares solution to a large, sparse, linear system of equations.</td>
</tr>
<tr>
<td>lsmr(A, b[, damp, atol, btol, conlim, ...])</td>
<td>Iterative solver for least-squares problems.</td>
</tr>
</tbody>
</table>

```
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)
```

Find the least-squares solution to a large, sparse, linear system of equations.

The function solves \(Ax = b\) or \(\min ||b - Ax||^2\) or \(\min ||Ax - b||^2 + \delta^2 ||x||^2\).

The matrix A may be square or rectangular (over-determined or under-determined), and may have any rank.

1. Unsymmetric equations -- solve \(Ax = b\)
2. Linear least squares -- solve \(Ax = b\) in the least-squares sense
3. Damped least squares -- solve \((A + \delta I)x = b\) 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 \(A^T x\).
  - \(b\) : (m,) ndarray
    - Right-hand side vector b.
  - **damp** : float

5.28. Sparse matrices (**scipy.sparse**)
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 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 atol = btol = conlim = 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 $(A'A + \text{damp}^2 \text{I})^{-1}$.

### 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 $\text{damp} == 0$.

**anorm**: float

Estimate of Frobenius norm of $\text{Abar} = [[A]; [\text{damp} \text{I}]]$.

**acond**: float

Estimate of $\text{cond}(\text{Abar})$.

**arnorm**: float

Estimate of $\|A'x - \text{damp}^2 x\|$.

**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 \( r_0 = b - A \times x_0 \).
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 \( A \times M(\text{inverse}) \times z = b \), 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

[R28], [R29], [R30]

scipy.sparse.linalg.lsmr \((A, b, \text{damp}=0.0, \text{atol}=1e-06, \text{btol}=1e-06, \text{conlim}=100000000.0, \text{maxiter}=\text{None}, \text{show}=\text{False})\)

Iterative solver for least-squares problems.

lsmr solves the system of linear equations \( A \times x = b \). If the system is inconsistent, it solves the least-squares problem \( \min ||b - A \times x||_2 \). A is a rectangular matrix of dimension \( m \times n \), 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**: \((m, )\) ndarray
  - Vector \( b \) in the linear system.
- **damp**: float
  - Damping factor for regularized least-squares. lsmr solves the regularized least-squares problem:

\[
\min ||(b) - (A \times x)||_2
\]

where \( \text{damp} \) is a scalar. If \( \text{damp} \) 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 \( \text{atol} \) and \( \text{btol} \). Let \( r = b - A \times x \) be the residual vector for the current approximate solution
If $Ax = b$ seems to be consistent, lsmr terminates when $\|r\| \leq atol \cdot \|A\| \cdot \|x\| + btol \cdot \|b\|$. Otherwise, lsmr terminates when $\|A^T r\| \leq atol \cdot \|A\| \cdot \|r\|$. If both tolerances are $1.0e-6$ (say), the final $\|r\|$ 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.

$\text{conlim}$ : float, optional

lsmr 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 $1.0e+8$. If $\text{conlim}$ is None, the default value is $1e+8$. Maximum precision can be obtained by setting $atol = btol = \text{conlim} = 0$, 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.

$\text{show}$ : bool, optional

Print iterations logs if $\text{show}=\text{True}$.

Returns

$x$ : ndarray of float

Least-square solution returned.

$\text{istop}$ : int

istop gives the reason for stopping:

- $\text{istop} = 0$ means $x=0$ is a solution.
- $\text{istop} = 1$ means $x$ is an approximate solution to $Ax = b$, according to $atol$ and $btol$.
- $\text{istop} = 2$ means $x$ approximately solves the least-squares problem according to $atol$.
- $\text{istop} = 3$ means $\text{cond}(A)$ seems to be greater than $\text{CONLIM}$.
- $\text{istop} = 4$ is the same as 1 with $atol = btol = \text{eps} \text{ (machine precision)}$.
- $\text{istop} = 5$ is the same as 2 with $atol = \text{eps}$.
- $\text{istop} = 6$ is the same as 3 with $\text{CONLIM} = 1/\text{eps}$.
- $\text{istop} = 7$ means $\text{ITN}$ reached $maxiter$ before the other stopping conditions were satisfied.

$\text{itn}$ : int

Number of iterations used.

$\text{normr}$ : float

$\|b-Ax\|$

$\text{normar}$ : float

$\|A^T (b - Ax)\|$

$\text{norma}$ : float

$\|A\|$

$\text{conda}$ : float

Condition number of $A$.

$\text{normx}$ : float

$\|x\|$
Notes
New in version 0.11.0.

References
[R26], [R27]

Matrix factorizations  Eigenvalue problems:

\[
\text{eigs}(A[, k, M, sigma, which, v0, ncv, ...]) \quad \text{Find } k \text{ eigenvalues and eigenvectors of the square matrix } A.
\]

\[
\text{eigsh}(A[, k, M, sigma, which, v0, ncv, ...]) \quad \text{Find } k \text{ eigenvalues and eigenvectors of the real symmetric square matrix or complex hermitian matrix } A.
\]

\[
\text{lobpcg}(A, X[, B, M, Y, tol, maxiter, ...]) \quad \text{Locally Optimal Block Preconditioned Conjugate Gradient Method (LOBPCG)}
\]

\[
\text{scipy.sparse.linalg.eigs}(A, k=6, M=None, sigma=None, which='LM', v0=None, ncv=None, maxiter=None, tol=0, return_eigenvectors=True, Minv=None, OPinv=None, OPpart=None)
\]

Find \(k\) eigenvalues and eigenvectors of the square matrix \(A\).

Solves \(A \times x[i] = w[i] \times x[i]\), 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
  - An array, sparse matrix, or LinearOperator representing the operation \(A \times x\), where \(A\) is a real or complex square matrix.
- \(k\): int, optional
  - The number of eigenvalues and eigenvectors desired. \(k\) must be smaller than \(N\). 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 \(M \times x\) 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 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 \(M \times x = b\). 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 \(x = Minv \times b\).
- \(sigma\): real or complex, optional
  - Find eigenvalues near \(sigma\) using shift-invert mode. This requires an operator to compute the solution of the linear system \([A - sigma \times M] \times x = b\), 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 \(x = OPinv \times b = [A - sigma \times M]^{-1} \times b\). 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),

$$w'[i] = \frac{1}{2} \times \left[ \frac{1}{(w[i]-\sigma)} + \frac{1}{(w[i]-\text{conj}(\sigma))} \right].$$

If $A$ is real and OPpart == 'i',

$$w'[i] = \frac{1}{2i} \times \left[ \frac{1}{(w[i]-\sigma)} - \frac{1}{(w[i]-\text{conj}(\sigma))} \right].$$

If $A$ is complex, $w'[i] = \frac{1}{(w[i]-\sigma)}$.

$v0$: 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($n$, 2*k + 1)

$which$: 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

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 con-
verged 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 [R14] SNEUPD, DNEUPD, CNEUPD, ZNEUPD, functions which use the Implicitly Restarted Arnoldi Method to find the eigenvalues and eigenvectors [R15].

References

[R14], [R15]

Examples

Find 6 eigenvectors of the identity matrix:

```python
>>> import scipy.sparse as sparse
>>> id = np.eye(13)
>>> vals, vecs = sparse.linalg.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(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 \( A \times x[i] = M \times w[i] \times x[i] \), the generalized eigenvalue problem for \( w[i] \) eigenvalues with corresponding eigenvectors \( x[i] \).

Parameters

- **A**: An N x N matrix, array, sparse matrix, or LinearOperator representing the operation \( A \times x \), where \( A \) is a real symmetric matrix. 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

---

5.28. Sparse matrices (scipy.sparse) 1037
Find eigenvalues near sigma using shift-invert mode. This requires an operator to compute the solution of the linear system \((A - sigma \cdot M)x = b\), 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 \(x = OPinv \cdot b = (A - sigma \cdot M)^{-1} \cdot b\). Note that when sigma is specified, the keyword ‘which’ refers to the shifted eigenvalues \(w'[i]\) where:

\[
\begin{align*}
\text{if mode} &= \text{‘normal’}, \quad w'[i] = 1 / (w[i] - sigma) \\
\text{if mode} &= \text{‘cayley’}, \quad w'[i] = (w[i] + sigma) / (w[i] - sigma) \\
\text{if mode} &= \text{‘buckling’}, \quad w'[i] = w[i] / (w[i] - sigma) 
\end{align*}
\]

(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 \(ncv > 2k\). Default: \(\min(n, 2k + 1)\)

\(which\) : 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: \(n \times 10\)

\(tol\) : float
Relative accuracy for eigenvalues (stopping criterion). The default value of 0 implies machine precision.

\(Minv\) : \(N \times N\) matrix, array, sparse matrix, or LinearOperator
See notes in \(M\), above

\(OPinv\) : \(N \times N\) matrix, array, sparse matrix, or LinearOperator
See notes in sigma, above.

\(return_eigenvectors\) : bool
Return eigenvectors (True) in addition to eigenvalues

\(mode\) : 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 \(OP \cdot x'[i] = w'[i] \cdot B \cdot x'[i]\) and transforms the resulting Ritz vectors \(x'[i]\) and Ritz values \(w'[i]\) into the desired eigenvectors and eigenvalues of the problem \(A \cdot x[i] = w[i] \cdot M \cdot x[i]\). The modes are as follows:

- ‘normal’: \(\text{OP} = (A - sigma \cdot M)^{-1} \cdot B = M, w'[i] = 1 / (w[i] - sigma)\)
SciPy Reference Guide, Release 0.16.0

'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 [R16] SSEUPD and DSEUPD functions which use the Implicitly Restarted Lanczos Method to find the eigenvalues and eigenvectors [R17].

References

[R16], [R17]

Examples

```python
>>> import scipy.sparse as sparse
>>> id = np.eye(13)
>>> vals, vecs = sparse.linalg.eigsh(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.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 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
SciPy Reference Guide, Release 0.16.0

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^n when 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 http://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

[R23], [R24], [R25]

Examples

>>> # Solve A x = lambda B x with constraints and preconditioning.
>>> n = 100
>>> vals = [nm.arange( n, dtype = nm.float64 ) + 1]
>>> # Matrix A.
>>> operatorA = spdiags(vals, 0, n, n)

>>> # Matrix B
>>> operatorB = nm.eye(n, n)

>>> # Constraints.
>>> Y = nm.eye(n, 3)

>>> # Preconditioner - inverse of A.
>>> ivals = [1./vals[0]]

>>> def precond(x):
...     invA = spdiags(ivals, 0, n, n)
...     y = invA * x
...     if sp.issparse(y):
...         y = y.toarray()

...     return as2d(y)

>>> # Alternative way of providing the same preconditioner.
>>> #precond = spdiags(ivals, 0, n, n)

>>> tt = time.clock()

>>> eigs, vecs = lobpcg(X, operatorA, operatorB, blockVectorY=Y,
                      operatorT=precond,
                      residualTolerance=1e-4, maxIterations=40,
                      largest=False, verbosityLevel=1)

>>> print 'solution time:', time.clock() - tt

>>> print eigs

Singular values problems:

svds(A[, k, ncv, tol, which, v0, maxiter, ...]) - Compute the largest k singular values/vectors for a sparse matrix.

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.

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, 2*k + 1)

tol : float, optional


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) right 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.
- "u": only return the u matrix, without computing vh (if N > M).
- "vh": only return the vh matrix, without computing u (if N <= M).

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.

Complete or incomplete LU factorizations

**scipy.sparse.linalg.splu(A[, permc_spec, diag_pivot_thresh, ...])** Compute the LU decomposition of a sparse, square matrix.

**scipy.sparse.linalg.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(A, permc_spec=None, diag_pivot_thresh=None, drop_tol=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 * A^T• 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 [R35]

**drop_tol**: float, optional
(deprecated) No effect.

relax : int, optional
Expert option for customizing the degree of relaxing supernodes. See SuperLU user’s guide for details [R35]

panel_size : int, optional
Expert option for customizing the panel size. See SuperLU user’s guide for details [R35]

options : dict, optional
Dictionary containing additional expert options to SuperLU. See SuperLU user guide [R35] (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

invA : scipy.sparse.linalg.SuperLU
Object, which has a solve method.

See also:

spilu  incomplete LU decomposition

Notes

This function uses the SuperLU library.

References

[R35]

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 decomposition. (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

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.
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
>>> (Pc.T * (lu.L * lu.U) * Pr.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 `scipy.sparse.csc_matrix`
- **U**: Upper triangular factor as a `scipy.sparse.csc_matrix`

### SuperLU

- **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.
  
  The column permutation matrix can be reconstructed via:
  ```python
  >>> Pc = np.zeros((n, n))
  >>> Pc[np.arange(n), perm_c] = 1
  ```

- **perm_r**: Permutation Pr represented as an array of indices.
  
  The row permutation matrix can be reconstructed via:
  ```python
  >>> Pr = np.zeros((n, n))
  >>> Pr[perm_r, np.arange(n)] = 1
  ```

- **L**: Lower triangular factor with unit diagonal as a `scipy.sparse.csc_matrix`
  
  New in version 0.14.0.

- **U**: Upper triangular factor as a `scipy.sparse.csc_matrix`
  
  New in version 0.14.0.

### Methods

- **solve** *(rhs[, trans])*  
  Solves linear system of equations with one or several right-hand sides.

  ```python
  SuperLU.solve (rhs[, trans])
  ```

  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 * x == rhs (default)
    'T': A^T * x == rhs
    'H': A^H * x == rhs

Returns
    x : ndarray, shape=rhs.shape
    Solution vector(s)

.. _arpack:

ArpackNoConvergence(msg, eigenvalues, ...) : ARPACK iteration did not converge
ArpackError(info[, infodict]) : ARPACK error

Exceptions
    exception scipy.sparse.linalg.ArpackNoConvergence(msg, eigenvalues, eigenvectors)
        ARPACK iteration did not converge

Attributes

+-----------------+--------------------------------------------------+
| attribute       | description                                      |
+-----------------+--------------------------------------------------+
| eigenvalues     | (ndarray) Partial result. Converged eigenvalues. |
+-----------------+--------------------------------------------------+
exception scipy.sparse.linalg.ArpackError (info, infodict={‘e’}: {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.’, -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.’, -13: “NEV and WHICH = ‘BE’ are incompatible.”, -12: ‘IPARAM(1) must be equal to 0 or 1.’, -1: ‘N must be positive.’, -10: ‘IPARAM(7) must be 1, 2, 3.’, -9: ‘Starting vector is zero.’, -8: ‘Error return from LAPACK eigenvalue calculation.’, -7: ‘Length of private work array WORKL is not sufficient.’, -6: ‘BMAT must be one of ‘I’ or ‘G’.’, -5: ‘WHICH must be one of ‘LM’, ‘SM’, ‘LR’, ‘SR’, ‘LI’, ‘SI’’, -4: ‘The maximum number of Arnoldi update iterations allowed must be greater than zero.’, -3: ‘NCV-NEV >= 2 and less than or equal to N.’, -2: ‘NEV must be positive.’, -11: “IPARAM(7) = 1 and BMAT = ‘G’ are incompatible.”}, ‘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.’, -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.’, -13: “NEV and WHICH = ‘BE’ are incompatible.”, -12: ‘IPARAM(1) must be equal to 0 or 1.’, -2: ‘NEV must be positive.’, -10: ‘IPARAM(7) must be 1, 2, 3.’, -9: ‘Starting vector is zero.’, -8: ‘Error return from LAPACK eigenvalue calculation.’, -7: ‘Length of private work array WORKL is not sufficient.’, -6: ‘BMAT must be one of ‘I’ or ‘G’.’, -5: ‘WHICH must be one of ‘LM’, ‘SM’, ‘LR’, ‘SR’, ‘LI’, ‘SI’’, -4: ‘The maximum number of Arnoldi update iterations allowed must be greater than zero.’, -3: ‘NCV-NEV >= 2 and less than or equal to N.’, -2: ‘NEV must be positive.’, -11: “IPARAM(7) = 1 and BMAT = ‘G’ are incompatible.”}, ‘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.’, -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.’, -13: “NEV and WHICH = ‘BE’ are incompatible.”, -12: ‘IPARAM(1) must be equal to 0 or 1.’, -2: ‘NEV must be positive.’, -10: ‘IPARAM(7) must be 1, 2, 3.’, -9: ‘Starting vector is zero.’, -8: ‘Error return from LAPACK eigenvalue calculation.’, -7: ‘Length of private work array WORKL is not sufficient.’, -6: ‘BMAT must be one of ‘I’ or ‘G’.’, -5: ‘WHICH must be one of ‘LM’, ‘SM’, ‘LR’, ‘SR’, ‘LI’, ‘SI’’, -4: ‘The maximum number of Arnoldi update iterations allowed must be greater than zero.’, -3: ‘NCV-NEV >= 2 and less than or equal to N.’, -2: ‘NEV must be positive.’, -11: “IPARAM(7) = 1 and BMAT = ‘G’ are incompatible.”}

5.28. Sparse matrices (scipy.sparse)
### Functions

- `all(a[, axis, out, keepdims])`: Test whether all array elements along a given axis evaluate to True.
- `amax(a[, axis, out, keepdims])`: Return the maximum of an array or maximum along an axis.
- `amin(a[, axis, out, keepdims])`: Return the minimum of an array or minimum along an axis.
- `array(object[, dtype, copy, order, subok, ndmin])`: Create an array.
- `asarray(a[, dtype, order])`: Convert the input to an array.
- `aslinearoperator(A)`: Return A as a LinearOperator.
- `bicg(A, b[, x0, tol, maxiter, xtype, M, ...])`: Use BIConjugate Gradient iteration to solve \( A x = b \).
- `bicgstab(A, b[, x0, tol, maxiter, xtype, M, callback])`: Use BIConjugate Gradient STABilized iteration to solve \( A x = b \).
- `cg(A, b[, x0, tol, maxiter, xtype, M, ...])`: Use Conjugate Gradient iteration to solve \( A x = b \).
- `cgs(A, b[, x0, tol, maxiter, xtype, M, callback])`: Use Conjugate Gradient Squared iteration to solve \( A x = b \).
- `dot(a, b[, out])`: Dot product of two arrays.
- `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 \( A \).
- `empty(shape[, dtype, order])`: Return a new array of given shape and type, without initializing entries.
- `empty_like(a[, dtype, order, subok])`: Return a new array with the same shape and type as a given array.
- `expm(A)`: Compute the matrix exponential using Pade approximation.
- `expm_multiply(A, B[, start, stop, num, endpoint])`: Compute the action of the matrix exponential of \( A \) on \( B \).
- `factorized(A)`: Return a function for solving a sparse linear system, with \( A \) pre-factorized.
- `fastCopyAndTranspose(a)`: Return the current object that defines floating-point error handling.
- `gmres(A, b[, x0, tol, restart, maxiter, ...])`: Use Generalized Minimal RESidual iteration to solve \( A x = b \).
- `inv(A)`: Compute the inverse of a sparse matrix.
- `issparse(x)`: Determine whether the object is sparse.
- `linalg(A, b[, x0, tol, maxiter, M, ...])`: Solve a matrix equation using the LGMRES algorithm.
- `lsqr(A, b[, damp, atol, btol, conlim, ...])`: Iterative solver for least-squares problems.
- `lsmr(A, b[, damp, atol, btol, conlim, ...])`: Find the least-squares solution to a large, sparse, linear system of equations.
- `minres(A, b[, x0, shift, tol, maxiter, ...])`: Use MINimum RESidual iteration to solve \( A x = b \).
- `norm(x[, ord])`: 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.
- `product(a[, axis, dtype, out, keepdims])`: Return the product of array elements over a given axis.
- `qmr(A, b[, x0, tol, maxiter, xtype, M1, M2, ...])`: Use Quasi-Minimal Residual iteration to solve \( A x = b \).
- `ravel(a[, order])`: Return a flattened array.
- `rollaxis(a, axis[, start])`: Roll the specified axis backwards, until it lies in a given position.
- `size(a[, axis])`: Return the number of elements along a given axis.
- `spilu(A[, drop_tol, fill_factor, drop_rule, ...])`: Compute an incomplete LU decomposition for a sparse, square matrix.
- `splu(A[", perm_pspec, diag-pivot-thresh, use_umfpack])`: Compute the LU decomposition of a sparse, square matrix.
- `spsolve(A, b[, permc_spec, use_umfpack])`: Solve the sparse linear system \( A x = b \), where \( b \) may be a vector or a matrix.
- `sum(a[, axis, dtype, out, keepdims])`: Sum of array elements over a given axis.
- `svds(A[, k, ncv, which, v0, maxiter, ...])`: Compute the largest \( k \) singular values/vectors for a sparse matrix.
- `transpose(a[, axes])`: Permute the dimensions of an array.
- `use_solver(**kwargs)`: Valid keyword arguments with defaults (other ignored):`
- `zeros(shape[, dtype, order])`: Return a new array of given shape and type, filled with zeros.

### Classes

- `LinearOperator(dtype, shape)`: Common interface for performing matrix vector products.

Continued on next page
Table 5.174 – continued from previous page

<table>
<thead>
<tr>
<th>SuperLU</th>
<th>LU factorization of a sparse matrix.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tester</td>
<td>alias of NoseTester</td>
</tr>
<tr>
<td>broadcast</td>
<td>Produce an object that mimics broadcasting.</td>
</tr>
<tr>
<td>cdouble</td>
<td>alias of complex128</td>
</tr>
<tr>
<td>complexfloating</td>
<td>Attributes</td>
</tr>
<tr>
<td>csingle</td>
<td>alias of complex64</td>
</tr>
<tr>
<td>double</td>
<td>alias of float64</td>
</tr>
<tr>
<td>errstate(**kwargs)</td>
<td>Context manager for floating-point error handling.</td>
</tr>
<tr>
<td>finfo</td>
<td>Machine limits for floating point types.</td>
</tr>
<tr>
<td>inexact</td>
<td>Attributes</td>
</tr>
<tr>
<td>intc</td>
<td>alias of int32</td>
</tr>
<tr>
<td>longdouble</td>
<td>alias of float128</td>
</tr>
<tr>
<td>single</td>
<td>alias of float32</td>
</tr>
</tbody>
</table>

Exceptions

<table>
<thead>
<tr>
<th>ArpackError(info[, infodict])</th>
<th>ARPACK error</th>
</tr>
</thead>
<tbody>
<tr>
<td>ArpackNoConvergence(msg, eigenvalues, ...)</td>
<td>ARPACK iteration did not converge</td>
</tr>
<tr>
<td>MatrixRankWarning</td>
<td></td>
</tr>
</tbody>
</table>

5.28.2 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.

5.28. Sparse matrices (scipy.sparse)
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:

```python
>>> np.dot(A.toarray(), v)
array([ 1, -3, -1], dtype=int64)
```

but then all the performance advantages would be lost.

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 x = b for 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:
>>> 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([0,0,1,3,1,0,0])
>>> J = array([0,2,1,3,1,0,0])
>>> V = array([1,1,1,1,1,1,1])
>>> 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).

## 5.29 Sparse linear algebra (**scipy.sparse.linalg**)  

### 5.29.1 Abstract linear operators

<table>
<thead>
<tr>
<th><strong>LinearOperator</strong><code>&lt;dtype, shape&gt;</code></th>
<th>Common interface for performing matrix vector products</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>aslinearoperator(A)</code></td>
<td>Return A as a LinearOperator.</td>
</tr>
</tbody>
</table>

**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 $A\times x=b$. Such solvers only require the computation of matrix vector products, $A\times v$ 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 * 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 LinearOperator with unspecified dtype>
>>> 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)`
- `adjoint()` Hermitian adjoint.

Continued on next page
Table 5.178 – continued from previous page

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>dot(x)</code></td>
<td>Matrix-matrix or matrix-vector multiplication.</td>
</tr>
<tr>
<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>transpose()</code></td>
<td>Transpose this linear operator.</td>
</tr>
</tbody>
</table>

**LinearOperator.``__call__``(x)**

**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**

A_H : LinearOperator

Hermitian adjoint of self.

**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**

A\times: array

1-d or 2-d array (depending on the shape of x) that represents the result of applying this linear operator on x.

**LinearOperator.``matmat``(X)**

Matrix-matrix multiplication.

Performs the operation $y = A \times X$ where $A$ is an $M \times N$ linear operator and $X$ dense $N \times K$ 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.

**LinearOperator.``matvec``(x)**

Matrix-vector multiplication.

Performs 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 : {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.
LinearOperator.

LinearOperator

rmatvec(x)

Adjoint matrix-vector multiplication.

Performs the operation \( y = A^H \cdot x \) where \( A \) is an \( M \times N \) 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.

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(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.

Examples

```python
>>> from scipy import matrix
>>> M = matrix( [[1,2,3],[4,5,6]], dtype='int32' )
>>> aslinearoperator( M )
<2x3 LinearOperator with dtype=int32>
```
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.

New in version 0.12.0.

scipy.sparse.linalg.expm($A$)
Compute the matrix exponential using Pade approximation.

Parameters
A : (M,M) array_like or sparse matrix

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
[R254]

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
[R255], [R256]
5.29.3 Matrix norms

`onenormest(A[, t, itmax, compute_v, compute_w])`  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 $\|Av\|_1 = est \cdot \|v\|_1$. 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**

[R267], [R268]

5.29.4 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.

`factorized(A)`  Return a fuction for solving a sparse linear system, with $A$ pre-factorized.

**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.size` must be `(n,)` or `(n, 1)`

**perm_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.

**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
>>> 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])
>>> x1 = solve( rhs1 ) # Uses the LU factors.
array([ 1., -2., -2.])
```

Iterative methods for linear equation systems:

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>bicg(A, b[, x0, tol, maxiter, xtype, M,...])</code></td>
<td>Use BIConjugate Gradient iteration to solve $A x = b$</td>
</tr>
<tr>
<td><code>bicgstab(A, b[, x0, tol, maxiter, xtype, M,...])</code></td>
<td>Use BIConjugate Gradient STABilized iteration to solve $A x = b$</td>
</tr>
<tr>
<td><code>cg(A, b[, x0, tol, maxiter, xtype, M, callback])</code></td>
<td>Use Conjugate Gradient iteration to solve $A x = b$</td>
</tr>
<tr>
<td><code>cgs(A, b[, x0, tol, maxiter, M, callback])</code></td>
<td>Use Conjugate Gradient Squared iteration to solve $A x = b$</td>
</tr>
<tr>
<td><code>gmres(A, b[, x0, tol, restart, maxiter, ...])</code></td>
<td>Use Generalized Minimal RESidual iteration to solve $A x = b$.</td>
</tr>
<tr>
<td><code>lgmres(A, b[, x0, tol, maxiter, M, ...])</code></td>
<td>Solve a matrix equation using the LGMRES algorithm.</td>
</tr>
</tbody>
</table>
Table 5.182 – continued from previous page

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>minres(A, b[, x0, shift, tol, maxiter, ...])</td>
<td>Use MINimum RESidual iteration to solve Ax=b</td>
</tr>
<tr>
<td>qmr(A, b[, x0, tol, maxiter, xtype, M1, M2, ...])</td>
<td>Use Quasi-Minimal Residual iteration to solve A x = b</td>
</tr>
</tbody>
</table>

**scipy.sparse.linalg.bicg** (A, b, x0=None, tol=1e-05, maxiter=None, xtype=None, M=None, callback=None)

Use BIConjugate Gradient iteration to solve A x = 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.

**Other Parameters**
- **x0**: {array, matrix}
  - Starting guess for the solution.
- **tol**: float
  - Tolerance to achieve. The algorithm terminates when either the relative or the absolute 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.
- **xtype**: {‘f’, ‘d’, ‘F’, ‘D’}
  - This parameter is deprecated – avoid using it.
  - The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype=’f’,’d’,’F’ or ‘D’. This parameter has been superseded by LinearOperator.

**scipy.sparse.linalg.bicgstab** (A, b, x0=None, tol=1e-05, maxiter=None, xtype=None, M=None, callback=None)

Use BIConjugate Gradient STABilized iteration to solve A x = b

**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**: float
  Tolerance to achieve. The algorithm terminates when either the relative or the absolute 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 \( \text{callback}(x_k) \), where \( x_k \) is the current solution vector.
- **xtype**: \{‘f’, ‘d’, ‘F’, ‘D’\}
  This parameter is deprecated – avoid using it.
  The type of the result. If None, then it will be determined from \( A \).dtype.char and \( b \). If \( A \) does not have a typecode method then it will compute \( A \).matvec(x0) to get a typecode. To save the extra computation when \( A \) does not have a typecode attribute use \( xtype=0 \) for the same type as \( b \) or use \( xtype=’F’,’d’,’F’,’D’ \). This parameter has been superseded by LinearOperator.

**scipy.sparse.linalg.cg**(\( A, b, x0=\text{None}, \text{tol}=1e-05, \text{maxiter}=\text{None}, \text{xtype}=\text{None}, M=\text{None}, \text{callback}=\text{None} \))

Use Conjugate Gradient iteration to solve \( A x = b \)

**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**: float
  Tolerance to achieve. The algorithm terminates when either the relative or the absolute 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.

**xtype**: {'f', 'd', 'F', 'D'}
This parameter is deprecated – avoid using it.
The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f', 'd', 'F', or 'D'. This parameter has been superseded by LinearOperator.

```python
scipy.sparse.linalg.cgs(A, b, x0=None, tol=1e-05, maxiter=None, xtype=None, M=None, callback=None)
```

Use Conjugate Gradient Squared iteration to solve \( A x = b \)

**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 : float
  Tolerance to achieve. The algorithm terminates when either the relative or the absolute 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.
- xtype : {'f', 'd', 'F', 'D'}
  This parameter is deprecated – avoid using it.
The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f', 'd', 'F', or 'D'. This parameter has been superseded by LinearOperator.
scipy.sparse.linalg.gmres(A, b, x0=None, tol=1e-05, restart=None, maxiter=None, xtype=None, M=None, callback=None, restart=None)

Use Generalized Minimal RESidual iteration to solve $A x = b$.

**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**: float
  Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below `tol`.
- **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.
- **xtype**: {'f', 'd', 'F', 'D'}
  This parameter is DEPRECATED — avoid using it.
  The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f', 'd', 'F', or 'D'. This parameter has been superseded by LinearOperator.
- **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 \( P^{-1} \times x \).
import scipy.sparse.linalg as spla
M_x = lambda x: spla.spsolve(P, x)
M = spla.LinearOperator((n, n), M_x)
```

The LGMRES algorithm [R257] [R258] 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 \( N \times N \) 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.
- \( tol \) : float, optional
  - Tolerance to achieve. The algorithm terminates when either the relative or the absolute residual is below \( tol \).
- \( maxiter \) : 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 [R257], 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
SciPy Reference Guide, Release 0.16.0

•>0 : convergence to tolerance not achieved, number of iterations
•<0 : illegal input or breakdown

Notes
The LGMRES algorithm [R257] [R258] 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
[R257], [R258]

scipy.sparse.linalg.minres(A, b, x0=None, shift=0.0, tol=1e-05, maxiter=None, xtype=None,
M=None, callback=None, show=False, check=False)

Use MINimum RESidual iteration to solve Ax=b

MINRES minimizes norm(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 : {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).
x0 : {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 either the relative or the absolute 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.
xtype : {‘f’,’d’,’F’,’D’}
This parameter is deprecated – avoid using it.
The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f','d','F',or ‘D’. This parameter has been superseded by LinearOperator.

Notes

THIS FUNCTION IS EXPERIMENTAL AND SUBJECT TO CHANGE!

References

Solution of sparse indefinite systems of linear equations,
http://www.stanford.edu/group/SOL/software/minres.html

This file is a translation of the following MATLAB implementation:
http://www.stanford.edu/group/SOL/software/minres/matlab/

scipy.sparse.linalg.qmr(A, b, x0=None, tol=1e-05, maxiter=None, xtype=None, M1=None, M2=None, callback=None)

Use Quasi-Minimal Residual iteration to solve A x = 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 A\times and A^T \times.

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 either the relative or the absolute 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.

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.

xtype : {'f', 'd', 'F', 'D'}
This parameter is DEPRECATED – avoid using it.
The type of the result. If None, then it will be determined from A.dtype.char and b. If A does not have a typecode method then it will compute A.matvec(x0) to get a typecode. To save the extra computation when A
SciPy Reference Guide, Release 0.16.0

does not have a typecode attribute use xtype=0 for the same type as b or use xtype='f','d','F',or 'D'. This parameter has been superseded by LinearOperator.

See also:

LinearOperator

Iterative methods for least-squares problems:

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>lsqr</strong></td>
<td>Find the least-squares solution to a large, sparse, linear system of equations.</td>
</tr>
<tr>
<td><strong>lsmr</strong></td>
<td>Iterative solver for least-squares problems.</td>
</tr>
</tbody>
</table>

scipy.sparse.linalg.lsqr(A, b[, damp, atol, btol, conlim, ...])  
Find the least-squares solution to a large, sparse, linear system of equations.

The function solves

\[ Ax = b \]  

or

\[ \min \| b - Ax \|^2 \]  

or

\[ \min \| Ax - b \|^2 + \|x\|^2 \]  

The matrix A may be square or rectangular (over-determined or under-determined), and may have any rank.

1. Unsymmetric equations -- solve \( A \times x = b \)
2. Linear least squares -- solve \( A \times x = b \)  
in the least-squares sense
3. Damped least squares -- solve \( \begin{pmatrix} A & \text{damp} & I \end{pmatrix} \times \begin{pmatrix} x \end{pmatrix} = \begin{pmatrix} b \end{pmatrix} \)  
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 \( A \times x \) and \( A^T \times x \).
- **b**: (m,) ndarray  
  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 cond(A) and the size of damp.)
- **conlim**: 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.
- **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 \( (A'A + \text{damp}^2 \times I)^{-1} \).

**Returns**

- **x**: ndarray of float  
  The final solution.
- **istop**: int  
  5.29. Sparse linear algebra (scipy.sparse.linalg) 1065
Gives the reason for termination. 1 means x is an approximate solution to \( Ax = b \). 2 means x approximately solves the least-squares problem.

\[
\text{itn} : \text{int}
\]
Iteration number upon termination.

\[
\text{r1norm} : \text{float}
\]
\( \text{norm}(r), \text{where } r = b - Ax. \)

\[
\text{r2norm} : \text{float}
\]
\[ \text{sqrt}(\text{norm}(r)^2 + \text{damp}^2 \times \text{norm}(x)^2) \]. Equal to \( \text{r1norm} \) if \( \text{damp} == 0 \).

\[
\text{anorm} : \text{float}
\]
Estimate of Frobenius norm of \( Abar = [[A]; [\text{damp} \times I]]. \)

\[
\text{acond} : \text{float}
\]
Estimate of \( \text{cond}(Abar). \)

\[
\text{arnorm} : \text{float}
\]
Estimate of \( \text{norm}(A' \times r - \text{damp}^2 \times x). \)

\[
\text{xnorm} : \text{float}
\]
\( \text{norm}(x) \)

\[
\text{var} : \text{ndarray of float}
\]
If \( \text{calc_var} \) is True, estimates all diagonals of \( (A' A)^{(-1)} \) (if \( \text{damp} == 0 \)) or more generally \( (A' A + \text{damp}^2 \times I)^{(-1)} \). 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 \( \text{damp} = 0 \).)

**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 \( \text{damp} \) 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.

If some initial estimate \( x_0 \) is known and if \( \text{damp} == 0 \), one could proceed as follows:

1. Compute a residual vector \( r0 = b - A \times x0 \).
2. Use LSQR to solve the system \( A \times dx = r0 \).
3. Add the correction \( dx \) to obtain a final solution \( x = x0 + dx \).

This requires that \( x0 \) be available before and after the call to LSQR. To judge the benefits, suppose LSQR takes \( k1 \) iterations to solve \( A^*x = b \) and \( k2 \) iterations to solve \( A^*dx = r0 \). If \( x0 \) is “good”, \( \text{norm}(r0) \) will be smaller than \( \text{norm}(b) \). If the same stopping tolerances \( \text{atol} \) and \( \text{btol} \) are used for each system, \( k1 \) and \( k2 \) will be similar, but the final solution \( x0 + dx \) 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 \( A^*x = b \), the larger value \( \text{btol} \times \text{norm}(b)/\text{norm}(r0) \) should be suitable for \( A^*dx = r0 \).

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 \( A + M(\text{inverse}) \times z = b \), 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

[R264], [R265], [R266]

```python
scipy.sparse.linalg.lsmr(A, b, damp=0.0, atol=1e-06, btol=1e-06, conlim=100000000.0, maxiter=None, show=False)
```

Iterative solver for least-squares problems.

\( \text{lsmr} \) 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.

- \( b \) : \((m,) \) ndarray
  
  Vector \( b \) in the linear system.

- \( \text{damp} \) : float
  
  Damping factor for regularized least-squares. \( \text{lsmr} \) solves the regularized least-squares problem:

  \[
  \min \ |\ |b - (A x)||_2
  \]

  \[
  |(0) (damp*I) |_2
  \]

  where \( \text{damp} \) is a scalar. If \( \text{damp} \) is None or 0, the system is solved without regularization.

- \( \text{atol, btol} \) : float, optional
  
  Stopping tolerances. \( \text{lsmr} \) continues iterations until a certain backward error estimate is smaller than some quantity depending on \( \text{atol} \) and \( \text{btol} \). Let \( r = b - Ax \) be the residual vector for the current approximate solution \( x \). If \( Ax = b \) seems to be consistent, \( \text{lsmr} \) terminates when \( \text{norm}(r) \leq \text{atol} \times \text{norm}(A) \times \text{norm}(x) + \text{btol} \times \text{norm}(b) \). Otherwise, \( \text{lsmr} \) terminates when \( \text{norm}(A^T r) \leq \text{atol} \times \text{norm}(A) \times \text{norm}(r) \). 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 \( \text{LAMBDA} \).) If \( \text{atol} \) or \( \text{btol} \) 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 \( \text{atol} = 1e-7 \). This prevents the algorithm from doing unnecessary work beyond the uncertainty of the input data.

- \( \text{conlim} \) : float, optional
  
  \( \text{lsmr} \) 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 \( 1.0e+8 \). If \( \text{conlim} \) is None, the default value is \( 1e+8 \). Maximum precision can be obtained by setting \( \text{atol} = \text{btol} = \text{conlim} = 0 \), but the number of iterations may then be excessive.

- \( \text{maxiter} \) : int, optional
  
  \( \text{lsmr} \) terminates if the number of iterations reaches \( \text{maxiter} \). The default is \( \text{maxiter} = \min(m, n) \). For ill-conditioned systems, a larger value of \( \text{maxiter} \) may be needed.
Returns

show : bool, optional
    Print iterations logs if show=True.

x : ndarray of float
    Least-square solution returned.

istop : int
    istop gives the reason for stopping:
    istop = 0 means x=0 is a solution.
    = 1 means x is an approximate solution to A*x = B,
      according to atol and btol.
    = 2 means x approximately solves the least-squares problem
      according to atol.
    = 3 means COND(A) seems to be greater than CONLIM.
    = 4 is the same as 1 with atol = btol = eps (machine
      precision)
    = 5 is the same as 2 with atol = eps.
    = 6 is the same as 3 with CONLIM = 1/eps.
    = 7 means ITN reached maxiter before the other stopping
      conditions were satisfied.

itn : int
    Number of iterations used.

normr : float
    norm(b-Ax)

normar : float
    norm(A^T (b - Ax))

norma : float
    norm(A)

conda : float
    Condition number of A.

normx : float
    norm(x)

Notes

New in version 0.11.0.

References

[R262], [R263]

5.29.5 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 (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 $A \times \{i\} = w[i] \times M \times \{i\}$, 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 $A \times x$, 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. 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 $M \times x$ 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 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 $M \times x = b$. 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 or complex, optional
  Find eigenvalues near sigma using shift-invert mode. This requires an operator to compute the solution of the linear system $[A - sigma \times M] \times x = b$, 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
  
  \[x = OPinv \times b = [A - sigma \times M]^{-1} \times b.\]

  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),**
  \n  \[w'[i] = \frac{1}{2} \times \left[ \frac{1}{w[i] - sigma} + \frac{1}{w[i] - \text{conj}(sigma)} \right].\]

  **If A is real and OPpart == 'i',**
  \n  \[w'[i] = \frac{1}{2i} \times \left[ \frac{1}{w[i] - sigma} - \frac{1}{w[i] - \text{conj}(sigma)} \right].\]

  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, 2k + 1)

- **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

5.29. Sparse linear algebra (scipy.sparse.linalg)
When \( \sigma \neq \text{None} \), ‘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: \( n \times 10 \)

- **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.

**Returns**

- **\( w \)**: ndarray
  - See notes in sigma, above
  - Array of \( k \) eigenvalues.

- **\( v \)**: ndarray
  - See notes in sigma, above
  - 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 \[R250\] SNEUPD, DNEUPD, CNEUPD, ZNEUPD, functions which use the Implicitly Restarted Arnoldi Method to find the eigenvalues and eigenvectors \[R251\].

**References**

[R250], [R251]

**Examples**

Find 6 eigenvectors of the identity matrix:

```python
>>> id = np.eye(13)
>>> vals, vecs = scipy.sparse.linalg.eigs(id, k=6)
>>> vals
array([[ 1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j]])
>>> 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**

- $A$: An N x N matrix, array, sparse matrix, or LinearOperator representing the operation $A \times x$, where $A$ is a real symmetric matrix. 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 $[A - sigma \times M] x = b$, 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 $x = OPinv \times b = \frac{1}{[A - sigma \times M]} - 1 \times b$. 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’, $w'[i] = \frac{(w[i] + sigma)}{(w[i] - sigma)}$.
    - 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 $ncv > 2\times k$. Default: $\min(n, 2\times k + 1)$.
- $which$: 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: \( n \times 10 \)

**tol**: float
- Relative accuracy for eigenvalues (stopping criterion). The default value of 0 implies machine precision.

**M**: N x N matrix, array, sparse matrix, or LinearOperator
- See notes in M, above

**B**: N x N matrix, array, sparse matrix, or LinearOperator
- See notes in sigma, above.

**return_eigenvectors**: bool
- Return eigenvectors (True) in addition to eigenvalues

**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 \( OP \times x'[i] = w'[i] \times B \times x'[i] \) and transforms the resulting Ritz vectors \( x'[i] \) and Ritz values \( w'[i] \) into the desired eigenvectors and eigenvalues of the problem \( A \times x[i] = w[i] \times M \times x[i] \).

The modes are as follows:

- **normal**: \( OP = [A - sigma \times M]^\text{-1} \times M, B = M, w'[i] = 1 / (w[i] - sigma) \)
- **buckling**: \( OP = [A - sigma \times M]^\text{-1} \times A, B = A, w'[i] = w[i] / (w[i] - sigma) \)
- **cayley**: \( OP = [A - sigma \times M]^\text{-1} \times [A + sigma \times M], B = M, w'[i] = (w[i] + sigma) / (w[i] - sigma) \)

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 [R252] SSEUPD and DSEUPD functions which use the Implicitly Restarted Lanczos Method to find the eigenvalues and eigenvectors [R253].

**References**

[R252], [R253]
Examples

```python
>>> import scipy.sparse as sparse
>>> id = np.eye(13)
>>> vals, vecs = sparse.linalg.eigsh(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.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 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 $3m$ 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 $5m > n$, 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 http://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

[R259], [R260], [R261]

Examples

```python
>>> # Solve $A x = \lambda B x$ with constraints and preconditioning.
>>> n = 100
>>> vals = [nm.arange( n, dtype = nm.float64 ) + 1]
>>> # Matrix $A$.
>>> operatorA = spdiags( vals, 0, n, n )
>>> # Matrix $B$
>>> operatorB = nm.eye( n, n )
>>> # Constraints.
>>> Y = nm.eye( n, 3 )
>>> # Initial guess for eigenvectors, should have linearly independent columns. Column dimension = number of requested eigenvalues.
>>> X = sc.rand( n, 3 )
>>> # Preconditioner - inverse of $A$.
>>> ivals = [1./vals[0]]
>>> def precond( x ):
...     invA = spdiags( ivals, 0, n, n )
...     y = invA * x
...     if sp.issparse( y ):
...         y = y.toarray()
...
...     return as2d( y )

>>> # Alternative way of providing the same preconditioner.
>>> #precond = spdiags( ivals, 0, n, n )

>>> tt = time.clock()
>>> eigs, vecs = lobpcg(X, operatorA, operatorB, blockVectorY=Y,
...                    operatorT=precond,

```

```
```python
residualTolerance=1e-4, maxIterations=40,
largest=False, verbosityLevel=1)
print 'solution time:', time.clock() - tt
print eigs
```

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(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.
- **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, 2*k + 1)
- **tol**: float, optional
- **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) right 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).

**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.

Complete or incomplete LU factorizations

```python
scipy.sparse.linalg.splu(A[, permc_spec, diag_pivot_thresh,...])
```
Compute the LU decomposition of a sparse, square matrix.

```python
scipy.sparse.linalg.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(A, permc_spec=None, diag_pivot_thresh=None, drop_tol=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 [R271]
- **drop_tol**: float, optional
  (deprecated) No effect.
- **relax**: int, optional
  Expert option for customizing the degree of relaxing supernodes. See SuperLU user’s guide for details [R271]
- **panel_size**: int, optional
  Expert option for customizing the panel size. See SuperLU user’s guide for details [R271]
- **options**: dict, optional
  Dictionary containing additional expert options to SuperLU. See SuperLU user guide [R271] (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

- **invA**: scipy.sparse.linalg.SuperLU
  Object, which has a solve method.

See also:

- **spilu**: incomplete LU decomposition

Notes

This function uses the SuperLU library.

References

[R271]
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 decomposition. (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, prow, column, area, secondary, dynamic, interp. (Default: basic, area)
    See SuperLU documentation for details.

Remaining other options

**Returns**

invA_approx : scipy.sparse.linalg.SuperLU
    Object, which has a solve method.

See also:

spilu 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.

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.spilu(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:

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:

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:

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:

(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

<table>
<thead>
<tr>
<th>Attribute</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>shape</td>
<td>Shape of the original matrix as a tuple of ints.</td>
</tr>
<tr>
<td>nnz</td>
<td>Number of nonzero elements in the matrix.</td>
</tr>
<tr>
<td>perm_c</td>
<td>Permutation Pc represented as an array of indices.</td>
</tr>
<tr>
<td>perm_r</td>
<td>Permutation Pr represented as an array of indices.</td>
</tr>
<tr>
<td>L</td>
<td>Lower triangular factor with unit diagonal as a scipy.sparse.csc_matrix.</td>
</tr>
<tr>
<td>U</td>
<td>Upper triangular factor as a scipy.sparse.csc_matrix.</td>
</tr>
</tbody>
</table>

SuperLU.shape
Shape of the original matrix as a tuple of ints.

SuperLU.nnz
Number of nonzero elements in the matrix.

SuperLU.perm_c
Permutation Pc represented as an array of indices.
The column permutation matrix can be reconstructed via:

```python
>>> Pc = np.zeros((n, n))
>>> Pc[np.arange(n), perm_c] = 1
```

SuperLU.perm_r

Permutation Pr represented as an array of indices.

The row permutation matrix can be reconstructed via:

```python
>>> Pr = np.zeros((n, n))
>>> Pr[perm_r, np.arange(n)] = 1
```

SuperLU.L

Lower triangular factor with unit diagonal as a `scipy.sparse.csc_matrix`.

New in version 0.14.0.

SuperLU.U

Upper triangular factor as a `scipy.sparse.csc_matrix`.

New in version 0.14.0.

Methods

```python
solve(rhs[, trans])  Solves linear system of equations with one or several right-hand sides.
```

SuperLU.solve `(rhs[, trans])`

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 * x == rhs (default)
  - 'T': A^T * x == rhs
  - 'H': A^H * x == rhs

Returns

- `x` : ndarray, shape `rhs.shape`
  Solution vector(s)

5.29.6 Exceptions

```
ArpackNoConvergence(msg, eigenvalues, ...)
ArpackError(info[, infodict])
```

exception `scipy.sparse.linalg.ArpackNoConvergence (msg, eigenvalues, eigenvectors)`

ARPACK iteration did not converge

Attributes

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>eigenvalues</td>
<td>(ndarray) Partial result. Converged eigenvalues.</td>
</tr>
</tbody>
</table>
exception scipy.sparse.linalg.ArpackError (info, infodict={‘e’: {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.’, -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.’, -13: ‘NEV and WHICH = ‘BE’ are incompatible.’, -12: ‘IPARAM(1) must be equal to 0 or 1.’, -1: ‘N must be positive.’, -10: ‘IPARAM(7) must be 1, 2, 3.’, -9: ‘Starting vector is zero.’, -8: ‘Error return from LAPACK eigenvalue calculation.’, -7: ‘Length of private work array WORKL is not sufficient.’, -6: ‘B MAT must be one of ‘I’ or ‘G’.’, -5: ‘WHICH must be one of ‘LM’, ‘SM’, ‘LR’, ‘SR’, ‘LI’, ‘SI’’, -4: ‘The maximum number of Arnoldi update iterations allowed must be greater than zero.’, -3: ‘NCV-NEV >= 2 and less than or equal to N.’, -2: ‘NEV must be positive.’, -11: ‘IPARAM(7) = 1 and B MAT = ‘G’ are incompatible.’}, ‘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.’, -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.’, -13: ‘NEV and WHICH = ‘BE’ are incompatible.’, -12: ‘IPARAM(1) must be equal to 0 or 1.’, -2: ‘NEV must be positive.’, -10: ‘IPARAM(7) must be 1, 2, 3.’, -9: ‘Starting vector is zero.’, -8: ‘Error return from LAPACK eigenvalue calculation.’, -7: ‘Length of private work array WORKL is not sufficient.’, -6: ‘B MAT must be one of ‘I’ or ‘G’.’, -5: ‘WHICH must be one of ‘LM’, ‘SM’, ‘LR’, ‘SR’, ‘LI’, ‘SI’’, -4: ‘The maximum number of Arnoldi update iterations allowed must be greater than zero.’, -3: ‘NCV-NEV >= 2 and less than or equal to N.’, -2: ‘NEV must be positive.’, -11: ‘IPARAM(7) = 1 and B MAT = ‘G’ are incompatible.’}, ‘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.’, -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.’, -13: ‘NEV and WHICH = ‘BE’ are incompatible.’, -12: ‘IPARAM(1) must be equal to 0 or 1.’, -2: ‘NEV must be positive.’, -10: ‘IPARAM(7) must be 1, 2, 3.’, -9: ‘Starting vector is zero.’, -8: ‘Error return from LAPACK eigenvalue calculation.’, -7: ‘Length of private work array WORKL is not sufficient.’, -6: ‘B MAT must be one of ‘I’ or ‘G’.’, -5: ‘WHICH must be one of ‘LM’, ‘SM’, ‘LR’, ‘SR’, ‘LI’, ‘SI’’, -4: ‘The maximum number of Arnoldi update iterations allowed must be greater than zero.’, -3: ‘NCV-NEV >= 2 and less than or equal to N.’, -2: ‘NEV must be positive.’, -11: ‘IPARAM(7) = 1 and B MAT = ‘G’ are incompatible.’}, ‘f’: {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.’, -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.’, -13: ‘NEV and WHICH = ‘BE’ are incompatible.’, -12: ‘IPARAM(1) must be equal to 0 or 1.’, -2: ‘NEV must be positive.’, -10: ‘IPARAM(7) must be 1, 2, 3.’, -9: ‘Starting vector is zero.’, -8: ‘Error return from LAPACK eigenvalue calculation.’, -7: ‘Length of private work array WORKL is not sufficient.’, -6: ‘B MAT must be one of ‘I’ or ‘G’.’, -5: ‘WHICH must be one of ‘LM’, ‘SM’, ‘LR’, ‘SR’, ‘LI’, ‘SI’’, -4: ‘The maximum number of Arnoldi update iterations allowed must be greater than zero.’, -3: ‘NCV-NEV >= 2 and less than or equal to N.’, -2: ‘NEV must be positive.’, -11: ‘IPARAM(7) = 1 and B MAT = ‘G’ are incompatible.’}, ‘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.’, -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.’, -13: ‘NEV and WHICH = ‘BE’ are incompatible.’, -12: ‘IPARAM(1) must be equal to 0 or 1.’, -2: ‘NEV must be positive.’, -10: ‘IPARAM(7) must be 1, 2, 3.’, -9: ‘Starting vector is zero.’, -8: ‘Error return from LAPACK eigenvalue calculation.’, -7: ‘Length of private work array WORKL is not sufficient.’, -6: ‘B MAT must be one of ‘I’ or ‘G’.’, -5: ‘WHICH must be one of ‘LM’, ‘SM’, ‘LR’, ‘SR’, ‘LI’, ‘SI’’, -4: ‘The maximum number of Arnoldi update iterations allowed must be greater than zero.’, -3: ‘NCV-NEV >= 2 and less than or equal to N.’, -2: ‘NEV must be positive.’, -11: ‘IPARAM(7) = 1 and B MAT = ‘G’ are incompatible.’}, ‘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.’, -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.’, -13: ‘NEV and WHICH = ‘BE’ are incompatible.’, -12: ‘IPARAM(1) must be equal to 0 or 1.’, -2: ‘NEV must be positive.’, -10: ‘IPARAM(7) must be 1, 2, 3.’, -9: ‘Starting vector is zero.’, -8: ‘Error return from LAPACK eigenvalue calculation.’, -7: ‘Length of private work array WORKL is not sufficient.’, -6: ‘B MAT must be one of ‘I’ or ‘G’.’, -5: ‘WHICH must be one of ‘LM’, ‘SM’, ‘LR’, ‘SR’, ‘LI’, ‘SI’’, -4: ‘The maximum number of Arnoldi update iterations allowed must be greater than zero.’, -3: ‘NCV-NEV >= 2 and less than or equal to N.’, -2: ‘NEV must be positive.’, -11: ‘IPARAM(7) = 1 and B MAT = ‘G’ are incompatible.’}, ‘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.’, -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.’, -13: ‘NEV and WHICH = ‘BE’ are incompatible.’, -12: ‘IPARAM(1) must be equal to 0 or 1.’, -2: ‘NEV must be positive.’, -10: ‘IPARAM(7) must be 1, 2, 3.’, -9: ‘Starting vector is zero.’, -8: ‘Error return from LAPACK eigenvalue calculation.’, -7: ‘Length of private work array WORKL is not sufficient.’, -6: ‘B MAT must be one of ‘I’ or ‘G’.’, -5: ‘WHICH must be one of ‘LM’, ‘SM’, ‘LR’, ‘SR’, ‘LI’, ‘SI’’, -4: ‘The maximum number of Arnoldi update iterations allowed must be greater than zero.’, -3: ‘NCV-NEV >= 2 and less than or equal to N.’, -2: ‘NEV must be positive.’, -11: ‘IPARAM(7) = 1 and B MAT = ‘G’ are incompatible.’}.
5.30 Compressed Sparse Graph Routines (scipy.sparse.csgraph)

Fast graph algorithms based on sparse matrix representations.

5.30.1 Contents

- `connected_components(csgraph[, directed, ...])` Analyze the connected components of a sparse graph
- `laplacian(csgraph[, normed, return_diag, ...])` Return the Laplacian matrix of a directed graph.
- `shortest_path(csgraph[, method, directed, ...])` Perform a shortest-path graph search on a positive directed or undirected graph.
- `dijkstra(csgraph[, directed, indices, ...])` Dijkstra algorithm using Fibonacci Heaps
- `floyd_warshall(csgraph[, directed, ...])` Compute the shortest path lengths using the Floyd-Warshall algorithm
- `bellman_ford(csgraph[, directed, indices, ...])` Compute the shortest path lengths using the Bellman-Ford algorithm.
- `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(csgraph[, overwrite])` Returns the permutation array that orders a sparse CSR or CSC matrix in Reverse-Cuthill McKee ordering.
- `maximum_bipartite_matching(csgraph[, overwrite])` Returns an array of row or column permutations that makes the diagonal of a nonsingular square CSC sparse matrix zero free.

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` : str, 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

[R204] 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
  The N x N laplacian matrix of graph.
- **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)[::-1]
>>> 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(csgraph, method='auto', directed=True, return_predecessors=False, unweighted=False, overwrite=False)

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', 'lD'], 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 $O[N(N^2 k)]$, 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’.

**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
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.

**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.

**scipy.sparse.csgraph.dijkstra**

```
dijkstra(csgraph, directed=True, indices=None, return_predecessors=False, unweighted=False)
```

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]. 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.

- **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). .. versionadded:: 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.

**scipy.sparse.csgraph.floyd_warshall**

```
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 prede-
   cessors, 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

scipy.sparse.csgraph.bellman_ford(csgraph, directed=True, indices=None, re-
turn_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 prede-
   cessors, which can be used to reconstruct the shortest paths. Row i of the
SciPy Reference Guide, Release 0.16.0

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.

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

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.

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 predecesor 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.

```python
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].

- **return_predecessors** : bool, optional
  If True (default), then return the predecesor 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.

```python
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)---5---(1)             (3)---(1)                 
   \ /                       \ /                        
   6 2                       2                           
   \ /                       /                            
   (2)                       (2)

In compressed sparse representation, the solution looks like this:

   >>> 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 (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:

<table>
<thead>
<tr>
<th>input graph</th>
<th>depth first tree from (0)</th>
</tr>
</thead>
<tbody>
<tr>
<td>(0)</td>
<td>(0)</td>
</tr>
<tr>
<td>/ \</td>
<td>/ \</td>
</tr>
<tr>
<td>3 8</td>
<td>8</td>
</tr>
<tr>
<td>/ \</td>
<td>/ \</td>
</tr>
<tr>
<td>(3)---5---(1)</td>
<td>(3)---(1)</td>
</tr>
<tr>
<td>\ /</td>
<td>\ /</td>
</tr>
<tr>
<td>6 2</td>
<td>6 2</td>
</tr>
<tr>
<td>\ /</td>
<td>\ /</td>
</tr>
<tr>
<td>(2)</td>
<td>(2)</td>
</tr>
</tbody>
</table>

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**(`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**

<table>
<thead>
<tr>
<th>span_tree</th>
<th>csr matrix</th>
</tr>
</thead>
<tbody>
<tr>
<td>The N x N compressed-sparse representation of the undirected minimum spanning tree over the input (see notes below).</td>
<td></td>
</tr>
</tbody>
</table>

**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>(0)</td>
<td>(0)</td>
</tr>
<tr>
<td>/ \</td>
<td>/</td>
</tr>
<tr>
<td>3 8</td>
<td>3</td>
</tr>
<tr>
<td>/ \</td>
<td>/</td>
</tr>
<tr>
<td>(3)---5---(1)</td>
<td>(3)---5---(1)</td>
</tr>
<tr>
<td>\ /</td>
<td>\ /</td>
</tr>
<tr>
<td>6 2</td>
<td>2</td>
</tr>
<tr>
<td>\ /</td>
<td>\ /</td>
</tr>
<tr>
<td>(2)</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, 0, 3],
       [0, 0, 2, 5],
       [0, 0, 0, 0],
       [0, 0, 0, 0]])
```

scipy.sparse.csgraph.reverse_cuthill_mckee() 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**

<table>
<thead>
<tr>
<th>graph</th>
<th>sparse matrix</th>
</tr>
</thead>
<tbody>
<tr>
<td>Input sparse in CSC or CSR sparse matrix format.</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>symmetric_mode</th>
<th>bool, optional</th>
</tr>
</thead>
<tbody>
<tr>
<td>Is input matrix guaranteed to be symmetric.</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>perm</th>
<th>ndarray</th>
</tr>
</thead>
<tbody>
<tr>
<td>Is input matrix guaranteed to be symmetric.</td>
<td></td>
</tr>
</tbody>
</table>
Array of permuted row and column indices.

Notes
New in version 0.15.0.

References

scipy.sparse.csgraph.maximum_bipartite_matching()
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'}

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

5.30.2 Graph Representations

This module uses graphs which are stored in a matrix format. A graph with N nodes can be represented by an (N 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:

```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) /  \
  | 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]. 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. 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.
5.31 Spatial algorithms and data structures (scipy.spatial)

5.31.1 Nearest-neighbor Queries

**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:

```python
>>> import sys
>>> sys.setrecursionlimit(10000)
```

**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.
- `inner_node(split_dim, split, less, greater)`
- `leafnode(idx)`
- `node`

Continued on next page
**Table 5.192 – continued from previous page**

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>query(x[, k, eps, p, distance_upper_bound])</code></td>
<td>Query the kd-tree for nearest neighbors</td>
</tr>
<tr>
<td><code>query_ball_point(x, r[, p, eps])</code></td>
<td>Find all points within distance r of point(s) x.</td>
</tr>
<tr>
<td><code>query_ball_tree(other, r[, p, eps])</code></td>
<td>Find all pairs of points whose distance is at most r</td>
</tr>
<tr>
<td><code>query_pairs(r[, p, eps])</code></td>
<td>Find all pairs of points within a distance.</td>
</tr>
<tr>
<td><code>sparse_distance_matrix(other, max_distance)</code></td>
<td>Compute a sparse distance matrix</td>
</tr>
</tbody>
</table>

**KDTREE.count_neighbors** *(other, r, p=2.0)*

Count how many nearby pairs can be formed.

Count the number of pairs (x1,x2) can be formed, with x1 drawn from self and x2 drawn from *other*, and where `distance(x1, x2, p) <= 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<=p<=infinity`, 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).

**KDTREE.query** *(x, k=1, eps=0, p=2, distance_upper_bound=inf)*

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+eps)` times the distance to the real kth nearest neighbor.
- `p`: float, `1<=p<=infinity`, 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+(*(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]])
```

```python
>>> pts = np.array([[0, 0], [2.1, 2.9]])
```

```python
>>> tree.query(pts)
(array([ 2. , 0.14142136]), array([ 0, 13]))
```

```python
>>> tree.query(pts[0])
(2.0, 0)
```

`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 + eps), and branches are added in bulk if their furthest points are nearer than r * (1 + eps).

**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[0:4, 0:4]
>>> points = zip(x.ravel(), y.ravel())
>>> tree = spatial.KDTree(points)
>>> tree.query_ball_point([2, 0], 1)
[4, 8, 9, 12]
```

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 \( \text{other.data} \).

KDTree.query_pairs \((r, p=2.0, eps=0)\)
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.

KDTree.sparse_distance_matrix \((other, max_distance, p=2.0)\)
Compute a sparse distance matrix

Computes a distance matrix between two KDTrees, leaving as zero any distance greater than \( \text{max_distance} \).
class `scipy.spatial.cKDTree`

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 and 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.

Attributes

- **data**
- **indices**
- **leafsize**
- **m**
- **maxes**
- **mins**
- **n**
- **tree**
cKDTree.data

cKDTree.indices

cKDTree.leafsize

cKDTree.m

cKDTree.maxes

cKDTree.mins

cKDTree.n

cKDTree.tree

**Methods**

<table>
<thead>
<tr>
<th>Method Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>count_neighbors(self, other, r[, p])</td>
<td>Count how many nearby pairs can be formed.</td>
</tr>
<tr>
<td>query(self, x[, k, eps, p, ...])</td>
<td>Query the kd-tree for nearest neighbors</td>
</tr>
<tr>
<td>query_ball_point(self, x, r[, p, eps])</td>
<td>Find all points within distance r of point(s) x.</td>
</tr>
<tr>
<td>query_ball_tree(self, other, r[, p, eps])</td>
<td>Find all pairs of points whose distance is at most r.</td>
</tr>
<tr>
<td>query_pairs(self, r[, p, eps])</td>
<td>Find all pairs of points whose distance is at most r.</td>
</tr>
<tr>
<td>sparse_distance_matrix(self, other, max_distance)</td>
<td>Compute a sparse distance matrix</td>
</tr>
</tbody>
</table>

**cKDTree.count_neighbors** *(self, other, r, p=2.)*

Count how many nearby pairs can be formed.

Count the number of pairs (x1,x2) can be formed, with x1 drawn from self and x2 drawn from other, and where distance(x1, x2, p) <= 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
- **r**: float or one-dimensional array of floats
- **p**: float, 1<=p<=infinity

**Returns**

- **result**: int or 1-D array of ints

**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.

Query the kd-tree for nearest neighbors.

**Parameters**

- **x**: array_like, last dimension self.m
- **k**: integer
- **eps**: non-negative float
Return approximate nearest neighbors; the \( k \)-th returned value is guaranteed to be no further than \((1+\text{eps})\) times the distance to the real \( k \)-th nearest neighbor.

\( p \): float, \( 1 \leq p \leq \infty \)

Which Minkowski \( p \)-norm to use. \( 1 \) is the sum-of-absolute-values “Manhattan” distance \( 2 \) is the usual Euclidean distance \( \infty \) is the maximum-coordinate-difference distance

\( \text{distance\_upper\_bound} \): 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**

\( d \): array of floats

The distances to the nearest neighbors. If \( x \) has shape tuple+(self.m,), then \( d \) has shape tuple+(k,). 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,). Missing neighbors are indicated with self.n.

cKDTree.query_ball_point (self, \( x \), \( r \), \( p=2. \), \( \text{eps=0} \) )

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 \([1, \infty]\).

\( \text{eps} \): 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 \( r \ast (1 + \text{eps}) \).

**Returns**

\( \text{results} \): 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_point.

**Examples**

```python
>>> from scipy import spatial
>>> x, y = np.mgrid[0:4, 0:4]
>>> points = zip(x.ravel(), y.ravel())
>>> tree = spatial.cKDTree(points)
>>> tree.query_ball_point([2, 0], 1)
[4, 8, 9, 12]
```
cKDTree.query_ball_tree (self, other, r, p=2., 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 <= p <= infinity.
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 * (1+eps). 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.

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 <= p <= infinity.
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 * (1+eps). eps has to be non-negative.

Returns
results : set
    Set of pairs (i,j), with i < j, for which the corresponding positions are close.

cKDTree.sparse_distance_matrix (self, other, max_distance, p=2.)
Compute a sparse distance matrix

Computes a distance matrix between two KDTrees, leaving as zero any distance greater than max_distance.

Parameters
other : cKDTree
max_distance : positive float
p : float, 1<=p<=infinity

Returns
result : dok_matrix
    Sparse matrix representing the results in “dictionary of keys” format. FIXME: Internally, built as a COO matrix, it would be more efficient to return this COO matrix.

Distance computations (scipy.spatial.distance)

Function Reference  Distance matrix computation from a collection of raw observation vectors stored in a rectangular array.

pdist(X[, metric, p, w, V, VI])  Pairwise distances between observations in n-dimensional space.
cdist(XA, XB[, metric, p, V, VI, w])  Computes distance between each pair of the two collections of inputs.
`scipy.spatial.distance.pdist(X, metric='euclidean', p=2, w=None, V=None, VI=None)`

Pairwise distances between observations in n-dimensional space.

The following are common calling conventions.

1. `Y = pdist(X, '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 = pdist(X, 'minkowski', p)`
   Computes the distances using the Minkowski distance $||u - v||_p$ (p-norm) where $p \geq 1$.

3. `Y = pdist(X, 'cityblock')`
   Computes the city block or Manhattan distance between the points.

4. `Y = pdist(X, 'seuclidean', V=None)`
   Computes the standardized Euclidean distance. The standardized Euclidean distance between two n-vectors $u$ and $v$ is
   \[ \sqrt{\frac{\sum (u_i - v_i)^2}{V[i]}} \]
   where $V[i]$ is the variance computed over all the i’th components of the points. If not passed, it is automatically computed.

5. `Y = pdist(X, 'sqeuclidean')`
   Computes the squared Euclidean distance $||u - v||^2$ between the vectors.

6. `Y = pdist(X, 'cosine')`
   Computes the cosine distance between vectors u and v,
   \[ 1 - \frac{u \cdot v}{||u||_2 ||v||_2} \]
   where $||*||_2$ is the 2-norm of its argument *, and $u \cdot v$ is the dot product of u and v.

7. `Y = pdist(X, '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 = 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 = 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 where at least one of them is non-zero.

10. `Y = 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. \[ Y = \text{pdist}(X, \text{‘canberra’}) \]

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. \[ Y = \text{pdist}(X, \text{‘braycurtis’}) \]

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. \[ Y = \text{pdist}(X, \text{‘mahalanobis’, VI=None}) \]

Computes the Mahalanobis distance between the points. The Mahalanobis distance between two points \( u \) and \( v \) is \((u - v)(1/V)(u - v)^T\) 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. \[ Y = \text{pdist}(X, \text{‘yule’}) \]

Computes the Yule distance between each pair of boolean vectors. (see yule function documentation)

15. \[ Y = \text{pdist}(X, \text{‘matching’}) \]

Computes the matching distance between each pair of boolean vectors. (see matching function documentation)

16. \[ Y = \text{pdist}(X, \text{‘dice’}) \]

Computes the Dice distance between each pair of boolean vectors. (see dice function documentation)

17. \[ Y = \text{pdist}(X, \text{‘kulsinski’}) \]

Computes the Kulsinski distance between each pair of boolean vectors. (see kulsinski function documentation)

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. \( Y = \text{pdist}(X, \text{`wminkowski'}) \)

Computes the weighted Minkowski distance between each pair of vectors. (see \text{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:

\[
dm = \text{pdist}(X, \lambda u, v: \text{np.sqrt}(((u-v)**2).\text{sum}))
\]

Note that you should avoid passing a reference to one of the distance functions defined in this library. For example:

\[
dm = \text{pdist}(X, \text{sokalsneath})
\]

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:

\[
dm = \text{pdist}(X, \text{`sokalsneath'})
\]

**Parameters**

- \( X \) : ndarray
  An \( m \) by \( n \) array of \( m \) original observations in an \( n \)-dimensional space.
- \( \text{metric} \) : str or function, optional
  The distance metric to use. The distance function can be `braycurtis', `canberra', `chebyshev', `cityblock', `correlation', `cosine', `dice', `euclidean', `hamming', `jaccard', `kulsinski', `mahalanobis', `matching', `minkowski', `rogerstanimoto', `russellrao', `seuclidean', `sokalmichener', `sokalsneath', `sqeuclidean', `yule'.
- \( w \) : ndarray, optional
  The weight vector (for weighted Minkowski).
- \( p \) : double, optional
  The p-norm to apply (for Minkowski, weighted and unweighted)
- \( V \) : ndarray, optional
  The variance vector (for standardized Euclidean).
- \( VI \) : ndarray, optional
  The inverse of the covariance matrix (for Mahalanobis).

**Returns**

- \( Y \) : ndarray
  Returns a condensed distance matrix \( Y \). For each \( i \) and \( j \) (where \( i < j < n \)), the metric \( \text{dist}(u=X[i], v=X[j]) \) is computed and stored in entry \( ij \).

**See also:**

\texttt{squareform} converts between condensed distance matrices and square distance matrices.

**Notes**

See \texttt{squareform} for information on how to calculate the index of this entry or to convert the condensed distance matrix to a redundant square matrix.

\texttt{scipy.spatial.distance.cdist} \((XA, XB, metric='euclidean', p=2, V=None, VI=None, w=None)\)

Computes distance between each pair of the two collections of inputs.

The following are common calling conventions:
1. $Y = \text{cdist}(XA, XB, 'euclidean')$

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. $Y = \text{cdist}(XA, XB, 'minkowski', p)$

Computes the distances using the Minkowski distance $||u - v||_p$ ($p$-norm) where $p \geq 1$.

3. $Y = \text{cdist}(XA, XB, 'cityblock')$

Computes the city block or Manhattan distance between the points.

4. $Y = \text{cdist}(XA, XB, 'seuclidean', V=None)$

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. $Y = \text{cdist}(XA, XB, 'sqeuclidean')$

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 $|| \ast ||_2$ is the 2-norm of its argument $\ast$, 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. \( Y = \text{cdist}(X_A, X_B, \ 'braycurtis') \)

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. \( Y = \text{cdist}(X_A, X_B, \ 'mahalanobis', \ VI=None) \)

Computes the Mahalanobis distance between the points. The Mahalanobis distance between two points \( u \) and \( v \) is \((u - v)(1/V)(u - v)^T\) where \((1/V)\) (the \( V \) variable) is the inverse covariance. If \( V \) is not None, \( V \) will be used as the inverse covariance matrix.

14. \( Y = \text{cdist}(X_A, X_B, \ 'yule') \)

Computes the Yule distance between the boolean vectors. (see \texttt{yule} function documentation)

15. \( Y = \text{cdist}(X_A, X_B, \ 'matching') \)

Computes the matching distance between the boolean vectors. (see \texttt{matching} function documentation)

16. \( Y = \text{cdist}(X_A, X_B, \ 'dice') \)

Computes the Dice distance between the boolean vectors. (see \texttt{dice} function documentation)

17. \( Y = \text{cdist}(X_A, X_B, \ 'kulsinski') \)

Computes the Kulsinski distance between the boolean vectors. (see \texttt{kulsinski} function documentation)

18. \( Y = \text{cdist}(X_A, X_B, \ 'rogerstanimoto') \)

Computes the Rogers-Tanimoto distance between the boolean vectors. (see \texttt{rogerstanimoto} function documentation)

19. \( Y = \text{cdist}(X_A, X_B, \ 'russellrao') \)

Computes the Russell-Rao distance between the boolean vectors. (see \texttt{russellrao} function documentation)

20. \( Y = \text{cdist}(X_A, X_B, \ 'sokalmichener') \)

Computes the Sokal-Michener distance between the boolean vectors. (see \texttt{sokalmichener} function documentation)

21. \( Y = \text{cdist}(X_A, X_B, \ 'sokalsneath') \)

Computes the Sokal-Sneath distance between the vectors. (see \texttt{sokalsneath} function documentation)

22. \( Y = \text{cdist}(X_A, X_B, \ 'wminkowski') \)

Computes the weighted Minkowski distance between the vectors. (see \texttt{wminkowski} function documentation)

23. \( Y = \text{cdist}(X_A, X_B, \ f) \)

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:
dm = cdist(XA, XB, lambda u, v: 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:

dm = cdist(XA, XB, 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:

dm = cdist(XA, XB, 'sokalsneath')

**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
- **w**: ndarray, optional
  - The weight vector (for weighted Minkowski).
- **p**: scalar, optional
  - The \( p \)-norm to apply (for Minkowski, weighted and unweighted).
- **V**: ndarray, optional
  - The variance vector (for standardized Euclidean).
- **VI**: ndarray, optional
  - The inverse of the covariance matrix (for Mahalanobis).

**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.

**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]])
```

```python
scipy.spatial.distance.squareform(X, force='no', checks=True)
```

Converts 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 checks is 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. \(v = \text{squareform}(X)\)

Given a square d-by-d symmetric distance matrix X, \(v=\text{squareform}(X)\) returns a d * (d-1) / 2 (or \(\binom{n}{2}\)) sized vector v.

\(v[\binom{n}{2}-\binom{i}{2}+(j-i-1)]\) is the distance between points i and j. If X is non-square or asymmetric, an error is returned.

2. \(X = \text{squareform}(v)\)

Given a d*d(-1)/2 sized v for some integer d>=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 \(v[\binom{n}{2}-\binom{i}{2}+(j-u-1)]\) and all diagonal elements are zero.

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.

```python
is_valid_dm(D[, tol, throw, name, warning])
```

Returns True if input array is a valid distance matrix.

---

5.31. Spatial algorithms and data structures (**scipy.spatial**) 1107
is_valid_y(y[, warning, throw, name]) Returns True if the input array is a valid condensed distance matrix.

num_obs_dm(d) Returns the number of original observations that correspond to a square, redundant distance matrix.

num_obs_y(Y) Returns the number of original observations that correspond to a condensed distance matrix.

distance.is_valid_dm(D, tol=0.0, throw=False, name='D', warning=False)
Returns True if input array is a valid distance matrix.

Distance matrices must be 2-dimensional numpy arrays containing doubles. They must have a zero-diagonal, and they must be symmetric.

Parameters
- **D**: ndarray
  The candidate object to test for validity.
- **tol**: float, optional
  The distance matrix should be symmetric. `tol` is the maximum difference between entries `ij` and `ji` for the distance metric to be considered symmetric.
- **throw**: bool, optional
  An exception is thrown if the distance matrix passed is not valid.
- **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.

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`.

distance.is_valid_y(y, warning=False, throw=False, name=None)
Returns True if the input array is a valid condensed distance matrix.

Condensed distance matrices must be 1-dimensional numpy arrays containing doubles. 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.

distance.num_obs_dm(d)
Returns the number of original observations that correspond to a square, redundant distance matrix.

Parameters
- **d**: ndarray

Returns
- **num_obs_dm**: int
  The target distance matrix.
The number of observations in the redundant distance matrix.

```python
scipy.spatial.distance.num_obs_y(Y)
```

Returns 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 vectors `u` and `v`. Computing distances over a large collection of vectors is inefficient for these functions. Use `pdist` for this purpose.

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>braycurtis(u, v)</code></td>
<td>Computes the Bray-Curtis distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>canberra(u, v)</code></td>
<td>Computes the Canberra distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>chebyshev(u, v)</code></td>
<td>Computes the Chebyshev distance.</td>
</tr>
<tr>
<td><code>cityblock(u, v)</code></td>
<td>Computes the City Block (Manhattan) distance.</td>
</tr>
<tr>
<td><code>correlation(u, v)</code></td>
<td>Computes the correlation distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>cosine(u, v)</code></td>
<td>Computes the Cosine distance between 1-D arrays.</td>
</tr>
<tr>
<td><code>dice(u, v)</code></td>
<td>Computes the Dice dissimilarity between two boolean 1-D arrays.</td>
</tr>
<tr>
<td><code>euclidean(u, v)</code></td>
<td>Computes the Euclidean distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>hamming(u, v)</code></td>
<td>Computes the Hamming distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>jaccard(u, v)</code></td>
<td>Computes the Jaccard-Needham dissimilarity between two boolean 1-D arrays.</td>
</tr>
<tr>
<td><code>kulsinski(u, v)</code></td>
<td>Computes the Kulsinski dissimilarity between two boolean 1-D arrays.</td>
</tr>
<tr>
<td><code>mahalanobis(u, v, VI)</code></td>
<td>Computes the Mahalanobis distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>matching(u, v)</code></td>
<td>Computes the Matching dissimilarity between two boolean 1-D arrays.</td>
</tr>
<tr>
<td><code>minkowski(u, v, p)</code></td>
<td>Computes the Minkowski distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>rogerstanimoto(u, v)</code></td>
<td>Computes the Rogers-Tanimoto dissimilarity between two boolean 1-D arrays.</td>
</tr>
<tr>
<td><code>russellrao(u, v)</code></td>
<td>Computes the Russell-Rao dissimilarity between two boolean 1-D arrays.</td>
</tr>
<tr>
<td><code>seuclidean(u, v, V)</code></td>
<td>Returns the standardized Euclidean distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>sokalmichener(u, v)</code></td>
<td>Computes the Sokal-Michener dissimilarity between two boolean 1-D arrays.</td>
</tr>
<tr>
<td><code>sokalsneath(u, v)</code></td>
<td>Computes the Sokal-Sneath dissimilarity between two boolean 1-D arrays.</td>
</tr>
<tr>
<td><code>sqeuclidean(u, v)</code></td>
<td>Computes the squared Euclidean distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>wminkowski(u, v, p, w)</code></td>
<td>Computes the weighted Minkowski distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>yule(u, v)</code></td>
<td>Computes the Yule dissimilarity between two boolean 1-D arrays.</td>
</tr>
</tbody>
</table>

**scipy.spatial.distance.braycurtis(u, v)**

Computes the Bray-Curtis distance between two 1-D arrays.

Bray-Curtis distance is defined as

\[ \frac{\sum |u_i - v_i|}{\sum |u_i + v_i|} \]

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.

**Returns**

- `braycurtis`: double
  - The Bray-Curtis distance between 1-D arrays `u` and `v`.

**scipy.spatial.distance.canberra(u, v)**

Computes 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.

**Returns**
- \( \text{canberra} \): 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.

```python
scipy.spatial.distance.chebyshev(u, v)
```
Computes 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.

**Returns**
- \( \text{chebyshev} \): double
  The Chebyshev distance between vectors \( u \) and \( v \).

```python
scipy.spatial.distance.cityblock(u, v)
```
Computes 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.

**Returns**
- \( \text{cityblock} \): double
  The City Block (Manhattan) distance between vectors \( u \) and \( v \).

```python
scipy.spatial.distance.correlation(u, v)
```
Computes 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.

**Returns**
- \( \text{correlation} \): double
  The correlation distance between 1-D array \( u \) and \( v \).
scipy.spatial.distance.cosine(u, v)

Computes 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.

**Returns**

- **cosine**: double
  - The Cosine distance between vectors \( u \) and \( v \).

scipy.spatial.distance.dice(u, v)

Computes 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,) ndarray, bool
  - Input 1-D array.
- **v**: (N,) ndarray, bool
  - Input 1-D array.

**Returns**

- **dice**: double
  - The Dice dissimilarity between 1-D arrays \( u \) and \( v \).

scipy.spatial.distance.euclidean(u, v)

Computes the Euclidean distance between two 1-D arrays.

The Euclidean distance between 1-D arrays \( u \) and \( v \), is defined as

\[
||u - v||_2
\]

**Parameters**

- **u**: (N,) array_like
  - Input array.
- **v**: (N,) array_like
  - Input array.

**Returns**

- **euclidean**: double
  - The Euclidean distance between vectors \( u \) and \( v \).

scipy.spatial.distance.hamming(u, v)

Computes 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

\[
\frac{c_{10} + c_{01}}{n}
\]

where \( c_{ij} \) is the number of occurrences of \( u[k] = i \) and \( v[k] = j \) for \( k < n \).

**Parameters**

- **u**: (N,) array_like
  - Input array.
- **v**: (N,) array_like
  - Input array.

**Returns**

- **hamming**: double
  - Input array.
The Hamming distance between vectors \( u \) and \( v \).

\[
\text{scipy.spatial.distance.jaccard}(u, v)
\]
Computes 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.

**Returns**
- \( \text{jaccard} \) : double
  The Jaccard distance between vectors \( u \) and \( v \).

\[
\text{scipy.spatial.distance.kulsinski}(u, v)
\]
Computes 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.

**Returns**
- \( \text{kulsinski} \) : double
  The Kulsinski distance between vectors \( u \) and \( v \).

\[
\text{scipy.spatial.distance.mahalanobis}(u, v, V)
\]
Computes 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.
- \( V \) : ndarray
  The inverse of the covariance matrix.

**Returns**
- \( \text{mahalanobis} \) : double
  The Mahalanobis distance between vectors \( u \) and \( v \).

\[
\text{scipy.spatial.distance.matching}(u, v)
\]
Computes the Matching dissimilarity between two boolean 1-D arrays.

The Matching dissimilarity between two boolean 1-D arrays \( u \) and \( v \), is defined as

\[
\frac{c_{TF} + c_{FT}}{n}
\]

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.

**Returns**

- **matching**: double
  - The Matching dissimilarity between vectors $u$ and $v$.

### scipy.spatial.distance.minkowski($u$, $v$, $p$)

Computes 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 $||u - v||_p$.

**Returns**

- **d**: double
  - The Minkowski distance between vectors $u$ and $v$.

### scipy.spatial.distance.rogerstanimoto($u$, $v$)

Computes 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

$$ R = \frac{c_{TT} + c_{FF}}{c_{TT} + c_{FF} + R} $$

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.

**Returns**

- **rogerstanimoto**: double
  - The Rogers-Tanimoto dissimilarity between vectors $u$ and $v$.

### scipy.spatial.distance.russellrao($u$, $v$)

Computes 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.

**Returns**

- **russellrao**: double
  - The Russell-Rao dissimilarity between vectors $u$ and $v$.

### scipy.spatial.distance.seuclidean($u$, $v$, $V$)

Returns the standardized Euclidean distance between two 1-D arrays.

The standardized Euclidean distance between $u$ and $v$.

**Parameters**

- **u**: (N,) array_like
  - Input array.
Input array.
\[ v: (N,) \text{array_like} \]
Input array.
\[ V: (N,) \text{array_like} \]
\[ V \] is an 1-D array of component variances. It is usually computed among a larger collection vectors.

Returns

- **euclidean**: double
  The standardized Euclidean distance between vectors \( u \) and \( v \).

**scipy.spatial.distance.sokalmichener** \((u, v)\)

Computes 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

- \( u: (N,) \text{array_like, bool} \)
  Input array.
- \( v: (N,) \text{array_like, bool} \)

Returns

- **sokalmichener**: double
  The Sokal-Michener dissimilarity between vectors \( u \) and \( v \).

**scipy.spatial.distance.sokalsneath** \((u, v)\)

Computes 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

- \( u: (N,) \text{array_like, bool} \)
  Input array.
- \( v: (N,) \text{array_like, bool} \)

Returns

- **sokalsneath**: double
  The Sokal-Sneath dissimilarity between vectors \( u \) and \( v \).

**scipy.spatial.distance.sqeuclidean** \((u, v)\)

Computes the squared Euclidean distance between two 1-D arrays.

The squared Euclidean distance between \( u \) and \( v \) is defined as

\[
||u - v||_2^2
\]

Parameters

- \( u: (N,) \text{array_like} \)
  Input array.
- \( v: (N,) \text{array_like} \)

Returns

- **sqeuclidean**: double
  The squared Euclidean distance between vectors \( u \) and \( v \).

**scipy.spatial.distance.wminkowski** \((u, v, p, w)\)

Computes 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**

- \( \text{wminkowski} : \) double
  - The weighted Minkowski distance between vectors \( u \) and \( v \).

```python
scipy.spatial.distance.yule(u, v)
```
Computes the Yule dissimilarity between two boolean 1-D arrays.

The Yule dissimilarity is defined as

\[
R = \frac{c_{TT} * c_{FF} + R}{2}
\]
where \( c_{ij} \) is the number of occurrences of \( u[k] = i \) and \( v[k] = j \) for \( k < n \) and \( R = 2.0 * c_{TF} * c_{FT} \).

**Parameters**

- \( u : (N,) \) array_like, bool
  - Input array.
- \( v : (N,) \) array_like, bool
  - Input array.

**Returns**

- \( \text{yule} : \) double
  - The Yule dissimilarity between vectors \( u \) and \( v \).

**Functions**

- `braycurtis(u, v)` Computes the Bray-Curtis distance between two 1-D arrays.
- `callable(object) -> bool)` Return whether the object is callable (i.e., some kind of function).
- `canberra(u, v)` Computes the Canberra distance between two 1-D arrays.
- `cdist(XA, XB[, metric, p, V, VI, w])` Computes distance between each pair of the two collections of inputs.
- `chebyshev(u, v)` Computes the Chebyshev distance.
- `cityblock(u, v)` Computes the City Block (Manhattan) distance.
- `correlation(u, v)` Computes the correlation distance between two 1-D arrays.
- `cosine(u, v)` Computes the Cosine distance between 1-D arrays.
- `dice(u, v)` Computes the Dice dissimilarity between two boolean 1-D arrays.
- `euclidean(u, v)` Computes the Euclidean distance between two 1-D arrays.
- `hamming(u, v)` Computes the Hamming distance between two 1-D arrays.
- `is_valid_dm(D[, tol, throw, name, warning])` Returns True if input array is a valid distance matrix.
- `is_valid_y(Y[, warning, throw, name])` Returns True if the input array is a valid condensed distance matrix.
- `jaccard(u, v)` Computes the Jaccard-Needham dissimilarity between two boolean 1-D arrays.
- `kulsinski(u, v)` Computes the Kulinski dissimilarity between two boolean 1-D arrays.
- `mahalanobis(u, v, VI)` Computes the Mahalanobis distance between two 1-D arrays.
- `matching(u, v)` Computes the Matching dissimilarity between two boolean 1-D arrays.
- `minkowski(u, v, p)` Computes the Minkowski distance between two 1-D arrays.
- `norm(a[, ord])` Matrix or vector norm.
- `num_obs_dm(d)` Returns the number of original observations that correspond to a square, redundant distance matrix.
- `num_obs_y(Y)` Returns the number of original observations that correspond to a condensed distance matrix.
- `pdist(X[, metric, p, V, VI])` Pairwise distances between observations in n-dimensional space.
- `rogerstanimoto(u, v)` Computes the Rogers-Tanimoto dissimilarity between two boolean 1-D arrays.
- `russellrao(u, v)` Computes the Russell-Rao dissimilarity between two boolean 1-D arrays.
- `seuclidean(u, v, V)` Returns the standardized Euclidean distance between two 1-D arrays.
<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>sokalmichener</code></td>
<td>Computes the Sokal-Michener dissimilarity between two boolean 1-D arrays.</td>
</tr>
<tr>
<td><code>sokalsneath</code></td>
<td>Computes the Sokal-Sneath dissimilarity between two boolean 1-D arrays.</td>
</tr>
<tr>
<td><code>sqeuclidean</code></td>
<td>Computes the squared Euclidean distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>squareform</code></td>
<td>Converts a vector-form distance vector to a square-form distance matrix, and vice-versa.</td>
</tr>
<tr>
<td><code>wminkowski</code></td>
<td>Computes the weighted Minkowski distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>yule</code></td>
<td>Computes the Yule dissimilarity between two boolean 1-D arrays.</td>
</tr>
</tbody>
</table>

### Classes

#### 5.31.2 Delaunay Triangulation, Convex Hulls and Voronoi Diagrams

**Class** `scipy.spatial.Delaunay` (points[, furthest_site=\_\_false\_\_], incremental=\_\_false\_\_, qhull_options=\_\_none\_\_)  
Delaunay tesselation 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  
  New in version 0.12.0.  
  incremental : bool, optional  
  Allow adding new points incrementally. This takes up some additional re-  
  sources.  
  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” for ndim > 4 and “Qbb  
  Qc Qz” otherwise. Incremental mode omits “Qz”.  

**Raises**  
QhullError  
Raised when Qhull encounters an error condition, such as geometrical de-  
  generacy when options to resolve are not enabled.  

ValueError  
Raised if an incompatible array is given as input.

**Notes**  
The tesselation is computed using the Qhull library Qhull library.  

**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.

Do not call the `add_points` method from a __del__ destructor.
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.copy())
>>> plt.plot(points[:,0], points[:,1], 'o')
>>> plt.show()
```

![Triangulation plot](image)

Point indices and coordinates for the two triangles forming the triangulation:

```python
>>> tri.simplices
array([[3, 2, 0],
       [3, 1, 0]], dtype=int32)
>>> points[tri.simplices]
array([[[ 1. , 1. ],
       [ 1. , 0. ],
       [ 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:
>>> p = np.array(((0.1, 0.2), (1.5, 0.5)))
>>> tri.find_simplex(p)
array([ 1, -1], dtype=int32)

We can also compute barycentric coordinates in triangle 1 for these points:

```python
>>> b = tri.transform[1,:2].dot(p - tri.transform[1,2])
>>> np.c_[b, 1 - b.sum(axis=1)]
array([[ 0.1 , 0.2 , 0.7 ],
       [ 1.27272727, 0.27272727, -0.54545455]])
```

The coordinates for the first point are all positive, meaning it is indeed inside the triangle.

**Attributes**

- **transform**
  Affine transform from $x$ to the barycentric coordinates $c$.
  
  **Type**
  
  ndarray of double, shape (nsimplex, ndim+1, ndim)

  This is defined by:

  $T c = x - r$

  At vertex $j$, $c_j = 1$ and the other coordinates zero.

  For simplex $i$, `transform[i,:ndim,:ndim]` contains inverse of the matrix $T$, and `transform[i,ndim,:]` contains the vector $r$.

- **vertex_to_simplex**
  Lookup array, from a vertex, to some simplex which it is a part of.
  
  **Type**
  
  ndarray of int, shape (npoints,)

- **convex_hull**
  Vertices of facets forming the convex hull of the point set.
  
  **Type**
  
  ndarray of int, shape (nfaces, ndim)

  The array contains the indices of the points belonging to the $(N-1)$-dimensional facets that form the convex hull of the triangulation.

  **Note:** Computing convex hulls via the Delaunay triangulation is inefficient and subject to increased numerical instability. Use `ConvexHull` instead.

- **vertex_neighbor_vertices**
  Neighboring vertices of vertices.
  
  Tuple of two ndarrays of int: (indices, indptr). The indices of neighboring vertices of vertex $k$ are `indptr[indices[k]:indices[k+1]]`. 
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).
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. .. versionadded:: 0.12.0
vertices Same as simplices, but deprecated.

Methods

add_points(points[, restart]) Process a set of additional new points.
close() Finish incremental processing.
find_simplex(self, xi[, bruteforce, tol]) Find the simplices containing the given points.
lift_points(self, x) Lift points to the Qhull paraboloid.
plane_distance(self, xi) Compute hyperplane distances to the point xi from all simplices.

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.

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.

Delaunay.find_simplex(self, xi[, bruteforce, tol=None])
Find the simplices containing the given points.

Parameters
tri : DelaunayInfo
Delaunay triangulation
.. _qh_findbestfacet:

qh_findbestfacet

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.

.. _ConvexHull:

ConvexHull

The convex hull is computed using the Qhull library.

Do not call the `add_points` method from a `__del__` destructor.

References

[Qhull]

Examples

Convex hull of a random set of points:

>>> from scipy.spatial import ConvexHull
>>> points = np.random.rand(30, 2)  # 30 random points in 2-D
>>> hull = ConvexHull(points)

Plot it:
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

<table>
<thead>
<tr>
<th>Attribute</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>points</code></td>
<td>(ndarray of double, shape (npoints, ndim)) Coordinates of input points.</td>
</tr>
<tr>
<td><code>vertices</code></td>
<td>(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.</td>
</tr>
<tr>
<td><code>simplices</code></td>
<td>(ndarray of ints, shape (nfacet, ndim)) Indices of points forming the simplical facets of the convex hull.</td>
</tr>
<tr>
<td><code>neighbors</code></td>
<td>(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.</td>
</tr>
<tr>
<td><code>equations</code></td>
<td>(ndarray of double, shape (nfacet, ndim+1)) [normal, offset] forming the hyperplane equation of the facet (see Qhull documentation for more).</td>
</tr>
<tr>
<td><code>coplanar</code></td>
<td>(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.</td>
</tr>
</tbody>
</table>

### Methods

- `add_points(points[, restart])` Process a set of additional new points.
- `close()` Finish incremental processing.
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.

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.

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.
Do not call the add_points method from a __del__ destructor.

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:

>>> import matplotlib.pyplot as plt
>>> 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, 0], [-1, 1], [1, -1, 0], [3, -1, 2], [-1, 3], [-1, 2], [3, 2, 0, 1], [2, -1, 0], [3, -1, 1]]
>>> vor.ridge_vertices
[[-1, 0], [-1, 0], [-1, 1], [-1, 1], [0, 1], [-1, 3], [-1, 2], [2, 3], [-1, 3], [-1, 2], [0, 2],
```

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]],
```

5.31. Spatial algorithms and data structures (scipy.spatial) 1123
[5, 4],
[8, 7],
[2, 1],
[4, 1],
[4, 7]), dtype=int32)

Attributes

<table>
<thead>
<tr>
<th>Attribute</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>points</td>
<td>(ndarray of double, shape (npoints, ndim)) Coordinates of input points.</td>
</tr>
<tr>
<td>vertices</td>
<td>(ndarray of double, shape (nvertices, ndim)) Coordinates of the Voronoi vertices.</td>
</tr>
<tr>
<td>ridge_points</td>
<td>(ndarray of ints, shape (nridges, 2)) Indices of the points between which each Voronoi ridge lies.</td>
</tr>
<tr>
<td>ridge_vertices</td>
<td>(list of list of ints, shape (nridges, *)) Indices of the Voronoi vertices forming each Voronoi ridge.</td>
</tr>
<tr>
<td>regions</td>
<td>(list of list of ints, shape (nregions, *)) Indices of the Voronoi vertices forming each Voronoi region. -1 indicates vertex outside the Voronoi diagram.</td>
</tr>
<tr>
<td>point_region</td>
<td>(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.</td>
</tr>
</tbody>
</table>

Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>add_points</td>
<td>Process a set of additional new points.</td>
</tr>
<tr>
<td>close()</td>
<td>Finish incremental processing.</td>
</tr>
</tbody>
</table>

Voronoi.add_points(points, restart=False)

Process a set of additional new points.

Parameters

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>points</td>
<td>ndarray</td>
</tr>
<tr>
<td>restart</td>
<td>bool, optional</td>
</tr>
</tbody>
</table>

Raises

<table>
<thead>
<tr>
<th>Error</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>QhullError</td>
<td>Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.</td>
</tr>
</tbody>
</table>

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.

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.

5.31.3 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

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.

convex_hull_plot_2d(hull, ax=None)
    Plot the given convex hull diagram in 2-D
    Parameters
        hull : scipy.spatial.ConvexHull instance
            Convex hull to plot
        ax : matplotlib.axes.Axes instance, optional
            Axes to plot on
    Returns
        fig : matplotlib.figure.Figure instance
            Figure for the plot
    See also:
        ConvexHull

Notes
Requires Matplotlib.

voronoi_plot_2d(vor, ax=None)
    Plot the given Voronoi diagram in 2-D
    Parameters
        vor : scipy.spatial.Voronoi instance
            Diagram to plot
        ax : matplotlib.axes.Axes instance, optional
            Axes to plot on
    Returns
        fig : matplotlib.figure.Figure instance
            Figure for the plot
    See also:
        Voronoi

Notes
Requires Matplotlib.

See also:

Tutorial
5.31.4 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], :]
# tesselation 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:

```python
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:

```python
(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**

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>tsearch(tri, xi)</code></td>
<td>Find simplices containing the given points.</td>
</tr>
<tr>
<td><code>distance_matrix(x, y[, p, threshold])</code></td>
<td>Compute the distance matrix.</td>
</tr>
<tr>
<td><code>minkowski_distance(x, y[, p])</code></td>
<td>Compute the L**p distance between two arrays.</td>
</tr>
<tr>
<td><code>minkowski_distance_p(x, y[, p])</code></td>
<td>Compute the p-th power of the L**p distance between two arrays.</td>
</tr>
<tr>
<td><code>procrustes(data1, data2)</code></td>
<td>Procrustes analysis, a similarity test for two data sets.</td>
</tr>
</tbody>
</table>

**scipy.spatial.tsearch(tri, xi)**

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`
- `scipy.spatial.distance_matrix(x, y, p=2, threshold=1000000)`

Compute the distance matrix.

Returns the matrix of all pair-wise distances.

**Parameters**

- `x`: (M, K) array_like
  - TODO: description needed
- `y`: (N, K) array_like
  - TODO: description needed
- `p`: float, 1 <= p <= infinity
  - Which Minkowski p-norm to use.
threshold : positive int
    If \( M \times N \times K > \text{threshold} \), algorithm uses a Python loop instead of large
temporary arrays.

Returns result : (M, N) ndarray
    Distance matrix.

Examples

```python
>>> distance_matrix([[0,0],[0,1]], [[1,0],[1,1]])
array([[ 1.        , 1.41421356],
       [ 1.41421356, 1.      ]])
```

scipy.spatial.minkowski_distance(x, y, p=2)
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 <= p <= infinity
    Which Minkowski p-norm to use.

Examples

```python
>>> minkowski_distance([[0,0],[0,0]], [[1,1],[0,1]])
array([1.41421356, 1.      ])  
```

scipy.spatial.minkowski_distance_p(x, y, p=2)
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 <= p <= infinity
    Which Minkowski p-norm to use.

Examples

```python
>>> minkowski_distance_p([[0,0],[0,0]], [[1,1],[0,1]])
array([2, 1])
```

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:

\* \( tr(\mathbf{A}^T \mathbf{A}) = 1 \).
\* Both sets of points are centered around the origin.
Procrustes ([R273], [R274]) then applies the optimal transform to the second matrix (including scaling/dilation,
rotations, and reflections) to minimize \( M^2 = \sum (\text{data1} - \text{data2})^2 \), 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 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 \( t\text{r}(AA^T) = 1 \).

- **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

**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 \( t\text{r}(AA^T) = 1 \).
- 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**

[R273], [R274]

**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)
>>> round(disparity)
0.0
```

## 5.32 Distance computations (scipy.spatial.distance)

### 5.32.1 Function Reference

Distance matrix computation from a collection of raw observation vectors stored in a rectangular array.
**pdist**(X[, metric, p, w, V, VI])  
Pairwise distances between observations in n-dimensional space.

**cdist**(XA, XB[, metric, p, V, VI, w])  
Computes distance between each pair of the two collections of inputs.

**squareform**(X[, force, checks])  
Converts a vector-form distance vector to a square-form distance matrix, and vice-versa.

```python
scipy.spatial.distance.pdist(X, metric='euclidean', p=2, w=None, V=None, VI=None)
```

Pairwise distances between observations in n-dimensional space.

The following are common calling conventions.

1. \( Y = \text{pdist}(X, \text{metric='euclidean'}) \)

   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. \( Y = \text{pdist}(X, \text{metric='minkowski', p}) \)

   Computes the distances using the Minkowski distance \( ||u - v||_p \) (p-norm) where \( p \geq 1 \).

3. \( Y = \text{pdist}(X, \text{metric='cityblock'}) \)

   Computes the city block or Manhattan distance between the points.

4. \( Y = \text{pdist}(X, \text{metric='seuclidean', V=None}) \)

   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. \( Y = \text{pdist}(X, \text{metric='squaredeuclidean'}) \)

   Computes the squared Euclidean distance \( ||u - v||^2 \) between the vectors.

6. \( Y = \text{pdist}(X, \text{metric='cosine'}) \)

   Computes the cosine distance between vectors \( u \) and \( v \),

   \[
   1 - \frac{u \cdot v}{||u||_2 ||v||_2}
   \]

   where \( ||*||_2 \) is the 2-norm of its argument \( * \), and \( u \cdot v \) is the dot product of \( u \) and \( v \).

7. \( Y = \text{pdist}(X, \text{metric='correlation'}) \)

   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. \( Y = \text{pdist}(X, \text{metric='hamming'}) \)

   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. \( Y = \text{pdist}(X, \text{metric='jaccard'}) \)

   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. \( Y = \text{pdist}(X, \text{metric='chebyshev'}) \)

    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 $(u - v)(1/V)(u - v)^T$ 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. $Y = \text{pdist}(X, 'matching')$

Computes the matching distance between each pair of boolean vectors. (see matching function documentation)

16. $Y = \text{pdist}(X, 'dice')$

Computes the Dice distance between each pair of boolean vectors. (see dice function documentation)

17. $Y = \text{pdist}(X, 'kulsinski')$

Computes the Kulsinski distance between each pair of boolean vectors. (see kulsinski function documentation)

18. $Y = \text{pdist}(X, 'rogerstanimoto')$

Computes the Rogers-Tanimoto distance between each pair of boolean vectors. (see rogerstanimoto function documentation)

19. $Y = \text{pdist}(X, 'russellrao')$

Computes the Russell-Rao distance between each pair of boolean vectors. (see russellrao function documentation)

20. $Y = \text{pdist}(X, 'sokalmichener')$

Computes the Sokal-Michener distance between each pair of boolean vectors. (see sokalmichener function documentation)

21. $Y = \text{pdist}(X, 'sokalsneath')$

Computes the Sokal-Sneath distance between each pair of boolean vectors. (see sokalsneath function documentation)
22. `Y = pdist(X, 'wminkowski')`

Computes the weighted Minkowski distance between each pair of vectors. (see `wminkowski` function documentation)

23. `Y = 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 = pdist(X, lambda u, v: 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 = pdist(X, 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 = pdist(X, 'sokalsneath')
```

### Parameters

- **X**: ndarray
  - An m by n array of m original observations in an n-dimensional space.
- **metric**: str or function, optional
  - The distance metric to use. The distance function can be `braycurtis`, `canberra`, `chebyshev`, `cityblock`, `correlation`, `cosine`, `dice`, `euclidean`, `hamming`, `jaccard`, `kulsinski`, `mahalanobis`, `matching`, `minkowski`, `rogerstanimoto`, `russellrao`, `seuclidean`, `sokalmichener`, `sokalsneath`, `sqeuclidean`, `yule`.
- **w**: ndarray, optional
  - The weight vector (for weighted Minkowski).
- **p**: double, optional
  - The p-norm to apply (for Minkowski, weighted and unweighted)
- **V**: ndarray, optional
  - The variance vector (for standardized Euclidean).
- **VI**: ndarray, optional
  - The inverse of the covariance matrix (for Mahalanobis).

### Returns

- **Y**: ndarray
  - Returns a condensed distance matrix Y. For each i and j (where \(i < j < n\)), the metric `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.

```python
scipy.spatial.distance.cdist(XA, XB, metric='euclidean', p=2, V=None, VI=None, w=None)
```

Computes distance between each pair of the two collections of inputs.

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. \( Y = \text{cdist}(XA, XB, \text{'minkowski'}, p) \)

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

\[
\sqrt{\sum (u_i - v_i)^2/V[i]},
\]

\( V \) 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. \( Y = \text{cdist}(XA, XB, \text{'cosine'}) \)

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 \( * \), and \( u \cdot v \) is the dot product of \( u \) and \( v \).

7. \( Y = \text{cdist}(XA, XB, \text{'correlation'}) \)

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 \( \bar{u} \) is the mean of the elements of vector \( v \), and \( x \cdot y \) is the dot product of \( x \) and \( y \).

8. \( Y = \text{cdist}(XA, XB, \text{'hamming'}) \)

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. \( Y = \text{cdist}(XA, XB, \text{'jaccard'}) \)

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. \( Y = \text{cdist}(XA, XB, \text{'chebyshev'}) \)

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. \( Y = \text{cdist}(XA, XB, \text{'canberra'}) \)

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. \( Y = \text{cdist}(XA, XB, \text{'braycurtis'}) \)

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. \( Y = \text{cdist}(XA, XB, \text{'mahalanobis'}, VI=None) \)

Computes the Mahalanobis distance between the points. The Mahalanobis distance between two points \( u \) and \( v \) is \((u - v)(1/V)(u - v)^T\) 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. \( Y = \text{cdist}(XA, XB, \text{'yule'}) \)

Computes the Yule distance between the boolean vectors. (see \texttt{yule} function documentation)

15. \( Y = \text{cdist}(XA, XB, \text{'matching'}) \)

Computes the matching distance between the boolean vectors. (see \texttt{matching} function documentation)

16. \( Y = \text{cdist}(XA, XB, \text{'dice'}) \)

Computes the Dice distance between the boolean vectors. (see \texttt{dice} function documentation)

17. \( Y = \text{cdist}(XA, XB, \text{'kulsinski'}) \)

Computes the Kulinski distance between the boolean vectors. (see \texttt{kulsinski} function documentation)

18. \( Y = \text{cdist}(XA, XB, \text{'rogerstanimoto'}) \)

Computes the Rogers-Tanimoto distance between the boolean vectors. (see \texttt{rogerstanimoto} function documentation)

19. \( Y = \text{cdist}(XA, XB, \text{'russellrao'}) \)

Computes the Russell-Rao distance between the boolean vectors. (see \texttt{russellrao} function documentation)

20. \( Y = \text{cdist}(XA, XB, \text{'sokalmichener'}) \)

Computes the Sokal-Michener distance between the boolean vectors. (see \texttt{sokalmichener} function documentation)

21. \( Y = \text{cdist}(XA, XB, \text{'sokalsneath'}) \)

Computes the Sokal-Sneath distance between the vectors. (see \texttt{sokalsneath} function documentation)

22. \( Y = \text{cdist}(XA, XB, \text{'wminkowski'}) \)

Computes the weighted Minkowski distance between the vectors. (see \texttt{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 \( f \). For example, Euclidean distance between the vectors could be computed as follows:
Note that you should avoid passing a reference to one of the distance functions defined in this library. For example:

```python
dm = cdist(XA, XB, 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 = cdist(XA, XB, 'sokalsneath')
```

**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', 'kulsinski', 'mahalanobis', 'matching', 'minkowski', 'rogerstanimoto', 'russellrao', 'seuclidean', 'sokalmichener', 'sokalsneath', 'sqeuclidean', 'wminkowski', 'yule'.
- **w**: ndarray, optional
  - The weight vector (for weighted Minkowski).
- **p**: scalar, optional
  - The \( p \)-norm to apply (for Minkowski, weighted and unweighted)
- **V**: ndarray, optional
  - The variance vector (for standardized Euclidean).
- **VI**: ndarray, optional
  - The inverse of the covariance matrix (for Mahalanobis).

**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.

**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:
>>> 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(X, force='no', checks=True)
Converts 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 checks is 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 * (d-1) / 2 (or $\binom{n}{2}$) sized vector v.

   v[{n choose 2} -{n-i choose 2} + (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*d(-1)/2 sized v for some integer d>=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 choose 2} -{n-i choose 2} + (j-u-1)] and all diagonal elements are zero.

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.

is_valid_dm(D[, tol, throw, name, warning])  Returns True if input array is a valid distance matrix.
### is_valid_dm

```python
scipy.spatial.distance.is_valid_dm(D, tol=0.0, throw=False, name='D', warning=False)
```

Returns True if input array is a valid distance matrix.

Distance matrices must be 2-dimensional numpy arrays containing doubles. They must have a zero-diagonal, and they must be symmetric.

**Parameters**

- `D`: ndarray
  - The candidate object to test for validity.
- `tol`: float, optional
  - The distance matrix should be symmetric. `tol` is the maximum difference between entries $ij$ and $ji$ for the distance metric to be considered symmetric.
- `throw`: bool, optional
  - An exception is thrown if the distance matrix passed is not valid.
- `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`.

### is_valid_y

```python
scipy.spatial.distance.is_valid_y(y, warning=False, throw=False, name=None)
```

Returns True if the input array is a valid condensed distance matrix.

Condensed distance matrices must be 1-dimensional numpy arrays containing doubles. 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.

### num_obs_dm

```python
scipy.spatial.distance.num_obs_dm(d)
```

Returns 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 original observations that correspond to a square, redundant distance matrix.
The number of observations in the redundant distance matrix.

**scipy.spatial.distance.num_obs_y(Y)**

Returns 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 vectors u and v. Computing distances over a large collection of vectors is inefficient for these functions. Use `pdist` for this purpose.

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>braycurtis(u, v)</code></td>
<td>Computes the Bray-Curtis distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>canberra(u, v)</code></td>
<td>Computes the Canberra distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>chebyshev(u, v)</code></td>
<td>Computes the Chebyshev distance.</td>
</tr>
<tr>
<td><code>cityblock(u, v)</code></td>
<td>Computes the City Block (Manhattan) distance.</td>
</tr>
<tr>
<td><code>correlation(u, v)</code></td>
<td>Computes the correlation distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>cosine(u, v)</code></td>
<td>Computes the Cosine distance between 1-D arrays.</td>
</tr>
<tr>
<td><code>dice(u, v)</code></td>
<td>Computes the Dice dissimilarity between two boolean 1-D arrays.</td>
</tr>
<tr>
<td><code>euclidean(u, v)</code></td>
<td>Computes the Euclidean distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>hamming(u, v)</code></td>
<td>Computes the Hamming distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>jaccard(u, v)</code></td>
<td>Computes the Jaccard-Needham dissimilarity between two boolean 1-D arrays.</td>
</tr>
<tr>
<td><code>kulsinski(u, v)</code></td>
<td>Computes the Kulinski dissimilarity between two boolean 1-D arrays.</td>
</tr>
<tr>
<td><code>mahalanobis(u, v, VI)</code></td>
<td>Computes the Mahalanobis distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>matching(u, v)</code></td>
<td>Computes the Matching dissimilarity between two boolean 1-D arrays.</td>
</tr>
<tr>
<td><code>minkowski(u, v, p)</code></td>
<td>Computes the Minkowski distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>rogerstanimoto(u, v)</code></td>
<td>Computes the Rogers-Tanimoto dissimilarity between two boolean 1-D arrays.</td>
</tr>
<tr>
<td><code>russellrao(u, v)</code></td>
<td>Computes the Russell-Rao dissimilarity between two boolean 1-D arrays.</td>
</tr>
<tr>
<td><code>seuclidean(u, v, V)</code></td>
<td>Returns the standardized Euclidean distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>sokalmichener(u, v)</code></td>
<td>Computes the Sokal-Michener dissimilarity between two boolean 1-D arrays.</td>
</tr>
<tr>
<td><code>sokalsneath(u, v)</code></td>
<td>Computes the Sokal-Sneath dissimilarity between two boolean 1-D arrays.</td>
</tr>
<tr>
<td><code>wminkowski(u, v, p, w)</code></td>
<td>Computes the weighted Minkowski distance between two 1-D arrays.</td>
</tr>
<tr>
<td><code>yule(u, v)</code></td>
<td>Computes the Yule dissimilarity between two boolean 1-D arrays.</td>
</tr>
</tbody>
</table>

**scipy.spatial.distance.braycurtis(u, v)**

Computes 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.

**Returns**  
braycurtis : double

The Bray-Curtis distance between 1-D arrays u and v.

**scipy.spatial.distance.canberra(u, v)**

Computes 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.

**Returns**
- \( \text{canberra} \) : 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.

```
scipy.spatial.distance.chebyshev(u, v)
```
Computes 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.

**Returns**
- \( \text{chebyshev} \) : double
  - The Chebyshev distance between vectors \( u \) and \( v \).

```
scipy.spatial.distance.cityblock(u, v)
```
Computes 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.

**Returns**
- \( \text{cityblock} \) : double
  - The City Block (Manhattan) distance between vectors \( u \) and \( v \).

```
scipy.spatial.distance.correlation(u, v)
```
Computes 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.

**Returns**
- \( \text{correlation} \) : double
  - The correlation distance between 1-D array \( u \) and \( v \).
scipy.spatial.distance.cosine(u, v)
Computes 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.

**Returns**

- **cosine**: double
  The Cosine distance between vectors $u$ and $v$.

scipy.spatial.distance.dice(u, v)
Computes 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,) ndarray, bool
  Input 1-D array.
- **v**: (N,) ndarray, bool
  Input 1-D array.

**Returns**

- **dice**: double
  The Dice dissimilarity between 1-D arrays $u$ and $v$.

scipy.spatial.distance.euclidean(u, v)
Computes the Euclidean distance between two 1-D arrays.

The Euclidean distance between 1-D arrays $u$ and $v$, is defined as

$$||u - v||_2$$

**Parameters**

- **u**: (N,) array_like
  Input array.
- **v**: (N,) array_like
  Input array.

**Returns**

- **euclidean**: double
  The Euclidean distance between vectors $u$ and $v$.

scipy.spatial.distance.hamming(u, v)
Computes 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,) array_like
  Input array.
- **v**: (N,) array_like
  Input array.

**Returns**

- **hamming**: double
  The Hamming distance between vectors $u$ and $v$. 

5.32. Distance computations (scipy.spatial.distance)
The Hamming distance between vectors \( u \) and \( v \).

**scipy.spatial.distance.jaccard** \((u, v)\)

Computes 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.

**Returns**
- \( \text{jaccard} \) : double
  - The Jaccard distance between vectors \( u \) and \( v \).

**scipy.spatial.distance.kulsinski** \((u, v)\)

Computes the Kulinsky dissimilarity between two boolean 1-D arrays.

The Kulinsky 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.

**Returns**
- \( \text{kulsinski} \) : double
  - The Kulinsky distance between vectors \( u \) and \( v \).

**scipy.spatial.distance.mahalanobis** \((u, v, VI)\)

Computes 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**
- \( \text{mahalanobis} \) : double
  - The Mahalanobis distance between vectors \( u \) and \( v \).

**scipy.spatial.distance.matching** \((u, v)\)

Computes the Matching dissimilarity between two boolean 1-D arrays.

The Matching dissimilarity between two boolean 1-D arrays \( u \) and \( v \), is defined as

\[
\frac{c_{TF} + c_{FT}}{n}
\]

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.

Returns

- **matching**: double
  - The Matching dissimilarity between vectors u and v.

**scipy.spatial.distance.minkowski** *(u, v, p)*

Computes 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 $||u - v||_p$.

Returns

- **d**: double
  - The Minkowski distance between vectors u and v.

**scipy.spatial.distance.rogerstanimoto** *(u, v)*

Computes 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

$$R = \frac{c_{TT} + c_{FF} + R}{2(c_{TF} + c_{FT})}.$$

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.

Returns

- **rogerstanimoto**: double
  - The Rogers-Tanimoto dissimilarity between vectors u and v.

**scipy.spatial.distance.russellrao** *(u, v)*

Computes 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.

Returns

- **russellrao**: double
  - The Russell-Rao dissimilarity between vectors u and v.

**scipy.spatial.distance.seuclidean** *(u, v, V)*

Returns 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.

scipy.spatial.distance.sokalmichener(u, v)
  Computes 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.

Returns sokalmichener: double
  The Sokal-Michener dissimilarity between vectors u and v.

scipy.spatial.distance.sokalsneath(u, v)
  Computes 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.

Returns sokalsneath: double
  The Sokal-Sneath dissimilarity between vectors u and v.

scipy.spatial.distance.sqeuclidean(u, v)
  Computes the squared Euclidean distance between two 1-D arrays.

The squared Euclidean distance between \( u \) and \( v \) is defined as

\[ ||u - v||_2^2. \]

Parameters
- u : (N,) array_like
  Input array.
- v : (N,) array_like
  Input array.

Returns sqeuclidean: double
  The squared Euclidean distance between vectors u and v.

scipy.spatial.distance.wminkowski(u, v, p, w)
  Computes 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 $v$.

scipy.spatial.distance.yule(u, v)
Computes the Yule dissimilarity between two boolean 1-D arrays.

The Yule dissimilarity is defined as

$$R = \frac{c_{TT} * c_{FF} + R}{2}$$

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.

Returns

- **yule**: double
  - The Yule dissimilarity between vectors $u$ and $v$.

### 5.33 Special functions (scipy.special)

Nearly all of the functions below are universal functions and follow broadcasting and automatic array-looping rules. Exceptions are noted.

#### 5.33.1 Error handling

Errors are handled by returning nans, or other appropriate values. Some of the special function routines will emit warnings when an error occurs. By default this is disabled. To enable such messages use `errprint(1)`, and to disable such messages use `errprint(0)`.

Example:

```python
>>> print scipy.special.bdtr(-1,10,0.3)
>>> scipy.special.errprint(1)
>>> print scipy.special.bdtr(-1,10,0.3)
```

<table>
<thead>
<tr>
<th>errprint(inflag)</th>
<th>Sets or returns the error printing flag for special functions.</th>
</tr>
</thead>
<tbody>
<tr>
<td>SpecialFunctionWarning</td>
<td>Warning that can be issued with errprint(True)</td>
</tr>
</tbody>
</table>

scipy.special.errprint(inflag=None)
Sets or returns the error printing flag for special functions.

Parameters

- **inflag**: bool, optional
  - Whether warnings concerning evaluation of special functions in scipy.special are shown. If omitted, no change is made to the current setting.

Returns

- **old_flag**
Previous value of the error flag

```
exception scipy.special.SpecialFunctionWarning
    Warning that can be issued with errprint(True)
```

## 5.33.2 Available functions

### Airy functions

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>airy(z)</td>
<td>Airy functions and their derivatives.</td>
</tr>
<tr>
<td>airye(z)</td>
<td>Exponentially scaled Airy functions and their derivatives.</td>
</tr>
<tr>
<td>ai_zeros(nt)</td>
<td>Compute the zeros of Airy Functions Ai(x) and Ai′(x), a and a′ respectively, and the associated values of Ai(a′) and Ai′(a).</td>
</tr>
<tr>
<td>bi_zeros(nt)</td>
<td>Compute the zeros of Airy Functions Bi(x) and Bi′(x), b and b′ respectively, and the associated values of Ai(b′) and Ai′(b).</td>
</tr>
<tr>
<td>itairy(x)</td>
<td>Integrals of Airy functions.</td>
</tr>
</tbody>
</table>

**scipy.special.airy(z)**

- **airy(z)**: Airy functions and their derivatives.

  **Parameters**
  - `z`: float or complex  
  
  **Returns**
  - `Ai, Aip, Bi, Bip`  
  
  Airy functions Ai and Bi, and their derivatives Aip and Bip

  **Notes**
  
  The Airy functions Ai and Bi are two independent solutions of \( y''(x) = x y \).

**scipy.special.airye(z)**

- **airye(z)**: Exponentially scaled Airy functions and their derivatives.

  **Scaling:**
  
  \[
  \begin{align*}
  eAi &= Ai \times \exp\left(2.0/3.0 \times z \times \text{sqrt}(z)\right) \\
  eAip &= Aip \times \exp\left(2.0/3.0 \times z \times \text{sqrt}(z)\right) \\
  eBi &= Bi \times \exp\left(-\text{abs}\left(2.0/3.0 \times z \times \text{sqrt}(z)\right).\text{real}\right) \\
  eBip &= Bip \times \exp\left(-\text{abs}\left(2.0/3.0 \times z \times \text{sqrt}(z)\right).\text{real}\right)
  \end{align*}
  \]

  **Parameters**
  - `z`: float or complex  
  
  **Returns**
  - `eAi, eAip, eBi, eBip`  
  
  Airy functions Ai and Bi, and their derivatives Aip and Bip

**scipy.special.ai_zeros(nt)**

- **ai_zeros(nt)**: Compute the zeros of Airy Functions Ai(x) and Ai′(x), a and a′ respectively, and the associated values of Ai(a′) and Ai′(a).

  **Returns**
  - `a[0-L]` – the lth zero of Ai(x)  
  - `ap[0-L]` – the lth zero of Ai′(x)  
  - `ai[0-L]` – Ai(ap[l-1])  
  - `aip[0-L]` – Ai′(a[l-1])

**scipy.special.bi_zeros(nt)**

- **bi_zeros(nt)**: Compute the zeros of Airy Functions Bi(x) and Bi′(x), b and b′ respectively, and the associated values of Ai(b′) and Ai′(b).
**SciPy Reference Guide, Release 0.16.0**

**Returns**
- b[l-1] – the lth zero of Bi(x)
- bp[l-1] – the lth zero of Bi'(x)
- bi[l-1] = Bi(bp[l-1])
- bip[l-1] = Bi'(b[l-1])

`scipy.special.itairy(x) = <ufunc 'itairy'>`

Integrals of Airy functions

Calculates the integral of Airy functions from 0 to x

**Returns**
- Apt, Bpt  
  Integrals for positive arguments
- Ant, Bnt  
  Integrals for negative arguments

**Elliptic Functions and Integrals**

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>ellipj(u, m)</code></td>
<td>Jacobian elliptic functions</td>
</tr>
<tr>
<td><code>ellipk(m)</code></td>
<td>Complete elliptic integral of the first kind</td>
</tr>
<tr>
<td><code>ellipkm1(p)</code></td>
<td>Complete elliptic integral of the first kind around m = 1</td>
</tr>
<tr>
<td><code>ellipkinc(phi, m)</code></td>
<td>Incomplete elliptic integral of the first kind</td>
</tr>
<tr>
<td><code>ellipe(m)</code></td>
<td>Complete elliptic integral of the second kind</td>
</tr>
<tr>
<td><code>ellipeinc(phi, m)</code></td>
<td>Incomplete elliptic integral of the second kind</td>
</tr>
</tbody>
</table>

`scipy.special.ellipj(u, m) = <ufunc 'ellipj'>`

Jacobian elliptic functions

Calculates the Jacobian elliptic functions of parameter m between 0 and 1, and real u.

**Parameters**
- m, u

**Returns**
- sn, cn, dn, ph

Parameters:
- m, u

The returned functions:
- sn(u|m), cn(u|m), dn(u|m)

The value ph is such that if u = ellik(ph, m), then sn(u|m) = sin(ph) and cn(u|m) = cos(ph).

`scipy.special.ellipk(m)`

Complete elliptic integral of the first kind

This function is defined as

\[ K(m) = \int_0^{\pi/2} \frac{dt}{\sqrt{1 - m \sin(t)^2}} \]

**Parameters**
- m : array_like

**Returns**
- K : array_like

The parameter of the elliptic integral.

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

5.33. Special functions (`scipy.special`) 1145
For more precision around point $m = 1$, use $\texttt{ellipkm1}$.

scipy.special.\texttt{ellipkm1}(p) = <ufunc 'ellipkm1'>

Complete elliptic integral of the first kind around $m = 1$

This function is defined as

$$K(p) = \int_0^{\pi/2} \left[ 1 - m \sin(t)^2 \right]^{-1/2} dt$$

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:
- $\texttt{ellipk}$ Complete elliptic integral of the first kind
- $\texttt{ellipkinc}$ Incomplete elliptic integral of the first kind
- $\texttt{ellipe}$ Complete elliptic integral of the second kind
- $\texttt{ellipeinc}$ Incomplete elliptic integral of the second kind

scipy.special.\texttt{ellipkinc}(phi, m) = <ufunc 'ellipkinc'>

Incomplete elliptic integral of the first kind

This function is defined as

$$K(\phi, m) = \int_0^\phi \left[ 1 - m \sin(t)^2 \right]^{-1/2} dt$$

**Parameters**
- **phi**: array_like
  amplitude of the elliptic integral
- **m**: array_like

**Returns**
- **K**: ndarray
  parameter of the elliptic integral
  Value of the elliptic integral.

See also:
- $\texttt{ellipkm1}$ Complete elliptic integral of the first kind, near $m = 1$
- $\texttt{ellipk}$ Complete elliptic integral of the first kind
- $\texttt{ellipe}$ Complete elliptic integral of the second kind
- $\texttt{ellipeinc}$ Incomplete elliptic integral of the second kind

Notes
This function is also called $F(\phi, m)$.

scipy.special.\texttt{ellipe}(m) = <ufunc 'ellipe'>

Complete elliptic integral of the second kind

This function is defined as

$$E(m) = \int_0^{\pi/2} \left[ 1 - m \sin(t)^2 \right]^{1/2} dt$$

**Parameters**
- **m**: array_like

**Returns**
- **E**: ndarray
  Defines the parameter of the elliptic integral.
  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
- `ellipeinc` Incomplete elliptic integral of the second kind

\[
\text{scipy.special.ellipeinc}(\phi, m) = \text{<ufunc 'ellipeinc'>}
\]

Incomplete elliptic integral of the second kind

This function is defined as

\[
E(\phi, m) = \int_{0}^{\phi} \left[ 1 - m \sin^2(t) \right]^{1/2} dt
\]

**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

### Bessel Functions

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>jv(v, z)</code></td>
<td>Bessel function of the first kind of real order v</td>
</tr>
<tr>
<td><code>jve(v, z)</code></td>
<td>Exponentially scaled Bessel function of order v</td>
</tr>
<tr>
<td><code>yn(n, x)</code></td>
<td>Bessel function of the second kind of integer order n</td>
</tr>
<tr>
<td><code>yv(v, z)</code></td>
<td>Bessel function of the second kind of real order</td>
</tr>
<tr>
<td><code>yve(v, z)</code></td>
<td>Exponentially scaled Bessel function of the second kind of real order</td>
</tr>
<tr>
<td><code>kn(n, x)</code></td>
<td>Modified Bessel function of the second kind of integer order n</td>
</tr>
<tr>
<td><code>kv(v, z)</code></td>
<td>Modified Bessel function of the second kind of real order v</td>
</tr>
<tr>
<td><code>kve(v, z)</code></td>
<td>Exponentially scaled modified Bessel function of the second kind.</td>
</tr>
<tr>
<td><code>iv(v, z)</code></td>
<td>Modified Bessel function of the first kind of real order</td>
</tr>
<tr>
<td><code>ive(v, z)</code></td>
<td>Exponentially scaled modified Bessel function of the first kind</td>
</tr>
<tr>
<td><code>hankel1(v, z)</code></td>
<td>Hankel function of the first kind</td>
</tr>
<tr>
<td><code>hankel1e(v, z)</code></td>
<td>Exponentially scaled Hankel function of the first kind</td>
</tr>
<tr>
<td><code>hankel2(v, z)</code></td>
<td>Hankel function of the second kind</td>
</tr>
<tr>
<td><code>hankel2e(v, z)</code></td>
<td>Exponentially scaled Hankel function of the second kind</td>
</tr>
</tbody>
</table>

\[
\text{scipy.special.jv}(v, z) = \text{<ufunc 'jv'>}
\]

Bessel function of the first kind of real order v

\[
\text{scipy.special.jve}(v, z) = \text{<ufunc 'jve'>}
\]

Exponentially scaled Bessel function of order v

Defined as:

\[
jve(v, z) = jv(v, z) \times \exp(-\text{abs}(z.imag))
\]
**scipy.special.yn(n, x)**
Bessel function of the second kind of integer order

Returns the Bessel function of the second kind of integer order \( n \) at \( x \).

**scipy.special.yv(v, z)**
Bessel function of the second kind of real order

Returns the Bessel function of the second kind of real order \( v \) at complex \( z \).

**scipy.special.yve(v, z)**
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 \( z \):

\[
yve(v, z) = yv(v, z) \times \exp(-\text{abs}(z\text{.imag}))
\]

**scipy.special.kn(n, x)**
Modified Bessel function of the second kind of integer order \( n \)

These are also sometimes called functions of the third kind.

**scipy.special.kv(v, z)**
Modified Bessel function of the second kind of real order \( v \)

Returns the modified Bessel function of the second kind (sometimes called the third kind) for real order \( v \) at complex \( z \).

**scipy.special.kve(v, z)**
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 \( v \) at complex \( z \):

\[
kve(v, z) = kv(v, z) \times \exp(z)
\]

**scipy.special.iv(v, z)**
Modified Bessel function of the first kind of real order

Parameters:
- \( v \): float  
  Order. If \( z \) is of real type and negative, \( v \) must be integer valued.
- \( z \): float or complex  
  Argument.

**scipy.special.ive(v, z)**
Exponentially scaled modified Bessel function of the first kind

Defined as:

\[
ive(v, z) = iv(v, z) \times \exp(-\text{abs}(z\text{.real}))
\]

**scipy.special.hankel1(v, z)**
Hankel function of the first kind

Parameters:
- \( v \): float  
  Order
- \( z \): float or complex  
  Argument
scipy.special.hankel1e(v, z) = <ufunc ‘hankel1e’>
Exponentially scaled Hankel function of the first kind
Defined as:
\[ hankel1e(v, z) = hankel1(v, z) \times \exp(-1j \times z) \]

**Parameters**
- **v**: float
  - Order
- **z**: complex
  - Argument

scipy.special.hankel2(v, z) = <ufunc ‘hankel2’>
Hankel function of the second kind

**Parameters**
- **v**: float
  - Order
- **z**: complex
  - Argument

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**: float
  - Order
- **z**: complex
  - Argument

The following is not an universal function:

\[ \text{lmbda}(v, x) \quad \text{Compute sequence of lambda functions with arbitrary order v and their derivatives.} \]

scipy.special.lmbda(v, x)
Compute sequence of lambda functions with arbitrary order v and their derivatives. \( L_0(x) \), \( L_v(x) \) are computed with \( v=0 \) or \( v=int(v) \).

### Zeros of Bessel Functions

These are not universal functions:

- **jn_jnp_zeros(nt)**: Compute nt (\( \leq 1200 \)) zeros of the Bessel functions \( J_n \) and \( J_n' \) and arrange them in order of their magnitudes.
- **jyn_zeros(n, nt)**: Compute nt zeros of the Bessel functions \( J_n(x) \), \( J_n'(x) \), \( Y_n(x) \), and \( Y_n'(x) \), respectively.
- **jn_zeros(n, nt)**: Compute nt zeros of the Bessel function \( J_n(x) \).
- **jn_zeros(n, nt)**: Compute nt zeros of the Bessel function \( J_n'(x) \).
- **yn_zeros(n, nt)**: Compute nt zeros of the Bessel function \( Y_n(x) \).
- **ynp_zeros(n, nt)**: Compute nt zeros of the Bessel function \( Y_n'(x) \).
- **y0_zeros(nt[, complex])**: Returns nt (complex or real) zeros of \( Y_0(z) \), \( z_0 \), and the value of \( Y_0'(z_0) = -Y_1(z_0) \) at each zero.
- **y1_zeros(nt[, complex])**: Returns nt (complex or real) zeros of \( Y_1(z) \), \( z_1 \), and the value of \( Y_1'(z_1) = Y_0(z_1) \) at each zero.
- **yip_zeros(nt[, complex])**: Returns nt (complex or real) zeros of \( Y_1(z) \), \( z_1' \), and the value of \( Y_1(z_1') \) at each zero.
scipy.special.jnjp_zeros(nt)
Compute nt (<=1200) zeros of the Bessel functions Jn and Jn' and arrange them in order of their magnitudes.

Returns
- zo[l-1] : ndarray
  Value of the lth zero of Jn(x) and Jn'(x). Of length nt.
- n[l-1] : ndarray
  Order of the Jn(x) or Jn'(x) associated with lth zero. Of length nt.
- m[l-1] : ndarray
  Serial number of the zeros of Jn(x) or Jn'(x) associated with lth zero. Of length nt.
- t[l-1] : ndarray
  0 if lth zero in zo is zero of Jn(x), 1 if it is a zero of Jn'(x). Of length nt.

See also:
- jn_zeros, jnp_zeros
- jyn_zeros(n, nt)
  Compute nt zeros of the Bessel functions Jn(x), Jn'(x), Yn(x), and Yn'(x), respectively. Returns 4 arrays of length nt.
  See jn_zeros, jnp_zeros, yn_zeros, ynp_zeros to get separate arrays.
- jn_zeros(n, nt)
  Compute nt zeros of the Bessel function Jn(x).
- jnp_zeros(n, nt)
  Compute nt zeros of the Bessel function Jn'(x).
- yn_zeros(n, nt)
  Compute nt zeros of the Bessel function Yn(x).
- ynp_zeros(n, nt)
  Compute nt zeros of the Bessel function Yn'(x).
- y0_zeros(nt, complex=0)
  Returns nt (complex or real) zeros of Y0(z), z0, and the value of Y0'(z0) = -Y1(z0) at each zero.
- y1_zeros(nt, complex=0)
  Returns nt (complex or real) zeros of Y1(z), z1, and the value of Y1'(z1) = Y0(z1) at each zero.
- yip_zeros(nt, complex=0)
  Returns nt (complex or real) zeros of Y1'(z), z1', and the value of Y1(z1') at each zero.

Faster versions of common Bessel Functions

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>j0(x)</td>
<td>Bessel function the first kind of order 0</td>
</tr>
<tr>
<td>j1(x)</td>
<td>Bessel function of the first kind of order 1</td>
</tr>
<tr>
<td>y0(x)</td>
<td>Bessel function of the second kind of order 0</td>
</tr>
<tr>
<td>y1(x)</td>
<td>Bessel function of the second kind of order 1</td>
</tr>
<tr>
<td>i0(x)</td>
<td>Modified Bessel function of order 0</td>
</tr>
<tr>
<td>i0e(x)</td>
<td>Exponentially scaled modified Bessel function of order 0.</td>
</tr>
<tr>
<td>i1(x)</td>
<td>Modified Bessel function of order 1</td>
</tr>
<tr>
<td>i1e(x)</td>
<td>Exponentially scaled modified Bessel function of order 0.</td>
</tr>
<tr>
<td>k0(x)</td>
<td>Modified Bessel function K of order 0</td>
</tr>
<tr>
<td>k0e(x)</td>
<td>Exponentially scaled modified Bessel function K of order 0.</td>
</tr>
<tr>
<td>k1(x)</td>
<td>Modified Bessel function of the first kind of order 1</td>
</tr>
<tr>
<td>k1e(x)</td>
<td>Exponentially scaled modified Bessel function K of order 1</td>
</tr>
</tbody>
</table>
5.33. Special functions (scipy.special) 1151

scipy.special.j0(x) = <ufunc 'j0'>
    Bessel function the first kind of order 0

scipy.special.j1(x) = <ufunc 'j1'>
    Bessel function of the first kind of order 1

scipy.special.y0(x) = <ufunc 'y0'>
    Bessel function of the second kind of order 0
    Returns the Bessel function of the second kind of order 0 at x.

scipy.special.y1(x) = <ufunc 'y1'>
    Bessel function of the second kind of order 1
    Returns the Bessel function of the second kind of order 1 at x.

scipy.special.i0(x) = <ufunc 'i0'>
    Modified Bessel function of order 0

scipy.special.i0e(x) = <ufunc 'i0e'>
    Exponentially scaled modified Bessel function of order 0.
    Defined as:
    \[ i0e(x) = \exp(-|x|) \times i0(x). \]

scipy.special.i1(x) = <ufunc 'i1'>
    Modified Bessel function of order 1

scipy.special.i1e(x) = <ufunc 'i1e'>
    Exponentially scaled modified Bessel function of order 0.
    Defined as:
    \[ i1e(x) = \exp(-|x|) \times i1(x) \]

scipy.special.k0(x) = <ufunc 'k0'>
    Modified Bessel function K of order 0
    Modified Bessel function of the second kind (sometimes called the third kind) of order 0.

scipy.special.k0e(x) = <ufunc 'k0e'>
    Exponentially scaled modified Bessel function K of order 0
    Defined as:
    \[ k0e(x) = \exp(x) \times k0(x) . \]

scipy.special.k1(x) = <ufunc 'k1'>
    Modified Bessel function of the first kind of order 1

scipy.special.k1e(x) = <ufunc 'k1e'>
    Exponentially scaled modified Bessel function K of order 1
    Defined as:
    \[ k1e(x) = \exp(x) \times k1(x) \]

Continued on next page
Integrals of Bessel Functions

<table>
<thead>
<tr>
<th>Bessel Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>\texttt{itj0y0}(x)</td>
<td>Integrals of Bessel functions of order 0</td>
</tr>
<tr>
<td>\texttt{it2j0y0}(x)</td>
<td>Integrals related to Bessel functions of order 0</td>
</tr>
<tr>
<td>\texttt{iti0k0}(x)</td>
<td>Integrals of modified Bessel functions of order 0</td>
</tr>
<tr>
<td>\texttt{it2i0k0}(x)</td>
<td>Integrals related to modified Bessel functions of order 0</td>
</tr>
<tr>
<td>\texttt{besselpoly}(a, lmb, nu)</td>
<td>Weighed integral of a Bessel function.</td>
</tr>
</tbody>
</table>

\texttt{scipy.special.itj0y0}(x) = \texttt{ufunc \textasciitilde \texttt{itj0y0}}

Integrals of Bessel functions of order 0

Returns \texttt{ij0}, \texttt{iy0}

\texttt{scipy.special.it2j0y0}(x) = \texttt{ufunc \textasciitilde \texttt{it2j0y0}}

Integrals related to Bessel functions of order 0

Returns \texttt{ij0}, \texttt{iy0}

\texttt{scipy.special.iti0k0}(x) = \texttt{ufunc \textasciitilde \texttt{iti0k0}}

Integrals of modified Bessel functions of order 0

Returns \texttt{ii0}, \texttt{ik0}

\texttt{scipy.special.it2i0k0}(x) = \texttt{ufunc \textasciitilde \texttt{it2i0k0}}

Integrals related to modified Bessel functions of order 0

Returns \texttt{ii0}, \texttt{ik0}

\texttt{scipy.special.besselpoly}(a, lmb, nu) = \texttt{ufunc \textasciitilde \texttt{besselpoly}}

Weighed 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>Derivative</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>\texttt{jvp}(v, z[, n])</td>
<td>Return the nth derivative of ( J_v(z) ) with respect to ( z ).</td>
</tr>
<tr>
<td>\texttt{yvp}(v, z[, n])</td>
<td>Return the nth derivative of ( Y_v(z) ) with respect to ( z ).</td>
</tr>
<tr>
<td>\texttt{kvp}(v, z[, n])</td>
<td>Return the nth derivative of ( K_v(z) ) with respect to ( z ).</td>
</tr>
<tr>
<td>\texttt{ivp}(v, z[, n])</td>
<td>Return the nth derivative of ( I_v(z) ) with respect to ( z ).</td>
</tr>
<tr>
<td>\texttt{h1vp}(v, z[, n])</td>
<td>Return the nth derivative of ( H1_v(z) ) with respect to ( z ).</td>
</tr>
<tr>
<td>\texttt{h2vp}(v, z[, n])</td>
<td>Return the nth derivative of ( H2_v(z) ) with respect to ( z ).</td>
</tr>
</tbody>
</table>
scipy.special.jvp(v, z, n=1)
Return the nth derivative of Jv(z) with respect to z.

scipy.special.yvp(v, z, n=1)
Return the nth derivative of Yv(z) with respect to z.

scipy.special.kvp(v, z, n=1)
Return the nth derivative of Kv(z) with respect to z.

scipy.special.ivp(v, z, n=1)
Return the nth derivative of Iv(z) with respect to z.

scipy.special.h1vp(v, z, n=1)
Return the nth derivative of H1v(z) with respect to z.

scipy.special.h2vp(v, z, n=1)
Return the nth derivative of H2v(z) with respect to z.

### Spherical Bessel Functions

These are not universal functions:

- `sph_jn(n, z)` Compute the spherical Bessel function jn(z) and its derivative for all orders up to and including n.
- `sph_yn(n, z)` Compute the spherical Bessel function yn(z) and its derivative for all orders up to and including n.
- `sph_jyn(n, z)` Compute the spherical Bessel functions, jn(z) and yn(z) and their derivatives for all orders up to and including n.
- `sph_in(n, z)` Compute the spherical Bessel function in(z) and its derivative for all orders up to and including n.
- `sph_kn(n, z)` Compute the spherical Bessel function kn(z) and its derivative for all orders up to and including n.
- `sph_inkn(n, z)` Compute the spherical Bessel functions, in(z) and kn(z) and their derivatives for all orders up to and including n.

### Riccati-Bessel Functions

These are not universal functions:

- `riccati_jn(n, x)` Compute the Ricatti-Bessel function of the first kind and its derivative for all orders up to and including n.
- `riccati_yn(n, x)` Compute the Ricatti-Bessel function of the second kind and its derivative for all orders up to and including n.

- `scipy.special.riccati_jn(n, x)`
  Compute the Ricatti-Bessel function of the first kind and its derivative for all orders up to and including n.
scipy.special.riccati_yn(n, x)
Compute the Ricatti-Bessel function of the second kind and its derivative for all orders up to and including n.

Struve Functions

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>struve(v, x)</td>
<td>Struve function</td>
</tr>
<tr>
<td>modstruve(v, x)</td>
<td>Modified Struve function</td>
</tr>
<tr>
<td>itstruve0(x)</td>
<td>Integral of the Struve function of order 0</td>
</tr>
<tr>
<td>it2struve0(x)</td>
<td>Integral related to Struve function of order 0</td>
</tr>
<tr>
<td>itmodstruve0(x)</td>
<td>Integral of the modified Struve function of order 0</td>
</tr>
</tbody>
</table>

scipy.special.struve(v, x) = <ufunc ‘struve’>
Struve function
Computes the struve function Hv(x) of order v at x, x must be positive unless v is an integer.

scipy.special.modstruve(v, x) = <ufunc ‘modstruve’>
Modified Struve function
Returns the modified Struve function Lv(x) of order v at x, x must be positive unless v is an integer.

scipy.special.itstruve0(x) = <ufunc ‘itstruve0’>
Integral of the Struve function of order 0

\[
\text{Returns} \quad i \\
\int \text{H}_0(t), \ t=0..x
\]

scipy.special.it2struve0(x) = <ufunc ‘it2struve0’>
Integral related to Struve function of order 0

\[
\text{Returns} \quad i \\
\int \text{H}_0(t)/t, \ t=x..\infty
\]

scipy.special.itmodstruve0(x) = <ufunc ‘itmodstruve0’>
Integral of the modified Struve function of order 0

\[
\text{Returns} \quad i \\
\int \text{L}_0(t), \ t=0..x
\]

Raw Statistical Functions

See also:

scipy.stats: Friendly versions of these functions.

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>btdtr(k, n, p)</td>
<td>Binomial distribution cumulative distribution function.</td>
</tr>
<tr>
<td>btdtrc(k, n, p)</td>
<td>Binomial distribution survival function.</td>
</tr>
<tr>
<td>btdtri(k, n, y)</td>
<td>Inverse function to btdtr vs.</td>
</tr>
<tr>
<td>btdtrik(y, n, p)</td>
<td>Inverse function to btdtr vs k</td>
</tr>
<tr>
<td>btdtrin(k, y, p)</td>
<td>Inverse function to btdtr vs n</td>
</tr>
<tr>
<td>btdtr(a,b,x)</td>
<td>Cumulative beta distribution.</td>
</tr>
<tr>
<td>btdtrib(a, b, p)</td>
<td>p-th quantile of the beta distribution.</td>
</tr>
<tr>
<td>btdtria(p, b, x)</td>
<td>Inverse of btdtr vs a</td>
</tr>
<tr>
<td>btdtrib(a, p, x)</td>
<td>Inverse of btdtr vs b</td>
</tr>
<tr>
<td>fdtr(dfm, dfd, x)</td>
<td>F cumulative distribution function</td>
</tr>
</tbody>
</table>
Table 5.222 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>fdtrc(dfn, dfd, x)</td>
<td>F survival function</td>
</tr>
<tr>
<td>fdtrc(dfn, dfd, p)</td>
<td>Inverse to fdtr vs x</td>
</tr>
<tr>
<td>gdtr(a,b,x)</td>
<td>Gamma distribution cumulative density function.</td>
</tr>
<tr>
<td>gdtrc(a,b,x)</td>
<td>Gamma distribution survival function.</td>
</tr>
<tr>
<td>gdtria(p, b, x[, out])</td>
<td>Inverse of gdtr vs a.</td>
</tr>
<tr>
<td>gdtrib(a, p, x[, out])</td>
<td>Inverse of gdtr vs b.</td>
</tr>
<tr>
<td>gdtrix(a, b, p[, out])</td>
<td>Inverse of gdtr vs x.</td>
</tr>
<tr>
<td>nbdt(k, n, p)</td>
<td>Negative binomial cumulative distribution function</td>
</tr>
<tr>
<td>nbdtrc(k, n, p)</td>
<td>Negative binomial survival function.</td>
</tr>
<tr>
<td>nbdtri(k, n, y)</td>
<td>Inverse of nbdt vs p</td>
</tr>
<tr>
<td>nbdtrk(y,n,p)</td>
<td>Inverse of nbdt vs k</td>
</tr>
<tr>
<td>nbdtrn(k,y,p)</td>
<td>Inverse of nbdt vs n</td>
</tr>
<tr>
<td>ncf(F)</td>
<td>Cumulative distribution function of the non-central F distribution.</td>
</tr>
<tr>
<td>ncfdridf(df, p, dfn)</td>
<td>Calculate degrees of freedom (denominator) for the noncentral F-distribution.</td>
</tr>
<tr>
<td>ncfdrdfn(df, p, dfn)</td>
<td>Calculate degrees of freedom (numerator) for the noncentral F-distribution.</td>
</tr>
<tr>
<td>ncfdr(dfn, dfd, nc, f)</td>
<td>Inverse cumulative distribution function of the non-central F distribution.</td>
</tr>
<tr>
<td>nct(dff, nc, t)</td>
<td>Cumulative distribution function of the non-central t distribution.</td>
</tr>
<tr>
<td>nctdrt(dff, p, nc, t)</td>
<td>Calculate degrees of freedom for non-central t distribution.</td>
</tr>
<tr>
<td>nctdrti(dff, nc, p, t)</td>
<td>Inverse cumulative distribution function of the non-central t distribution.</td>
</tr>
<tr>
<td>nctdtrinc(dff, p, t)</td>
<td>Calculate non-centrality parameter for non-central t distribution.</td>
</tr>
<tr>
<td>nrdtrmn(p, x, std)</td>
<td>Calculate mean of normal distribution given other params.</td>
</tr>
<tr>
<td>nrdtrisd(p, x, mn)</td>
<td>Calculate standard deviation of normal distribution given other params.</td>
</tr>
<tr>
<td>pdtr(k, m)</td>
<td>Poisson cumulative distribution function</td>
</tr>
<tr>
<td>pdtrc(k, m)</td>
<td>Poisson survival function</td>
</tr>
<tr>
<td>pdttri(k, y)</td>
<td>Inverse to pdtr vs m</td>
</tr>
<tr>
<td>pdtr(k, m)</td>
<td>Inverse to pdtr vs k</td>
</tr>
<tr>
<td>stdtr(dff, t)</td>
<td>Student t distribution cumulative density function</td>
</tr>
<tr>
<td>stdtridf(dff, p)</td>
<td>Inverse of stdtr vs df</td>
</tr>
<tr>
<td>stdtrit(dff, p)</td>
<td>Inverse of stdtr vs t</td>
</tr>
<tr>
<td>chdtr(v, x)</td>
<td>Chi square cumulative distribution function</td>
</tr>
<tr>
<td>chdtrc(v, x)</td>
<td>Chi square survival function</td>
</tr>
<tr>
<td>chdtri(v, p)</td>
<td>Inverse to chdtrc</td>
</tr>
<tr>
<td>chdtriv(p, x)</td>
<td>Inverse to chdtr vs v</td>
</tr>
<tr>
<td>ndtr(x)</td>
<td>Gaussian cumulative distribution function</td>
</tr>
<tr>
<td>log_card_r(x)</td>
<td>Logarithm of Gaussian cumulative distribution function</td>
</tr>
<tr>
<td>ndtri(y)</td>
<td>Inverse of ndtr vs x</td>
</tr>
<tr>
<td>chndtr(dff, x, df, nc)</td>
<td>Non-central chi square cumulative distribution function</td>
</tr>
<tr>
<td>chndtridf(x, p, nc)</td>
<td>Inverse to chndtr vs df</td>
</tr>
<tr>
<td>chndtrinc(x, df, p)</td>
<td>Inverse to chndtr vs nc</td>
</tr>
<tr>
<td>chndtrix(x, df, nc)</td>
<td>Inverse to chndtr vs x</td>
</tr>
<tr>
<td>smirnov(n, e)</td>
<td>Kolmogorov-Smirnov complementary cumulative distribution function</td>
</tr>
<tr>
<td>smirnovi(n, y)</td>
<td>Inverse to smirnov</td>
</tr>
<tr>
<td>kolmogorov(y)</td>
<td>Complementary cumulative distribution function of Kolmogorov distribution</td>
</tr>
<tr>
<td>kolmogi(p)</td>
<td>Inverse function to kolmogorov</td>
</tr>
<tr>
<td>tklmbda(x, lmbda)</td>
<td>Tukey-Lambda cumulative distribution function</td>
</tr>
<tr>
<td>logit(x)</td>
<td>Logit ufunc for ndarrays</td>
</tr>
<tr>
<td>expit(x)</td>
<td>Expit ufunc for ndarrays</td>
</tr>
<tr>
<td>boxcox(x, lmbda)</td>
<td>Compute the Box-Cox transformation.</td>
</tr>
<tr>
<td>boxcoxl(x, lmbda)</td>
<td>Compute the Box-Cox transformation of 1 + x.</td>
</tr>
</tbody>
</table>
**scipy.special.bdtr**

Binomial distribution cumulative distribution function.

Sum of the terms 0 through k of the Binomial probability density.

\[
y = \sum_{j=0}^{k} \binom{n}{j} p^j (1-p)^{(n-j)}, j=0..k
\]

**Parameters**
- \(k\) : int
  - Terms to include
- \(n\) : int
  - Probability
- \(p\) : float
  - Sum of terms

**Returns**
- \(y\) : float

**scipy.special.bdtrc**

Binomial distribution survival function.

Sum of the terms \(k+1\) through \(n\) of the Binomial probability density

\[
y = \sum_{j=k+1}^{n} \binom{n}{j} p^j (1-p)^{(n-j)}, j=k+1..n
\]

**Parameters**
- \(k\) : int
  - Terms to include
- \(n\) : int
  - Probability
- \(p\) : float
  - Sum of terms

**Returns**
- \(y\) : float

**scipy.special.bdtri**

Inverse function to \(\text{bdtr} vs. p\)

Finds probability \(p\) such that for the cumulative binomial probability \(\text{bdtr}(k, n, p) == y\).  

**scipy.special.bdtrik**

Inverse function to \(\text{bdtr} vs k\)

**scipy.special.bdtrin**

Inverse function to \(\text{bdtr} vs n\)

**scipy.special.btdtr**

Cumulative beta distribution.

Returns the area from zero to \(x\) under the beta density function:

\[
\frac{\Gamma(a+b)}{(\Gamma(a)\times\Gamma(b)))\times\text{integral}(t**(a-1) \times (1-t)**(b-1), t=0..x)}
\]

**See also:**
- betainc
- betaincinv
- betaincinv

**scipy.special.btdtria**

Inverse of \(\text{btdtr}\) vs \(a\)

\(p\)-th quantile of the beta distribution.

This is effectively the inverse of \(\text{btdtr}\) returning the value of \(x\) for which \(\text{btdtr}(a,b,x) = p\).

**See also:**
- betaincinv
scipy.special.btdtrb$(a, p, x) = \text{ufunc ‘btdtrib’}$
Inverse of btdtr vs b

scipy.special.fdtr$(dfn, dfd, x) = \text{ufunc ‘fdtr’}$
F cumulative distribution function
Returns the area from zero to x under the F density function (also known as Snedcor’s density or the variance ratio density). This is the density of X = (unum/dfn)/( uden/dfd), where unum and uden are random variables having Chi square distributions with dfn and dfd degrees of freedom, respectively.

scipy.special.fdtrc$(dfn, dfd, x) = \text{ufunc ‘fdtrc’}$
F survival function
Returns the complemented F distribution function.

scipy.special.fdtri$(dfn, dfd, p) = \text{ufunc ‘fdtri’}$
Inverse to fdtr vs x
Finds the F density argument x such that fdtr(dfn, dfd, x) == p.

scipy.special.gdtr$(a, b, x) = \text{ufunc ‘gdtr’}$
Gamma distribution cumulative density function.
Returns the integral from zero to x of the gamma probability density function:

$$a^b / \gamma(b) * \int_0^x t^{b-1} \exp(-at) dt$$

The arguments a and b are used differently here than in other definitions.

scipy.special.gdtrc$(a, b, x) = \text{ufunc ‘gdtrc’}$
Gamma distribution survival function.
Integral from x to infinity of the gamma probability density function.

See also:
gdtr, gdtri

scipy.special.gdtria$(p, b, x, out=None) = \text{ufunc ‘gdtria’}$
Inverse of gdtr vs a.
Returns the inverse with respect to the parameter $a$ of $p = \text{gdtr}(a, b, x)$, the cumulative distribution function of the gamma distribution.

Parameters

- **p** : array_like
  Probability values.
- **b** : array_like
  $b$ 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 $gdtr(a, b, x)$.

**Examples**
First evaluate $gdtr$.

```python
>>> p = gdtr(1.2, 3.4, 5.6)
>>> print(p)
0.94378087442
```
Verify the inverse.

```python
>>> gdtria(p, 3.4, 5.6)
1.2
```

**gdtrib**
In reverse of $gdtr$ vs $b$.

Returns the inverse with respect to the parameter $b$ of $p = gdtr(a, b, x)$, the cumulative distribution function of the gamma distribution.

**Parameters**
- $a$: array_like
  $a$ parameter values of $gdtr(a, b, x)$. $1/a$ 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 $p = gdtr(a, b, x)$. $b$ is the “shape” parameter of the gamma distribution.

**See also**:
- $gdtr$: CDF of the gamma distribution.
- $gdtria$: Inverse with respect to $a$ of $gdtr(a, b, x)$.
- $gdtrix$: Inverse with respect to $x$ of $gdtr(a, b, x)$.

**Examples**
First evaluate $gdtr$.

```python
>>> p = gdtr(1.2, 3.4, 5.6)
>>> print(p)
0.94378087442
```
Verify the inverse.

```python
>>> gdtria(p, 3.4, 5.6)
3.3999999999723882
```

**gdtrix**
Inverse of $gdtr$ vs $x$.

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
  - Parameter values of \( gdtr(a, b, x) \). \( 1/a \) is the “scale” parameter of the gamma distribution.
- **b**: array_like
  - 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 \( gdtr(a, b, x) \).

Examples

First evaluate \( gdtr \).

```python
>>> 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 \((k, n, p)\) = <ufunc ‘nbdtr’>

Negative binomial cumulative distribution function

Returns the sum of the terms 0 through \( k \) of the negative binomial distribution:

\[
\sum_{j=0}^{\infty} \binom{n+j-1}{j} p^n (1-p)^j \]

In a sequence of Bernoulli trials this is the probability that \( k \) or fewer failures precede the \( n \)th success.

scipy.special.nbdtrc \((k, n, p)\) = <ufunc ‘nbdtrc’>

Negative binomial survival function

Returns the sum of the terms \( k+1 \) to infinity of the negative binomial distribution.

scipy.special.nbdtri \((k, n, y)\) = <ufunc ‘nbdtri’>

Inverse of nbdtr vs \( p \)

Finds the argument \( p \) such that \( nbdtr(k, n, p) = y \).

scipy.special.nbdtrik \((y, n, p)\) = <ufunc ‘nbdtrik’>

Inverse of nbdtr vs \( k \)

Finds the argument \( k \) such that \( nbdtr(k, n, p) = y \).
scipy.special.nbdtrin\(k, y, p\) = \texttt{ufunc ‘nbdtrin’}

Inverse of \texttt{nbdtr} vs \(n\)

Finds the argument \(n\) such that \texttt{nbdtr}(\(k, n, p\)) = \(y\).

scipy.special.ncfdtr\((\texttt{dfn}, \texttt{dfd}, \texttt{nc}, f)\) = \texttt{ufunc ‘ncfdtr’}

Cumulative distribution function of the non-central F distribution.

**Parameters**

- \texttt{dfn} : array_like
  Degrees of freedom of the numerator sum of squares. Range (0, inf).
- \texttt{dfd} : array_like
  Degrees of freedom of the denominator sum of squares. Range (0, inf).
- \texttt{nc} : array_like
  Noncentrality parameter. Should be in range (0, 1e4).
- \texttt{f} : array_like
  Quantiles, i.e. the upper limit of integration.

**Returns**

- \texttt{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:**

- \texttt{ncfdtridf} Inverse CDF (iCDF) of the non-central F distribution.
- \texttt{ncfdtridfn} Calculate \(\texttt{dfn}\), given CDF and iCDF values.
- \texttt{ncfdtridfd} Calculate \(\texttt{dfd}\), given CDF and iCDF values.
- \texttt{ncfdtrinc} Calculate noncentrality parameter, given CDF, iCDF, \(\texttt{dfn}\), \(\texttt{dfd}\).

**Examples**

```python
>>> from scipy import special
>>> from scipy import stats
>>> import matplotlib.pyplot as plt

Plot the CDF of the non-central F distribution, for \(\text{nc}=0\). Compare with the F-distribution from scipy.stats:

```
scipy.special.ncfdtridfd($p, f, dfn, nc$) = <ufunc ‘ncfdtridfd’>
Calculate degrees of freedom (denominator) for the noncentral F-distribution.

See ncfdr for more details.

scipy.special.ncfdtridfn($p, f, dfd, nc$) = <ufunc ‘ncfdtridfn’>
Calculate degrees of freedom (numerator) for the noncentral F-distribution.

See ncfdr for more details.

scipy.special.ncfdtri($p, dfn, dfd, nc$) = <ufunc ‘ncfdtri’>
Inverse cumulative distribution function of the non-central F distribution.

See ncfdr for more details.

scipy.special.ncfdtrinc($p, f, dfn, dfd$) = <ufunc ‘ncfdtrinc’>
Calculate non-centrality parameter for non-central F distribution.

See ncfdr for more details.

scipy.special.nctdtr($df, nc, t$) = <ufunc ‘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.
- ncfdtridf
  Calculate degrees of freedom, given CDF and iCDF values.
- ncfdtrinc
  Calculate non-centrality parameter, given CDF iCDF values.
Examples

```python
>>> 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
def plot_cdf(x, df, nc):
    nct_stats = stats.t.cdf(x, df)
    nct_special = special.nctdtr(df, nc, x)
    fig = plt.figure()
    ax = fig.add_subplot(111)
    ax.plot(x, nct_stats, 'b-', lw=3)
    ax.plot(x, nct_special, 'r-')
    plt.show()
```

```python
>>> x = np.linspace(-5, 5, num=500)
>>> df = 3
>>> nct_stats = stats.t.cdf(x, df)
>>> nct_special = special.nctdtr(df, 0, x)

>>> 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**

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**

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(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(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

Returns
    mn : float or ndarray
        The mean of the normal distribution.

See also:
    nrdtrimn, ndtr

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.

mn : float or ndarray

Returns
    std : array_like
        The mean of the normal distribution.

See also:
    nrdtris, ndtr

scipy.special.pdtz(k, m) = <ufunc 'pdtz'>
Poisson cumulative distribution function

    Returns the sum of the first k terms of the Poisson distribution:
    \text{sum}(\exp(-m) * m**j / j!, j=0..k) = \text{gammaincc}(k+1, m).
    Arguments must both be positive and k an integer.

scipy.special.pdtzc(k, m) = <ufunc 'pdtzc'>
Poisson survival function

    Returns the sum of the terms from k+1 to infinity of the Poisson distribution:
    \text{sum}(\exp(-m) * m**j / j!, j=k+1..\text{inf}) = \text{gammainc}(k+1, m).
    Arguments must both be positive and k an integer.
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 gammaincinv(k+1, y). k must be a nonnegative integer and y between 0 and 1.

scipy.special.pdtrik(p, m) = <ufunc 'pdtrik'>
Inverse to pdtr vs k
Returns the quantile k such that pdtr(k, m) = p

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:

\[\frac{\Gamma((df+1)/2)}{\sqrt{df\pi} \Gamma(df/2)} \int_{-\infty}^{t} (1+x^2/df)^{-(df/2+1/2)} dx\]

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(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(v, x) = <ufunc 'chdtr'>
Chi square cumulative distribution function
Returns the area under the left hand tail (from 0 to x) of the Chi square probability density function with v degrees of freedom:

\[\frac{1}{2^{(v/2)} \Gamma(v/2)} \int_{0}^{x} t^{(v/2-1)} e^{-t/2} dt\]

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:

\[\frac{1}{2^{(v/2)} \Gamma(v/2)} \int_{x}^{\infty} t^{(v/2-1)} e^{-t/2} dt\]

scipy.special.chdtri(v, p) = <ufunc 'chdtri'>
Inverse to chdtrc
Returns the argument x such that chdtrc(v, x) == p.

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(x) = <ufunc 'ndtr'>
Gaussian cumulative distribution function
Returns the area under the standard Gaussian probability density function, integrated from minus infinity to x:

\[\frac{1}{\sqrt{2\pi}} \int_{-\infty}^{x} e^{-t^2/2} dt\]
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:

\[ \log\left(\frac{1}{\sqrt{2\pi}} \int_{-\infty}^{x} e^{-t^2 / 2} dt \right) \]

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(x, df, nc) = ufunc 'chndtr'
Non-central chi square cumulative distribution function

scipy.special.chndtridf(x, p, nc) = ufunc 'chndtridf'
Inverse to chndtr vs df

scipy.special.chndtrinc(x, df, p) = ufunc 'chndtrinc'
Inverse to chndtr vs nc

scipy.special.chndtrix(p, df, nc) = ufunc 'chndtrix'
Inverse to chndtr vs x

scipy.special.smirnov(n, e) = ufunc 'smirnov'
Kolmogorov-Smirnov complementary cumulative distribution function

Returns the exact Kolmogorov-Smirnov complementary cumulative distribution function (Dn+ or Dn-) 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 e.

scipy.special.smirnovi(n, y) = ufunc 'smirnovi'
Inverse to smirnov

Returns e such that smirnov(n, e) = y.

scipy.special.kolmogorov(y) = ufunc 'kolmogorov'
Complementary cumulative distribution function of Kolmogorov distribution

Returns the complementary cumulative distribution function of Kolmogorov’s limiting distribution (Kn* for large n) 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.

scipy.special.kolmogi(p) = ufunc 'kolmogi'
Inverse function to kolmogorov

Returns y such that kolmogorov(y) == p.

scipy.special.tklmbda(x, lmbda) = ufunc ‘tklmbda’
Tukey-Lambda cumulative distribution function

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) = -inf, logit(1) = inf, and logit(p) for p<0 or p>1 yields nan.

Parameters
   x : ndarray

Returns
   out : ndarray
The ndarray to apply logit to element-wise.
An ndarray of the same shape as x. Its entries are logit of the corresponding entry of x.

Notes
As a ufunc logit takes a number of optional keyword arguments. For more information see ufuncs
New in version 0.10.0.

scipy.special.expit(x) = <ufunc 'expit'>
Expit ufunc for ndarrays.
The expit function, also known as the logistic function, is defined as expit(x) = 1/(1+exp(-x)). It is the inverse of the logit function.

Parameters  x : ndarray
Returns  out : ndarray

An ndarray of the same shape as x. Its entries are expit of the corresponding entry of x.

Notes
As a ufunc expit takes a number of optional keyword arguments. For more information see ufuncs
New in version 0.10.0.

scipy.special.boxcox(x, lmbda) = <ufunc 'boxcox'>
Compute the Box-Cox transformation.
The Box-Cox transformation is:

\[ y = \begin{cases} 
(x**lmbda - 1) / lmbda & \text{if } lmbda \neq 0 \\
\log(x) & \text{if } lmbda = 0 
\end{cases} \]

Returns nan if x < 0. Returns -inf if x == 0 and lmbda < 0.

Parameters  x : array_like
            Data to be transformed.
            lmbda : array_like
Returns  y : array
           Power parameter of the Box-Cox transform.
           Transformed data.

Notes
New in version 0.14.0.

Examples

>>> boxcox([1, 4, 10], 2.5)
array([ 0.        , 12.41321329, 126.0910641])

scipy.special.boxcoxl(x, lmbda) = <ufunc 'boxcoxl'>
Compute the Box-Cox transformation of 1 + x.
The Box-Cox transformation computed by boxcoxl is:

\[ y = \begin{cases} 
((1+x)**lmbda - 1) / lmbda & \text{if } lmbda \neq 0 \\
\log(1+x) & \text{if } lmbda = 0 
\end{cases} \]
Returns \( \text{nan} \) if \( x < -1 \). Returns \(-\infty\) if \( x == -1 \) and \( \text{lmbda} < 0 \).

**Parameters**
- \( x \): array_like
  Data to be transformed.
- \( \text{lmbda} \): array_like
  Power parameter of the Box-Cox transform.

**Returns**
- \( y \): array
  Transformed data.

**Notes**
New in version 0.14.0.

**Examples**
```python
>>> 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])
```

### Information Theory Functions

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>entr(x)</code></td>
<td>Elementwise function for computing entropy.</td>
</tr>
<tr>
<td><code>rel_entr(x, y)</code></td>
<td>Elementwise function for computing relative entropy.</td>
</tr>
<tr>
<td><code>kl_div(x, y)</code></td>
<td>Elementwise function for computing Kullback-Leibler divergence.</td>
</tr>
<tr>
<td><code>huber(delta, r)</code></td>
<td>Huber loss function.</td>
</tr>
<tr>
<td><code>pseudo_huber(delta, r)</code></td>
<td>Pseudo-Huber loss function.</td>
</tr>
</tbody>
</table>

**scipy.special.entr(x)**
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**
- \( \text{res} \): 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 0.14.0.

**scipy.special.rel_entr(x, y)**
Elementwise function for computing relative entropy.

\[
\text{rel}_\text{entr}(x, y) = \begin{cases} 
x \log(x/y) & x > 0, y > 0 \\
0 & x = 0, y \geq 0 \\
\infty & \text{otherwise}
\end{cases}
\]

5.33. Special functions (*scipy.special*)
**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 0.14.0.

`scipy.special.kl_div(x, y) = <ufunc `kl_div`>`

Elementwise function for computing Kullback-Leibler divergence.

\[
\text{kl}_\text{div}(x, y) = \begin{cases} 
  x \log(x/y) - x + y & x > 0, y > 0 \\
  y & x = 0, y \geq 0 \\
  \infty & \text{otherwise}
\end{cases}
\]

**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 0.14.0.

`scipy.special.huber(delta, r) = <ufunc `huber`>`

Huber loss function.

\[
\text{huber}(\delta, r) = \begin{cases} 
  \infty & \delta < 0 \\
  \frac{1}{2}r^2 & 0 \leq \delta, |r| \leq \delta \\
  \delta(|r| - \frac{1}{2}\delta) & \text{otherwise}
\end{cases}
\]

**Parameters**

- delta : ndarray
  
  Input array, indicating the quadratic vs. linear loss changepoint.

- r : ndarray
  
  Input array, possibly representing residuals.

**Returns**

- res : ndarray
  
  The computed Huber loss function values.

**Notes**

This function is convex in r.

New in version 0.15.0.
scipy.special.pseudo_huber(delta, r) = <ufunc ‘pseudo_huber’>

Pseudo-Huber loss function.

\[
\text{pseudo\_huber}(\delta, r) = \delta^2 \left( \sqrt{1 + \left( \frac{r}{\delta} \right)^2} - 1 \right)
\]

**Parameters**
- \( \delta \) : 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

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>gamma(z)</td>
<td>Gamma function</td>
</tr>
<tr>
<td>gammaln(z)</td>
<td>Logarithm of absolute value of gamma function</td>
</tr>
<tr>
<td>gammasgn(x)</td>
<td>Sign of the gamma function.</td>
</tr>
<tr>
<td>gammainc(a, x)</td>
<td>Incomplete gamma function.</td>
</tr>
<tr>
<td>gammaincinv(a, y)</td>
<td>Inverse to gammainc</td>
</tr>
<tr>
<td>gammaincc(a, x)</td>
<td>Complemented incomplete gamma integral.</td>
</tr>
<tr>
<td>gammainccinv(a, y)</td>
<td>Inverse to gammaincc</td>
</tr>
<tr>
<td>beta(a, b)</td>
<td>Beta function.</td>
</tr>
<tr>
<td>betain(a, b)</td>
<td>Natural logarithm of absolute value of beta function.</td>
</tr>
<tr>
<td>betainc(a, b, x)</td>
<td>Incomplete beta integral.</td>
</tr>
<tr>
<td>betaincinv(a, b, y)</td>
<td>Inverse function to beta integral.</td>
</tr>
<tr>
<td>psi(z)</td>
<td>Digamma function</td>
</tr>
<tr>
<td>rgamma(z)</td>
<td>Gamma function inverted</td>
</tr>
<tr>
<td>polygamma(n, x)</td>
<td>Polygamma function which is the nth derivative of the digamma (psi) function.</td>
</tr>
<tr>
<td>multigammaln(a, d)</td>
<td>Returns the log of multivariate gamma, also sometimes called the generalized gamma.</td>
</tr>
<tr>
<td>digamma(z)</td>
<td>Digamma function</td>
</tr>
<tr>
<td>poch(z, m)</td>
<td>Rising factorial ((z)_m)</td>
</tr>
</tbody>
</table>

scipy.special.gamma(z) = <ufunc ‘gamma’>

Gamma function

The gamma function is often referred to as the generalized factorial since \( z \cdot \gamma(z) = \gamma(z+1) \)
and \( \gamma(n+1) = n! \) for natural number \( n \).

scipy.special.gammaln(z) = <ufunc ‘gammaln’>

Logarithm of absolute value of gamma function

Defined as:

\[
\ln(\text{abs}(\gamma(z)))
\]

See also:

gammasgn
scipy.special.gammasgn(x) = <ufunc 'gammasgn'>
Sign of the gamma function.

See also:

gammaln

scipy.special.gammainc(a, x) = <ufunc 'gammainc'>
Incomplete gamma function

Defined as:

\[
\frac{1}{\Gamma(a)} \int_{0}^{x} e^{-t} t^{a-1} dt
\]

\(a\) must be positive and \(x\) must be \(\geq 0\).

scipy.special.gammaincinv(a, y) = <ufunc 'gammaincinv'>
Inverse to gammainc

Returns \(x\) such that \(\text{gammainc}(a, x) = y\).

scipy.special.gammaincc(a, x) = <ufunc 'gammaincc'>
Complemented incomplete gamma integral

Defined as:

\[
\frac{1}{\Gamma(a)} \int_{x}^{\infty} e^{-t} t^{a-1} dt = 1 - \text{gammainc}(a, x)
\]

\(a\) must be positive and \(x\) must be \(\geq 0\).

scipy.special.gammaincinv(a, y) = <ufunc 'gammaincinv'>
Inverse to gammaincc

Returns \(x\) such that \(\text{gammaincc}(a, x) = y\).

scipy.special.beta(a, b) = <ufunc 'beta'>
Beta function.

\[
\text{beta}(a,b) = \frac{\Gamma(a) \times \Gamma(b)}{\Gamma(a+b)}
\]

scipy.special.betainc(a, b, x) = <ufunc 'betainc'>
Incomplete beta integral.

Compute the incomplete beta integral of the arguments, evaluated from zero to \(x\):

\[
\frac{\Gamma(a+b)}{(\Gamma(a) \times \Gamma(b))} \times \int_{0}^{x} t^{a-1} (1-t)^{b-1} dt.
\]

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 betaf(a, b).

scipy.special.betaincinv(a, b, y) = <ufunc 'betaincinv'>
Inverse function to beta integral.

Compute \(x\) such that \(\text{betainc}(a,b,x) = y\).
scipy.special.psi(z) = <ufunc ‘psi’>
    Digamma function
    The derivative of the logarithm of the gamma function evaluated at z (also called the digamma function).

scipy.special.rgamma(z) = <ufunc ‘rgamma’>
    Gamma function inverted
    Returns 1/gamma(x)

scipy.special.polygamma(n, x)
    Polygamma function which 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

    >>> from scipy import special
    >>> x = [2, 3, 25.5]
    >>> special.polygamma(1, x)
    array([ 0.64493407, 0.39493407, 0.03999467])
    >>> special.polygamma(0, x) == special.psi(x)
    array([ True, True, True], dtype=bool)

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_{\mathbb{R}^d_+} e^{-\sum_i x_i} \prod_i x_i^{a_i} dV

    with the condition a > (d-1)/2, and \mathbb{R}^d_+ being the set of all the positive definite matrices of dimension s. 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 + (d-1)/2)).

    References

scipy.special.digamma(z) = <ufunc ‘psi’>

Digamma function

The derivative of the logarithm of the gamma function evaluated at z (also called the digamma function).

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:

\[(z)_m = z \times (z + 1) \times \ldots \times (z + m - 1)\]

Error Function and Fresnel Integrals

<table>
<thead>
<tr>
<th>erf(z)</th>
<th>Returns the error function of complex argument.</th>
</tr>
</thead>
<tbody>
<tr>
<td>erfc(x)</td>
<td>Complementary error function, 1 - erf(x).</td>
</tr>
<tr>
<td>erfcx(x)</td>
<td>Scaled complementary error function, (\exp(x^2)) erfc(x).</td>
</tr>
<tr>
<td>erfi(z)</td>
<td>Imaginary error function, (-i) (\text{erf}(iz)).</td>
</tr>
<tr>
<td>erfinv(y)</td>
<td>Inverse function for (\text{erf})</td>
</tr>
<tr>
<td>erfcinv(y)</td>
<td>Inverse function for (\text{erfc})</td>
</tr>
<tr>
<td>wofz(z)</td>
<td>Faddeeva function</td>
</tr>
<tr>
<td>dawson(x)</td>
<td>Dawson’s integral</td>
</tr>
<tr>
<td>fresnel(z)</td>
<td>Fresnel sin and cos integrals</td>
</tr>
<tr>
<td>fresnel_zeros(nt)</td>
<td>Compute nt complex zeros of the sine and cosine Fresnel integrals (S(z)) and (C(z)).</td>
</tr>
<tr>
<td>modfresnelp(x)</td>
<td>Modified Fresnel positive integrals</td>
</tr>
<tr>
<td>modfresnelm(x)</td>
<td>Modified Fresnel negative integrals</td>
</tr>
</tbody>
</table>

scipy.special.erf(z) = <ufunc ‘erf’>

Returns the error function of complex argument.

It is defined as \(2/\sqrt{\pi}\) \(\int_{0}^{\infty} \exp(-t^2) dt = 0..z\).

Parameters
- x : ndarray

Returns
- res : ndarray

Input array.

The values of the error function at the given points \(x\).

See also:
- erfc, erfinv, erfcinv

Notes

The cumulative of the unit normal distribution is given by \(\Phi(z) = 1/2[1 + \text{erf}(z/\sqrt{2})]\).

References

[R282], [R283], [R284]

scipy.special.erfc(x) = <ufunc ‘erfc’>

Complementary error function, \(1 - \text{erf}(x)\).
**References**

[R285]

```python
scipy.special.erfcx(x) = <ufunc 'erfcx'>
```
Scaled complementary error function, exp(x^2) erfc(x).

**Notes**

New in version 0.12.0.

**References**

[R286]

```python
scipy.special.erfi(z) = <ufunc 'erfi'>
```
Imaginary error function, -i erf(i z).

**Notes**

New in version 0.12.0.

**References**

[R287]

```python
scipy.special.erfinv(y)
```
Inverse function for erf

```python
scipy.special.erfcinv(y)
```
Inverse function for erfc

```python
scipy.special.wofz(z) = <ufunc 'wofz'>
```
Faddeeva function

Returns the value of the Faddeeva function for complex argument:

\[ \exp(-z^2) \cdot \text{erfc}(-i z) \]

**References**

[R292]

```python
scipy.special.dawsn(x) = <ufunc 'dawsn'>
```
Dawson’s integral.

Computes:

\[ \exp(-x^2) \cdot \text{integral}\left(\exp(t^2), t=0..x\right). \]

**References**

[R277]

```python
scipy.special.fresnel(z) = <ufunc 'fresnel'>
```
Fresnel sin and cos integrals

Defined as:

\[
\begin{align*}
\text{ssa} &= \text{integral}(\sin(\pi/2 \cdot t^2), t=0..z) \\
\text{csa} &= \text{integral}(\cos(\pi/2 \cdot t^2), t=0..z)
\end{align*}
\]
Parameters

\[ z : \text{float or complex array_like} \]

Argument

Returns

\[ \text{ssa, csa} \]

Fresnel sin and cos integral values

```
scipy.special.fresnel_zeros(nt)

Compute nt complex zeros of the sine and cosine Fresnel integrals \( S(z) \) and \( C(z) \).
```

```
scipy.special.modfresnelp(x) = <ufunc 'modfresnelp'>

Modified Fresnel positive integrals

Returns

\[ \text{fp} \]

Integral \( F_+(x) := \int_x^\infty \exp(1j t^2) \, dt \)

\[ \text{kp} \]

Integral \( K_+(x) := \frac{1}{\sqrt{\pi}} \exp(-1j (x^2 + \pi/4)) \times fp \)

```

```
scipy.special.modfresnelm(x) = <ufunc 'modfresnelm'>

Modified Fresnel negative integrals

Returns

\[ \text{fm} \]

Integral \( F_-(x) := \int_x^\infty \exp(-1j t^2) \, dt \)

\[ \text{km} \]

Integral \( K_-(x) := \frac{1}{\sqrt{\pi}} \exp(1j (x^2 + \pi/4)) \times fp \)

```

These are not universal functions:

```
scipy.special.erf_zeros(nt)

Compute nt complex zeros of the error function \( \text{erf}(z) \).
```

```
scipy.special.fresnelc_zeros(nt)

Compute nt complex zeros of the cosine Fresnel integral \( C(z) \).
```

```
scipy.special.fresnels_zeros(nt)

Compute nt complex zeros of the sine Fresnel integral \( S(z) \).
```

```
scipy.special.lpmv(m, v, x)

Associated legendre function of integer order.

```

```
scipy.special.sph_harm(m, n, theta, phi)

Compute spherical harmonics.
```

Legendre Functions

```
scipy.special.lpmv(m, v, x) = <ufunc 'lpmv'>

Associated legendre function of integer order.

Parameters

\[ m : \text{int} \]

Order

\[ v : \text{real} \]

Degree. Must be \( v > -m-1 \) or \( v < m \)

\[ x : \text{complex} \]

Argument. Must be \( |x| \leq 1 \).
```

```
scipy.special.sph_harm(m, n, theta, phi) = <ufunc 'sph_harm'>

```
Compute spherical harmonics.

\[ Y_{m}^{n} (\theta, \phi) = \sqrt{\frac{2n + 1 (n - m)!}{4\pi (n + m)!}} e^{im\theta} P_{n}^{m} (\cos(\phi)) \]

**Parameters**
- \( m \): int
  - \(|m| \leq n\); the order of the harmonic.
- \( n \): int
  - where \( n \geq 0\); the degree of the harmonic. This is often called \( l \) (lower case L) in descriptions of spherical harmonics.
- \( \theta \): float
  - \([0, 2\pi]\); the azimuthal (longitudinal) coordinate.
- \( \phi \): float
  - \([0, \pi]\); the polar (colatitudinal) coordinate.

**Returns**
- \( y_{mn} \): complex float
  - The harmonic \( Y_{m}^{n} \) sampled at \( \theta \) and \( \phi \)

**Notes**

There are different conventions for the meaning of input arguments \( \theta \) and \( \phi \). We take \( \theta \) to be the azimuthal angle and \( \phi \) to be the polar angle. It is common to see the opposite convention - that is \( \theta \) as the polar angle and \( \phi \) as the azimuthal angle.

**References**

[R291]

These are not universal functions:

- **clpmn**: Associated Legendre function of the first kind, \( P_{m}^{n}(z) \)
- **lpn**: Compute sequence of Legendre functions of the first kind (polynomials), \( P_{n}(z) \) and derivatives for all degrees from 0 to \( n \).
- **lqn**: Compute sequence of Legendre functions of the second kind, \( Q_{n}(z) \) and derivatives for all degrees from 0 to \( n \).
- **lpmn**: Associated Legendre function of the first kind, \( P_{m}^{n}(z) \)
- **lqmn**: Associated Legendre functions of the second kind, \( Q_{m}^{n}(z) \) and its derivative, \( Q_{m}^{n}'(z) \) of order \( m \) and degree \( n \).

**scipy.special.clpmn**

Associated Legendre function of the first kind, \( P_{m}^{n}(z) \)

Computes the (associated) Legendre function of the first kind of order \( m \) and degree \( n \):

\[ P_{m}^{n}(z) = P_{-n}^{m}(z) \]

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 to \( m \) and degrees from 0 to \( n \).

**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
- \( z \): 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**
- \( P_{mn \_z} \): \((m+1, n+1)\) array
  - Values for all orders 0 to \( m \) and degrees 0 to \( n \)
Pmn_d_z : (m+1, n+1) array
  Derivatives for all orders 0..m and degrees 0..n

See also:

lpmn  associated Legendre functions of the first kind for real z

Notes
By default, i.e. for type=3, phase conventions are chosen according to [R275] 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

[R275]
scipy.special.lpn(n, z)
Compute sequence of Legendre functions of the first kind (polynomials), Pn(z) and derivatives for all degrees from 0 to n (inclusive).
See also special.legendre for polynomial class.

scipy.special.lqn(n, z)
Compute sequence of Legendre functions of the second kind, Qn(z) and derivatives for all degrees from 0 to n (inclusive).

scipy.special.lpmn(m, n, z)
Associated Legendre function of the first kind, Pmn(z)
Computes the associated Legendre function of the first kind of order m and degree n:

Pmn(z) = P_n^{m}(z)

and its derivative, Pmn’(z). Returns two arrays of size (m+1, n+1) containing Pmn(z) and Pmn’(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| <= n; the order of the Legendre function.
  n : int
    where n >= 0; the degree of the Legendre function. Often called l (lower case L) in descriptions of the associated Legendre function
  z : float

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:

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, inf) and (-inf, -1) is such that the result is always real.
References

[R290]

scipy.special.lqmn(m,n,z)
Associated Legendre functions of the second kind, \(Qmn(z)\) and its derivative, \(Qmn' (z)\) of order \(m\) and degree \(n\). Returns two arrays of size \((m+1, n+1)\) containing \(Qmn(z)\) and \(Qmn' (z)\) for all orders from \(0..m\) and degrees from \(0..n\).

\(z\) can be complex.

Ellipsoidal Harmonics

```
scipy.special.ellip_harm(h2, k2, n, p, s[, signm, signn])
```
Ellipsoidal harmonic functions \(E^p_n(l)\)

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
  Sign of prefactor of functions. Can be +/-1. See Notes.
  the harmonic \(E^p_n(s)\)

**See also:**

- `ellip_harm_2`
- `ellip_normal`

**Notes**

The geometric interpretation of the ellipsoidal functions is explained in [R279], [R280], [R281]. 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

[R278], [R279], [R280], [R281]

Examples

```python
>>> from scipy.special import ellip_harm
>>> w = ellip_harm(5, 8, 1, 1, 2.5)
>>> w
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 - 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 (h2, k2, n, p, s)`

Ellipsoidal harmonic functions $F^p_n(s)$

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:**

`ellip_harm`, `ellip_normal`

**Notes**

Lame functions of the second kind are related to the functions of the first kind:

$$F^p_n(s) = (2n + 1)E^p_n(s) \int_0^{1/s} \frac{du}{(E^p_n(1/u))^2 \sqrt{(1 - u^2k^2)(1 - u^2h^2)}}$$

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's `ellip_normal(h2, k2, n, p)` function

Ellipsoidal harmonic normalization constants $\gamma^p_n$

The normalization constant is defined as

$$
\gamma^p_n = 8 \int_0^h dx \int_h^k dy \frac{(y^2 - x^2)(E_p^n(y)E_p^n(x))^2}{\sqrt{((k^2 - y^2)(y^2 - h^2)(h^2 - x^2)(k^2 - x^2))}}
$$

**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 $\gamma^p_n$

**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:

- `assoc_laguerre(x, n[, k])`: Returns the n-th order generalized (associated) Laguerre polynomial.
- `eval_legendre(n, x[, out])`: Evaluate Legendre polynomial at a point.
- `eval_chebyt(n, x[, out])`: Evaluate Chebyshev T polynomial at a point.
- `eval_chebyu(n, x[, out])`: Evaluate Chebyshev U polynomial at a point.
- `eval_chebyc(n, x[, out])`: Evaluate Chebyshev C polynomial at a point.
- `eval_chebys(n, x[, out])`: Evaluate Chebyshev S polynomial at a point.
- `eval_jacobi(n, alpha, beta, x[, out])`: Evaluate Jacobi polynomial at a point.
- `eval_laguerre(n, x[, out])`: Evaluate Laguerre polynomial at a point.
- `eval_genlaguerre(n, alpha, x[, out])`: Evaluate generalized Laguerre polynomial at a point.
- `eval_hermite(n, x[, out])`: Evaluate Hermite polynomial at a point.
<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>eval_hermitenorm(n, x[, out])</code></td>
<td>Evaluate normalized Hermite polynomial at a point.</td>
</tr>
<tr>
<td><code>eval_gegenbauer(n, alpha, x[, out])</code></td>
<td>Evaluate Gegenbauer polynomial at a point.</td>
</tr>
<tr>
<td><code>eval_sh_legendre(n, x[, out])</code></td>
<td>Evaluate shifted Legendre polynomial at a point.</td>
</tr>
<tr>
<td><code>eval_sh_chebyt(n, x[, out])</code></td>
<td>Evaluate shifted Chebyshev T polynomial at a point.</td>
</tr>
<tr>
<td><code>eval_sh_chebyu(n, x[, out])</code></td>
<td>Evaluate shifted Chebyshev U polynomial at a point.</td>
</tr>
<tr>
<td><code>eval_sh_jacobi(n, p, q, x[, out])</code></td>
<td>Evaluate shifted Jacobi polynomial at a point.</td>
</tr>
</tbody>
</table>

**Notes**

`assoc_laguerre` is a simple wrapper around `eval_genlaguerre`, with reversed argument order `(x, n, k=0.0) --> (n, k, x)`. This routine is numerically stable for `x` in `[-1, 1]` at least up to order 10000.

```python
scipy.special.assoc_laguerre(x, n, k=0.0)
Returns the n-th order generalized (associated) Laguerre polynomial.

The polynomial $L(\alpha)_n(x)$ is orthogonal over $[0, \infty)$, with weighting function $\exp(-x) \cdot x^\alpha$ with $\alpha > -1$.
```

The polynomial $L(\alpha)_n(x)$ is orthogonal over $[0, \infty)$, with weighting function $\exp(-x) \cdot x^\alpha$ with $\alpha > -1$.
scipy.special.eval_sh_jacobi(n, p, q, x, out=None) = <ufunc 'eval_sh_jacobi'>
Evaluate shifted Jacobi polynomial at a point.

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 × 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.

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>scipy.special.legendre(n[, monic])</td>
<td>Legendre polynomial coefficients</td>
</tr>
<tr>
<td>scipy.special.chebyt(n[, monic])</td>
<td>Return nth order Chebyshev polynomial of first kind, Tn(x). Orthogonal over [-1, 1] with weight function (1-x^2)^(-1/2).</td>
</tr>
<tr>
<td>scipy.special.chebyu(n[, monic])</td>
<td>Return nth order Chebyshev polynomial of second kind, Un(x). Orthogonal over [-1, 1] with weight function (1-x^2)^(-1/2).</td>
</tr>
<tr>
<td>scipy.special.jacobi(n, alpha, beta[, monic])</td>
<td>Returns the nth order Jacobi polynomial, P^(alpha,beta)_n(x) orthogonal over [-1,1] with weighting function (1-x)**alpha (1+x)**beta with alpha,beta &gt; -1.</td>
</tr>
<tr>
<td>scipy.special.sh_legendre(n[, monic])</td>
<td>Returns the nth order shifted Legendre polynomial, P^*_n(x), orthogonal over [0,1] with weighting function 1.</td>
</tr>
<tr>
<td>scipy.special.sh_chebyt(n[, monic])</td>
<td>Return nth order shifted Chebyshev polynomial of first kind, Tn(x).</td>
</tr>
<tr>
<td>scipy.special.sh_chebyu(n[, monic])</td>
<td>Return nth order shifted Chebyshev polynomial of second kind, Un(x).</td>
</tr>
<tr>
<td>scipy.special.sh_jacobi(n, p, q[, monic])</td>
<td>Returns the nth order Jacobi polynomial, G_n(p,q,x) orthogonal over [0,1] with weighting function (1-x)<strong>(p-q) (x)</strong>(q-1) with p&gt;q-1 and q &gt; 0.</td>
</tr>
</tbody>
</table>

scipy.special.legendre(n, monic=False)
Legendre polynomial coefficients

Returns the nth-order Legendre polynomial, P_n(x), orthogonal over [-1, 1] with weight function 1.

- **Parameters**
  - n: Order of the polynomial
  - monic : bool, optional
    If True, output is a monic polynomial (normalized so the leading coefficient is 1). Default is False.

- **Returns**
  - P : orthopoly1d
    The Legendre polynomial object

**Examples**

Generate the 3rd-order Legendre polynomial 1/2*(5x^3 + 0x^2 - 3x + 0):

```python
>>> legendre(3)
poly1d([ 2.5, 0., -1.5, -0. ])
```

scipy.special.chebyt(n, monic=False)

Return nth order Chebyshev polynomial of first kind, Tn(x). Orthogonal over [-1,1] with weight function (1-x**2)***(-1/2).

scipy.special.chebyu(n, monic=False)

Return nth order Chebyshev polynomial of second kind, Un(x). Orthogonal over [-1,1] with weight function (1-x**2)***(1/2).

scipy.special.chebyc(n, monic=False)

Return nth order Chebyshev polynomial of first kind, Cn(x). Orthogonal over [-2,2] with weight function (1-(x/2)**2)***(-1/2).
scipy.special.chebys(n, monic=False)
Return nth order Chebyshev polynomial of second kind, Sn(x). Orthogonal over [-2,2] with weight function
\((1-(x/2)**2)**(1/2)\).

scipy.special.jacobi(n, alpha, beta, monic=False)
Returns the nth order Jacobi polynomial, P^\alpha_\beta(n)(x) orthogonal over [-1,1] with weighting function
\((1-x)*alpha*(1+x)**beta with alpha, beta > -1\).

scipy.special.laguerre(n, monic=False)
Return the nth order Laguerre polynomial, L_n(x), orthogonal over [0,inf) with weighting function exp(-x)

scipy.special.genlaguerre(n, alpha, monic=False)
Returns the nth order generalized (associated) Laguerre polynomial, L_\alpha(n)(x), orthogonal over [0,inf)
with weighting function exp(-x) x^alpha with alpha > -1

scipy.special.hermite(n, monic=False)
Return the nth order Hermite polynomial, H_n(x), orthogonal over (-inf,inf) with weighting function exp(-x**2)

scipy.special.hermite(n, monic=False)
Return the nth order normalized Hermite polynomial, H_n(x), orthogonal over (-inf,inf) with weighting func-
tion exp(-(x/2)**2)

scipy.special.gegenbauer(n, alpha, monic=False)
Return the nth order Gegenbauer (ultraspherical) polynomial, C_\alpha(n)(x), orthogonal over [-1,1] with
weighting function (1-x**2)**(alpha-1/2) with alpha > -1/2

scipy.special.sh_legendre(n, monic=False)
Returns the nth order shifted Legendre polynomial, P^*_n(x), orthogonal over [0,1] with weighting function 1.

scipy.special.sh_chebyt(n, monic=False)
Return nth order shifted Chebyshev polynomial of first kind, T_n(x). Orthogonal over [0,1] with weight function
\((x-x**2)**(-1/2)\).

scipy.special.sh_chebyu(n, monic=False)
Return nth order shifted Chebyshev polynomial of second kind, U_n(x). Orthogonal over [0,1] with weight
function \((x-x**2)**(1/2)\).

scipy.special.sh_jacobi(n, p, q, monic=False)
Returns the nth order Jacobi polynomial, G_n(p,q,x) orthogonal over [0,1] with weighting function \((1-x)^**(p-q)
(x)**(q-1) with p>q-1 and q > 0.

Warning: Computing values of high-order polynomials (around order > 20) using polynomial coefficients is
numerically unstable. To evaluate polynomial values, the eval_\* functions should be used instead.

Hypergeometric Functions

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>hyp2f1(a, b, c, z)</td>
<td>Gauss hypergeometric function 2F1(a, b; c; z).</td>
</tr>
<tr>
<td>hyp1f1(a, b, x)</td>
<td>Confluent hypergeometric function 1F1(a, b; x).</td>
</tr>
<tr>
<td>hyperu(a, b, x)</td>
<td>Confluent hypergeometric function U(a, b, x) of the second kind</td>
</tr>
<tr>
<td>hyp0f1(v, z)</td>
<td>Confluent hypergeometric limit function 0F1.</td>
</tr>
<tr>
<td>hyp2f0(a, b, x, type)</td>
<td>Hypergeometric function 2F0 in y and an error estimate</td>
</tr>
<tr>
<td>hyp1f2(a, b, c, x)</td>
<td>Hypergeometric function 1F2 and error estimate</td>
</tr>
<tr>
<td>hyp3f0(a, b, c, x)</td>
<td>Hypergeometric function 3F0 in y and an error estimate</td>
</tr>
</tbody>
</table>

scipy.special.hyp2f1(a, b, c, z) = <ufunc ‘hyp2f1’>
Gauss hypergeometric function 2F1(a, b; c; z).
scipy.special.hyp1f1(a, b, x) = <ufunc ‘hyp1f1’>
Confluent hypergeometric function 1F1(a, b; x)

scipy.special.hyperu(a, b, x) = <ufunc ‘hyperu’>
Confluent hypergeometric function U(a, b; x) of the second kind

scipy.special.hyp0f1(v, z)
Confluent hypergeometric limit function 0F1.

Parameters
v, z : array_like
    Input values.

Returns
hyp0f1 : ndarray
    The confluent hypergeometric limit function.

Notes
This function is defined as:

\[
0F_1(v, z) = \sum_{k=0}^{\infty} \frac{z^k}{(v)_k k!}.
\]

It's also the limit as q -> infinity of \( 1F1(q; v; z/q) \), and satisfies the differential equation \( f''(z) + vf'(z) = f(z) \).

scipy.special.hyp2f0(a, b, x, type) = <ufunc ‘hyp2f0’>
Hypergeometric function 2F0 in y and an error estimate

The parameter \( \text{type} \) determines a convergence factor and can be either 1 or 2.

Returns
y : Value of the function
err : Error estimate

scipy.special.hyp1f2(a, b, c, x) = <ufunc ‘hyp1f2’>
Hypergeometric function 1F2 and error estimate

Returns
y : Value of the function
err : Error estimate

scipy.special.hyp3f0(a, b, c, x) = <ufunc ‘hyp3f0’>
Hypergeometric function 3F0 in y and an error estimate

Returns
y : Value of the function
err : Error estimate

Parabolic Cylinder Functions

| pbdv(v, x) | Parabolic cylinder function D |
| pbvv(v, x) | Parabolic cylinder function V |
| pbwa(a, x) | Parabolic cylinder function W |

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 \(dp\).

\[\begin{align*}
\text{Returns} & \quad d \\
& \quad \text{Value of the function} \\
& \quad dp \\
& \quad \text{Value of the derivative vs } x
\end{align*}\]

\texttt{scipy.special.pbvv}(v,x) = \texttt{<ufunc ‘pbvv’>}
Parabolic cylinder function \(V\)

Returns the parabolic cylinder function \(Vv(x)\) in \(v\) and the derivative, \(Vv'(x)\) in \(vp\).

\[\begin{align*}
\text{Returns} & \quad v \\
& \quad \text{Value of the function} \\
& \quad vp \\
& \quad \text{Value of the derivative vs } x
\end{align*}\]

\texttt{scipy.special.pbwa}(a,x) = \texttt{<ufunc ‘pbwa’>}
Parabolic cylinder function \(W\)

Returns the parabolic cylinder function \(W(a,x)\) in \(w\) and the derivative, \(W'(a,x)\) in \(wp\).

\[\begin{align*}
\text{Warning:} & \quad \text{May not be accurate for large (>5) arguments in } a \text{ and/or } x.
\end{align*}\]

\[\begin{align*}
\text{Returns} & \quad w \\
& \quad \text{Value of the function} \\
& \quad wp \\
& \quad \text{Value of the derivative vs } x
\end{align*}\]

These are not universal functions:

\texttt{pbdv_seq}(v,x) Compute sequence of parabolic cylinder functions \(Dv(x)\) and their derivatives for \(Dv0(x)\)\(_0\)..\(Dv(x)\) with \(v0=\text{v-int(v)}\).

\texttt{pbvv_seq}(v,x) Compute sequence of parabolic cylinder functions \(Dv(x)\) and their derivatives for \(Dv0(x)\)\(_0\)..\(Dv(x)\) with \(v0=\text{v-int(v)}\).

\texttt{pbdn_seq}(n,z) Compute sequence of parabolic cylinder functions \(Dn(z)\) and their derivatives for \(D0(z)\)\(_0\)..\(Dn(z)\).

\texttt{scipy.special.pbdv_seq}(v,x)
Compute sequence of parabolic cylinder functions \(Dv(x)\) and their derivatives for \(Dv0(x)\)\(_0\)..\(Dv(x)\) with \(v0=\text{v-int(v)}\).

\texttt{scipy.special.pbvv_seq}(v,x)
Compute sequence of parabolic cylinder functions \(Dv(x)\) and their derivatives for \(Dv0(x)\)\(_0\)..\(Dv(x)\) with \(v0=\text{v-int(v)}\).

\texttt{scipy.special.pbdn_seq}(n,z)
Compute sequence of parabolic cylinder functions \(Dn(z)\) and their derivatives for \(D0(z)\)\(_0\)..\(Dn(z)\).

\textbf{Mathieu and Related Functions}

\texttt{mathieu_a}(m,q) Characteristic value of even Mathieu functions
\texttt{mathieu_b}(m,q) Characteristic value of odd Mathieu functions

\texttt{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.

\texttt{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:

- `mathieu_even_coef(m, q)`: Compute expansion coefficients for even Mathieu functions and modified Mathieu functions.
- `mathieu_odd_coef(m, q)`: Compute expansion coefficients for even Mathieu functions and modified Mathieu functions.

The following return both function and first derivative:

- `mathieu_cem(m, q, x)`: Even Mathieu function and its derivative
- `mathieu_sem(m, q, x)`: Odd Mathieu function and its derivative
- `mathieu_modcem1(m, q, x)`: Even modified Mathieu function of the first kind and its derivative
- `mathieu_modcem2(m, q, x)`: Even modified Mathieu function of the second kind and its derivative
- `mathieu_modsem1(m, q, x)`: Odd modified Mathieu function of the first kind and its derivative
- `mathieu_modsem2(m, q, x)`: Odd modified Mathieu function of the second kind and its derivative

The following return both function and first derivative:

- `mathieu_cem(m, q, x) = <ufunc 'mathieu_cem'>`: Even Mathieu function and its derivative
- `mathieu_sem(m, q, x) = <ufunc 'mathieu_sem'>`: Odd 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

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 \( (m, q, x) \) = <ufunc 'mathieu_modcem1'>
Even modified Mathieu function of the first kind and its derivative

Evaluates the even modified Mathieu function of the first kind, \( Mc_1m(x, q) \), 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 \( (m, q, x) \) = <ufunc 'mathieu_modcem2'>
Even modified Mathieu function of the second kind and its derivative

Evaluates the even modified Mathieu function of the second kind, \( Mc_2m(x,q) \), and its derivative at \( x \) (given in degrees) for order \( m \) and parameter \( q \).

**Returns**

- \( y \) Value of the function
- \( yp \) Value of the derivative vs \( x \)

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
- \( yp \) Value of the derivative vs \( x \)

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
- \( yp \) Value of the derivative vs \( x \)

### Spheroidal Wave Functions

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pro_ang1(m,n,c)</td>
<td>Prolate spheroidal angular function of the first kind and its derivative</td>
</tr>
<tr>
<td>pro_rad1(m,n,c)</td>
<td>Prolate spheroidal radial function of the first kind and its derivative</td>
</tr>
<tr>
<td>pro_rad2(m,n,c)</td>
<td>Prolate spheroidal radial function of the second kind and its derivative</td>
</tr>
<tr>
<td>obl_ang1(m, n, c, x)</td>
<td>Oblate spheroidal angular function of the first kind and its derivative</td>
</tr>
<tr>
<td>obl_rad1(m,n,c)</td>
<td>Oblate spheroidal radial function of the first kind and its derivative</td>
</tr>
<tr>
<td>obl_rad2(m,n,c)</td>
<td>Oblate spheroidal radial function of the second kind and its derivative</td>
</tr>
<tr>
<td>pro_cv(m,n,c)</td>
<td>Characteristic value of prolate spheroidal function</td>
</tr>
<tr>
<td>obl_cv(m, n, c)</td>
<td>Characteristic value of oblate spheroidal function</td>
</tr>
<tr>
<td>pro_cv_seq(m, n, c)</td>
<td>Compute a sequence of characteristic values for the prolate spheroidal wave functions for mode m and n’=m+n</td>
</tr>
<tr>
<td>obl_cv_seq(m, n, c)</td>
<td>Compute a sequence of characteristic values for the oblate spheroidal wave functions for mode m and n’=m+n</td>
</tr>
</tbody>
</table>
**scipy.special.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>=0 and n>m, spheroidal parameter c and |x| < 1.0.

**Returns**

- s: Value of the function
- sp: Value of the derivative vs x

**scipy.special.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>=0 and n>=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**

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>=0 and n>=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**

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>=0 and n>=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**

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>=0 and n>=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**

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>=0 and n>=m, spheroidal parameter c and |x| < 1.0.

**Returns**

- s: Value of the function
scipy.special.pro_cv(m, n, c) = <ufunc ‘pro_cv’>
Characteristic value of prolate spheroidal function

Computes the characteristic value of prolate spheroidal wave functions of order m, n (n>=m) and spheroidal parameter c.

scipy.special.obl_cv(m, n, c) = <ufunc ‘obl_cv’>
Characteristic value of oblate spheroidal function

Computes the characteristic value of oblate spheroidal wave functions of order m, n (n>=m) and spheroidal parameter c.

scipy.special.pro_cv_seq(m, n, c) computes a sequence of characteristic values for the prolate spheroidal wave functions for mode m and n'=m..n and spheroidal parameter c.

scipy.special.obl_cv_seq(m, n, c) computes a sequence of characteristic values for the oblate spheroidal wave functions for mode m and n'=m..n and spheroidal parameter c.

The following functions require pre-computed characteristic value:

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pro_ang1_cv(m, n, c, cv, x)</td>
<td>Prolate spheroidal angular function pro_ang1 for precomputed characteristic value</td>
</tr>
<tr>
<td>pro_rad1_cv(m, n, c, cv, x)</td>
<td>Prolate spheroidal radial function pro_rad1 for precomputed characteristic value</td>
</tr>
<tr>
<td>pro_rad2_cv(m, n, c, cv, x)</td>
<td>Prolate spheroidal radial function pro_rad2 for precomputed characteristic value</td>
</tr>
<tr>
<td>obl_ang1_cv(m, n, c, x)</td>
<td>Oblate spheroidal angular function obl_ang1 for precomputed characteristic value</td>
</tr>
<tr>
<td>obl_rad1_cv(m, n, c, cv, x)</td>
<td>Oblate spheroidal radial function obl_rad1 for precomputed characteristic value</td>
</tr>
<tr>
<td>obl_rad2_cv(m, n, c, cv, x)</td>
<td>Oblate spheroidal radial function obl_rad2 for precomputed characteristic value</td>
</tr>
</tbody>
</table>

scipy.special.pro_ang1_cv(m, n, c, cv, x) = <ufunc ‘pro_ang1_cv’>

Prolate spheroidal angular function pro_ang1 for precomputed characteristic value

Computes the prolate 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.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(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 \( m \geq 0 \) and \( n \geq m \), 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

```python
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 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 \( |x| < 1.0 \). Requires pre-computed characteristic value.

**Returns**
- \( s \) Value of the function
- \( sp \) Value of the derivative vs x

```python
scipy.special.obl_rad1_cv(m, n, c, cv, x) = <ufunc 'obl_rad1_cv'>
```

Oblate spheroidal radial function obl_rad1 for precomputed characteristic value

Kelvin Functions

- `kelvin(x)` Kelvin functions as complex numbers
- `kelvin_zeros(nt)` Compute \( nt \) zeros of all the Kelvin functions returned in a length 8 tuple of arrays of length \( nt \).
- `ber(x)` Kelvin function ber.
- `bei(x)` Kelvin function bei
- `berp(x)` Derivative of the Kelvin function ber
- `beip(x)` Derivative of the Kelvin function bei
- `ker(x)` Kelvin function ker
- `kei(x)` Kelvin function ker
- `kerp(x)` Derivative of the Kelvin function ker

Continued on next page
Table 5.240 – continued from previous page

keip(x) Derivative of the Kelvin function kei

scipy.special.kelvin(x) = <ufunc ‘kelvin’>
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, kelvin(x)[0].real = ber x and kelvin(x)[0].imag = bei x with
similar relationships for ker and kei.

scipy.special.kelvin_zeros(nt)
Compute nt zeros of all the Kelvin functions returned in a length 8 tuple of arrays of length nt. The tuple
containse the arrays of zeros of (ber, bei, ker, kei, ber’, bei’, ker’, kei’)

scipy.special.ber(x) = <ufunc ‘ber’>
Kelvin function ber.

scipy.special.bei(x) = <ufunc ‘bei’>
Kelvin function bei

scipy.special.berp(x) = <ufunc ‘berp’>
Derivative of the Kelvin function ber

scipy.special.beip(x) = <ufunc ‘beip’>
Derivative of the Kelvin function bei

scipy.special.ker(x) = <ufunc ‘ker’>
Kelvin function ker

scipy.special.kei(x) = <ufunc ‘kei’>
Kelvin function kei

scipy.special.kerp(x) = <ufunc ‘kerp’>
Derivative of the Kelvin function ker

scipy.special.keip(x) = <ufunc ‘keip’>
Derivative of the Kelvin function kei

These are not universal functions:

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ber_zeros(nt)</td>
<td>Compute nt zeros of the Kelvin function ber x</td>
</tr>
<tr>
<td>bei_zeros(nt)</td>
<td>Compute nt zeros of the Kelvin function bei x</td>
</tr>
<tr>
<td>berp_zeros(nt)</td>
<td>Compute nt zeros of the Kelvin function ber’ x</td>
</tr>
<tr>
<td>beip_zeros(nt)</td>
<td>Compute nt zeros of the Kelvin function bei’ x</td>
</tr>
<tr>
<td>ker_zeros(nt)</td>
<td>Compute nt zeros of the Kelvin function ker x</td>
</tr>
<tr>
<td>kei_zeros(nt)</td>
<td>Compute nt zeros of the Kelvin function kei x</td>
</tr>
<tr>
<td>kerp_zeros(nt)</td>
<td>Compute nt zeros of the Kelvin function ker’ x</td>
</tr>
<tr>
<td>keip_zeros(nt)</td>
<td>Compute nt zeros of the Kelvin function kei’ x</td>
</tr>
</tbody>
</table>

scipy.special.ber_zeros(nt)
Compute nt zeros of the Kelvin function ber x

scipy.special.bei_zeros(nt)
Compute nt zeros of the Kelvin function bei x

scipy.special.berp_zeros(nt)
Compute nt zeros of the Kelvin function ber’ x
SciPy Reference Guide, Release 0.16.0

scipy.special.beip_zeros(nt)
Compute nt zeros of the Kelvin function bei' x

scipy.special.ker_zeros(nt)
Compute nt zeros of the Kelvin function ker x

scipy.special.kei_zeros(nt)
Compute nt zeros of the Kelvin function kei x

scipy.special.kerp_zeros(nt)
Compute nt zeros of the Kelvin function ker' x

scipy.special.keip_zeros(nt)
Compute nt zeros of the Kelvin function kei' x

Combinatorics

_ comb(N, k[, exact, repetition])_ The number of combinations of N things taken k at a time.

_ perm(N, k[, exact])_ Permutations of N things taken k at a time, i.e., k-permutations of N.

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, ndarray
  The total number of combinations.

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 (N, k, exact=False)
Permutations of N things taken k at a time, i.e., k-permutations of N.

5.33. Special functions (scipy.special) 1191
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
```

**Other Special Functions**

- **agm(a, b)**: Arithmetic, Geometric Mean
- **bernoulli(n)**: Return an array of the Bernoulli numbers B0..Bn
- **binom(n, k)**: Binomial coefficient
- **diric(x, n)**: Return the periodic sinc function, also called the Dirichlet function.
- **euler(n)**: Return an array of the Euler numbers E0..En (inclusive)
- **expn(n, x)**: Exponential integral E_n
- **exp1(z)**: Exponential integral E_1 of complex argument z
- **expi(z)**: Exponential integral Ei
- **factorial(n[, exact])**: The factorial function, n! = special.gamma(n+1).
- **factorial2(n[, exact])**: Double factorial.
- **factorialk(n[k], exact)**: n(!!...!) = multifactorial of order k
- **shichi(x)**: Hyperbolic sine and cosine integrals
- **sici(x)**: Sine and cosine integrals
- **spence(x)**: Dilogarithm integral
- **lambertw(z[, k, tol])**: Lambert W function [R599].
- **zeta(x, q)**: Hurwitz zeta function
- **zetac(x)**: Riemann zeta function minus 1.

**scipy.special.agm(a, b)**

Arithmetic, Geometric Mean

Start with a_0=a and b_0=b and iteratively compute

a_(n+1) = (a_n+b_n)/2  b_(n+1) = sqrt(a_n*b_n)

until a_n=b_n. The result is agm(a,b)
\[ \text{agm}(a,b) = \text{agm}(b,a) \quad \text{agm}(a,a) = a \quad \text{min}(a,b) < \text{agm}(a,b) < \text{max}(a,b) \]

\textit{scipy.special.bernoulli}(n)
Return an array of the Bernoulli numbers B0..Bn

\textit{scipy.special.binom}(n,k) = <ufunc 'binom'>
Binomial coefficient

\textit{scipy.special.diric}(x,n)
Return the periodic sinc function, also called the Dirichlet function.

The Dirichlet function is defined as:

\[ \text{diric}(x) = \frac{\sin(x \times n/2)}{(n \times \sin(x / 2))}, \]

where \( n \) is a positive integer.

\textbf{Parameters}
\begin{itemize}
  \item \textbf{x} : array_like
    Input data
  \item \textbf{n} : int
    Integer defining the periodicity.
\end{itemize}

\textbf{Returns}
\begin{itemize}
  \item \textbf{diric} : ndarray
    \end{itemize}

\textbf{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.diric(x, n))
...     plt.title('diric, n={}'.format(n))
>>> plt.show()
```
scipy.special.euler$(n)$
Return an array of the Euler numbers $E_0..E_n$ (inclusive)

scipy.special.expn$(n, x)$ = <ufunc 'expn'>
Exponential integral $E_n$
Returns the exponential integral for integer $n$ and non-negative $x$ and $n$:

$$\int \frac{\exp(-x t)}{t^n} \, dt$$

scipy.special.expl$(z)$ = <ufunc 'expl'>
Exponential integral $E_1$ of complex argument $z$

$$\int \frac{\exp(-z t)}{t} \, dt$$

scipy.special.expi$(x)$ = <ufunc 'expi'>
Exponential integral $Ei$
Defined as:

\[ \text{integral}\left(\exp(t)/t, t=\text{inf}..x\right) \]

See \texttt{expn} for a different exponential integral.

\texttt{scipy.special.factorial}(n, exact=False)

The factorial function, \( n! = \text{special.gamma}(n+1) \).

If exact is 0, then floating point precision is used, otherwise exact long integer is computed.

- Array argument accepted only for \texttt{exact=False} case.
- If \( n<0 \), the return value is 0.

**Parameters**

- \texttt{n} : int or array_like of ints
  Calculate \( n! \). Arrays are only supported with \texttt{exact} set to False. If \( n < 0 \), the return value is 0.

- \texttt{exact} : bool, optional
  The result can be approximated rapidly using the gamma-formula above. If \texttt{exact} is set to True, calculate the answer exactly using integer arithmetic. Default is False.

**Returns**

- \texttt{nf} : float or int
  Factorial of \( n \), as an integer or a float depending on \texttt{exact}.

**Examples**

```python
>>> from scipy.special import factorial
>>> arr = np.array([3,4,5])
>>> factorial(arr, exact=False)
array([ 6., 24., 120.])
>>> factorial(5, exact=True)
120L
```

\texttt{scipy.special.factorial2}(n, exact=False)

Double factorial.

This is the factorial with every second value skipped, i.e., \( 7!! = 7 \times 5 \times 3 \times 1 \). It can be approximated numerically as:

\[
\begin{align*}
\text{n!!} & = \text{special.gamma}(n/2+1) \times 2^\left(\lfloor (n+1)/2 \rfloor\right) / \sqrt{\pi} \quad \text{n odd} \\
& = 2^\left( (n/2) \times (n/2) \right) \quad \text{n even}
\end{align*}
\]

**Parameters**

- \texttt{n} : int or array_like
  Calculate \( n!! \). Arrays are only supported with \texttt{exact} set to False. If \( n < 0 \), the return value is 0.

- \texttt{exact} : bool, optional
  The result can be approximated rapidly using the gamma-formula above (default). If \texttt{exact} is set to True, calculate the answer exactly using integer arithmetic.

**Returns**

- \texttt{nff} : float or int
  Double factorial of \( n \), as an int or a float depending on \texttt{exact}.

**Examples**

```python
>>> from scipy.special import factorial2
>>> factorial2(7, exact=False)
array(105.00000000000001)
```
scipy.special.factorial2(7, exact=True)
105L

scipy.special.factorialk(n, k, exact=True)

\( n(!!...!) \) = multifactorial of order \( k \) \( k \) times

**Parameters**

- \( n \) : int  
  Calculate multifactorial. If \( n < 0 \), the return value is 0.
- \( k \) : int  
  Order of multifactorial.
- \( \text{exact} \) : bool, optional  
  If \( \text{exact} \) is set to True, calculate the answer exactly using integer arithmetic.

**Returns**

- \( \text{val} \) : int  
  Multi factorial of \( n \).

**Raises**

- NotImplementedError  
  Raises when \( \text{exact} \) is False

**Examples**

```python
>>> from scipy.special import factorialk
>>> factorialk(5, 1, exact=True)
120L
>>> factorialk(5, 3, exact=True)
10L
```

scipy.special.shichi(x) = <ufunc 'shichi'>

Hyperbolic sine and cosine integrals

**Returns**

- \( \text{shi} \)  
  \( \int \sinh(t)/t, t=0..x \)
- \( \text{chi} \)  
  \( eul + \ln x + \int \frac{(cosh(t)-1)}{t}, t=0..x \) where \( eul \) is Euler’s constant.

scipy.special.sici(x) = <ufunc 'sici'>

Sine and cosine integrals

**Returns**

- \( \text{si} \)  
  \( \int \sin(t)/t, t=0..x \)
- \( \text{ci} \)  
  \( eul + \ln x + \int \frac{(\cos(t) - 1)}{t}, t=0..x \) where \( eul \) is Euler’s constant.

scipy.special.spence(x) = <ufunc 'spence'>

Dilogarithm integral

Returns the dilogarithm integral:

\[-\int \log t / (t-1), t=1..x\]

scipy.special.lambertw(z, k=0, tol=1e-8)

Lambert \( W \) function [R288].

The Lambert \( W \) function \( W(z) \) is defined as the inverse function of \( w \ast \exp(w) \). In other words, the value of \( W(z) \) is such that \( z = W(z) \ast \exp(W(z)) \) for any complex number \( z \).

The Lambert \( W \) function is a multivalued function with infinitely many branches. Each branch gives a separate solution of the equation \( z = w \ast \exp(w) \). Here, the branches are indexed by the integer \( k \).

**Parameters**

- \( z \) : array_like
Input argument.

- **k**: int, optional
  - Branch index.

- **tol**: float, optional
  - Evaluation tolerance.

**Returns**

- **w**: array
  - *w* will have the same shape as *z*.

**Notes**

All branches are supported by `lambertw`:
- `lambertw(z)` gives the principal solution (branch 0)
- `lambertw(z, k)` gives the solution on branch *k*

The Lambert W function has two partially real branches: the principal branch (*k* = 0) is real for real *z* > -1/e, and the *k* = -1 branch is real for -1/e < *z* < 0. All branches except *k* = 0 have a logarithmic singularity at *z* = 0.

**Possible issues**

The evaluation can become inaccurate very close to the branch point at -1/e. In some corner cases, `lambertw` might currently fail to converge, or can end up on the wrong branch.

**Algorithm**

Halley’s iteration is used to invert *w* * exp(*w*), using a first-order asymptotic approximation (O(log(*w*)) or O(*w*)) as the initial estimate.

The definition, implementation and choice of branches is based on [R289].

**References**

[R288], [R289]

**Examples**

The Lambert W function is the inverse of *w* exp(*w*):

```python
>>> from scipy.special import lambertw
>>> w = lambertw(1)
>>> w
(0.56714329040978384+0j)
>>> w * np.exp(w)
(1.0+0j)
```

Any branch gives a valid inverse:

```python
>>> w = lambertw(1, k=3)
>>> w
(-2.8535817554090377+17.113535539412148j)
>>> w*np.exp(w)
(1.0000000000000002+1.609823385706477e-15j)
```

**Applications to equation-solving**

The Lambert W function may be used to solve various kinds of equations, such as finding the value of the infinite power tower *z*^*z*^...:

```python
>>> def tower(z, n):
...     if n == 0:
...         return z
...     return z**tower(z, n-1)
```

5.33. Special functions (`scipy.special`)
...         return z ** tower(z, n-1)
...
>>> tower(0.5, 100)
0.641185744504986
>>> -lambertw(-np.log(0.5)) / np.log(0.5)
(0.64118574450498589+0j)

scipy.special.zeta (x, q) = <ufunc ‘zeta’>
Hurwitz zeta function

The Riemann zeta function of two arguments (also known as the Hurwitz zeta function).
This function is defined as

\[ \zeta(x, q) = \sum_{k=0}^{\infty} \frac{1}{(k+q)^x}, \]

where \( x > 1 \) and \( q > 0 \).

See also:
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 \( x > 1 \).

See also:
zeta

Convenience Functions

- **cbrt (x)**: Cube root of x
- **exp10 (x)**: \(10**x\)
- **exp2 (x)**: \(2**x\)
- **radian (d, m, s)**: Convert from degrees to radians
- **cosdg (x)**: Cosine of the angle x given in degrees.
- **sindg (x)**: Sine of angle given in degrees
- **tandg (x)**: Tangent of angle x given in degrees.
- **cotdg (x)**: Cotangent of the angle x given in degrees.
- **log1p (x)**: Calculates log(1+x) for use when x is near zero
- **expml (x)**: \(\exp(x) - 1\) for use when x is near zero.
- **cosml (x)**: \(\cos(x) - 1\) for use when x is near zero.
- **round (x)**: Round to nearest integer
- **xlogy (x, y)**: Compute \(x \times \log(y)\) so that the result is 0 if \(x = 0\).
- **xlog1py (x, y)**: Compute \(x \times \log1p(y)\) so that the result is 0 if \(x = 0\).
scipy.special.exp10(x) = <ufunc ‘exp10’>
10**x

scipy.special.exp2(x) = <ufunc ‘exp2’>
2**x

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(x) = <ufunc ‘cosdg’>
Cosine of the angle x given in degrees.

scipy.special.sindg(x) = <ufunc ‘sindg’>
Sine of angle given in degrees

scipy.special.tandg(x) = <ufunc ‘tandg’>
Tangent of angle x given in degrees.

scipy.special.cotdg(x) = <ufunc ‘cotdg’>
Cotangent of the angle x given in degrees.

scipy.special.log1p(x) = <ufunc ‘log1p’>
Calculates log(1+x) for use when x is near zero

scipy.special.expm1(x) = <ufunc ‘expm1’>
exp(x) - 1 for use when x is near zero.

scipy.special.cosm1(x) = <ufunc ‘cosm1’>
cos(x) - 1 for use when x is near zero.

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(x, y) = <ufunc ‘xlogy’>
Compute x*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*log(y)

Notes
New in version 0.13.0.

scipy.special.xlog1py(x, y) = <ufunc ‘xlog1py’>
Compute x*log1p(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*log1p(y)
New in version 0.13.0.

5.34 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):

<table>
<thead>
<tr>
<th>Class</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rv_continuous</code></td>
<td>A generic continuous random variable class meant for subclassing.</td>
</tr>
<tr>
<td><code>rv_discrete</code></td>
<td>A generic discrete random variable class meant for subclassing.</td>
</tr>
</tbody>
</table>

`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:

_logpdf, _cdf, _logcdf, _ppf, _rvs, _isf, _sf, _logsf

Rarely would you override _isf, _sf or _logsf, but you could.

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:

\[
\text{rv = generic(<shape(s)>, loc=0, scale=1)}
\]

frozen RV 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):
...       return np.exp(-x**2 / 2.) / np.sqrt(2.0 * np.pi)
>>> gaussian = gaussian_gen(name='gaussian')
```

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 automagically 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:

```python
>>> gaussian.pdf(x, loc, scale)
```

essentially computes

```python
y = (x - loc) / scale
```

and

```python
gaussian._pdf(y) / scale.
```

Attributes

- `random_state` Get or set the RandomState object for generating random variates.

```python
rv_continuous.random_state
```

Get or set the RandomState object for generating random variates.

This can be either None or an existing RandomState object.

If None (or np.random), use the RandomState singleton used by np.random. If already a RandomState instance, use it. If an int, use a new RandomState instance seeded with seed.

Methods

- `rvs(*args, **kws)` Random variates of given type.
- `pdf(x, *args, **kws)` Probability density function at x of the given RV.
- `logpdf(x, *args, **kws)` Log of the probability density function at x of the given RV.
- `cdf(x, *args, **kws)` Cumulative distribution function of the given RV.
- `logcdf(x, *args, **kws)` Log of the cumulative distribution function at x of the given RV.
- `sf(x, *args, **kws)` Survival function (1 - `cdf`) at x of the given RV.
- `logsf(x, *args, **kws)` Log of the survival function of the given RV.
- `ppf(q, *args, **kws)` Percent point function (inverse of `cdf`) at q of the given RV.
- `isf(q, *args, **kws)` Inverse survival function (inverse of `sf`) at q of the given RV.
- `moment(n, *args, **kws)` n-th order non-central moment of distribution.
- `stats(*args, **kws)` Some statistics of the given RV.
- `entropy(*args, **kws)` Differential entropy of the RV.
- `expect([func, args, loc, scale, lb, ub, ...])` Calculate expected value of a function with respect to the distribution.
- `median(*args, **kws)` Median of the distribution.
- `mean(*args, **kws)` Mean of the distribution.
- `std(*args, **kws)` Standard deviation of the distribution.
- `var(*args, **kws)` Variance of the distribution.
- `interval(alpha, *args, **kws)` Confidence interval with equal areas around the median.
- `__call__(*args, **kws)` Freeze the distribution for the given arguments.
- `fit(data, *args, **kws)` Return MLEs for shape, location, and scale parameters from data.
- `fit_loc_scale(data, *args)` Estimate loc and scale parameters from data using 1st and 2nd moments.
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.

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 : array_like
   Probability density function evaluated at x

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

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

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

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

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

rv_continuous.ppf(q, *args, **kwds)
Percent point function (inverse of cdf) at q of the given RV.

Parameters
q : array_like
The lower tail probability

\[ \text{arg1, arg2, arg3,... : array_like} \]

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

\[ \text{loc : array_like, optional} \]

location parameter (default=0)

\[ \text{scale : array_like, optional} \]

scale parameter (default=1)

\textbf{Returns}

\[ x : \text{array_like} \]

Quantile corresponding to the lower tail probability \( q \).

\textit{rv_continuous.isf}(q, *args, **kwds)

Inverse survival function (inverse of \textit{sf}) at \( q \) of the given RV.

\textbf{Parameters}

\[ q : \text{array_like} \]

upper tail probability

\[ \text{arg1, arg2, arg3,... : array_like} \]

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

\[ \text{loc : array_like, optional} \]

location parameter (default=0)

\[ \text{scale : array_like, optional} \]

scale parameter (default=1)

\textbf{Returns}

\[ x : \text{ndarray or scalar} \]

Quantile corresponding to the upper tail probability \( q \).

\textit{rv_continuous.moment}(n, *args, **kwds)

\( n \)-th order non-central moment of distribution.

\textbf{Parameters}

\[ n : \text{int, } n \geq 1 \]

Order of moment.

\[ \text{arg1, arg2, arg3,... : float} \]

The shape parameter(s) for the distribution (see docstring of the instance object for more information).

\[ \text{loc : array_like, optional} \]

location parameter (default=0)

\[ \text{scale : array_like, optional} \]

scale parameter (default=1)

\textbf{Returns}

\[ x \]

Quantile corresponding to the upper tail probability \( q \).

\textit{rv_continuous.stats}(*args, **kwds)

Some statistics of the given RV.

\textbf{Parameters}

\[ \text{arg1, arg2, arg3,... : array_like} \]

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

\[ \text{loc : array_like, optional} \]

location parameter (default=0)

\[ \text{scale : array_like, optional} \]

scale parameter (default=1)

\[ \text{moments : str, optional} \]

composed of letters ['mvsk'] defining which moments to compute: 'm' = mean, 'v' = variance, 's' = (Fisher's) skew, 'k' = (Fisher's) kurtosis. (default is 'mv')

\textbf{Returns}

\[ stats \]

of requested moments.

\textit{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 (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
```

`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.

The expected value of a function $f(x)$ with respect to a distribution `dist` is defined as:

\[ E[x] = \int f(x) * \text{dist.pdf}(x) \]

**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 `integrate.quad`.

`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 : 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

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
default=0
location parameter (default=0)

scale : array_like, optional
scale parameter (default=1)

Returns

mean : float
the mean of the distribution

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
default=0
location parameter (default=0)

scale : array_like, optional
scale parameter (default=1)

Returns

std : float
standard deviation of the distribution

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
default=0
location parameter (default=0)

scale : array_like, optional
scale parameter (default=1)

Returns

var : float
the variance of the distribution

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 \(100 \times \alpha\) % of the rv's possible values.

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.

rv_continuous.fit(data, *args, **kwds)
Return MLEs for shape, 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 is equivalent to f0 and fb is 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 shape, loc, scale : tuple of floats
MLEs for any shape statistics, followed by those for location and scale.

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
>>> 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):

>>> a1, b1, loc1, scale1 = beta.fit(x)

We can also use some prior knowledge about the dataset: let’s keep loc and scale fixed:

>>> a1, b1, loc1, scale1 = beta.fit(x, floc=0, fscale=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:

>>> a1, b1, loc1, scale1 = beta.fit(x, fa=1, floc=0, fscale=1)

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 in-
   stance object for more information).

Returns
Lhat : float
   Estimated location parameter for the data.
Shat : float
   Estimated scale parameter for the data.

rv_continuous.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).

class scipy.stats.rv_discrete(a=0, b=inf, 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 vari-
ables. It can also be used to construct an arbitrary distribution defined by a list of support points and correspond-
ing 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 infinity
   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 
\( \text{sum}(pk) = 1 \).

**inc** : integer, optional
Increrment 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 argu-
ment restriction is violated, default is np.nan.

**name** : str, optional
The name of the instance. This string is used to construct the default exam-
ple 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 pro-
vided, 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 compati-
bility, 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, the main differences being:
• 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 \( \text{Prob}(X=x_k) = pk \) 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, 0.0, 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.

`rv_discrete.random_state`

Get or set the RandomState object for generating random variates.

This can be either None or an existing RandomState object.

If None (or np.random), use the RandomState singleton used by np.random. If already a RandomState instance, use it. If an int, use a new RandomState instance seeded with seed.

Methods

- `rvs(*args, **kwargs)` Random variates of given type.
- `pmf(k, *args, **kwds)` Probability mass function at k of the given RV.
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 : array_like, optional
Location parameter (default=0).
size : int or tuple of ints, optional
Defining number of random variates (Default is 1). Note that size has to be given as keyword, not as positional argument.
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.

rv_discrete.pmf(k,*args,**kwargs)
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=0).

Returns
pmf : array_like
Probability mass function evaluated at k

rv_discrete.logpmf(k,*args,**kwargs)
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.

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.

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.

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.

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.
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.

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.

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 instance object for more information).
loc : array_like, optional
    Location parameter (default=0)
scale : array_like, optional (continuous RVs only)
    Scale parameter (default=1)

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 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.

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 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
```

**rv_discrete.expect** *(func=None, args=(), loc=0, lb=None, ub=None, conditional=False)*
Calculate expected value of a function with respect to the distribution for discrete distribution.

**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 integration, default is set to the support of the distribution, inclusive \((lb \leq k \leq ub)\).
- **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, \(f(k)\), conditional on being in the given interval \((k \text{ such that } lb \leq k \leq ub)\). Default is False.

**Returns**
- **expect**: float
  Expected value.

**Notes**
- Function is not vectorized
- Accuracy: uses self.moment_tol as stopping criterion for heavy tailed distribution e.g. zipf(4), accuracy for mean, variance in example is only 1e-5, increasing precision (moment_tol) makes zipf very slow
- suppnmin=100 internal parameter for minimum number of points to evaluate could be added as keyword parameter, to evaluate functions with non-monotonic shapes, points include integers in \((-suppnmin, suppnmin)\)
- Uses maxcount=1000 limits the number of points that are evaluated to break loop for infinite sums (a maximum of suppnmin+1000 positive plus suppnmin+1000 negative integers are evaluated)

**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

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 in-
stance 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

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 in-
stance 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

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 in-
stance 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

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 in-
stance 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 $100 \times \alpha$ % of the rv's possible values.

```
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.

### 5.34.1 Continuous distributions

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>alpha</code></td>
<td>An alpha continuous random variable.</td>
</tr>
<tr>
<td><code>anglit</code></td>
<td>An anglit continuous random variable.</td>
</tr>
<tr>
<td><code>arcsine</code></td>
<td>An arcsine continuous random variable.</td>
</tr>
<tr>
<td><code>beta</code></td>
<td>A beta continuous random variable.</td>
</tr>
<tr>
<td><code>betaprime</code></td>
<td>A beta prime continuous random variable.</td>
</tr>
<tr>
<td><code>bradford</code></td>
<td>A Bradford continuous random variable.</td>
</tr>
<tr>
<td><code>burr</code></td>
<td>A Burr continuous random variable.</td>
</tr>
<tr>
<td><code>cauchy</code></td>
<td>A Cauchy continuous random variable.</td>
</tr>
<tr>
<td><code>chi</code></td>
<td>A chi continuous random variable.</td>
</tr>
<tr>
<td><code>chi2</code></td>
<td>A chi-squared continuous random variable.</td>
</tr>
<tr>
<td><code>cosine</code></td>
<td>A cosine continuous random variable.</td>
</tr>
<tr>
<td><code>dgamma</code></td>
<td>A double gamma continuous random variable.</td>
</tr>
<tr>
<td><code>dweibull</code></td>
<td>A double Weibull continuous random variable.</td>
</tr>
<tr>
<td><code>erlang</code></td>
<td>An Erlang continuous random variable.</td>
</tr>
<tr>
<td><code>expon</code></td>
<td>An exponential continuous random variable.</td>
</tr>
<tr>
<td><code>exponnorm</code></td>
<td>An exponentially modified Normal continuous random variable.</td>
</tr>
<tr>
<td><code>exponweib</code></td>
<td>An exponentiated Weibull continuous random variable.</td>
</tr>
<tr>
<td><code>exponpow</code></td>
<td>An exponential power continuous random variable.</td>
</tr>
<tr>
<td><code>f</code></td>
<td>An F continuous random variable.</td>
</tr>
<tr>
<td><code>fatiguelife</code></td>
<td>A fatigue-life (Birnbaum-Saunders) continuous random variable.</td>
</tr>
<tr>
<td><code>fisk</code></td>
<td>A Fisk continuous random variable.</td>
</tr>
<tr>
<td><code>foldcauchy</code></td>
<td>A folded Cauchy continuous random variable.</td>
</tr>
<tr>
<td><code>foldnorm</code></td>
<td>A folded normal continuous random variable.</td>
</tr>
<tr>
<td><code>frechet_r</code></td>
<td>A Frechet right (or Weibull minimum) continuous random variable.</td>
</tr>
<tr>
<td><code>frechet_l</code></td>
<td>A Frechet left (or Weibull maximum) continuous random variable.</td>
</tr>
<tr>
<td><code>genlogistic</code></td>
<td>A generalized logistic continuous random variable.</td>
</tr>
<tr>
<td><code>gennorm</code></td>
<td>A generalized normal continuous random variable.</td>
</tr>
<tr>
<td><code>genpareto</code></td>
<td>A generalized Pareto continuous random variable.</td>
</tr>
<tr>
<td><code>genexpon</code></td>
<td>A generalized exponential continuous random variable.</td>
</tr>
<tr>
<td><code>genextreme</code></td>
<td>A generalized extreme value continuous random variable.</td>
</tr>
<tr>
<td><code>gausshyper</code></td>
<td>A Gauss hypergeometric continuous random variable.</td>
</tr>
<tr>
<td><code>gamma</code></td>
<td>A gamma continuous random variable.</td>
</tr>
<tr>
<td><code>gengamma</code></td>
<td>A generalized gamma continuous random variable.</td>
</tr>
<tr>
<td><code>genhalflogistic</code></td>
<td>A generalized half-logistic continuous random variable.</td>
</tr>
<tr>
<td><code>gilbrat</code></td>
<td>A Gilbrat continuous random variable.</td>
</tr>
<tr>
<td><code>gompertz</code></td>
<td>A Gompertz (or truncated Gumbel) continuous random variable.</td>
</tr>
<tr>
<td><code>gumbel_r</code></td>
<td>A right-skewed Gumbel continuous random variable.</td>
</tr>
<tr>
<td><code>gumbel_l</code></td>
<td>A left-skewed Gumbel continuous random variable.</td>
</tr>
</tbody>
</table>
Table 5.250 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<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>johnsonsfb</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>kstwobign</td>
<td>Kolmogorov-Smirnov one-sided test.</td>
</tr>
<tr>
<td>laplace</td>
<td>A Laplace continuous random variable.</td>
</tr>
<tr>
<td>logistic</td>
<td>A logistic (or Sech-squared) continuous random variable.</td>
</tr>
<tr>
<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>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>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>reciprocal</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>t</td>
<td>A Student’s T 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-Lambha 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>wald</td>
<td>A Wald continuous random variable.</td>
</tr>
<tr>
<td>weibull_min</td>
<td>A Frechet right (or Weibull minimum) continuous random variable.</td>
</tr>
<tr>
<td>weibull_max</td>
<td>A Frechet left (or 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._continuous_distns.alpha_gen object at 0x7fa40ebcfa0>
An alpha continuous random variable.
```
As an instance of the `rv_continuous` class, `alpha` 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 `alpha` is:

\[ \text{alpha.pdf}(x, a) = \frac{1}{x^2 \Phi(a) \sqrt{2\pi}} \exp\left(-\frac{1}{2} \left(\frac{a - 1}{x}\right)^2\right), \]

where \( \Phi(a) \) 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, \( \text{alpha.pdf}(x, a, \text{loc}, \text{scale}) \) is identically equivalent to \( \text{alpha.pdf}(y, a) / \text{scale} \) with \( y = (x - \text{loc}) / \text{scale} \).

**Examples**

```python
>>> from scipy.stats import alpha
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
define 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, normed=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><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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, a, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, a, loc=0, scale=1)</code></td>
<td>Survival function (1 – cdf — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, a, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<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>
</tr>
<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, 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>
</tr>
<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>

```python
scipy.stats.anglit = <scipy.stats._continuous_distns.anglit_gen object at 0x7fa40ebcfd90>
```

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:

\[ \text{anglit.pdf}(x) = \sin(2x + \pi/2) = \cos(2x), \]
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, \( \text{anglit.pdf}(x, \text{loc}, \text{scale}) \) is identically equivalent to \( \text{anglit.pdf}(y) / \text{scale} \) 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:

```none```
>>> 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))
```

Generate random numbers:

```python
>>> r = anglit.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, normed=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(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 density function.</td>
</tr>
<tr>
<td>logcdf(x, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>
<tr>
<td>mean(loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</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.arcsine = <scipy.stats._continuous_distns.arcsine_gen object at 0x7fa40ebcf9f0>

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:

\[
\text{arcsine.pdf}(x) = \frac{1}{\pi \sqrt{x(1-x)}}
\]

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 \(y = (x - \text{loc}) / \text{scale}\).

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))
>>> True
```  
Generate random numbers:

```python
>>> r = arcsine.rvs(size=1000)
```  
And compare the histogram:

```python
>>> ax.hist(r, normed=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()</code></td>
<td>Random variates.</td>
</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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — 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, 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>
</tbody>
</table>

```python
cnumpy.stats.beta = <scipy.stats._continuous_distns.beta_gen object at 0x7fa40ebe51d0>
```

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:

\[
\frac{\Gamma(a+b) \cdot x^{(a-1)} \cdot (1-x)^{(b-1)}}{\Gamma(a) \cdot \Gamma(b)}
\]
for \(0 < x < 1, a > 0, b > 0\), where \(\Gamma(z)\) is the gamma function \(\text{scipy.special.gamma}\).

*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 \(\text{loc}\) and \(\text{scale}\) parameters. Specifically, \(\text{beta.pdf}(x, a, b, \text{loc}, \text{scale})\) is identically equivalent to \(\text{beta.pdf}(y, a, b) / \text{scale}\) with \(y = (x - \text{loc}) / \text{scale}\).

Examples

```python
>>> from scipy.stats import beta
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
Calculate a few first moments:
>>> a, b = 2.31, 0.627
>>> mean, var, skew, kurt = beta.stats(a, b, moments='mvsk')
Display the probability density function (pdf):
>>> 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:
>>> rv = beta(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
Check accuracy of cdf and ppf:
>>> 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:
>>> r = beta.rvs(a, b, size=1000)
And compare the histogram:
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

5.34. Statistical functions (scipy.stats)
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 density function.</td>
</tr>
<tr>
<td>logcdf(x, a, b, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, a, b, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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>
</tr>
<tr>
<td>expect(func, 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.betaprime = <scipy.stats._continuous_distns.betaprime_gen object at 0x7fa40ebe5590>

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.
The probability density function for betaprime is:

\[
\text{betaprime.pdf}(x, a, b) = x^{(a-1)} \times (1+x)^{-(a+b)} / \text{beta}(a, b)
\]

for \(x > 0, a > 0, b > 0\), where \(\text{beta}(a, b)\) 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, \(\text{betaprime.pdf}(x, a, b, \text{loc}, \text{scale})\) is identically equivalent to \(\text{betaprime.pdf}(y, a, b) / \text{scale}\) with \(y = (x - \text{loc}) / \text{scale}\).

Examples

>>> from scipy.stats import betaprime
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
Calculate a few first moments:
>>> a, b = 5, 6
>>> mean, var, skew, kurt = betaprime.stats(a, b, moments='mvsk')
Display the probability density function (pdf):
>>> 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:
>>> rv = betaprime(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
Check accuracy of cdf and ppf:
>>> vals = betaprime.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], betaprime.cdf(vals, a, b))
True
Generate random numbers:
>>> r = betaprime.rvs(a, b, size=1000)
And compare the histogram:
>>> ax.hist(r, normed=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 density function.</td>
</tr>
<tr>
<td>logcdf(x, a, b, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, a, b, loc=0, scale=1)</td>
<td>Survival function (1 — cdf — 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>
</tr>
<tr>
<td>expect(func, 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._continuous_distns.bradford_gen object at 0x7fa40ebe58d0>
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 \texttt{bradford} is:

\[
bradford.pdf(x, c) = \frac{c}{k \times (1+c \times x)},
\]

for \(0 < x < 1\), \(c > 0\) and \(k = \log(1+c)\).
\texttt{bradford} takes \(c\) 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, \texttt{bradford.pdf(x, c, loc, scale)} is identically equivalent to \texttt{bradford.pdf(y, c) / scale} with \(y = (x - \text{loc}) / \text{scale}\).

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))
```

Generate random numbers:

```python
>>> r = bradford.rvs(c, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, normed=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 density function.
- `logcdf(x, c, loc=0, scale=1)`: Log of the cumulative density function.
- `sf(x, c, loc=0, scale=1)`: Survival function \((1 - \text{cdf})\) — 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 \(\text{cdf}\)) — percentiles.
- `isf(q, c, loc=0, scale=1)`: Inverse survival function (inverse of \(\text{sf}\)).
- `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, 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.burr = <scipy.stats._continuous_distns.burr_gen object at 0x7fa40ebe5bd0>
```

A Burr 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 `burr` with \(d = 1\)
The probability density function for burr is:

\[
burr.pdf(x, c, d) = c \times d \times x^{-(c-1)} \times (1+x^{c-1})^{-d-1}
\]

for \(x > 0\).

burr 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 loc and scale parameters. Specifically, burr.pdf \((x, c, d, \text{loc}, \text{scale})\) is identically equivalent to burr.pdf \((y, c, d) / \text{scale}\) with \(y = (x - \text{loc}) / \text{scale}\).

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, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
```

```python
plt.show()
```
Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rvs(c, d, loc=0, scale=1, random_state=None)</td>
<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 density function.</td>
</tr>
<tr>
<td>logcdf(x, c, d, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, c, d, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>
<tr>
<td>median(c, d, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(c, d, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(c, d, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(c, d, loc=0, scale=1)</td>
<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>
</tr>
</tbody>
</table>

scipy.stats.cauchy = <scipy.stats._continuous_distns.cauchy_gen object at 0x7fa40ebe210>

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:

\[
\text{cauchy.pdf}(x) = \frac{1}{\pi (1 + x^2)}
\]

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `cauchy.pdf(x, loc, scale)` is identically equivalent to `cauchy.pdf(y) / scale` with \(y = (x - \text{loc}) / \text{scale}\).

Examples

```python
>>> from scipy.stats import cauchy
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> mean, var, skew, kurt = cauchy.stats(moments='mvsk')
```

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, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
### Methods

- **rvs**(loc=0, scale=1, size=1, random_state=None)
  - Random variates.
- **pdf**(x, loc=0, scale=1)
  - Probability density function.
- **logpdf**(x, loc=0, scale=1)
  - Log of the probability density function.
- **cdf**(x, loc=0, scale=1)
  - Cumulative density function.
- **logcdf**(x, loc=0, scale=1)
  - Log of the cumulative density function.
- **sf**(x, loc=0, scale=1)
  - Survival function (1 - cdf — sometimes more accurate).
- **logsf**(x, loc=0, scale=1)
  - Log of the survival function.
- **ppf**(q, loc=0, scale=1)
  - Percent point function (inverse of cdf — percentiles).
- **isf**(q, loc=0, scale=1)
  - Inverse survival function (inverse of sf).
- **moment**(n, loc=0, scale=1)
  - Non-central moment of order n
- **stats**(loc=0, scale=1, moments='mv')
  - Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
- **entropy**(loc=0, scale=1)
  - (Differential) entropy of the RV.
- **fit**(data, loc=0, scale=1)
  - Parameter estimates for generic data.
- **expect**(func, 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**(loc=0, scale=1)
  - Median of the distribution.
- **mean**(loc=0, scale=1)
  - Mean of the distribution.
- **var**(loc=0, scale=1)
  - Variance of the distribution.
- **std**(loc=0, scale=1)
  - Standard deviation of the distribution.
- **interval**(alpha, loc=0, scale=1)
  - Endpoints of the range that contains alpha percent of the distribution.

```python
scipy.stats.chi = <scipy.stats._continuous_distns.chi_gen object at 0x7fa40ebee450>
```

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 \texttt{chi} is:

\[
\text{chi.pdf}(x, \text{df}) = x^{(\text{df}-1)} \times \exp(-x^2/2) / (2^{(\text{df}/2-1)} \times \text{gamma}(\text{df}/2))
\]

for \(x > 0\).

Special cases of \texttt{chi} are:
- \texttt{chi(1, loc, scale)} is equivalent to \texttt{halfnorm}
- \texttt{chi(2, 0, scale)} is equivalent to \texttt{rayleigh}
- \texttt{chi(3, 0, scale)} is equivalent to \texttt{maxwell}

\texttt{chi} takes \texttt{df} 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, \texttt{chi.pdf}(x, df, loc, scale) is identically equivalent to \texttt{chi.pdf}(y, df) / scale with \(y = (x - \text{loc}) / \text{scale}\).

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:
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()

```

Methods

rvs(df, loc=0, scale=1, size=1, random_state=None)  
Random variates.

dpdf(x, df, loc=0, scale=1)  
Probability density function.

lopdf(x, df, loc=0, scale=1)  
Log of the probability density function.

cdf(x, df, loc=0, scale=1)  
Cumulative density function.

logcdf(x, df, loc=0, scale=1)  
Log of the cumulative density function.

sf(x, df, loc=0, scale=1)  
Survival function (1 - cdf — sometimes more accurate).

logsf(x, df, loc=0, scale=1)  
Log of the survival function.

ppf(q, df, loc=0, scale=1)  
Percent point function (inverse of cdf — percentiles).

isf(q, df, loc=0, scale=1)  
Inverse survival function (inverse of sf).

moment(n, df, loc=0, scale=1)  
Non-central moment of order n

stats(df, loc=0, scale=1, moments='mv')  
Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').

entropy(df, loc=0, scale=1)  
(Differential) entropy of the RV.

fit(data, df, loc=0, scale=1)  
Parameter estimates for generic data.

expect(func, df, 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(df, loc=0, scale=1)  
Median of the distribution.

mean(df, loc=0, scale=1)  
Mean of the distribution.

var(df, loc=0, scale=1)  
Variance of the distribution.

std(df, loc=0, scale=1)  
Standard deviation of the distribution.

interval(alpha, df, loc=0, scale=1)  
Endpoints of the range that contains alpha percent of the distribution
```

scipy.stats.chi2 = <scipy.stats._continuous_distns.chi2_gen object at 0x7fa40ebee710>

A chi-squared continuous random variable.

As an instance of the rv_continuous class, chi2 object inherits from it a collection of generic methods
Notes

The probability density function for \texttt{chi2} is:

\begin{equation}
\text{chi2.pdf}(x, df) = \frac{1}{(2\times\text{gamma}(df/2))} \times (x/2)^{(df/2-1)} \times \exp(-x/2)
\end{equation}

\texttt{chi2} takes \texttt{df} 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, \texttt{chi2.pdf}(x, df, loc, scale) is identically equivalent to \texttt{chi2.pdf}(y, df) / scale with y = (x - loc) / scale.

Examples

```python
>>> from scipy.stats import chi2
>>> import matplotlib.pyplot as plt

>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> df = 55
>>> mean, var, skew, kurt = chi2.stats(df, moments='mvsk')
```  
Display the probability density function (pdf):

```python
>>> 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:

```python
>>> rv = chi2(df)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```  
Check accuracy of cdf and ppf:

```python
>>> vals = chi2.ppf([0.001, 0.5, 0.999], df)
>>> np.allclose([0.001, 0.5, 0.999], chi2.cdf(vals, df))
```

True

Generate random numbers:

```python
>>> r = chi2.rvs(df, size=1000)
```  
And compare the histogram:

```python
>>> ax.hist(r, normed=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(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 density function.</td>
</tr>
<tr>
<td>logcdf(x, df, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, df, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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._continuous_distns.cosine_gen object at 0x7fa40ebee9d0>**

A cosine continuous random variable.

As an instance of the `rv_continuous` class, `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 `cosine` is:

\[
\text{cosine.pdf}(x) = \frac{1}{2\pi} \times (1+\cos(x))
\]

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 `loc` and `scale` parameters. Specifically, \(\text{cosine.pdf}(x, \text{loc}, \text{scale})\) is identically equivalent to \(\text{cosine.pdf}(y) / \text{scale}\) 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:
```n
```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))
```

Generate random numbers:
```python
>>> r = cosine.rvs(size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, normed=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(loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — 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, 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>
</tbody>
</table>

`scipy.stats.dgamma = <scipy.stats._continuous_distns.dgamma_gen object at 0x7fa40ebeebd0>`

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 \texttt{dgamma} is:

\[
dgammad.pdf(x, a) = \frac{1}{(2\cdot\gamma(a))} \cdot |x|^{a-1} \cdot \exp(-|x|)
\]

for \(a > 0\).
\texttt{dgamma} 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 \texttt{loc} and \texttt{scale} parameters. Specifically, \texttt{dgamma.pdf(x, a, loc, scale)} is identically equivalent to \texttt{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:

>>> a = 1.1
>>> mean, var, skew, kurt = dgamma.stats(a, moments='mvsk')

display the probability density function (pdf):

>>> 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:

>>> rv = dgamma(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')

check accuracy of cdf and ppf:

>>> 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:

>>> r = dgamma.rvs(a, size=1000)

and compare the histogram:

>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
```

5.34. Statistical functions (**scipy.stats**)
Methods

<table>
<thead>
<tr>
<th>Method</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 density function.</td>
</tr>
<tr>
<td>logcdf(x, a, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, a, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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.dweibull = <scipy.stats._continuous_distns.dweibull_gen object at 0x7fa40ebeee90>

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:

dweibull.pdf(x, c) = c / 2 * abs(x)**(c-1) * exp(-abs(x)**c)

dweibull takes c 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, 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:

>>> c = 2.07

>>> mean, var, skew, kurt = dweibull.stats(c, moments='mvsk')

Display the probability density function (pdf):

>>> 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:

>>> rv = dweibull(c)

>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')

Check accuracy of cdf and ppf:

>>> 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:

>>> r = dweibull.rvs(c, size=1000)

And compare the histogram:

>>> ax.hist(r, normed=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(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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, c, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, c, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — 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, 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>

```python
scipy.stats.erlang = <scipy.stats._continuous_distns.erlang_gen object at 0x7fa40e990190>
```

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>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, a, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, a, loc=0, scale=1)</code></td>
<td>Survival function ($1 - cdf$ — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, a, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<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>
</tr>
<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, 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>
</tr>
<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.expon = <scipy.stats._continuous_distns.expon_gen object at 0x7fa40ebfe190>
```

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:

```
expon.pdf(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=0, scale=1)` 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 $pdf = \lambda \exp(-\lambda \times x)$. This parameterization corresponds to using $scale = 1 / \lambda$. 

5.34. Statistical functions (`scipy.stats`)
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))
True
```Generate random numbers:

```python
>>> r = expon.rvs(size=1000)

And compare the histogram:

```python
>>> ax.hist(r, normed=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(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 density function.</td>
</tr>
<tr>
<td>logcdf(x, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, loc=0, scale=1)</td>
<td>Survival function ($1 - \text{cdf}$ — 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, 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>
<tr>
<td>mean(loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</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._continuous_distns.exponnorm_gen object at 0x7fa40ebfe390>
```

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 $\text{exponnorm}$ is:

$$\text{exponnorm.pdf}(x, K) = \frac{1}{2K} \exp\left(\frac{1}{2K^2}\right) \exp\left(-\frac{x}{K}\right) \cdot \text{erfc}\left(-\frac{x - 1/K}{\sqrt{2}}\right)$$

where the shape parameter $K > 0$.

It can be thought of as the sum of a normally distributed random value with mean $\text{loc}$ and sigma $\text{scale}$ and an exponentially distributed random number with a pdf proportional to $\exp(-\lambda \cdot x)$ where $\lambda = (K \cdot \text{scale})^{-1}$.

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, $\text{exponnorm.pdf}(x, K, \text{loc}, \text{scale})$ 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 $K = 1/\sigma\lambda$.

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.pdf([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, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

```
0.00  0.05  0.10  0.15  0.20  0.25  0.30
-4   -2    0   2   4   6   8   10
exponnorm pdf
frozen pdf
```

### Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<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 density function.</td>
</tr>
<tr>
<td>logcdf(x, K, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, K, loc=0, scale=1)</td>
<td>Survival function ((1 - cdf) — 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, 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 = <scipy.stats._continuous_distns.exponweib_gen object at 0x7fa40ebfe650>
```
An exponentiated Weibull continuous random variable.

As an instance of the `rv_continuous` class, `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.

**Notes**

The probability density function for `exponweib` is:

\[
\text{exponweib.pdf}(x, a, c) = \\
a \times c \times (1-\exp(-x^c))^{(a-1)} \times \exp(-x^c) \times x^{(c-1)}
\]

for \(x > 0, a > 0, c > 0\).

`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 `loc` and `scale` parameters. Specifically, `exponweib.pdf(x, a, c, loc, scale)` is identically equivalent to `exponweib.pdf(y, a, c) / scale` with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
>>> from scipy.stats import exponweib
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
Calculate a few first moments:
>>> a, c = 2.89, 1.95
>>> mean, var, skew, kurt = exponweib.stats(a, c, moments='mvsk')
Display the probability density function (pdf):
>>> 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:
>>> rv = exponweib(a, c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
Check accuracy of cdf and ppf:
>>> 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:
>>> r = exponweib.rvs(a, c, size=1000)
And compare the histogram:
```python
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Histogram and Legend](image)

### Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rvs(a, c, loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, a, c, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, a, c, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, a, c, loc=0, scale=1)</code></td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td><code>logcdf(x, a, c, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, a, c, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, a, c, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, a, c, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, a, c, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>moment(n, a, c, loc=0, scale=1)</code></td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td><code>stats(a, 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(a, c, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, a, c, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, a, 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(a, c, loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(a, c, loc=0, scale=1)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(a, c, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(a, c, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, a, 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.exponpow** = <scipy.stats._continuous_distns.exponpow_gen object at 0x7fa40ebfe990>

An exponential power continuous random variable.

### 5.34. Statistical functions (scipy.stats)

1251
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:

\[ \text{exponpow.pdf}(x, b) = b \times x^{b-1} \times \exp(1 + x^b - \exp(x^b)) \]

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.

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
def mean, var, skew, kurt = exponpow.stats(b, moments='mvsk')
def 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, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

```

0.0 0.2 0.4 0.6 0.8 1.0 1.2 1.4
0.0 0.2 0.4 0.6 0.8 1.0 1.2 1.4 1.6 1.8
exponpow pdf
frozen pdf
```

### Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rvs</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf</code></td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td><code>logcdf</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf</code></td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>moment</code></td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td><code>stats</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect</code></td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td><code>median</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
</tr>
</tbody>
</table>

```python
scipy.stats.f = <scipy.stats._continuous_distns.f_gen object at 0x7fa40e97e210>
```
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:

\[
F.pdf(x, df1, df2) = \frac{df2**(df2/2) * df1**(df1/2) * x**(df1/2-1)}{(df2+df1*x)**((df1+df2)/2) * B(df1/2, df2/2)}
\]

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:

>>> 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, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Histogram with step-filled bars and legend](image)

**Methods**

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, dfn, dfd, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, dfn, dfd, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — 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 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, 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>
<tr>
<td><code>mean(dfn, dfd, loc=0, scale=1)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(dfn, dfd, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</tr>
<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._continuous_distns.fatiguelife_gen object at 0x7fa40ebfc50>`

5.34. Statistical functions (`scipy.stats`) 1255
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:

```python
fatiguelife.pdf(x, c) =
    (x+1) / (2*c*sqrt(2*pi*x**3)) * exp(-(x-1)**2/(2*x*c**2))
```

for \( x > 0 \).

`fatiguelife` takes \( c \) 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, `fatiguelife.pdf(x, c, loc, scale)` is identically equivalent to `fatiguelife.pdf(y, c) / scale` with \( y = (x - loc) / scale \).

**References**

[R316]

**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))
True
```

Generate random numbers:
>>> r = fatiguelife.rvs(c, size=1000)

And compare the histogram:

>>> ax.hist(r, normed=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(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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, c, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, c, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — 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, 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>

```python
scipy.stats.fisk = <scipy.stats._continuous_distns.fisk_gen object at 0x7fa40ebe5f10>
```

A Fisk continuous random variable.

The Fisk distribution is also known as the log-logistic distribution, and equals the Burr distribution with d == 1.

`fisk` takes `c` as a shape parameter.

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:

\[
\text{fisk.pdf}(x, c) = c \times x^{-(c+1)} \times (1 + x^{-(c)})^{-2}
\]

for \( x > 0 \).

`fisk` takes `c` as a 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, `fisk.pdf(x, c, loc, scale)` is identically equivalent to `fisk.pdf(y, c) / scale` with \( y = (x - \text{loc}) / \text{scale} \).
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, normed=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, 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 density function.</td>
</tr>
<tr>
<td>logcdf(x, c, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, c, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>
<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.foldcauchy = <scipy.stats._continuous_distns.foldcauchy_gen object at 0x7fa40ebfef10>
A folded Cauchy continuous random variable.

As an instance of the rv_continuous class, 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.
Notes
The probability density function for foldcauchy is:

\[
\text{foldcauchy.pdf}(x, c) = \frac{1}{\pi(1+(x-c)^2)} + \frac{1}{\pi(1+(x+c)^2)}
\]

for \(x \geq 0\).

foldcauchy takes \(c\) as a shape parameter.

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))
```

True

Generate random numbers:

```python
r = foldcauchy.rvs(c, size=1000)
```

And compare the histogram:

```python
ax.hist(r, normed=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 density function.
- `logcdf(x, c, loc=0, scale=1)`
  - Log of the cumulative density function.
- `sf(x, c, loc=0, scale=1)`
  - Survival function (1 — cdf — 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(\textquoteleft m\textquoteright\textquoteleft), variance(\textquoteleft v\textquoteright\textquoteleft), skew(\textquoteleft s\textquoteright\textquoteleft), and/or kurtosis(\textquoteleft k\textquoteright\textquoteleft).
- `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, 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.foldnorm = <scipy.stats._continuous_distns.foldnorm_gen object at 0x7fa40e97e550>

A folded normal continuous random variable.

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:

\[ \text{foldnormal.pdf}(x, c) = \sqrt{2/\pi} \times \cosh(c \times x) \times \exp(-(x^2+c^2)/2) \]

for \( c \geq 0 \).

`foldnorm` takes \( c \) 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, `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:

```python
>>> c = 1.95
>>> mean, var, skew, kurt = foldnorm.stats(c, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> 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:

```python
>>> rv = foldnorm(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = foldnorm.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], foldnorm.cdf(vals, c))
True
```

Generate random numbers:

```python
>>> r = foldnorm.rvs(c, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, normed=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(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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, c, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, c, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — 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, 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.frechet_r = <scipy.stats.continuous_distns.frechet_r_gen object at 0x7fa40e97e810>

A Frechet right (or Weibull minimum) 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.

See also:

weibull_min
The same distribution as \texttt{frechet_r}.

\texttt{frechet_l}, \texttt{weibull_max}

\section*{Notes}

The probability density function for \texttt{frechet_r} is:

\[ \text{frechet_r.pdf}(x, c) = c \times x^{(c-1)} \times \exp(-x^c) \]

for \( x > 0, c > 0 \).

\texttt{frechet_r} takes \( c \) 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, \texttt{frechet_r.pdf}(x, c, \texttt{loc}, \texttt{scale}) is identically equivalent to \texttt{frechet_r.pdf}(y, c) / \texttt{scale} with \( y = (x - \texttt{loc}) / \texttt{scale} \).

\section*{Examples}

\begin{verbatim}
>>> from scipy.stats import frechet_r
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

>>> c = 1.89
>>> mean, var, skew, kurt = frechet_r.stats(c, moments='mvsk')

Display the probability density function (pdf):

>>> 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:

>>> rv = frechet_r(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')

Check accuracy of cdf and ppf:

>>> 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:

>>> r = frechet_r.rvs(c, size=1000)

And compare the histogram:
\end{verbatim}
```python
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Chart showing a histogram and legend](chart.png)

**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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, c, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, c, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — 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, 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.frechet_l = <scipy.stats._continuous_distns.frechet_l_gen object at 0x7fa40e97ed50>**

A Frechet left (or Weibull maximum) 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.

See also:

weibull_max

The same distribution as frechet_l.

frechet_r, weibull_min

Notes

The probability density function for frechet_l is:

\[ f(x, c) = c \times (-x)^{c-1} \times \exp(-(-x)^c) \]

for \( x < 0, c > 0 \).

frechet_l takes \( c \) 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, \( \text{frechet_l.pdf}(x, c, \text{loc}, \text{scale}) \) is identically equivalent to \( \text{frechet_l.pdf}(y, c) / \text{scale} \) with \( y = (x - \text{loc}) / \text{scale} \).

Examples

```python
>>> from scipy.stats import frechet_l
>>> import matplotlib.pyplot as plt

fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

>>> c = 3.63
>>> mean, var, skew, kurt = frechet_l.stats(c, moments='mvsk')

Display the probability density function (pdf):

>>> x = np.linspace(frechet_l.ppf(0.01, c),
... frechet_l.ppf(0.99, c), 100)
>>> ax.plot(x, frechet_l.pdf(x, c), 'r-', lw=5, alpha=0.6, label='frechet_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 = frechet_l(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen 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, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Histogram comparison](image)

**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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, c, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, c, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — 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, 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.genlogistic = <scipy.stats._continuous_distns.genlogistic_gen object at 0x7fa40e9872d0>`
A generalized logistic continuous random variable.

As an instance of the `rv_continuous` class, `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 `genlogistic` is:

\[
\text{genlogistic.pdf}(x, c) = c \times \exp(-x) / (1 + \exp(-x))^{c+1}
\]

for \(x > 0, c > 0\).

`genlogistic` takes \(c\) 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, `genlogistic.pdf(x, c, loc, scale)` is identically equivalent to `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))
```

Generate random numbers:

```python
>>> r = genlogistic.rvs(c, size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Histogram and Legend](image)

### 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 density function.
- **logcdf(x, c, loc=0, scale=1)**: Log of the cumulative density function.
- **sf(x, c, loc=0, scale=1)**: Survival function ($1 - cdf$ — 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, 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.

```python
scipy.stats.genlogistic = <scipy.stats._continuous_distns.genlogistic_gen object at 0x7fa40e8fd00>
```

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 [R324]:

\[
gennorm.pdf(x, \beta) = \frac{\beta}{2 \gamma(1/\beta)} \exp(-|x|^{\beta})
\]

`gennorm` takes `\beta` as a shape parameter. 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**
[R324]

**Examples**

```python
calculated = 1.3
mean, var, skew, kurt = gennorm.stats(calculated, moments='mvsk')
```

Display the probability density function (pdf):

```python
x = np.linspace(gennorm.ppf(0.01, calculated),
                gennorm.ppf(0.99, calculated), 100)
ax.plot(x, gennorm.pdf(x, calculated),
        '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(calculated)
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], calculated)
np.allclose([0.001, 0.5, 0.999], gennorm.cdf(vals, calculated))
```

Generate random numbers:

```python
r = gennorm.rvs(calculated, size=1000)
```
And compare the histogram:

```python
>>> ax.hist(r, normed=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(beta, loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, beta, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, beta, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, beta, loc=0, scale=1)</code></td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td><code>logcdf(x, beta, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, beta, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, beta, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, beta, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, beta, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>moment(n, beta, loc=0, scale=1)</code></td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td><code>stats(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(beta, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, beta, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, 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>
</tr>
<tr>
<td><code>median(beta, loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(beta, loc=0, scale=1)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(beta, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(beta, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, beta, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>
scipy.stats.genpareto = <scipy.stats.continuous_distns.genpareto_gen object at 0x7fa40e987590>
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.

\textit{Notes}

The probability density function for \texttt{genpareto} is:

\[
\text{genpareto.pdf}(x, c) = (1 + c \times x)^{(-1 - 1/c)}
\]
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 \(c = 0\), \texttt{genpareto} reduces to the exponential distribution, \texttt{expon}:

\[
\text{genpareto.pdf}(x, c=0) = \exp(-x)
\]
For \(c = -1\), \texttt{genpareto} is uniform on \([0, 1]\):

\[
\text{genpareto.cdf}(x, c=-1) = x
\]

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, loc, scale) is identically equivalent to \texttt{genpareto.pdf}(y, c) / scale with \(y = (x - \text{loc}) / \text{scale}\).

\textit{Examples}

```python
>>> from scipy.stats import genpareto
>>> import matplotlib.pyplot as plt

>>> fig, ax = plt.subplots(1, 1)

>>> c = 0.1

>>> mean, var, skew, kurt = genpareto.stats(c, moments='mvsk')

>>> 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')
```

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 cdf and 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:

>>> r = genpareto.rvs(c, size=1000)

And compare the histogram:

>>> ax.hist(r, normed=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(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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, c, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, c, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — 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, 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.genexpon** = `<scipy.stats._continuous_distns.genexpon_gen object at 0x7fa40e987850>`

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:

\[ f(x; a, b, c) = (a + b \times (1 - \exp(-c \times x))) \times \exp(-a \times x) \]

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` where \( y = (x - loc) / scale \).

### 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):

```python
>>> 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:

```python
>>> rv = genexpon(a, b, c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> 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))
```

Generate random numbers:

```python
>>> r = genexpon.rvs(a, b, c, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, normed=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, c, loc=0, scale=1, size=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 density function.</td>
</tr>
<tr>
<td>logcdf(x, a, b, c, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, a, b, c, loc=0, scale=1)</td>
<td>Survival function ((1 - \text{cdf})—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(\langle m\rangle), variance(\langle v\rangle), skew(\langle s\rangle), and/or kurtosis(\langle k\rangle).</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, 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>

A generalized extreme value continuous random variable.

As an instance of the \texttt{rv_continuous} class, \texttt{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:

\texttt{scipy.stats.genextreme} = <\texttt{scipy.stats._continuous_distns.genextreme_gen} object at 0x7fa40e987bd0>
gumbel_r

Notes
For c=0, genextreme is equal to gumbel_r. The probability density function for genextreme is:

\[
\begin{align*}
    \text{genextreme.pdf}(x, c) &= \\
    \exp(-\exp(-x)) &\quad \text{for } c=0 \\
    \exp(-(1-c*x)^{(1/c)})*(1-c*x)^{(1/c-1)} &\quad \text{for } x \leq 1/c, c > 0
\end{align*}
\]

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.

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 - loc) / scale.

Examples

```python
>>> from scipy.stats import genextreme
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
Calculate a few first moments:

>>> c = -0.1
>>> mean, var, skew, kurt = genextreme.stats(c, moments='mvsk')
Display the probability density function (pdf):

>>> 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:

>>> rv = genextreme(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
Check accuracy of cdf and ppf:

>>> 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:

>>> r = genextreme.rvs(c, size=1000)
And compare the histogram:
```
```python
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Histogram and Legend](image)

### 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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, c, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, c, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — 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, 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>

```python
scipy.stats.gausshyper = <scipy.stats._continuous_distns.gausshyper_gen object at 0x7fa40e9a2950>
```

A Gauss hypergeometric continuous random variable.

5.34. Statistical functions *(scipy.stats)*
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:

\[
\text{gausshyper.pdf}(x, a, b, c, z) = 
\frac{C}{B(a, b) F[2, 1](c, a; a+b; -z)} \cdot x^{a-1} \cdot (1-x)^{b-1} \cdot (1+z\cdot x)^{-(c)}
\]

for \(0 \leq x \leq 1, a > 0, b > 0,\) and \(C = 1 / (B(a, b) F[2, 1](c, a; a+b; -z))\)

`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 \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
>>> from scipy.stats import gausshyper
>>> import matplotlib.pyplot as plt

>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

>>> 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

```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” distribution 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=2, 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
>>> r = gausshyper.rvs(a, b, c, z, size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

```
0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0
0.0 0.5 1.0 1.5 2.0 2.5 3.0 3.5 4.0 4.5
```

gausshyper pdf
frozen pdf

### Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rvs(a, b, c, z, loc=0, scale=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, a, b, c, z, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, a, b, c, z, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, a, b, c, z, loc=0, scale=1)</code></td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td><code>logcdf(x, a, b, c, z, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, a, b, c, z, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, a, b, c, z, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, a, b, c, z, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, a, b, c, z, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>moment(n, a, b, c, z, loc=0, scale=1)</code></td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td><code>stats(a, b, c, z, 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, c, z, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, a, b, c, z, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, a, b, c, z, 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, c, z, loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(a, b, c, z, loc=0, scale=1)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(a, b, c, z, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(a, b, c, z, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, a, b, c, z, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

```python
scipy.stats.gamma = <scipy.stats._continuous_distns.gamma_gen object at 0x7fa40e987e90>
```
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:

\[
gamma.pdf(x, a) = x^{a-1} \times \exp(-x) / \gamma(a)
\]

for \( x \geq 0, a > 0 \). Here \( \gamma(a) \) refers to the gamma function.

`gamma` has a shape parameter \( a \) which needs to be set explicitly.

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, \( \gamma.pdf(y, a, \text{loc}, \text{scale}) \) is identically equivalent to \( \gamma.pdf(y, a) / \text{scale} \) with \( y = (x - \text{loc}) / \text{scale} \).

**Examples**

```python
>>> from scipy.stats import gamma
>>> import matplotlib.pyplot as plt

>>> a = 1.99
>>> mean, var, skew, kurt = gamma.stats(a, moments='mvsk')

>>> 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))
```

Generate random numbers:

```python
```
```python
>>> r = gamma.rvs(a, size=1000)

And compare the histogram:

```
### Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, a, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, a, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, a, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<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>
</tr>
<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, 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>
</tr>
<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.gengamma** = `<scipy.stats._continuous_distns.gengamma_gen object at 0x7fa40e990450>`

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:

\[
gengamma.pdf(x, a, c) = \frac{|c| x^{c*a-1} \exp(-x^c)}{\Gamma(a)}
\]

for \(x > 0, a > 0\), and \(c \neq 0\).

`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 loc and 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:
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, normed=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(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>
</tr>
<tr>
<td>cdf(x, a, c, loc=0, scale=1)</td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td>logcdf(x, a, c, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, a, c, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, a, c, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<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, 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>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(a, c, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<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.genhalflogistic = <scipy.stats._continuous_distns.genhalflogistic_gen object at 0x7fa40e990790>
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:

genhalflogistic.pdf(x, c) = 2 * (1-c*x)**(1/c-1) / (1+(1-c*x)**(1/c))**2

for 0 <= x <= 1/c, and c > 0.

genhalflogistic takes c 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, 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
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:
c = 0.773
mean, var, skew, kurt = genhalflogistic.stats(c, moments='mvsk')

Display the probability density function (pdf):

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:

rv = genhalflogistic(c)
ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')

Check accuracy of cdf and ppf:

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:

r = genhalflogistic.rvs(c, size=1000)

And compare the histogram:

ax.hist(r, normed=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(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 density function.</td>
</tr>
<tr>
<td>logcdf(x, c, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, c, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>
<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.gilbrat = <scipy.stats._continuous_distns.gilbrat_gen object at 0x7fa40e93cf50>
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:

gilbrat.pdf(x) = 1/(x*sqrt(2*pi)) * exp(-1/2*(log(x))**2)

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 - loc) / scale.

Examples

>>> from scipy.stats import gilbrat
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

>>> 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.ppf([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, normed=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(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 density function.</td>
</tr>
<tr>
<td>logcdf(x, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>
<tr>
<td>mean(loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</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>

```python
scipy.stats.gompertz = <scipy.stats._continuous_distns.gompertz_gen object at 0x7fa40e990a50>
```

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:

\[
gompertz.pdf(x, c) = c \times \exp(x) \times \exp(-c \times (\exp(x)-1))
\]

for \( x \geq 0, c > 0 \).

`gompertz` takes \( c \) 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, \( gompertz.pdf(x, c, \text{loc}, \text{scale}) \) is identically equivalent to \( gompertz.pdf(y, c) / \text{scale} \) with \( y = (x - \text{loc}) / \text{scale} \).

#### Examples

```python
>>> from scipy.stats import gompertz
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:
```
>>> c = 0.947
>>> mean, var, skew, kurt = gompertz.stats(c, moments='mvsk')

Display the probability density function (pdf):

>>> 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:

>>> rv = gompertz(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')

Check accuracy of cdf and ppf:

>>> 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:

>>> r = gompertz.rvs(c, size=1000)

And compare the histogram:

>>> ax.hist(r, normed=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(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 density function.</td>
</tr>
<tr>
<td>logcdf(x, c, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, c, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>
<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.gumbel_r = <scipy.stats._continuous_distns.gumbel_r_gen object at 0x7fa40e990d10>
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:

gumbel_r.pdf(x) = exp(-(x + exp(-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 - loc) / 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')
```

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.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], gumbel_r.cdf(vals))
True
```

Generate random numbers:

```python
>>> r = gumbel_r.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, normed=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(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 density function.</td>
</tr>
<tr>
<td>logcdf(x, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>
<tr>
<td>mean(loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</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.gumbel_l = <scipy.stats._continuous_distns.gumbel_l_gen object at 0x7fa40e990f10>

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:

\[
gumbel_l.pdf(x) = \exp(x - \exp(x))
\]

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 - loc) / 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(0.01),
... gumbel_l.ppf(0.99), 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.ppf([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, normed=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(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 density function.</td>
</tr>
<tr>
<td>logcdf(x, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>
<tr>
<td>mean(loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</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.halfcauchy = <scipy.stats._continuous_distns.halfcauchy_gen object at 0x7fa40e9a2150>

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:

\[
halfcauchy.pdf(x) = \frac{2}{\pi (1 + x^2)}
\]

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, halfcauchy.pdf(x, loc, scale) is identically equivalent to halfcauchy.pdf(y) / scale with y = (x - loc) / scale.

Examples

```python
>>> from scipy.stats import halfcauchy
>>> 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(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))
True
```

Generate random numbers:

```python
>>> r = halfcauchy.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, normed=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(loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — 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, 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>
</tbody>
</table>

```
scipy.stats.halflogistic = <scipy.stats._continuous_distns.halflogistic_gen object at 0x7fa40e9a2350>
```

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:

```python
halflogistic.pdf(x) = 2 * exp(-x) / (1+exp(-x))^2 = 1/2 * sech(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, `halflogistic.pdf(x, loc, scale)` is identically equivalent to `halflogistic.pdf(y) / scale` with `y = (x - loc) / 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, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
Methods

- `rvs(loc=0, scale=1, size=1, random_state=None)`
  - Random variates.
- `pdf(x, loc=0, scale=1)`
  - Probability density function.
- `logpdf(x, loc=0, scale=1)`
  - Log of the probability density function.
- `cdf(x, loc=0, scale=1)`
  - Cumulative density function.
- `logcdf(x, loc=0, scale=1)`
  - Log of the cumulative density function.
- `sf(x, loc=0, scale=1)`
  - Survival function (1 - cdf — sometimes more accurate).
- `logsf(x, loc=0, scale=1)`
  - Log of the survival function.
- `ppf(q, loc=0, scale=1)`
  - Percent point function (inverse of cdf — percentiles).
- `isf(q, loc=0, scale=1)`
  - Inverse survival function (inverse of sf).
- `moment(n, loc=0, scale=1)`
  - Non-central moment of order n.
- `stats(loc=0, scale=1, moments='mv')`
  - Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
- `entropy(loc=0, scale=1)`
  - (Differential) entropy of the RV.
- `fit(data, loc=0, scale=1)`
  - Parameter estimates for generic data.
- `expect(func, 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(loc=0, scale=1)`
  - Median of the distribution.
- `mean(loc=0, scale=1)`
  - Mean of the distribution.
- `var(loc=0, scale=1)`
  - Variance of the distribution.
- `std(loc=0, scale=1)`
  - Standard deviation of the distribution.
- `interval(alpha, loc=0, scale=1)`
  - Endpoints of the range that contains alpha percent of the distribution

**scipy.stats.halfnorm = <scipy.stats._continuous_distns.halfnorm_gen object at 0x7fa40e9a2550>**

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:

\[
\text{halfnorm.pdf}(x) = \sqrt{\frac{2}{\pi}} \times \exp\left(-\frac{x^2}{2}\right)
\]

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 \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
>>> from scipy.stats import halfnorm
>>> 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(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, normed=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(loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — 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, 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>
</tbody>
</table>

`scipy.stats.halfgennorm = <scipy.stats._continuous_distns.halfgennorm_gen object at 0x7fa40e90e2d0>`

The upper half of a generalized normal continuous random variable.

As an instance of the `rv_continuous` class, `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.

See also:

- `gennorm`  
  generalized normal distribution
- `expon`  
  exponential distribution
- `halfnorm`  
  half normal distribution

**Notes**

The probability density function for `halfgennorm` is:

\[
  \text{halfgennorm.pdf}(x, \text{beta}) = \frac{\text{beta}}{\Gamma(1/\text{beta})} \exp(-|x|^\text{beta})
\]

`gennorm` takes `beta` as a shape parameter. For `beta = 1`, it is identical to an exponential distribution. For `beta = 2`, it is identical to a half normal distribution (with `scale=1/sqrt(2)`).

**References**

[R325]
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:

```python
>>> 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:

```python
>>> r = halfgennorm.rvs(beta, size=1000)
```  
And compare the histogram:

```python
>>> ax.hist(r, normed=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, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, beta, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, beta, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, beta, loc=0, scale=1)</td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td>logcdf(x, beta, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, beta, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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._continuous_distns.hypsecant_gen object at 0x7fa40e9a2750>

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:

\[
\text{hypsecant.pdf}(x) = \frac{1}{\pi} \times \text{sech}(x)
\]

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, \(\text{hypsecant.pdf}(x, \text{loc}, \text{scale})\) is identically equivalent to \(\text{hypsecant.pdf}(y) / \text{scale}\) 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))
True
```

Generate random numbers:

```python
>>> r = hypsecant.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, normed=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</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf</td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td>logcdf</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf</td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td>logsf</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect</td>
<td>Expected value of a function (of one argument) with respect to the distribution.</td>
</tr>
<tr>
<td>median</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

scipy.stats.invgamma = <scipy.stats._continuous_distns.invgamma_gen object at 0x7fa40e9a2c50>

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 \texttt{invgamma} is:

\[
\text{invgamma.pdf}(x, a) = x^{-(a+1)} / \Gamma(a) * \exp(-1/x)
\]

for \(x > 0, a > 0\).

\texttt{invgamma} takes \(a\) as a shape parameter.

\texttt{invgamma} is a special case of \texttt{gengamma} with \(c == -1\).

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{invgamma.pdf}(x, a, \texttt{loc}, \texttt{scale}) is identically equivalent to \texttt{invgamma.pdf}(y, a) / \texttt{scale} with \(y = (x - \texttt{loc}) / \texttt{scale}\).

**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))
```

Generate random numbers:

```python
>>> r = invgamma.rvs(a, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, normed=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, 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 density function.</td>
</tr>
<tr>
<td>logcdf(x, a, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, a, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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.invgauss = <scipy.stats._continuous_distns.invgauss_gen object at 0x7fa40e9a2f50>

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:

\[
\text{invgauss.pdf}(x, \mu) = \frac{1}{\sqrt{2\pi x^3}} \exp\left(-\frac{(x-\mu)^2}{2x\mu^2}\right)
\]

for \(x > 0\).

`invgauss` takes \(\mu\) 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, `invgauss.pdf(x, \mu, \text{loc}, \text{scale})` is identically equivalent to `invgauss.pdf(y, \mu) / \text{scale}` with \(y = (x - \text{loc}) / \text{scale}\).

When \(\mu\) is too small, evaluating the cumulative density function will be inaccurate due to \(\text{cdf}(\mu \rightarrow 0) = \text{inf} \times 0\). 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:

```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, normed=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(mu, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, mu, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, mu, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, mu, loc=0, scale=1)</td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td>logcdf(x, mu, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, mu, loc=0, scale=1)</td>
<td>Survival function (1 – cdf — sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, mu, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, mu, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, mu, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, mu, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(mu, loc=0, scale=1, moments=’mv’)</td>
<td>Mean(’m’), variance(’v’), skew(’s’), and/or kurtosis(’k’).</td>
</tr>
<tr>
<td>entropy(mu, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, mu, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, mu, 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(mu, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(mu, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(mu, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(mu, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, mu, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

scipy.stats.invweibull = <scipy.stats._continuous_distns.invweibull_gen object at 0x7fa40e9b2250>

An inverted Weibull continuous random variable.

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 \texttt{invweibull} is:

\[
\text{invweibull.pdf}(x, c) = c \times x^{-(c-1)} \times \exp(-x^c)
\]

for \(x > 0, c > 0\).

\texttt{invweibull} takes \(c\) 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, \texttt{invweibull.pdf}(x, c, loc, scale) is identically equivalent to \texttt{invweibull.pdf}(y, c) / scale with \(y = (x - \text{loc}) / \text{scale}\).

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))
True
```

Generate random numbers:

```python
>>> r = invweibull.rvs(c, size=1000)
```

And compare the histogram:
```python
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

```python
scipy.stats.johnsonsb = <scipy.stats._continuous_distns.johnsonsb_gen object at 0x7fa40e9b2510>
```

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:

```
johnsonsb.pdf(x, a, b) = b / (x*(1-x)) * phi(a + b * log(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, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Plot](image)

**Methods**

<table>
<thead>
<tr>
<th>Function</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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, a, b, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, a, b, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — 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, 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>
</tr>
<tr>
<td><code>mean(a, b, loc=0, scale=1)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(a, b, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</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 alpha percent of the distribution</td>
</tr>
</tbody>
</table>

**scipy.stats.johnsonsu** = `<scipy.stats._continuous_distns.johnsonsu_gen object at 0x7fa40e9b2850>`

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:

\[
johnsonsu.pdf(x, a, b) = \frac{b}{\sqrt{x^2 + 1}} \times \\
\phi(a + b \times \log(x + \sqrt{x^2 + 1}))
\]

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 \(\text{loc}\) and \(\text{scale}\) parameters. Specifically, \(\text{johnsonsu.pdf}(x, a, b, \text{loc}, \text{scale})\) is identically equivalent to \(\text{johnsonsu.pdf}(y, a, b) / \text{scale}\) 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))
True
```

Generate random numbers:

```python
>>> r = johnsonsu.rvs(a, b, size=1000)
```
And compare the histogram:

```python
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Histogram Comparison](image)

### 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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, a, b, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, a, b, loc=0, scale=1)</code></td>
<td>Survival function ($1 - cdf$ — 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, 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>
</tr>
<tr>
<td><code>mean(a, b, loc=0, scale=1)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(a, b, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</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 alpha percent of the distribution</td>
</tr>
</tbody>
</table>
scipy.stats.ksone = <scipy.stats._continuous_distns.ksone_gen object at 0x7fa40ebcf450>

General Kolmogorov-Smirnov one-sided test.

As an instance of the rv_continuous class, ksome 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.

**Methods**

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rvs(n, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, n, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, n, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, n, loc=0, scale=1)</td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td>logcdf(x, n, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, n, loc=0, scale=1)</td>
<td>Survival function (1 – cdf — sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, n, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, n, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, n, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, n, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(n, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(n, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, n, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, n, 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(n, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(n, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(n, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(n, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, n, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

**Examples**

```python
>>> from scipy.stats import ksome

>>> import matplotlib.pyplot as plt

>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

>>> n = 1e+03

>>> mean, var, skew, kurt = ksome.stats(n, moments='mvsk')

Display the probability density function (pdf):
```

Continued on next page
Table 5.251 – continued from previous page

```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)
```

```python
>>> 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, normed=True, histtype='stepfilled', alpha=0.2)

>>> ax.legend(loc='best', frameon=False)

>>> plt.show()
```

SciPy Reference Guide, Release 0.16.0

scipy.stats.kstwobign = <scipy.stats._continuous_distns.kstwobign_gen object at 0x7fa40ebcf6d0>

Kolmogorov-Smirnov two-sided test for large N.

As an instance of the rv_continuous class, 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.

Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rvs</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf</td>
<td>Cumulative density function.</td>
</tr>
</tbody>
</table>
### Table 5.252 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>logcdf(x, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, loc=0, scale=1)</td>
<td>Survival function (1 − cdf — 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='mvsk')</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, 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>
<tr>
<td>mean(loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</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>

### 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)

... kstwobign.pdf(0.99), 100)

```python
>>> ax.plot(x, kstwobign.pdf(x), ...
```

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()
```

Continued on next page
Table 5.252 – continued from previous page

```python
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
Check accuracy of cdf and ppf:
>>> vals = kstwobign.ppf([0.001, 0.5, 0.999])

>>> np.allclose([0.001, 0.5, 0.999], kstwobign.cdf(vals))
True
Generate random numbers:
>>> r = kstwobign.rvs(size=1000)
And compare the histogram:
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

```python
scipy.stats.laplace = <scipy.stats._continuous_distns.laplace_gen object at 0x7fa40e9b2b90>
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:

\[
\text{laplace.pdf}(x) = \frac{1}{2} \times \exp(-\text{abs}(x))
\]

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 - loc) / scale.

Examples

```python
>>> from scipy.stats import laplace
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> mean, var, skew, kurt = laplace.stats(moments='mvsk')

Display the probability density function (pdf):

```python
>>> x = np.linspace(laplace.ppf(0.01), ...
   laplace.ppf(0.99), 100)
```
```python
>>> 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()
```...

```python
>>> 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))
```

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, normed=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(loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — 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, 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>
</tbody>
</table>

scipy.stats.logistic = <scipy.stats._continuous_distns.logistic_gen object at 0x7fa40e93c510>

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:

\[
\text{logistic.pdf}(x) = \frac{\exp(-x)}{(1+\exp(-x))^2}
\]

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
>>> from scipy.stats import logistic
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> mean, var, skew, kurt = logistic.stats(moments='mvsk')
```
Display the probability density function (pdf):

```python
>>> 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
>>> rv = logistic()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = logistic.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], logistic.cdf(vals))
True
```

Generate random numbers:

```python
>>> r = logistic.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, normed=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(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 density function.</td>
</tr>
<tr>
<td>logcdf(x, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>
<tr>
<td>mean(loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</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.loggamma = <scipy.stats._continuous_distns.loggamma_gen object at 0x7fa40e93c710>

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:

\[ \text{loggamma.pdf}(x, c) = \exp(c \cdot x - \exp(x)) / \gamma(c) \]

for all \( x, \ c > 0 \).

loggamma takes \( c \) 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, loggamma.pdf(x, c, loc, scale) is identically equivalent to loggamma.pdf(y, c) / scale with y = (x - loc) / scale.

Examples

```python
>>> from scipy.stats import loggamma
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:
>>> 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))
```

Generate random numbers:

```python
>>> r = loggamma.rvs(c, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, normed=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(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 density function.</td>
</tr>
<tr>
<td>logcdf(x, c, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, c, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>
<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.loglaplace = <scipy.stats._continuous_distns.loglaplace_gen object at 0x7fa40e93c9d0>

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:

\[
\text{loglaplace.pdf}(x, c) = \begin{cases} 
  \frac{c}{2} \times x^{c-1}, & \text{for } 0 < x < 1 \\
  \frac{c}{2} \times x^{-c-1}, & \text{for } x \geq 1 
\end{cases}
\]

for \( c > 0 \).

loglaplace takes \( c \) 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, \( \text{loglaplace.pdf}(x, c, \text{loc}, \text{scale}) \) is identically equivalent to \( \text{loglaplace.pdf}(y, c) / \text{scale} \) with \( y = (x - \text{loc}) / \text{scale} \).

References

Examples

>>> from scipy.stats import loglaplace
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

>>> c = 3.25
>>> mean, var, skew, kurt = loglaplace.stats(c, moments='mvsk')

Display the probability density function (pdf):

>>> 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:

>>> rv = loglaplace(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')

Check accuracy of cdf and ppf:

>>> 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:

>>> r = loglaplace.rvs(c, size=1000)

And compare the histogram:

>>> ax.hist(r, normed=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(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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, c, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, c, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — 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, 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.lognorm = <scipy.stats._continuous_distns.lognorm_gen object at 0x7fa40e93cc90>
```

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 \texttt{lognorm} is:

\[
\text{lognorm.pdf}(x, s) = \frac{1}{s \times x \times \sqrt{2 \times \pi}} \times \exp\left(-\frac{1}{2} \times \left(\frac{\log(x)}{s}\right)^2\right)
\]

for \(x > 0, s > 0\).

\texttt{lognorm} takes \(s\) 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, \texttt{lognorm.pdf}(x, s, \texttt{loc}, \texttt{scale}) is identically equivalent to \texttt{lognorm.pdf}(y, s) / \texttt{scale} with \(y = (x - \texttt{loc}) / \texttt{scale}\).

If \(\log(x)\) is normally distributed with mean \(\mu\) and variance \(\sigma^2\), then \(x\) is log-normally distributed with shape parameter \(\sigma\) and scale parameter \(\exp(\mu)\).

Examples

```python
>>> from scipy.stats import lognorm
>>> import matplotlib.pyplot as plt

>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

>>> s = 0.954
>>> mean, var, skew, kurt = lognorm.stats(s, moments='mvsk')

Display the probability density function (pdf):

>>> 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:

>>> rv = lognorm(s)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')

Check accuracy of cdf and ppf:

>>> 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:

>>> r = lognorm.rvs(s, size=1000)

And compare the histogram:

>>> ax.hist(r, normed=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(loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, s, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, s, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, s, loc=0, scale=1)</td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td>logcdf(x, s, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, s, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, s, loc=0, scale=1, lb=lb=None, ub=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>
<td>Median of the distribution.</td>
</tr>
<tr>
<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._continuous_distns.lomax_gen object at 0x7fa40e95d9d0>

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 Lomax distribution is a special case of the Pareto distribution, with \( \text{loc}=-1.0 \).

The probability density function for \texttt{lomax} is:

\[
\text{lomax.pdf}(x, c) = \frac{c}{(1 + x)^{c+1}}
\]

for \( x \geq 0, c > 0 \).

\texttt{lomax} takes \( c \) 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, \texttt{lomax.pdf}(x, c, \texttt{loc}, \texttt{scale}) is identically equivalent to \texttt{lomax.pdf}(y, c) / \texttt{scale} with \( y = (x - \text{loc}) / \texttt{scale} \).

**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, normed=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(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 density function.</td>
</tr>
<tr>
<td>logcdf(x, c, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, c, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>
<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.maxwell = <scipy.stats._continuous_distns.maxwell_gen object at 0x7fa40e94f190>

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 \texttt{chi} distribution, with \texttt{df = 3}, \texttt{loc = 0.0}, and given \texttt{scale = a}, where \texttt{a} is the parameter used in the Mathworld description [R333].

The probability density function for \texttt{maxwell} is:

\[
\text{maxwell.pdf}(x) = \sqrt{2/\pi}x^{\ast 2} \ast \exp(-x^{\ast 2}/2)
\]

for \(x > 0\).

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{maxwell.pdf}(x, \texttt{loc}, \texttt{scale}) is identically equivalent to \texttt{maxwell.pdf}(y) / \texttt{scale} with \(y = (x - \texttt{loc}) / \texttt{scale}\).

References
[R333]

Examples

```python
>>> from scipy.stats import maxwell
>>> import matplotlib.pyplot as plt

fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```n```n```python
>>> mean, var, skew, kurt = maxwell.stats(moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> x = np.linspace(maxwell.ppf(0.01), ...
... maxwell.ppf(0.99), 100)
>>> ax.plot(x, maxwell.pdf(x), ...
... 'r-', lw=5, alpha=0.6, label='maxwell 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 = maxwell()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = maxwell.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], maxwell.cdf(vals))
```

True

Generate random numbers:

```python
>>> r = maxwell.rvs(size=1000)
```

And compare the histogram:
>>> ax.hist(r, normed=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(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 density function.</td>
</tr>
<tr>
<td>logcdf(x, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>
<tr>
<td>mean(loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</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.mielke = <scipy.stats._continuous_distns.mielke_gen object at 0x7fa40e94f390>
```

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
Notes
The probability density function for `mielke` is:

\[
mielke.pdf(x, k, s) = k \times x^{k-1} / (1+x^s)^{1+k/s}
\]

for \(x > 0\).

`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, loc, scale)` is identically equivalent to `mielke.pdf(y, k, s) / scale` with \(y = (x - loc) / scale\).

Examples

```python
>>> from scipy.stats import mielke
>>> import matplotlib.pyplot as plt

>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> k, s = 10.4, 3.6
>>> mean, var, skew, kurt = mielke.stats(k, s, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> 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:

```python
>>> rv = mielke(k, s)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

```python
>>> vals = mielke.ppf([0.001, 0.5, 0.999], k, s)
>>> np.allclose([0.001, 0.5, 0.999], mielke.cdf(vals, k, s))
```

Generate random numbers:

```python
>>> r = mielke.rvs(k, s, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
**Methods**

- `rvs(k, s, loc=0, scale=1, size=1, random_state=None)` Random variates.
- `pdf(x, k, s, loc=0, scale=1)` Probability density function.
- `logpdf(x, k, s, loc=0, scale=1)` Log of the probability density function.
- `cdf(x, k, s, loc=0, scale=1)` Cumulative density function.
- `logcdf(x, k, s, loc=0, scale=1)` Log of the cumulative density function.
- `sf(x, k, s, loc=0, scale=1)` Survival function \((1 - \text{cdf}) - \text{sometimes more accurate}\).
- `logsf(x, k, s, loc=0, scale=1)` Log of the survival function.
- `ppf(q, k, s, loc=0, scale=1)` Percent point function (inverse of cdf — percentiles).
- `isf(q, k, s, loc=0, scale=1)` Inverse survival function (inverse of sf).
- `moment(n, k, s, loc=0, scale=1)` Non-central moment of order \(n\)
- `stats(k, s, loc=0, scale=1, moments='mv')` Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
- `entropy(k, s, loc=0, scale=1)` (Differential) entropy of the RV.
- `fit(data, k, s, loc=0, scale=1)` Parameter estimates for generic data.
- `expect(func, k, s, 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(k, s, loc=0, scale=1)` Median of the distribution.
- `mean(k, s, loc=0, scale=1)` Mean of the distribution.
- `var(k, s, loc=0, scale=1)` Variance of the distribution.
- `std(k, s, loc=0, scale=1)` Standard deviation of the distribution.
- `interval(alpha, k, s, loc=0, scale=1)` Endpoints of the range that contains alpha percent of the distribution.

```python
scipy.stats.nakagami = <scipy.stats._continuous_distns.nakagami_gen object at 0x7fa40e94f6d0>
```

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:

\[
nakagami.pdf(x, \nu) = 2 \times \nu^{\nu} / \Gamma(\nu) \times x^{2\nu-1} \times e^{-\nu x^2}
\]

for \(x > 0, \nu > 0\).

`nakagami` takes \(\nu\) 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, `nakagami.pdf(x, \nu, loc, scale)` is identically equivalent to `nakagami.pdf(y, \nu) / scale` with \(y = (x - loc) / scale\).

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, normed=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(nu, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, nu, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, nu, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, nu, loc=0, scale=1)</td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td>logcdf(x, nu, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, nu, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, nu, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, nu, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, nu, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, nu, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(nu, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(nu, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, nu, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, nu, 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(nu, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(nu, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(nu, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(nu, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, nu, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

scipy.stats.ncx2 = <scipy.stats._continuous_distns.ncx2_gen object at 0x7fa40e94f990>

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 \texttt{ncx2} is:

\[
n\texttt{cx2.pdf}(x, \texttt{df}, \texttt{nc}) = \exp\left(-\left(\texttt{nc}+x\right)/2\right) \ast \frac{1}{2} \ast \left(\frac{x}{\texttt{nc}}\right)^{\left(\texttt{df}-2\right)/4} \ast I\left(\frac{(\texttt{df}-2)}{2}\right)\left(\sqrt{\texttt{nc} \ast x}\right)
\]

for \( x > 0 \).

\texttt{ncx2} takes \texttt{df} and \texttt{nc} 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{ncx2.pdf}(x, \texttt{df}, \texttt{nc}, \texttt{loc}, \texttt{scale}) is identically equivalent to \texttt{ncx2.pdf}(y, \texttt{df}, \texttt{nc}) / \texttt{scale} with \( y = (x - \texttt{loc}) / \texttt{scale} \).

Examples

```python
>>> from scipy.stats import ncx2
>>> import matplotlib.pyplot as plt

>>> fig, ax = plt.subplots(1, 1)

>>> df, nc = 21, 1.06
>>> mean, var, skew, kurt = ncx2.stats(df, nc, moments='mvsk')

>>> 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')

>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')

>>> ax.legend(loc='best', frameon=False)

>>> plt.show()
```

5.34. Statistical functions (scipy.stats) 1339
### Methods

- **rvs(df, nc, loc=0, scale=1, size=1, random_state=None)**: Random variates.
- **pdf(x, df, nc, loc=0, scale=1)**: Probability density function.
- **logpdf(x, df, nc, loc=0, scale=1)**: Log of the probability density function.
- **cdf(x, df, nc, loc=0, scale=1)**: Cumulative density function.
- **logcdf(x, df, nc, loc=0, scale=1)**: Log of the cumulative density function.
- **sf(x, df, nc, loc=0, scale=1)**: Survival function (1 - cdf — sometimes more accurate).
- **logsf(x, df, nc, loc=0, scale=1)**: Log of the survival function.
- **ppf(q, df, nc, loc=0, scale=1)**: Percent point function (inverse of cdf — percentiles).
- **isf(q, df, nc, loc=0, scale=1)**: Inverse survival function (inverse of sf).
- **moment(n, df, nc, loc=0, scale=1)**: Non-central moment of order n.
- **stats(df, nc, loc=0, scale=1, moments=’mv’)**: Mean(’m’), variance(’v’), skew(’s’), and/or kurtosis(’k’).
- **entropy(df, nc, loc=0, scale=1)**: (Differential) entropy of the RV.
- **fit(data, df, nc, loc=0, scale=1)**: Parameter estimates for generic data.
- **expect(func, df, nc, 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(df, nc, loc=0, scale=1)**: Median of the distribution.
- **mean(df, nc, loc=0, scale=1)**: Mean of the distribution.
- **var(df, nc, loc=0, scale=1)**: Variance of the distribution.
- **std(df, nc, loc=0, scale=1)**: Standard deviation of the distribution.
- **interval(alpha, df, nc, loc=0, scale=1)**: Endpoints of the range that contains alpha percent of the distribution.

**scipy.stats.ncf = <scipy.stats._continuous_distns.ncf_gen object at 0x7fa40e94fcd0>**

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:

\[
\text{ncf.pdf}(x, df1, df2, nc) = \exp(nc/2 + nc*df1*x/(2*(df1*x+df2))) \times \\
\quad df1**(df1/2) \times df2**(df2/2) \times x**((df1/2-1) \times \\
\quad (df2+df1*x))**(-((df1+df2)/2)) \times \\
\quad \gamma(df1/2) \times \gamma(1+df2/2) \times \\
\quad 1^{(v1/2-1)}^{(v2/2)}(-nc*v1*x/(2*(v1*x+v2))) / \\
\quad (B(v1/2, v2/2) \times \gamma((v1+v2)/2))
\]

for df1, df2, nc > 0.

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)

Calculate a few first moments:

```python
>>> dfn, dfd, nc = 27, 27, 0.416
>>> mean, var, skew, kurt = ncf.stats(dfn, dfd, nc, moments='mvsk')
```

Display the probability density function (pdf):

```python
>>> 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, alpha=0.6, 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, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Histogram of ncf distribution](image)

### Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rvs(dfn, dfd, nc, loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, dfn, dfd, nc, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, dfn, dfd, nc, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, dfn, dfd, nc, loc=0, scale=1)</code></td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td><code>logcdf(x, dfn, dfd, nc, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, dfn, dfd, nc, loc=0, scale=1)</code></td>
<td>Survival function ($1 - cdf$ — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, dfn, dfd, nc, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, dfn, dfd, nc, loc=0, scale=1)</code></td>
<td>Inverse percent function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, dfn, dfd, nc, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>moment(n, dfn, dfd, nc, loc=0, scale=1)</code></td>
<td>Non-central moment of order $n$.</td>
</tr>
<tr>
<td><code>stats(dfn, dfd, nc, 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, nc, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, dfn, dfd, nc, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, dfn, dfd, nc, 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, nc, loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(dfn, dfd, nc, loc=0, scale=1)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(dfn, dfd, nc, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(dfn, dfd, nc, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, dfn, dfd, nc, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
</tr>
</tbody>
</table>

`scipy.stats.nct = <scipy.stats._continuous_distns.nct_gen object at 0x7fa40e95d350>`
A non-central Student’s T continuous random variable.

As an instance of the \texttt{rv_continuous} class, \texttt{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.

\textbf{Notes}

The probability density function for \texttt{nct} is:

\[
\text{nct.pdf}(x, df, nc) = \frac{df^{(df/2)} \cdot \text{gamma}(df+1)}{2^{df} \cdot \exp(nc^2/2) \cdot (df+x^2)^{(df/2)} \cdot \text{gamma}(df/2)}
\]

for df > 0.

\texttt{nct} takes \texttt{df} and \texttt{nc} 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{nct.pdf}(x, df, nc, loc, scale) is identically equivalent to \texttt{nct.pdf}(y, df, nc) / scale with y = (x - loc) / scale.

\textbf{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, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![nct pdf and frozen pdf](image)

**Methods**

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rvs(df, nc, loc=0, scale=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, df, nc, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, df, nc, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, df, nc, loc=0, scale=1)</code></td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td><code>logcdf(x, df, nc, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, df, nc, loc=0, scale=1)</code></td>
<td>Survival function (1 − cdf — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, df, nc, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, df, nc, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, df, nc, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>moment(n, df, nc, loc=0, scale=1)</code></td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td><code>stats(df, nc, 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(df, nc, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, df, nc, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, df, nc, 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(df, nc, loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(df, nc, loc=0, scale=1)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(df, nc, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(df, nc, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, df, nc, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

```python
scipy.stats.norm = <scipy.stats._continuous_distns.norm_gen object at 0x7fa40ebcf8d0>
```

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:

\[
\text{norm.pdf}(x) = \frac{\exp(-x^2/2)}{\sqrt{2\pi}}
\]

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 - loc) / scale`.

**Examples**

```python
>>> from scipy.stats import norm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
calculates = norm.stats(moments='mvsk')
``` Example

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, normed=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(loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — 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, 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>
</tbody>
</table>

`scipy.stats.pareto = <scipy.stats._continuous_distns.pareto_gen object at 0x7fa40e95d6d0>`

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 \texttt{pareto} is:

\[
\text{pareto.pdf}(x, b) = \frac{b}{x^{b+1}}
\]

for \( x \geq 1, b > 0 \).

\texttt{pareto} takes \( b \) 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, \texttt{pareto.pdf}(x, b, \texttt{loc}, \texttt{scale}) is identically equivalent to \texttt{pareto.pdf}(y, b) / \texttt{scale} with \( y = (x - \texttt{loc}) / \texttt{scale} \).

Examples

```python
>>> 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))
True
```

Generate random numbers:

```python
>>> r = pareto.rvs(b, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```
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 density function.
- `logcdf(x, b, loc=0, scale=1)`
  - Log of the cumulative density function.
- `sf(x, b, loc=0, scale=1)`
  - Survival function (1 - cdf — 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, 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.

```python
scipy.stats.pearson3 = <scipy.stats._continuous_distns.pearson3_gen object at 0x7fa40e95dc90>
```

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:

\[
\text{pearson3.pdf}(x, \text{skew}) = \frac{\text{abs}(\beta)}{\Gamma(\alpha)} \cdot (\beta \cdot (x - \zeta))^{(\alpha - 1)} \cdot \exp(-\beta \cdot (x - \zeta))
\]

where:

\[
\beta = \frac{2}{\left(\text{skew} \cdot \text{stddev}\right)} \\
\alpha = \left(\text{stddev} \cdot \beta\right)^2 \\
\zeta = \text{loc} - \frac{\alpha}{\beta}
\]

`pearson3` takes `skew` 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, `pearson3.pdf(x, skew, loc, scale)` is identically equivalent to `pearson3.pdf(y, skew) / scale` with `y = (x - loc) / 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:

```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=5, alpha=0.6, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:  5.34. Statistical functions (scipy.stats) 1349
Generate random numbers:

```python
>>> r = pearson3.rvs(skew, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, normed=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(skew, loc=0, scale=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, skew, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, skew, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, skew, loc=0, scale=1)</code></td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td><code>logcdf(x, skew, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, skew, loc=0, scale=1)</code></td>
<td>Survival function ($1 - \text{cdf}$ — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, skew, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, skew, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, skew, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>moment(n, skew, loc=0, scale=1)</code></td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td><code>stats(skew, 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(skew, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, skew, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, skew, 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(skew, loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(skew, loc=0, scale=1)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(skew, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(skew, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, skew, loc=0, scale=1)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

scipy.stats.powerlaw = `<scipy.stats._continuous_distns.powerlaw_gen object at 0x7fa40e95df50>`

A power-function continuous random variable.

As an instance of the `rv_continuous` class, `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.

### Notes

The probability density function for `powerlaw` is:

\[
powerlaw.pdf(x, a) = a \times x^{a-1}
\]

for $0 <= x <= 1, a > 0$.

`powerlaw` 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, \(\text{powerlaw.pdf}(x, a, \text{loc}, \text{scale})\) is identically equivalent to \(\text{powerlaw.pdf}(y, a) / \text{scale}\) with \(y = (x - \text{loc}) / \text{scale}\).

`powerlaw` is a special case of `beta` with $b == 1$.

### 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, normed=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><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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, a, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, a, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, a, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<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>
</tr>
<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, 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>
</tr>
<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>

```python
scipy.stats.powerlognorm = <scipy.stats._continuous_distns.powerlognorm_gen object at 0x7fa40e965250>
```

A power log-normal continuous random variable.

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:

\[
\text{powerlognorm.pdf}(x, c, s) = c / (x * s) * \phi(\log(x)/s) * (\Phi(-\log(x)/s))^{(c-1)},
\]

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 \( y = (x - \text{loc}) / \text{scale} \).

### Examples

```python
>>> from scipy.stats import powerlognorm
>>> 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(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, normed=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(c, s, loc=0, scale=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 density function.</td>
</tr>
<tr>
<td>logcdf(x, c, s, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, c, s, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>

scipy.stats.powernorm = <scipy.stats._continuous_distns.powernorm_gen object at 0x7fa40f3c6590>

A power normal continuous random variable.

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:

powernorm.pdf(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.

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, powernorm.pdf(x, c, loc, scale) is identically equivalent to powernorm.pdf(y, c) / scale with y = (x - loc) / scale.

Examples

```python
>>> from scipy.stats import powernorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:
>>> 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))
```

Generate random numbers:

```python
>>> r = powernorm.rvs(c, size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, normed=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(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 density function.</td>
</tr>
<tr>
<td>logcdf(x, c, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, c, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>
<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.rdist = <scipy.stats._continuous_distns.rdist_gen object at 0x7fa40e965850>

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:

\[
rdist.pdf(x, c) = (1-x**2)**(c/2-1) / B(1/2, c/2)
\]

for \(-1 \leq x \leq 1, c > 0\).

rdist takes c as a shape parameter.

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:
c = 0.9
mean, var, skew, kurt = rdist.stats(c, moments='mvsk')

Display the probability density function (pdf):

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:

rv = rdist(c)
ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')

Check accuracy of cdf and ppf:

vals = rdist.ppf([0.001, 0.5, 0.999], c)
np.allclose([0.001, 0.5, 0.999], rdist.cdf(vals, c))
True

Generate random numbers:

r = rdist.rvs(c, size=1000)

And compare the histogram:

ax.hist(r, normed=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(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 density function.</td>
</tr>
<tr>
<td>logcdf(x, c, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, c, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>
<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.reciprocal = <scipy.stats._continuous_distns.reciprocal_gen object at 0x7fa40e965d10>

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:

reciprocal.pdf(x, a, b) = 1 / (x*log(b/a))

for a <= x <= b, a, b > 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, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Graph showing probability density function and frozen pdf](image_url)
### Methods

<table>
<thead>
<tr>
<th>Function</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 density function.</td>
</tr>
<tr>
<td>logcdf(x, a, b, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, a, b, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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>
</tr>
<tr>
<td>expect(func, 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>

import scipy.stats as stats
rayleigh = stats.rayleigh
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:

\[
\text{rayleigh.pdf}(r) = r \times \exp(-r^2/2)
\]

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 \( y = (x - \text{loc}) / \text{scale} \).

**Examples**

```python
>>> from scipy.stats import rayleigh
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:
>>> 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, normed=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(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 density function.</td>
</tr>
<tr>
<td>logcdf(x, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>
<tr>
<td>mean(loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</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.rice = <scipy.stats._continuous_distns.rice_gen object at 0x7fa40e975090>`

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:

\[
rice.pdf(x, b) = x * \exp(-(x**2+b**2)/2) * I[0](x*b)
\]

for \(x > 0, b > 0\).

`rice` takes \(b\) 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, `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 \(R = (U**2 + V**2)**0.5\). 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, normed=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(b, loc=0, scale=1, size=1, random_state=None)</code></td>
<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>
</tr>
<tr>
<td><code>cdf(x, b, loc=0, scale=1)</code></td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td><code>logcdf(x, b, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, b, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, b, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<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, 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>
<td>Mean of the distribution.</td>
</tr>
<tr>
<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.recipinvgauss** = `<scipy.stats._continuous_distns.recipinvgauss_gen object at 0x7fa40e975350>`

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:

\[
\text{recipinvgauss.pdf}(x, \mu) = \frac{1}{\sqrt{2\pi x}} \exp\left(-\frac{(1-\mu x)^2}{2(\mu x^2)}\right)
\]

for \(x \geq 0\).

`recipinvgauss` takes \(\mu\) 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, `recipinvgauss.pdf(x, \mu, \text{loc}, \text{scale})` is identically equivalent to `recipinvgauss.pdf(y, \mu) / \text{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
codeblocks
```
### Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rvs(mu, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, mu, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, mu, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, mu, loc=0, scale=1)</td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td>logcdf(x, mu, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, mu, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, mu, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, mu, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, mu, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, mu, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(mu, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(mu, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, mu, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, mu, 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(mu, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(mu, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(mu, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(mu, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, mu, loc=0, scale=1)</td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
</tr>
</tbody>
</table>

**scipy.stats.semicircular = <scipy.stats._continuous_distns.semicircular_gen object at 0x7fa40e975610>**

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:

\[
\text{semicircular.pdf}(x) = \frac{2}{\pi} \sqrt{1-x^2} 
\]

for \(-1 \leq x \leq 1\).

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution 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))
True
```

Generate random numbers:

```python
>>> r = semicircular.rvs(size=1000)
```

And compare the histogram:

```python
>>> ax.hist(r, normed=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(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 density function.</td>
</tr>
<tr>
<td>logcdf(x, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>
<tr>
<td>mean(loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</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.t = <scipy.stats._continuous_distns.t_gen object at 0x7fa40e95d090>

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:

$$
  t.pdf(x, df) = \frac{\Gamma((df+1)/2)}{\sqrt{\pi*df} * \Gamma(df/2) * (1+x**2/df)**((df+1)/2)}
$$

for $df > 0$.

$t$ 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, $t.pdf(x, df, loc, scale)$ is identically equivalent to $t.pdf(y, df) / scale$ with $y = (x - loc) / scale$.

### Examples

```python
>>> from scipy.stats import t
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:
>>> df = 2.74
>>> mean, var, skew, kurt = t.stats(df, moments='mvsk')

Display the probability density function (pdf):

>>> 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:

>>> rv = t(df)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')

Check accuracy of cdf and ppf:

>>> 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:

>>> r = t.rvs(df, size=1000)

And compare the histogram:

>>> ax.hist(r, normed=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><code>rvs(df, loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pdf(x, df, loc=0, scale=1)</code></td>
<td>Probability density function.</td>
</tr>
<tr>
<td><code>logpdf(x, df, loc=0, scale=1)</code></td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td><code>cdf(x, df, loc=0, scale=1)</code></td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td><code>logcdf(x, df, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, df, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, df, loc=0, scale=1)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, df, loc=0, scale=1)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, df, loc=0, scale=1)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>moment(n, df, loc=0, scale=1)</code></td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td><code>stats(df, 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(df, loc=0, scale=1)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>fit(data, df, loc=0, scale=1)</code></td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td><code>expect(func, df, 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(df, loc=0, scale=1)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(df, loc=0, scale=1)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(df, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(df, loc=0, scale=1)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, df, 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._continuous_distns.triang_gen object at 0x7fa40e975810>`

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.

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:
>>> 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, normed=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(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 density function.</td>
</tr>
<tr>
<td>logcdf(x, c, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, c, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>
<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.truncexpon = <scipy.stats._continuous_distns.truncexpon_gen object at 0x7fa40e975ad0>
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:

\[
\text{truncexpon.pdf}(x, b) = \exp(-x) / (1 - \exp(-b))
\]

for \(0 < x < b\).

truncexpon takes \(b\) 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, \(\text{truncexpon.pdf}(x, b, \text{loc}, \text{scale})\) is identically equivalent to \(\text{truncexpon.pdf}(y, b) / \text{scale}\) 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:
>>> b = 4.69
>>> mean, var, skew, kurt = truncexpon.stats(b, moments='mvsk')

Display the probability density function (pdf):

>>> 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:

>>> rv = truncexpon(b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')

Check accuracy of cdf and ppf:

>>> vals = truncexpon.ppf([0.001, 0.5, 0.999], b)
>>> np.allclose([0.001, 0.5, 0.999], truncexpon.cdf(vals, b))
True

Generate random numbers:

>>> r = truncexpon.rvs(b, size=1000)

And compare the histogram:

>>> ax.hist(r, normed=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(b, loc=0, scale=1, size=1, random_state=None)</td>
<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>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, b, loc=0, scale=1)</td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td>logcdf(x, b, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, b, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — 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, 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>
<td>Standard deviation of the distribution.</td>
</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.truncnorm** = <scipy.stats._continuous_distns.truncnorm_gen object at 0x7fa40e975d90>
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 = (myclip_a - my_mean) / my_std, (myclip_b - my_mean) / my_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, **truncnorm.pdf**(x, a, b, loc, scale) is identically equivalent to **truncnorm.pdf**((x - loc) / scale) with y = (x - loc) / scale.

**Examples**

```python
>>> from scipy.stats import truncnorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:
>>> a, b = 0.1, 2
>>> mean, var, skew, kurt = truncnorm.stats(a, b, moments='mvsk')

Display the probability density function (pdf):

>>> 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:

>>> rv = truncnorm(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')

Check accuracy of cdf and ppf:

>>> 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:

>>> r = truncnorm.rvs(a, b, size=1000)

And compare the histogram:

>>> ax.hist(r, normed=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(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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, a, b, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, a, b, loc=0, scale=1)</code></td>
<td>Survival function ((1 - \text{cdf})) — 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 ((\text{inverse of cdf})\ — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, a, b, loc=0, scale=1)</code></td>
<td>Inverse survival function ((\text{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, a, b, loc=0, scale=1, lb=None, ub=None, conditional=False, +kwds)</code></td>
<td>Expected value of a function ((\text{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>
</tr>
<tr>
<td><code>mean(a, b, loc=0, scale=1)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(a, b, loc=0, scale=1)</code></td>
<td>Variance of the distribution.</td>
</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 alpha percent of the distribution</td>
</tr>
</tbody>
</table>

SciPy Reference Guide, Release 0.16.0

**tukeylambda**

A `Tukey-Lambda` 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 (lam=-1)
- logistic (lam=0.0)
- approx Normal (lam=0.14)
- u-shape (lam = 0.5)
- uniform from -1 to 1 (lam = 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, `tukeylambda.pdf(x, lam, loc, scale)` is identically equivalent to `tukeylambda.pdf(y, lam) / scale` with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
>>> from scipy.stats import tukeylambda
>>> import matplotlib.pyplot as plt

Calculate a few first moments:

```
>>> lam = 3.13
>>> mean, var, skew, kurt = tukeylambda.stats(lam, moments='mvsk')

Display the probability density function (pdf):

>>> 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:

>>> rv = tukeylambda(lam)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')

Check accuracy of cdf and ppf:

>>> vals = tukeylambda.ppf([0.001, 0.5, 0.999], lam)
>>> np.allclose([0.001, 0.5, 0.999], tukeylambda.cdf(vals, lam))
True

Generate random numbers:

>>> r = tukeylambda.rvs(lam, size=1000)

And compare the histogram:

>>> ax.hist(r, normed=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(lam, loc=0, scale=1, size=1, random_state=None)</td>
<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>
</tr>
<tr>
<td>cdf(x, lam, loc=0, scale=1)</td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td>logcdf(x, lam, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, lam, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, lam, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, lam, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, lam, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, lam, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(lam, loc=0, scale=1, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<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, 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>
</tr>
<tr>
<td>mean(lam, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<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>

```python
scipy.stats.uniform = <scipy.stats._continuous_distns.uniform_gen object at 0x7fa40e8fd3d0>
```

A uniform continuous random variable.

This distribution is constant between \( \text{loc} \) and \( \text{loc} + \text{scale} \).

As an instance of the \texttt{rv_continuous} class, \texttt{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)  
>>> ax.plot(x, uniform.pdf(x), 'r-', lw=5, alpha=0.6, label='uniform 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.

5.34. Statistical functions (scipy.stats) 1379
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, normed=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><code>rvs(loc=0, scale=1, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — 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, 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>
</tbody>
</table>

`scipy.stats.vonmises = <scipy.stats._continuous_distns.vonmises_gen object at 0x7fa40e8fd5d0>`

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.

**See also:**

`vonmises_line`

The same distribution, defined on a [-pi, pi] segment of the real line.

**Notes**

If `x` is not in range or `loc` is not in range it assumes they are angles and converts them to [-pi, pi] equivalents.

The probability density function for `vonmises` is:

```
vonmises.pdf(x, kappa) = exp(kappa * cos(x)) / (2*pi*I[0](kappa))
```

for -pi <= x <= pi, kappa > 0.

`vonmises` takes 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 `vonmises.pdf(y, kappa) / scale` with `y = (x - loc) / scale`. 

5.34. Statistical functions (`scipy.stats`)
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, normed=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(kappa, loc=0, scale=1, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pdf(x, kappa, loc=0, scale=1)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, kappa, loc=0, scale=1)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>cdf(x, kappa, loc=0, scale=1)</td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td>logcdf(x, kappa, loc=0, scale=1)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, kappa, loc=0, scale=1)</td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, kappa, loc=0, scale=1)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, kappa, loc=0, scale=1)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, kappa, loc=0, scale=1)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>moment(n, kappa, loc=0, scale=1)</td>
<td>Non-central moment of order n</td>
</tr>
<tr>
<td>stats(kappa, loc=0, scale=1, moments='mv')</td>
<td>Mean(’m’), variance(’v’), skew(’s’), and/or kurtosis(’k’).</td>
</tr>
<tr>
<td>entropy(kappa, loc=0, scale=1)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>fit(data, kappa, loc=0, scale=1)</td>
<td>Parameter estimates for generic data.</td>
</tr>
<tr>
<td>expect(func, kappa, 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(kappa, loc=0, scale=1)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(kappa, loc=0, scale=1)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(kappa, loc=0, scale=1)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(kappa, loc=0, scale=1)</td>
<td>Standard deviation of the distribution.</td>
</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._continuous_distns.wald_gen object at 0x7fa40e8fd1b0>
```

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 \texttt{wald} is:

\[
\text{wald.pdf}(x) = \frac{1}{\sqrt{2\pi x^3}} \exp\left(-\frac{(x-1)^2}{2x}\right)
\]

for \( x > 0 \).

\texttt{wald} is a special case of \texttt{invgauss} with \( \mu = 1 \).

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{wald.pdf}(x, loc, scale) is identically equivalent to \texttt{wald.pdf}(y) / scale with \( y = (x - \text{loc}) / \text{scale} \).

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, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()```
Methods

rvs(loc=0, scale=1, size=1, random_state=None)  Random variates.
pdf(x, loc=0, scale=1)  Probability density function.
logpdf(x, loc=0, scale=1)  Log of the probability density function.
cdf(x, loc=0, scale=1)  Cumulative density function.
logcdf(x, loc=0, scale=1)  Log of the cumulative density function.
sf(x, loc=0, scale=1)  Survival function (1 - cdf — sometimes more accurate).
logsf(x, loc=0, scale=1)  Log of the survival function.
ppf(q, loc=0, scale=1)  Percent point function (inverse of cdf — percentiles).
isf(q, loc=0, scale=1)  Inverse survival function (inverse of sf).
moment(n, loc=0, scale=1)  Non-central moment of order n
stats(loc=0, scale=1, moments='mv')  Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)  (Differential) entropy of the RV.
fit(data, loc=0, scale=1)  Parameter estimates for generic data.
expect(func, 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(loc=0, scale=1)  Median of the distribution.
mean(loc=0, scale=1)  Mean of the distribution.
var(loc=0, scale=1)  Variance of the distribution.
std(loc=0, scale=1)  Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)  Endpoints of the range that contains alpha percent of the distribution

scipy.stats.weibull_min = <scipy.stats._continuous_distns.frechet_r_gen object at 0x7fa40e97ead0>
A Frechet right (or 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_min

5.34. Statistical functions (scipy.stats)
The same distribution as `frechet_r`.

`frechet_l, weibull_max`

**Notes**

The probability density function for `frechet_r` is:

\[
\text{frechet_r.pdf}(x, c) = c * x^{(c-1)} * \exp(-x^c)
\]

for \(x > 0\), \(c > 0\).

`frechet_r` takes \(c\) 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, \(\text{weibull_min.pdf}(x, c, \text{loc}, \text{scale})\) is identically equivalent to \(\text{weibull_min.pdf}(y, c) / \text{scale}\) with \(y = (x - \text{loc}) / \text{scale}\).

**Examples**

```python
>>> from scipy.stats import weibull_min
>>> import matplotlib.pyplot as plt

>>> fig, ax = plt.subplots(1, 1)

>>> c = 1.79
>>> mean, var, skew, kurt = weibull_min.stats(c, moments='mvsk')

>>> 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')

>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen 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, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

![Weibull Min PDF](image)

### 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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, c, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, c, loc=0, scale=1)</code></td>
<td>Survival function ($1 - cdf$ — 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, 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.weibull_max` = `<scipy.stats._continuous_distns.frechet_l_gen object at 0x7fa40e987050>`

A Frechet left (or 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_max**

The same distribution as frechet_l.

frechet_r, weibull_min

Notes

The probability density function for frechet_l is:

frechet_l.pdf(x, c) = c * (-x)**(c-1) * exp(-(-x)**c)

for x < 0, c > 0.

frechet_l takes c 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, 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:

```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, normed=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

```
weibull_max pdf
frozen pdf
```

**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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, c, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, c, loc=0, scale=1)</code></td>
<td>Survival function (1 - cdf — 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, 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.wrapcauchy = <scipy.stats._continuous_distns.wrapcauchy_gen object at 0x7fa40e8fdd10>`
A wrapped Cauchy continuous random variable.

As an instance of the \texttt{rv_continuous} class, \texttt{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.

\textbf{Notes}

The probability density function for \texttt{wrapcauchy} is:

\begin{equation}
\text{wrapcauchy.pdf}(x, c) = \frac{1-c^2}{2\pi(1+c^2-2c\cos(x))}
\end{equation}

for $0 \leq x \leq 2\pi$, $0 < c < 1$.

\texttt{wrapcauchy} takes $c$ 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, \texttt{wrapcauchy.pdf}(x, c, loc, scale) is identically equivalent to \texttt{wrapcauchy.pdf}(y, c) / scale with $y = (x - \text{loc}) / \text{scale}$.

\textbf{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, normed=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(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 density function.</td>
</tr>
<tr>
<td><code>logcdf(x, c, loc=0, scale=1)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, c, loc=0, scale=1)</code></td>
<td>Survival function ($1 - \text{cdf}$ — 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, 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>

5.34. **Statistical functions** *(scipy.stats)*
5.34.2 Multivariate distributions

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>multivariate_normal</td>
<td>A multivariate 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>
</tbody>
</table>

```
scipy.stats.multivariate_normal = <scipy.stats._multivariate.multivariate_normal_gen object at 0x7fa40e148e90>
```

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:

```
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:

>>> x, y = np.mgrid[-1:1:.01, -1:1:.01]
>>> pos = np.empty(x.shape + (2,))
>>> pos[:, :, 0] = x; pos[:, :, 1] = 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>pdf(x, mean=None, cov=1,</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>allow_singular=False)</td>
<td></td>
</tr>
<tr>
<td>logpdf(x, mean=None, cov=1,</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>allow_singular=False)</td>
<td></td>
</tr>
<tr>
<td>rvs(mean=None, cov=1, size=1,</td>
<td>Draw random samples from a multivariate normal distribution.</td>
</tr>
<tr>
<td>random_state=None)</td>
<td></td>
</tr>
<tr>
<td>entropy()</td>
<td>Compute the differential entropy of the multivariate normal.</td>
</tr>
</tbody>
</table>

scipy.stats.dirichlet = <scipy.stats._multivariate.dirichlet_gen object at 0x7fa40e148fd0>

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 parameters fixed.
Notes

Each \( \alpha \) 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 \texttt{dirichlet} is

\[
f(x) = \frac{1}{B(\alpha)} \prod_{i=1}^{K} x_i^{\alpha_i - 1}
\]

where

\[
B(\alpha) = \prod_{i=1}^{K} \frac{\Gamma(\alpha_i)}{\Gamma(\sum_{i=1}^{K} \alpha_i)}
\]

and \( \alpha = (\alpha_1, \ldots, \alpha_K) \), the concentration parameters and \( K \) is the dimension of the space where \( x \) takes values.

Methods

<table>
<thead>
<tr>
<th>pdf(x, alpha)</th>
<th>Probability density function.</th>
</tr>
</thead>
<tbody>
<tr>
<td>logpdf(x, alpha)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>rvs(alpha, size=1,</td>
<td>Draw random samples from a Dirichlet distribution.</td>
</tr>
<tr>
<td>random_state=None)</td>
<td></td>
</tr>
<tr>
<td>mean(alpha)</td>
<td>The mean of the Dirichlet distribution</td>
</tr>
<tr>
<td>var(alpha)</td>
<td>The variance of the Dirichlet distribution</td>
</tr>
<tr>
<td>entropy(alpha)</td>
<td>Compute the differential entropy of the multivariate normal.</td>
</tr>
</tbody>
</table>

\texttt{scipy.stats.wishart} = <scipy.stats._multivariate.wishart_gen object at 0x7fa40e156110>

A 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 precision matrix (the inverse of the covariance matrix).

Parameters

\( x \): array_like  
Quantiles, with the last axis of \( x \) denoting the components.

\( \texttt{df} \): int
Degrees of freedom, must be greater than or equal to dimension of the scale matrix

\( \texttt{scale} \): array_like
Symmetric positive definite scale matrix of the distribution

\( \texttt{random_state} \) : 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:

\( \texttt{rv} = \texttt{wishart}(\texttt{df}=1, \texttt{scale}=1) \)

*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 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:

\[
f(S) = \frac{|S|^{\nu-p-1}}{2^{\nu p/2} \Gamma_p(\nu/2)} \exp\left(-\operatorname{tr}(\Sigma^{-1} S)/2\right)
\]
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
[R374], [R375]

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>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pdf(x, df, scale)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, df, scale)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>rvs(df, scale, size=1, random_state=None)</td>
<td>Draw random samples from a Wishart distribution.</td>
</tr>
<tr>
<td>entropy()</td>
<td>Compute the differential entropy of the Wishart distribution.</td>
</tr>
</tbody>
</table>

**scipy.stats.invwishart** = `<scipy.stats._multivariate.invwishart_gen object at 0x7fa40e156390>`

An inverse 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 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:

\[
 f(S) = \frac{|\Sigma|^{\frac{\nu}{2}}}{2^{\frac{\nu p}{2}|S|^{\frac{\nu + p + 1}{2}}}} \Gamma_p \left( \frac{\nu}{2} \right) \exp \left( -\frac{\text{tr}(\Sigma S^{-1})}{2} \right)
\]

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 shape = \( \frac{\nu}{2} \) and scale = \( \frac{1}{2} \).

New in version 0.16.0.
References

[R326], [R327]

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.
```

Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pdf(x, df, scale)</td>
<td>Probability density function.</td>
</tr>
<tr>
<td>logpdf(x, df, scale)</td>
<td>Log of the probability density function.</td>
</tr>
<tr>
<td>rvs(df, scale, size=1, random_state=None)</td>
<td>Draw random samples from an inverse Wishart distribution.</td>
</tr>
</tbody>
</table>

5.34.3 Discrete distributions

- `bernoulli` A Bernoulli discrete random variable.
- `binom` A binomial discrete random variable.
- `boltzmann` A Boltzmann (Truncated Discrete Exponential) random variable.
- `laplace` A Laplacian discrete random variable.
- `geom` A geometric discrete random variable.
- `hypergeom` A hypergeometric discrete random variable.
Table 5.254 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>logser</td>
<td>A Logarithmic (Log-Series, Series) discrete random variable.</td>
</tr>
<tr>
<td>nbinom</td>
<td>A negative binomial discrete random variable.</td>
</tr>
<tr>
<td>planck</td>
<td>A Planck discrete exponential random variable.</td>
</tr>
<tr>
<td>poisson</td>
<td>A Poisson discrete random variable.</td>
</tr>
<tr>
<td>randint</td>
<td>A uniform discrete random variable.</td>
</tr>
<tr>
<td>skellam</td>
<td>A Skellam discrete random variable.</td>
</tr>
<tr>
<td>zipf</td>
<td>A Zipf discrete random variable.</td>
</tr>
</tbody>
</table>

scipy.stats.bernoulli = <scipy.stats._discrete_distns.bernoulli_gen object at 0x7fa40e995310>

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:

\[
\text{bernoulli.pmf}(k) = 1-p \quad \text{if } k = 0 \\
= p \quad \text{if } k = 1
\]

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 \(\text{loc}\) parameter. Specifically, bernoulli.pmf\((k, p, \text{loc})\) is identically equivalent to bernoulli.pmf\((k - \text{loc}, p)\).

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')
```
Check accuracy of \texttt{cdf} and \texttt{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>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rvs(x, loc=0, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pmf(x, p, loc=0)</td>
<td>Probability mass function.</td>
</tr>
<tr>
<td>logpmf(x, p, loc=0)</td>
<td>Log of the probability mass function.</td>
</tr>
<tr>
<td>cdf(x, p, loc=0)</td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td>logcdf(x, p, loc=0)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, p, loc=0)</td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, 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>
<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, 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>
</tr>
<tr>
<td>median(p, loc=0)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(p, loc=0)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(p, loc=0)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(p, loc=0)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<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._discrete_distns.binom_gen object at 0x7fa40e995090>**

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:

\[
\text{binom.pmf}(k) = \binom{n}{k} p^k (1-p)^{n-k}
\]

for \(k\in\{0, 1, \ldots, n\}\).

`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))
True
```

Generate random numbers:

```python
>>> r = binom.rvs(n, p, size=1000)
```
Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rvs(n, p, loc=0, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pmf(x, n, p, loc=0)</code></td>
<td>Probability mass function.</td>
</tr>
<tr>
<td><code>logpmf(x, n, p, loc=0)</code></td>
<td>Log of the probability mass function.</td>
</tr>
<tr>
<td><code>cdf(x, n, p, loc=0)</code></td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td><code>logcdf(x, n, p, loc=0)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, n, p, loc=0)</code></td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, n, p, loc=0)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, n, p, loc=0)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, n, p, loc=0)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>stats(n, p, loc=0, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy(n, p, loc=0)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>expect(func, n, p, 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(n, p, loc=0)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(n, p, loc=0)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(n, p, loc=0)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(n, p, loc=0)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, n, p, loc=0)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

`scipy.stats.boltzmann = <scipy.stats._discrete_distns.boltzmann_gen object at 0x7fa40e9230d0>`

A Boltzmann (Truncated Discrete Exponential) random variable.

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:

\[ \text{boltzmann.pmf}(k) = \frac{(1 - \exp(-\lambda_*) \exp(-\lambda_*k)}{1 - \exp(-\lambda_*N)} \]

for \( k = 0, \ldots, N-1 \).

`boltzmann` takes \( \lambda_* \) and \( N \) as shape parameters.

The probability mass function above is defined in the “standardized” form. To shift distribution use the \( \text{loc} \) parameter. Specifically, `boltzmann.pmf(k, \lambda_*, N, \text{loc})` is identically equivalent to `boltzmann.pmf(k - \text{loc}, \lambda_*, N)`.  

Examples

```python
>>> from scipy.stats import boltzmann
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> lambda_, N = 1.4, 19
>>> mean, var, skew, kurt = boltzmann.stats(lambda_, N, moments='mvsk')
```
Display the probability mass function (pmf):

```python
>>> 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:

```python
>>> 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:

```python
>>> prob = boltzmann.cdf(x, lambda_, N)
>>> np.allclose(x, boltzmann.ppf(prob, lambda_, N))
True
```

Generate random numbers:

```python
>>> r = boltzmann.rvs(lambda_, N, size=1000)
```
Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rvs(lambda_, N, loc=0, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pmf(x, lambda_, N, loc=0)</td>
<td>Probability mass function.</td>
</tr>
<tr>
<td>logpmf(x, lambda_, N, loc=0)</td>
<td>Log of the probability mass function.</td>
</tr>
<tr>
<td>cdf(x, lambda_, N, loc=0)</td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td>logcdf(x, lambda_, N, loc=0)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, lambda_, N, loc=0)</td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, 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 cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, lambda_, N, loc=0)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<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>
</tr>
<tr>
<td>expect(func, 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>
</tr>
<tr>
<td>median(lambda_, N, loc=0)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(lambda_, N, loc=0)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(lambda_, N, loc=0)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(lambda_, N, loc=0)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, lambda_, N, loc=0)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

scipy.stats.dlaplace = <scipy.stats._discrete_distns.dlaplace_gen object at 0x7fa40e923810>

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:

dlaplace.pmf(k) = tanh(a/2) \times \exp(-a \times abs(k))

for a > 0.

dlaplace takes a 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, a, loc) is identically equivalent to dlaplace.pmf(k - loc, a).

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

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rvs(a, loc=0, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pmf(x, a, loc=0)</code></td>
<td>Probability mass function.</td>
</tr>
<tr>
<td><code>logpmf(x, a, loc=0)</code></td>
<td>Log of the probability mass function.</td>
</tr>
<tr>
<td><code>cdf(x, a, loc=0)</code></td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td><code>logcdf(x, a, loc=0)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, a, loc=0)</code></td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, a, loc=0)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, a, loc=0)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, a, loc=0)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>stats(a, loc=0, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy(a, loc=0)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>expect(func, a, 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(a, loc=0)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(a, loc=0)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(a, loc=0)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(a, loc=0)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, a, loc=0)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

```python
scipy.stats.geom = <scipy.stats._discrete_distns.geom_gen object at 0x7fa40e995790>
```

A geometric discrete random variable.

As an instance of the `rv_discrete` class, `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 `geom` is:

$$
g_{\text{geom}}(k) = (1-p)^{k-1}p$$

for \( k \geq 1 \).

`geom` takes \( p \) as shape parameter.

The probability mass function above is defined in the “standardized” form. To shift distribution use the `loc` parameter. Specifically, `geom.pmf(k, p, loc)` is identically equivalent to `geom.pmf(k - loc, p)`.

### Examples

```python
>>> from scipy.stats import geom
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)

Calculate a few first moments:

```python
>>> p = 0.5
>>> mean, var, skew, kurt = geom.stats(p, moments='mvsk')
```

Display the probability mass function (pmf):
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>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rvs(p, loc=0, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pmf(x, p, loc=0)</code></td>
<td>Probability mass function.</td>
</tr>
<tr>
<td><code>logpmf(x, p, loc=0)</code></td>
<td>Log of the probability mass function.</td>
</tr>
<tr>
<td><code>cdf(x, p, loc=0)</code></td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td><code>logcdf(x, p, loc=0)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, p, loc=0)</code></td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, p, loc=0)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, p, loc=0)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, p, loc=0)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>stats(p, loc=0, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy(p, loc=0)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>expect(func, p, 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(p, loc=0)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(p, loc=0)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(p, loc=0)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(p, loc=0)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, p, loc=0)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

```python
scipy.stats.hypergeom = <scipy.stats._discrete_distns.hypergeom_gen object at 0x7fa40e995650>
```

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 probability mass function is defined as:

\[
\text{pmf}(k, M, n, N) = \frac{\binom{n}{k} \binom{M - n}{N - k}}{\binom{M}{N}}, \quad \text{for max}(0, N - (M-n)) \leq k \leq \min(n, N)
\]

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:
```
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>rvs(M, n, N, loc=0, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pmf(x, M, n, N, loc=0)</td>
<td>Probability mass function.</td>
</tr>
<tr>
<td>logpmf(x, M, n, N, loc=0)</td>
<td>Log of the probability mass function.</td>
</tr>
<tr>
<td>cdf(x, M, n, N, loc=0)</td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td>logcdf(x, M, n, N, loc=0)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, M, n, N, loc=0)</td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, M, n, N, loc=0)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, M, n, N, loc=0)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, M, n, N, loc=0)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>stats(M, n, N, loc=0, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(M, n, N, loc=0)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>expect(func, M, n, 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>
</tr>
<tr>
<td>median(M, n, N, loc=0)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(M, n, N, loc=0)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(M, n, N, loc=0)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(M, n, N, loc=0)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, M, n, N, loc=0)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

scipy.stats.logser = <scipy.stats._discrete_distns.logser_gen object at 0x7fa40e995990>
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:

\[
\text{logser.pmf}(k) = - p^k / (k\log(1-p))
\]

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:

```
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))
True
```

Generate random numbers:

```python
>>> r = logser.rvs(p, size=1000)
```
Methods

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rvs(p, loc=0, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pmf(x, p, loc=0)</code></td>
<td>Probability mass function.</td>
</tr>
<tr>
<td><code>logpmf(x, p, loc=0)</code></td>
<td>Log of the probability mass function.</td>
</tr>
<tr>
<td><code>cdf(x, p, loc=0)</code></td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td><code>logcdf(x, p, loc=0)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, p, loc=0)</code></td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, p, loc=0)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, p, loc=0)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, p, loc=0)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>stats(p, loc=0, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy(p, loc=0)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>expect(func, p, 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(p, loc=0)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(p, loc=0)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(p, loc=0)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(p, loc=0)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, p, loc=0)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

`scipy.stats.nbinom = <scipy.stats._discrete_distns.nbinom_gen object at 0x7fa40e9953d0>`

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

The probability mass function for `nbinom` is:

\[ nbinom.pmf(k) = \binom{k+n-1}{n-1} \times p^n \times (1-p)^k \]

for \( k \geq 0 \).

`nbinom` 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, `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)
>>> fig, ax = plt.subplots(1, 1)
>>> n, p = 0.4, 0.4
>>> mean, var, skew, kurt = nbinom.stats(n, p, moments='mvsk')
```

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))
```

Generate random numbers:

```python
>>> r = nbinom.rvs(n, p, size=1000)
```
### Methods

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rvs(n, p, loc=0, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pmf(x, n, p, loc=0)</code></td>
<td>Probability mass function.</td>
</tr>
<tr>
<td><code>logpmf(x, n, p, loc=0)</code></td>
<td>Log of the probability mass function.</td>
</tr>
<tr>
<td><code>cdf(x, n, p, loc=0)</code></td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td><code>logcdf(x, n, p, loc=0)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, n, p, loc=0)</code></td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, n, p, loc=0)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, n, p, loc=0)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, n, p, loc=0)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>stats(n, p, loc=0, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy(n, p, loc=0)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>expect(func, n, p, 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(n, p, loc=0)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(n, p, loc=0)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(n, p, loc=0)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(n, p, loc=0)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, n, p, loc=0)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

```python
scipy.stats.planck = <scipy.stats._discrete_distns.planck_gen object at 0x7fa40e995e50>
```

A Planck discrete exponential random variable.

As an instance of the `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:

```python
planck.pmf(k) = (1-exp(-lambda_*k)) * exp(-lambda_*k)
```

for `k * 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>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rvs(lambda_, loc=0, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pmf(x, lambda_, loc=0)</td>
<td>Probability mass function.</td>
</tr>
<tr>
<td>logpmf(x, lambda_, loc=0)</td>
<td>Log of the probability mass function.</td>
</tr>
<tr>
<td>cdf(x, lambda_, loc=0)</td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td>logcdf(x, lambda_, loc=0)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, lambda_, loc=0)</td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, 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, 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>
</tr>
<tr>
<td>var(lambda_, loc=0)</td>
<td>Variance of the distribution.</td>
</tr>
<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._discrete_distns.poisson_gen object at 0x7fa40e995dd0>

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:

\[
poisson.pmf(k) = \exp(-\mu) \times \mu^k / k! \\
\]

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
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:

```python
>>> mu = 0.6
>>> mean, var, skew, kurt = poisson.stats(mu, moments='mvsk')
```
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>
<th>Function</th>
<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(x, mu, loc=0)</td>
<td>Probability mass function.</td>
</tr>
<tr>
<td>logpmf(x, mu, loc=0)</td>
<td>Log of the probability mass function.</td>
</tr>
<tr>
<td>cdf(x, mu, loc=0)</td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td>logcdf(x, mu, loc=0)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, mu, loc=0)</td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, 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, 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._discrete_distns.randint_gen object at 0x7fa40e923190>
```

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:

```
randint.pmf(k) = 1./(high - low)
```

for \( k = \text{low}, \ldots, \text{high} - 1 \).

`randint` takes `low` and `high` as shape parameters.

Note the difference to the numpy `random_integers` which returns integers on a closed interval \([\text{low}, \text{high}]\).

The probability mass function above is defined in the “standardized” form. To shift distribution use the `loc` parameter. Specifically, `randint.pmf(k, \text{low}, \text{high}, \text{loc})` is identically equivalent to `randint.pmf(k - \text{loc}, \text{low}, \text{high})`.

Examples

```python
>>> from scipy.stats import randint
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate a few first moments:
>>> low, high = 7, 31
>>> mean, var, skew, kurt = randint.stats(low, high, moments='mvsk')

Display the probability mass function (pmf):

>>> 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:

>>> 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:

>>> prob = randint.cdf(x, low, high)
>>> np.allclose(x, randint.ppf(prob, low, high))
True

Generate random numbers:

>>> r = randint.rvs(low, high, size=1000)
### Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rvs(low, high, loc=0, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pmf(x, low, high, loc=0)</code></td>
<td>Probability mass function.</td>
</tr>
<tr>
<td><code>logpmf(x, low, high, loc=0)</code></td>
<td>Log of the probability mass function.</td>
</tr>
<tr>
<td><code>cdf(x, low, high, loc=0)</code></td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td><code>logcdf(x, low, high, loc=0)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, low, high, loc=0)</code></td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, low, high, loc=0)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, low, high, loc=0)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, low, high, loc=0)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>stats(low, high, loc=0, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy(low, high, loc=0)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>expect(func, low, high, 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(low, high, loc=0)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(low, high, loc=0)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(low, high, loc=0)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(low, high, loc=0)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, low, high, loc=0)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution.</td>
</tr>
</tbody>
</table>

**scipy.stats**.skellam = <scipy.stats._discrete_distributions.skellam_gen object at 0x7fa40e9237d0>

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 k1 and k2 be two Poisson-distributed r.v. with expected values lam1 and lam2. Then, k1 - k2 follows a Skellam distribution with parameters mu1 = lam1 - rho*sqrt(lam1*lam2) and mu2 = lam2 - rho*sqrt(lam1*lam2), where rho is the correlation coefficient between k1 and k2. If the two Poisson-distributed r.v. are independent then rho = 0.

Parameters mu1 and mu2 must be strictly positive.


skellam takes mu1 and mu2 as shape parameters.

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:
>>> mu1, mu2 = 15, 8
>>> mean, var, skew, kurt = skellam.stats(mu1, mu2, moments='mvsk')

Display the probability mass function (pmf):

>>> 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:

>>> 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:

>>> prob = skellam.cdf(x, mu1, mu2)
>>> np.allclose(x, skellam.ppf(prob, mu1, mu2))
True

Generate random numbers:

>>> r = skellam.rvs(mu1, mu2, size=1000)
Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rvs(mu1, mu2, loc=0, size=1, random_state=None)</td>
<td>Random variates.</td>
</tr>
<tr>
<td>pmf(x, mu1, mu2, loc=0)</td>
<td>Probability mass function.</td>
</tr>
<tr>
<td>logpmf(x, mu1, mu2, loc=0)</td>
<td>Log of the probability mass function.</td>
</tr>
<tr>
<td>cdf(x, mu1, mu2, loc=0)</td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td>logcdf(x, mu1, mu2, loc=0)</td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td>sf(x, mu1, mu2, loc=0)</td>
<td>Survival function (1 - cdf — sometimes more accurate).</td>
</tr>
<tr>
<td>logsf(x, mu1, mu2, loc=0)</td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td>ppf(q, mu1, mu2, loc=0)</td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td>isf(q, mu1, mu2, loc=0)</td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td>stats(mu1, mu2, loc=0, moments='mv')</td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td>entropy(mu1, mu2, loc=0)</td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td>expect(func, mu1, mu2, 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(mu1, mu2, loc=0)</td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td>mean(mu1, mu2, loc=0)</td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td>var(mu1, mu2, loc=0)</td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td>std(mu1, mu2, loc=0)</td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td>interval(alpha, mu1, mu2, loc=0)</td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

scipy.stats.zipf = <scipy.stats._discrete_distns.zipf_gen object at 0x7fa40e923550>
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:

\[ \text{zipf.pmf}(k, a) = \frac{1}{(\zeta(a) \cdot k^a)} \]

for \( k \geq 1 \).

zipf takes \( a \) as shape parameter.

The probability mass function above is defined in the “standardized” form. To shift distribution use the loc parameter. Specifically, \( \text{zipf.pmf}(k, a, \text{loc}) \) is identically equivalent to \( \text{zipf.pmf}(k - \text{loc}, a) \).

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>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>rvs(a, loc=0, size=1, random_state=None)</code></td>
<td>Random variates.</td>
</tr>
<tr>
<td><code>pmf(x, a, loc=0)</code></td>
<td>Probability mass function.</td>
</tr>
<tr>
<td><code>logpmf(x, a, loc=0)</code></td>
<td>Log of the probability mass function.</td>
</tr>
<tr>
<td><code>cdf(x, a, loc=0)</code></td>
<td>Cumulative density function.</td>
</tr>
<tr>
<td><code>logcdf(x, a, loc=0)</code></td>
<td>Log of the cumulative density function.</td>
</tr>
<tr>
<td><code>sf(x, a, loc=0)</code></td>
<td>Survival function ($1 - cdf$ — sometimes more accurate).</td>
</tr>
<tr>
<td><code>logsf(x, a, loc=0)</code></td>
<td>Log of the survival function.</td>
</tr>
<tr>
<td><code>ppf(q, a, loc=0)</code></td>
<td>Percent point function (inverse of cdf — percentiles).</td>
</tr>
<tr>
<td><code>isf(q, a, loc=0)</code></td>
<td>Inverse survival function (inverse of sf).</td>
</tr>
<tr>
<td><code>stats(a, loc=0, moments='mv')</code></td>
<td>Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').</td>
</tr>
<tr>
<td><code>entropy(a, loc=0)</code></td>
<td>(Differential) entropy of the RV.</td>
</tr>
<tr>
<td><code>expect(func, a, 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(a, loc=0)</code></td>
<td>Median of the distribution.</td>
</tr>
<tr>
<td><code>mean(a, loc=0)</code></td>
<td>Mean of the distribution.</td>
</tr>
<tr>
<td><code>var(a, loc=0)</code></td>
<td>Variance of the distribution.</td>
</tr>
<tr>
<td><code>std(a, loc=0)</code></td>
<td>Standard deviation of the distribution.</td>
</tr>
<tr>
<td><code>interval(alpha, a, loc=0)</code></td>
<td>Endpoints of the range that contains alpha percent of the distribution</td>
</tr>
</tbody>
</table>

### 5.34.4 Statistical functions

Several of these functions have a similar version in scipy.stats.mstats which work for masked arrays.

- `describe(a[, axis, ddof])`: Computes several descriptive statistics of the passed array.
- `gmean(a[, axis, dtype])`: Compute the geometric mean along the specified axis.
- `hmean(a[, axis, dtype])`: Calculates the harmonic mean along the specified axis.
- `kurtosis(a[, axis, fisher, bias])`: Computes the kurtosis (Fisher or Pearson) of a dataset.
- `kurtosistest(a[, axis])`: Tests whether a dataset has normal kurtosis.
- `mode(a[, axis])`: Returns an array of the modal (most common) value in the passed array.
- `moment(a[, moment, axis])`: Calculates the nth moment about the mean for a sample.
- `skew(a[, axis, bias])`: Computes the skewness of a data set.
- `skewtest(a[, axis])`: Tests whether the skew is different from a normal distribution.
- `kstat(data[, n])`: Return the nth k-statistic ($1 <= n <= 4$ so far).
- `kstatvar(data[, n])`: Returns an unbiased estimator of the variance of the k-statistic.
- `tmean(a[, limits, inclusive])`: Compute the trimmed mean.
- `tvar(a[, limits, inclusive])`: Compute the trimmed variance
- `tmin(a[, lowerlimit, axis, inclusive])`: Compute the trimmed minimum
- `tmax(a[, upperlimit, axis, inclusive])`: Compute the trimmed maximum
- `tsstd(a[, limits, inclusive])`: Compute the trimmed sample standard deviation
- `tsem(a[, limits, inclusive])`: Compute the trimmed standard error of the mean.

**Note:** `nanmean`, `nanstd`, and `nanmedian` functions are deprecated beginning in version 1.0.0 of SciPy.
The coefficient of variation, the ratio of the biased standard deviation to the mean.

**scipy.stats.describe** *(a[, axis=0, ddof=1])*

Computes 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. Default is 1.

**Returns**

- **nobs**: int
  Number of observations (length of data along **axis**).
- **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
  Biased skewness, based on moment calculations with denominator equal to the number of observations, i.e. no degrees of freedom correction.
- **kurtosis**: ndarray or float
  Biased kurtosis (Fisher). The kurtosis is normalized so that it is zero for the normal distribution. No degrees of freedom or bias correction is used.

**See also:**

- **skew**, **kurtosis**

**scipy.stats.gmean** *(a[, axis=0, dtype=None])*

Compute the geometric mean along the specified axis.

Returns 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.

```python
scipy.stats.hmean(a, axis=0, dtype=None)
```
Calculates the harmonic mean along the specified axis.

That is: \( \frac{n}{(1/x1 + 1/x2 + \ldots + 1/xn)} \)

**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.

```python
scipy.stats.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`.
- `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
Returns

kurtosis : array

If False, then the calculations are corrected for statistical bias.

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

[R329] scipy.stats.kurtosistest (a, axis=0)

Tests 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 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

Valid only for n>20. The Z-score is set to 0 for bad entries.

scipy.stats.mode (a, axis=0)

Returns an array of the modal (most common) value in the passed array.

If there is more than one such value, only the first 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

>>> a = np.array([[6, 8, 3, 0],
... [3, 2, 1, 7],
... [8, 1, 8, 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:

>>> stats.mode(a, axis=None)

(array([3]), array([3]))
**scipy.stats.moment** *(a, moment=1, axis=0)*  
Calculates the nth moment about the mean for a sample. Generally used to calculate coefficients of skewness and kurtosis.

**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.

**scipy.stats.normaltest** *(a, axis=0)*  
Tests 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 [R351], [R352] test that combines skew and kurtosis to produce an omnibus test of normality.

**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.

**References**
- [R351], [R352]

**scipy.stats.skew** *(a, axis=0, bias=True)*  
Computes the skewness of a data set. For normally distributed data, the skewness should be about 0. A skewness value > 0 means that there is more weight in the left 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**
- [R362]

**scipy.stats.skewtest** *(a, axis=0)*  
Tests 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**

- **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**

The sample size must be at least 8.

```python
scipy.stats.kstat(data, n=2)
```

Return the nth k-statistic (1<=n<=4 so far).

The nth k-statistic is the unique symmetric unbiased estimator of the nth cumulant kappa_n.

**Parameters**

- **data**: array_like
  - Input array.
- **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.

**Notes**

The cumulants are related to central moments but are specifically defined using a power series expansion of the logarithm of the characteristic function (which is the Fourier transform of the PDF). In particular let \( \phi(t) \) be the characteristic function, then:

\[
\ln \phi(t) = \sum_{n=0}^{\infty} \kappa_n (it)^n / n! 
\]

The first few cumulants (\( \kappa_n \)) in terms of central moments (\( \mu_n \)) are:

\[
\begin{align*}
\kappa_1 &= \mu_1 \\
\kappa_2 &= \mu_2 \\
\kappa_3 &= \mu_3 \\
\kappa_4 &= \mu_4 - 3\mu_2^2 \\
\kappa_5 &= \mu_5 - 10\mu_2\mu_3 \\
\end{align*}
\]

**References**

- [mathworld.wolfram.com/k-Statistic.html](http://mathworld.wolfram.com/k-Statistic.html)
- [mathworld.wolfram.com/Cumulant.html](http://mathworld.wolfram.com/Cumulant.html)

```python
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.
SciPy Reference Guide, Release 0.16.0

n : int, {1, 2}, optional
    Default is equal to 2.

Returns
kstatvar : float
    The nth k-statistic variance.

See also:
kstat
scipy.stats.tmean (a, limits=None, inclusive=(True, True))
Compute the trimmed mean.
This function finds the arithmetic mean 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 (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).

Returns
tmean : float

scipy.stats.tvar (a, limits=None, inclusive=(True, True))
Compute 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).

Returns
tvar : float
    Trimmed variance.

Notes
tvar computes the unbiased sample variance, i.e. it uses a correction factor \( n / (n - 1) \).

scipy.stats.tmin (a, lowerlimit=None, axis=0, inclusive=True)
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.

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 lower limit are included. The default value is True.

Returns

- `tmax` : float

`scipy.stats.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

`scipy.stats.tstd(a, limits=None, inclusive=(True, True))`

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. 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).

Returns

- `tstd` : float

Notes

`tstd` computes the unbiased sample standard deviation, i.e. it uses a correction factor $n / (n - 1)$.

`scipy.stats.tsem(a, limits=None, inclusive=(True, True))`

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

Notes

`tsem` computes the unbiased sample standard deviation, i.e. it uses a correction factor $n / (n - 1)$.
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).

**Returns**

- **tsem** : float

**Notes**

tsem uses unbiased sample standard deviation, i.e. it uses a correction factor $n / (n - 1)$.

scipy.stats.nanmean(*args, **kwds)

nanmean is deprecated! scipy.stats.nanmean is deprecated in scipy 0.15.0 in favour of numpy.nanmean.

Compute the mean over the given axis ignoring nans.

**Parameters**

- **x** : ndarray

  Input array.

- **axis** [int or None, optional] Axis along which the mean is computed. Default is 0. If None, compute over the whole array $x$.

**Returns**

- **m** : float

  The mean of $x$, ignoring nans.

**Examples**

```python
>>> from scipy import stats
>>> a = np.linspace(0, 4, 3)
>>> a
array([ 0., 2., 4.])
>>> a[-1] = np.nan
>>> stats.nanmean(a)
1.0
```

scipy.stats.nanstd(*args, **kwds)

nanstd is deprecated! scipy.stats.nanstd is deprecated in scipy 0.15 in favour of numpy.nanstd. Note that numpy.nanstd has a different signature.

Compute the standard deviation over the given axis, ignoring nans.

**Parameters**

- **x** : array_like

  Input array.

- **axis** [int or None, optional] Axis along which the standard deviation is computed. Default is 0. If None, compute over the whole array $x$.

- **bias** [bool, optional] If True, the biased (normalized by N) definition is used. If False (default), the unbiased definition is used.

**Returns**

- **s** : float

  The standard deviation.
Examples

```python
>>> from scipy import stats
>>> a = np.arange(10, dtype=float)
>>> a[1:3] = np.nan
>>> np.std(a)
nan
>>> stats.nanstd(a)
2.9154759474226504
>>> stats.nanstd(a.reshape(2, 5), axis=1)
array([ 2.0817, 1.5811])
>>> stats.nanstd(a.reshape(2, 5), axis=None)
2.9154759474226504
```

`scipy.stats.nanmedian(*args, **kwds)`

`nanmedian` is deprecated! `scipy.stats.nanmedian` is deprecated in scipy 0.15 in favour of `numpy.nanmedian`.

Compute the median along the given axis ignoring nan values.

**Parameters**

- `x`: array_like
  Input array.

- `axis` ([int or None, optional])
  Axis along which the median is computed. Default is 0. If None, compute over the whole array `x`.

**Returns**

- `m`: float
  The median of `x` along `axis`.

Examples

```python
>>> from scipy import stats
>>> a = np.array([0, 3, 1, 5, 5, np.nan])
>>> stats.nanmedian(a)
array(3.0)
>>> b = np.array([0, 3, 1, 5, 5, np.nan, 5])
>>> stats.nanmedian(b)
array(4.0)
```

Example with axis:

```python
>>> c = np.arange(30.).reshape(5,6)
>>> idx = np.array([False, False, False, True, False] * 6).reshape(5,6)
>>> c[idx] = np.nan
>>> c
array([[ 0.,  1.,  2., nan,  4.,  5.],
       [ 6.,  7., nan,  9., 10., 11.],
       [12., nan, 14., 15., 16., 17.],
       [ nan, 19., 20., 21., 22., nan],
       [24., 25., 26., 27., nan, 29.]])
>>> stats.nanmedian(c, axis=1)
array([ 2. ,  9. , 15. , 20.5, 26. ])
```

`scipy.stats.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 \( a \).

### References

[R372]

```python
cumfreq(a[, numbins, defaultreallimits, weights])
```
Returns a cumulative frequency histogram, using the histogram function.

```python
histogram2(*args, **kwds)
```
**histogram2 is deprecated!**

```python
histogram(a[, numbins, defaultlimits, ...])
```
Separates the range into several bins and returns the number of instances in each.

```python
itemfreq(a)
```
Returns a 2-D array of item frequencies.

```python
percentileofscore(a, score[, kind])
```
The percentile rank of a score relative to a list of scores.

```python
scoreatpercentile(a, per[, limit, ...])
```
Calculate the score at a given percentile of the input sequence.

```python
relfreq(a[, numbins, defaultreallimits, weights])
```
Returns a relative frequency histogram, using the histogram function.

```python
scipy.stats.cumfreq(a, numbins=10, defaultreallimits=None, weights=None)
```
Returns a cumulative frequency histogram, using the histogram function.

**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
>>> from scipy import stats
>>> x = [1, 4, 2, 1, 3, 1]
>>> cumfreqs, lowlim, binsize, extrapoints = stats.cumfreq(x, numbins=4)
>>> cumfreqs
array([3., 4., 5., 6.])
>>> cumfreqs, lowlim, binsize, extrapoints = stats.cumfreq(x, numbins=4, defaultreallimits=(1.5, 5))
>>> cumfreqs
array([1., 2., 3., 3.])
>>> extrapoints
3
```

```python
scipy.stats.histogram2(*args, **kwds)
```
**histogram2 is deprecated!** scipy.stats.histogram2 is deprecated in scipy 0.16.0; use np.histogram2d instead
Compute histogram using divisions in bins. Count the number of times values from array \(a\) fall into numerical ranges defined by \(bins\). Range \(x\) is given by \(bins[x] \leq \text{range}_x < bins[x+1]\) where \(x = 0, N\) and \(N\) is the length of the \(bins\) array. The last range is given by \(bins[N] \leq \text{range}_N < \infty\). Values less than \(bins[0]\) are not included in the histogram.

**Parameters**

- \(a\) : array_like of rank 1
  - The array of values to be assigned into bins
- \(bins\) : [array_like of rank 1]
  - Defines the ranges of values to use during histogramming.

**Returns**

- \(histogram\) : ndarray of rank 1
  - Each value represents the occurrences for a given bin (range) of values.

```python
c scipy.stats.histogram(a, numbins=10, defaultlimits=None, weights=None, printextras=False)
```

Separates the range into several bins and returns the number of instances in each bin.

**Parameters**

- \(a\) : array_like
  - Array of scores which will be put into bins.
- \(numbins\) : int, optional
  - The number of bins to use for the histogram. Default is 10.
- \(defaultlimits\) : 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
- \(printextras\) : bool, optional
  - If True, if there are extra points (i.e. the points that fall outside the bin limits) a warning is raised saying how many of those points there are. Default is False.

**Returns**

- \(count\) : ndarray
  - Number of points (or sum of weights) in each bin.
- \(lowerlimit\) : float
  - Lowest value of histogram, the lower limit of the first bin.
- \(binsize\) : float
  - The size of the bins (all bins have the same size).
- \(extrapoints\) : int
  - The number of points outside the range of the histogram.

**See also:**

- `numpy.histogram`

**Notes**

This histogram is based on numpy’s histogram but has a larger range by default if default limits is not set.

```python
c scipy.stats.itemfreq(a)
```

Returns a 2-D array of item frequencies.

**Parameters**

- \(a\) : (N,) array_like

**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, 2, 0, 1, 4])
>>> stats.itemfreq(a)
array([[ 0.,  2.],
       [ 1.,  4.],
       [ 2.,  2.],
       [ 4.,  1.],
       [ 5.,  1.]])
```

```python
>>> np.bincount(a)
array([2, 4, 2, 0, 1, 1])
```

```python
>>> stats.itemfreq(a/10.)
array([[ 0. ,  2. ],
       [ 0.1,  4. ],
       [ 0.2,  2. ],
       [ 0.4,  1. ],
       [ 0.5,  1. ]])
```

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 http://en.wikipedia.org/wiki/Percentile_rank

Returns

- `pcos` : float
  Percentile-position of score (0-100) relative to `a`.

See also:

- `numpy.percentile`

Examples

Three-quarters of the given values lie below a given score:
>>> 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:

>>> stats.percentileofscore([1, 2, 3, 3, 4], 3)
70.0

Only 2/5 values are strictly less than 3:

>>> stats.percentileofscore([1, 2, 3, 3, 4], 3, kind='strict')
40.0

But 4/5 values are less than or equal to 3:

>>> stats.percentileofscore([1, 2, 3, 3, 4], 3, kind='weak')
80.0

The average between the weak and the strict scores is

>>> stats.percentileofscore([1, 2, 3, 3, 4], 3, kind='mean')
60.0

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: \(i + (j - i) \times \text{fraction}\) where \text{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 >= 1.9.

Examples

```python
>>> from scipy import stats
>>> a = np.arange(100)
>>> stats.scoreatpercentile(a, 50)
49.5
```

`scipy.stats.relfreq(a, numbins=10, defaultreallimits=None, weights=None)`

Returns a relative frequency histogram, using the histogram function.

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 \((a\text{.min()} - s, a\text{.max()} + s)\), where \(s = (1/2)(a\text{.max()} - a\text{.min()}) / (\text{numbins} - 1)\).
- `weights`: array_like, optional
  The weights for each value in `a`. Default is None, which gives each value a weight of 1.0

Returns

- `frequency`: ndarray
  Binned values of relative frequency.
- `lowerlimit`: float
  Lower real limit
- `binsize`: float
  Width of each bin.
- `extrapoints`: int
  Extra points.

Examples

```python
>>> from scipy import stats
>>> a = np.array([1, 4, 2, 1, 3, 1])
>>> relfreqs, lowlim, binsize, extrapoints = stats.relfreq(a, numbins=4)
>>> relfreqs
array([ 0.5 , 0.16666667, 0.16666667, 0.16666667])
>>> np.sum(relfreqs)  # relative frequencies should add up to 1
0.99999999999999989
```

```
bin_freq = binned_statistic(x, y, statistic='mean', bins=10, range=None)
```

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

---

5.34. Statistical functions (`scipy.stats`) 1439
A statistic of the values within each bin.

**Parameters**

- **x**: array_like
  A sequence of values to be binned.

- **values**: array_like
  The values on which the statistic will be computed. This must be the same shape as \( x \).

- **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. \( \text{values} \) array is not referenced.
  - ‘sum’: compute the sum of values for points within each bin. This is identical to a weighted histogram.
  - 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([0]), or NaN if this returns an error.

- **bins**: int or sequence of scalars, optional
  If \( \text{bins} \) is an int, it defines the number of equal-width bins in the given range (10 by default). If \( \text{bins} \) 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 \( \text{bins}[-1] \).

- **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 \( \text{length(statistic)} + 1 \).

- **binnumber**: 1-D ndarray of ints
  This assigns to each observation an integer that represents the bin in which this observation falls. Array has the same length as values.

**See also:**

- `numpy.histogram`
- `binned_statistic_2d`
- `binned_statistic_dd`

**Notes**

All but the last (righthand-most) bin is half-open. In other words, if \( \text{bins} \) 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 a basic example:
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, normed=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(x, y, values, statistic='mean', bins=10, range=None)

Compute a bidimensional binned statistic for a set 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 within each bin.

Parameters
x : (N,) array_like
   A sequence of values to be binned along the first dimension.
y : (M,) array_like
   A sequence of values to be binned along the second dimension.
values : (N,) array_like
   The values on which the statistic will be computed. This must be the same shape as x.
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.
• '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_edges = y_edges = bins),
• the bin edges in each dimension (x_edges, y_edges = bins).

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.

Returns
statistic : (nx, ny) ndarray
The values of the selected statistic in each two-dimensional bin
x_edges : (nx + 1) ndarray
The bin edges along the first dimension.
y_edges : (ny + 1) ndarray
The bin edges along the second dimension.
bin_number : 1-D ndarray of ints
This assigns to each observation an integer that represents the bin in which this observation falls. Array has the same length as values.

See also:
numpy.histogram2d, binned_statistic, binned_statistic_dd

Notes
New in version 0.11.0.

scipy.stats.binned_statistic_dd(sample, values, statistic='mean', bins=10, range=None)
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 : array_like
The values on which the statistic will be computed. This must be the same shape as x.
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.
• 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:
• 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).

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 : 1-D ndarray of ints This assigns to each observation an integer that represents the bin in which this observation falls. Array has the same length as values.

See also:
np.histogramdd, binned_statistic, binned_statistic_2d

Notes
New in version 0.11.0.

obrientransform(*args) Computes the O’Brien transform on input data (any number of arrays).
signaltonoise(*args, **kwds) signaltonoise is deprecated!
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.
sem(a[, axis, ddof]) Calculates the standard error of the mean (or standard error of measurement) of the values in the input array.
zmap(scores, compare[, axis, ddof]) Calculates the relative z-scores.
zscore(a[, axis, ddof]) Calculates the z score of each value in the sample, relative to the sample mean and standard deviation.

scipy.stats.obrientransform(*args) Computes 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 [R353], 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

[R353]

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.signaltonoise (*args, **kwds)`

`signaltonoise` is deprecated! scipy.stats.signaltonoise is deprecated in scipy 0.16.0

The signal-to-noise ratio of the input data.

Returns the signal-to-noise ratio of \( a \), here defined as the mean divided by the 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 for standard deviation. Default is 0.

**Returns**

- **s2n**: ndarray

  The mean to standard deviation ratio(s) along \( axis \), or 0 where the standard deviation is 0.

`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:

  \( (\text{center}, (\text{lower}, \text{upper})) \)
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.

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

T.E. Oliphant, “A Bayesian perspective on estimating mean, variance, and standard-deviation from data”,

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 data-points.

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

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.

Examples

>>> from scipy import stats
>>> data = [6, 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)

scipy.stats.sem(a, axis=0, ddof=1)

Calculates 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.
SciPy Reference Guide, Release 0.16.0

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.

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 stats.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.zmap(scores, compare, axis=0, ddof=0)
Calculates the relative z-scores.

Returns 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

5.34. Statistical functions (scipy.stats) 1447
>>> 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(a, axis=0, ddof=0)
Calculates the z score of each value in the sample, relative to the sample mean and standard deviation.

**Parameters**
- `a`: array_like
  An array like 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, 1.07259584, 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 ]])
```

scipy.stats.sigmaclip(a, low, high)
Iterative sigma-clipping of array elements.

scipy.stats.threshold(a, threshmin, threshmax, newval)
Clip array to a given value.

scipy.stats.trimboth(a, proportiontocut[, axis])
Slices off a proportion of items from both ends of an array.

scipy.stats.trim1(a, proportiontocut[, tail])
Slices off a proportion of items from ONE end of the passed array distribution.

The output array contains only those elements of the input array `c` that satisfy the conditions.
mean(c) - std(c)*low < c < mean(c) + std(c)*high

Starting from the full sample, all elements outside the critical range are removed. The iteration continues with a new critical range until no elements are outside the 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 used for clipping.
- `upper`: float
  - Upper threshold value used 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()
(9.964646464646464, 9.964646464646464, 9.966666666666666)
>>> upp, c.mean() + fact*c.std(), c.max()
(10.035353535353535, 10.035353535353535, 10.033333333333333)

>>> 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.threshold(a, threshmin=None, threshmax=None, newval=0)

Clip array to a given value.

Similar to numpy.clip(), except that values less than `threshmin` or greater than `threshmax` are replaced by `newval`, instead of by `threshmin` and `threshmax` respectively.

**Parameters**
- `a`: array_like
  - Data to threshold.
- `threshmin`: float, int or None, optional
  - Minimum threshold, defaults to None.
- `threshmax`: float, int or None, optional
  - Maximum threshold, defaults to None.
- `newval`: float or int, optional

**Returns**
- `out`: ndarray
  - Value to put in place of values in `a` outside of bounds. Defaults to 0.
  - The clipped input array, with values less than `threshmin` or greater than `threshmax` replaced with `newval`. 

5.34. Statistical functions (scipy.stats)
Examples

```python
>>> a = np.array([9, 9, 6, 3, 1, 6, 1, 0, 0, 8])
>>> from scipy import stats
>>> stats.threshold(a, threshmin=2, threshmax=8, newval=-1)
array([-1, -1, 6, 3, -1, 6, -1, -1, -1, 8])
```

```python
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). You must pre-sort the array if you want ‘proper’ trimming. 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`.

See also:
- `trim_mean`

**Examples**

```python
>>> from scipy import stats
>>> a = np.arange(20)
>>> b = stats.trimboth(a, 0.1)
>>> b.shape
(16,)
```

```python
scipy.stats.trim1(a, proportiontocut, tail='right')
```
Slices off a proportion of items from ONE end of the passed array distribution.

If `proportiontocut` = 0.1, slices off ‘leftmost’ or ‘rightmost’ 10% of scores. 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’.

**Returns**
- `trim1`: ndarray
  Trimmed version of array `a`
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**

[R314], [R315]

scipy.stats.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 : (N,) array_like
    Input
y : (N,) array_like
    Input
```

**Returns**

```
(Pearson’s correlation coefficient,
2-tailed p-value)
```

**References**

http://www.statsoft.com/textbook/glspchtml#Pearson%20Correlation

scipy.stats.spearmanr(a, b=None, axis=0)

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 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**  
\( a, b \): 1D or 2D array_like, b is optional

One or two 1-D or 2-D arrays containing multiple variables and observations. Each column of \( a \) and \( b \) represents a variable, and each row entry a single observation of those variables. See also \( axis \). 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 \( axis=0 \), the relationship is transposed: each row represents a variable, while the columns contain observations. If \( axis=None \), then both arrays will be raveled.

**Returns**  
\( \text{correlation} \): 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 \( \text{rho} \).

**Notes**  
Changes in scipy 0.8.0: rewrite to add tie-handling, and \( axis \).

**References**  
[R363]

**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, 0.06435364, 0.53617935],
       [ 0.55338591, 0. , 0.27592895, 0.80234077],
       [ 0.06435364, 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. ]])
```
```python
>>> stats.spearmanr(x2n, y2n, axis=None)
(0.10816770419260482, 0.1273562188027364)

>>> stats.spearmanr(x2n.ravel(), y2n.ravel())
(0.10816770419260482, 0.1273562188027364)

>>> xint = np.random.randint(10, size=(100, 2))
>>> stats.spearmanr(xint)
(0.052760927029710199, 0.60213045837062351)
```

`scipy.stats.pointbiserialr(x, y)`
Calculates a point biserial correlation coefficient and the associated 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`.

```python
Parameters

- **x**: array_like of bools
  Input array.
- **y**: array_like

Returns

- **correlation**: float
  R value
- **pvalue**: float
  2-tailed p-value
```

References

http://en.wikipedia.org/wiki/Point-biserial_correlation_coefficient

Examples

```python
>>> from scipy import stats

>>> a = np.array([0, 0, 0, 1, 1, 1, 1])
>>> b = np.arange(7)
>>> stats.pointbiserialr(a, b)
(0.8660254037844386, 0.011724811003954652)

>>> stats.pearsonr(a, b)
(0.86602540378443871, 0.011724811003954626)

>>> np.corrcoef(a, b)
array([[ 1. , 0.8660254],
       [ 0.8660254, 1. ]])
```

`scipy.stats.kendalltau(x, y, initial_lexsort=True)`
Calculates 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 tau-b version of Kendall’s tau which accounts for ties.

```python
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
  Whether to use lexsort or quicksort as the sorting method for the initial sort of the inputs. Default is lexsort (True), for which `kendalltau` is
```

5.34. Statistical functions (scipy.stats) 1453
of complexity $O(n \log(n))$. If False, the complexity is $O(n^2)$, but with a
smaller pre-factor (so quicksort may be faster for small arrays).

**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, $\tau = 0$.

**Notes**

The definition of Kendall’s tau that is used is:

$$\tau = \frac{P - Q}{\sqrt{(P + Q + T)(P + Q + U)}}$$

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**


**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
0.24821309157521476
```

**scipy.stats.linregress** ($x, y=None$)

Calculate a regression line.

This computes a 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.
- **stderr**: float
  Standard error of the estimate
Examples

```python
>>> from scipy import stats
>>> x = np.random.random(10)
>>> y = np.random.random(10)
>>> slope, intercept, r_value, p_value, std_err = stats.linregress(x,y)

# To get coefficient of determination (r_squared)

>>> print("r-squared:", r_value**2)
r-squared: 0.15286643777
```

**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 `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.

**Notes**
The implementation of theilslopes follows [R364]. The intercept is not defined in [R364], and here it is defined as \( \text{median}(y) - \text{medslope} \times \text{median}(x) \), which is given in [R366]. 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 [R364].

**References**
[R364], [R365], [R366]

**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
gt = 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()
```
scipy.stats.ttest_1samp(a, popmean, axis=0)
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 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

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]))
```n
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([ 4.9961383e-01, 1.49986458e-04]))
>>> stats.ttest_1samp(rvs.T,[[5.0],[0.0]],axis=1)
(array([-0.68014479, 4.11038784]), array([ 4.9961383e-01, 1.49986458e-04]))
>>> stats.ttest_1samp(rvs,[[5.0],[0.0]])
(array([-0.68014479, -0.04323899],
  [ 2.77025808, 4.11038784]), array([[ 4.9961383e-01, 9.65686743e-01],
  [ 7.89094663e-03, 1.49986458e-04]))
```

scipy.stats.ttest_ind(a, b, axis=0, equal_var=True)
Calculates 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 [R368]. If False, perform Welch’s t-test, which does not assume equal population variance [R369]. .. versionadded:: 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
[R368], [R369]

Examples

```python
>>> from scipy import stats
>>> np.random.seed(12345678)
```

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)
(0.26833823296239279, 0.78849443369564776)
```

```python
>>> stats.ttest_ind(rvs1, rvs2, equal_var = False)
(0.26833823296239279, 0.78849452749500748)
```

ttest_ind underestimates p for unequal variances:

```python
>>> rvs3 = stats.norm.rvs(loc=5, scale=20, size=500)
>>> stats.ttest_ind(rvs1, rvs3)
(-0.46580283298287162, 0.64145827413436174)
>>> 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:

```python
>>> 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)
(-0.69712570584654099, 0.48716927725402048)
```

T-test with different means, variance, and n:
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 2 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 [R370]. If False, perform Welch’s t-test, which does not assume equal population variance [R371].

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
[R370], [R371]

scipy.stats.ttest_rel (a, b, axis=0)

Calculates 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.

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
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
http://en.wikipedia.org/wiki/T-test#Dependent_t-test

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(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.

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:

>>> 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 $\text{cdf}_{\text{dgp}}(x) < \text{norm.cdf}(x)$:

```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')
(0.0072115233216311081, 0.9853115890396395)

Don’t reject equal distribution against alternative hypothesis: greater

```python
>>> stats.kstest(x, 'norm', mode='asymp')
(0.12464329735846891, 0.040989164077641749)

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')
(0.07201892916532626, 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:
SciPy Reference Guide, Release 0.16.0

```python
>>> np.random.seed(987654321)
>>> stats.kstest(stats.t.rvs(3,size=100),'norm')
(0.131016895759829, 0.058826222555312224)
```

scipy.stats.chisquare(f_obs,f_exp=None, ddof=0, axis=0)

Calculates 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.

**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**

[R307], [R308]

**Examples**

When just `f_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, 0.84914503608460956)
```

With `f_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_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([ 2.21487748, 9.25460205]), array([ 0.73009511, 0.09758498]))
```

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)
```

`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([ 0.73575888, 0.57240675 ]))
```

`f_obs` and `f_exp` are also broadcast. In the following, `f_obs` has shape (6,) and `f_exp` has shape (2, 6), so the result of broadcasting `f_obs` and `f_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, 0.09758498]))
```

scipy.stats.power_divergence(f_obs, f_exp=None, ddof=0, axis=0, lambda_=None)

Cressie-Read power divergence statistic and goodness of fit test.

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 \( k - 1 - \text{ddof} \) 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 numerical values, 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 <code>stats.chisquare</code>.</td>
</tr>
<tr>
<td>&quot;log-likelihood&quot;</td>
<td>0</td>
<td>Log-likelihood ratio. Also known as the G-test [R356]_.</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 [R358]_.</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 chisquare, in which case this test is not appropriate.

This function handles masked arrays. If an element of `f_obs` or `f_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**

[R354], [R355], [R356], [R357], [R358]

**Examples**

(See chisquare for more examples.)

When just `f_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, 0.848234779463769)
```

The expected frequencies can be given with the `f_exp` argument:

```python
>>> power_divergence([16, 18, 16, 14, 12, 12],
...                   f_exp=[16, 16, 16, 16, 16, 8],
...                   lambda_='log-likelihood')
(3.5, 0.62338762774958223)
```

When `f_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 `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)
```

`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 `ddof`.

```python
>>> power_divergence([16, 18, 16, 14, 12, 12], ddof=[0,1,2])
(2.0, array([ 0.84914504,  0.73575888,  0.5724067 ]))
```

`f_obs` and `f_exp` are also broadcast. In the following, `f_obs` has shape (6,) and `f_exp` has shape (2, 6), so the result of broadcasting `f_obs` and `f_exp` has shape (2, 6). To compute the desired chi-squared statistics, we must use `axis=1`:

```python
>>> power_divergence([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]))
```

```python
scipy.stats.ks_2samp(data1, data2)
```

Computes 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
- `ddof`: two arrays of sample observations assumed to be drawn from a continuous distribution, sample sizes can be different

**Returns**

- `statistic`: float
KS statistic

\[ pvalue : \text{float} \]

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 p-value 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)
(0.10333333333333333, 0.14498781825751686)
```

For an identical distribution, we cannot reject the null hypothesis since the p-value is high, 41%:

```python
>>> rvs4 = stats.norm.rvs(size=n2, loc=0.0, scale=1.0)
>>> stats.ks_2samp(rvs1, rvs4)
(0.0799999999999996, 0.4112694972985719)
```

**scipy.stats.mannwhitneyu**

```python
(x, y, use_continuity=True)
```

Computes 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.

**Returns**

- **statistic**: float
  - The Mann-Whitney statistics.
- **pvalue**: float
  - One-sided p-value assuming a asymptotic normal distribution.
**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. The reported p-value is for a one-sided hypothesis, to get the two-sided p-value multiply the returned p-value by 2.

```python
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.

---

**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
```

---

```python
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 [R359] 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`. 

---

5.34. Statistical functions (`scipy.stats`) 1467
The default is ‘average’.

An array of length equal to the size of a, containing rank scores.

Notes
All floating point types are converted to numpy.float64 before ranking. This may result in spurious ties if an input array of floats has a wider data type than numpy.float64 (e.g. numpy.float128).

References
[R359]

Examples

```python
>>> from scipy.stats import rankdata
>>> rankdata([0, 2, 3, 2])
array([ 1., 2.5, 4. , 2.5])
```

```python
>>> rankdata([0, 2, 3, 2], method='min')
array([ 1., 2. , 4. , 2.])
```

```python
>>> rankdata([0, 2, 3, 2], method='max')
array([ 1. , 3. , 4. , 3.])
```

```python
>>> rankdata([0, 2, 3, 2], method='dense')
array([ 1., 2., 3., 2.])
```

```python
>>> rankdata([0, 2, 3, 2], method='ordinal')
array([ 1., 2., 4., 3.])
```

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
[R360]

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”, “zsplit”\}, optional

- **“pratt”**: Pratt treatment: includes zero-differences in the ranking process (more conservative)
- **“wilcox”**: Wilcox treatment: discards all zero-differences
- **“zsplit”**: 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**

[R373]

**scipy.stats.kruskal(*args)**

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.

**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**

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**

[R328]

**scipy.stats.friedmanchisquare(*args)**

Computes 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

[R319] scipy.stats.combine_pvalues (pvalues, method='fisher', weights=None)
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
Optional array of weights used only for Stouffer’s Z-score method.

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) [R309] uses a chi-squared statistic to compute a combined p-value. The closely related Stouffer’s Z-score method [R310] 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 [R311] [R312].

Fisher’s method may be extended to combine p-values from dependent tests [R313]. Extensions such as Brown’s method and Kost’s method are not currently implemented.

New in version 0.15.0.

References

[R309], [R310], [R311], [R312], [R313]

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ansari(x, y)</td>
<td>Perform the Ansari-Bradley test for equal scale parameters</td>
</tr>
<tr>
<td>bartlett(*args)</td>
<td>Perform Bartlett’s test for equal variances</td>
</tr>
<tr>
<td>levene(*args, **kwds)</td>
<td>Perform Levene test for equal variances.</td>
</tr>
<tr>
<td>shapiro(x[, a, reta])</td>
<td>Perform the Shapiro-Wilk test for normality.</td>
</tr>
</tbody>
</table>
### Table 5.262 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>anderson(x[, dist])</code></td>
<td>Anderson-Darling test for data coming from a particular distribution</td>
</tr>
<tr>
<td><code>anderson_ksamp(samples[, midrank])</code></td>
<td>The Anderson-Darling test for k-samples.</td>
</tr>
<tr>
<td><code>binom_test(x[, n, p])</code></td>
<td>Perform a test that the probability of success is p.</td>
</tr>
<tr>
<td><code>fligner(*args, **kwds)</code></td>
<td>Perform Fligner’s test for equal variances.</td>
</tr>
<tr>
<td><code>median_test(*args, **kwds)</code></td>
<td>Mood’s median test.</td>
</tr>
<tr>
<td><code>mood(x, y[, axis])</code></td>
<td>Perform Mood’s test for equal scale parameters.</td>
</tr>
</tbody>
</table>

#### `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

**Returns**  
- `statistic`: float  
  Arrays of sample data
- `pvalue`: float  
  The Ansari-Bradley test statistic

**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**

[R300]

#### `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 is more robust.

**Parameters**  
- `sample1, sample2, ...`: array_like

**Returns**  
- `statistic`: float  
  Arrays of sample data. May be different lengths.
- `pvalue`: float  
  The test statistic.

**References**

[R301], [R302]

#### `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 in the case where there are significant deviations from normality.

**Parameters**  
- `sample1, sample2, ...`: array_like
  The sample data, possibly with different lengths
center : {'mean', 'median', 'trimmed'}, optional
Which function of the data to use in the test. 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 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.

**References**

[R330], [R331], [R332]

```python
scipy.stats.shapiro(x, a=None, reta=False)
```

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.
- **a**: array_like, optional
  Array of internal parameters used in the calculation. If these are not given, they will be computed internally. If x has length n, then a must have length n/2.
- **reta**: bool, optional
  Whether or not to return the internally computed a values. The default is False.

**Returns**

- **W**: float
  The test statistic.
- **p-value**: float
  The p-value for the hypothesis test.
- **a**: array_like, optional
  If reta is True, then these are the internally computed “a” values that may be passed into this function on future calls.

**See also:**

anderson The Anderson-Darling test for normality

**References**

[R361]

```python
scipy.stats.anderson(x, dist='norm')
```

Anderson-Darling test for data coming from a particular distribution

The Anderson-Darling test is a modification of the Kolmogorov-Smirnov test kstest for 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
**dist**: `{'norm', 'expon', 'logistic', 'gumbel', 'extreme1'}`, optional
the type of distribution to test against. The default is ‘norm’ and ‘extreme1’
is a synonym for ‘gumbel’

**Returns**

- **statistic**: float
  The Anderson-Darling test statistic
- **critical_values**: list
  The critical values for this distribution
- **significance_level**: list
  The significance levels for the corresponding critical values in percents.
The function returns critical values for a differing set of significance levels depending on the distribution that is being tested against.

**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 A2 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.

**References**

[R293], [R294], [R295], [R296], [R297], [R298]

```python
scipy.stats.anderson_ksamp(samples, midrank=True)
```

The Anderson-Darling test for k-samples.

The k-sample Anderson-Darling test is a modification of the one-sample Anderson-Darling test. It tests the null hypothesis that k-samples are drawn from the same population without having to specify the distribution function of that population. The critical values depend on the number of 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.

**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**

[R299] 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 [R299], 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.

New in version 0.14.0.

References

[R299]

Examples

>>> 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 3.1%:

```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]),
 0.03134990135800783)
```

The null hypothesis cannot be rejected for three samples from an identical distribution. The approximate p-value (87%) has to be computed by extrapolation and may not be very accurate:

```python
>>> stats.anderson_ksamp([np.random.normal(size=50),
...                         np.random.normal(size=30), np.random.normal(size=20)])
(-0.73091722665244196,
 array([-0.44925884, 1.3052767 , 1.9434184 , 2.57696569, 3.41634856]),
 0.8789283903979661)
```

scipy.stats.binom_test (x, n=None, p=0.5)
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

Returns

- p-value : float
  The p-value of the hypothesis test

References

[R303]

scipy.stats.fligner(*args, **kwds)
Perform Fligner’s test for equal variances.
Fligner’s test tests the null hypothesis that all input samples are from populations with equal variances. Fligner’s test is non-parametric in contrast to Bartlett’s test `bartlett` and Levene’s test `levene`.

**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**
- `Xsq`: float
  The test statistic.
- `p-value`: float
  The p-value for the hypothesis test.

**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.

**References**
[R317], [R318]

`scipy.stats.median_test(*args, **kwds)`
Mood’s median test.
Test that two or more samples come from populations with the same median.
Let \( n = \text{len}(\text{args}) \) 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”.
- `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

5.34. Statistical functions (`scipy.stats`)
family to be used instead. See power_divergence for details. Default is 1 (Pearson’s chi-squared statistic).

The test statistic. The statistic that is returned is determined by lambda_. The default is Pearson’s chi-squared statistic.

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.

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

[R334], [R335]

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:

Group 1: 10 14 14 18 20 22 24 25 31 31 32 39 43 43 48 49
Group 2: 28 30 31 33 34 35 36 40 44 55 57 61 91 92 99
Group 3: 0 3 9 22 23 25 25 33 34 34 40 45 46 48 62 67 84

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, 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
>>> 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`.

```python
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 \( \text{axis}=1 \), 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
>>> 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([-5.84332354, -5.6840814 ]), array([5.11694980e-09, 1.31517628e-08]))
```

scipy.stats.boxcox(x, lmbda=None, alpha=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 \( 100 \times (1-alpha)\% \) 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.

\( (\text{min}_{\text{ci}}, \text{max}_{\text{ci}}) \): 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:

\[ y = \frac{x^{\lambda} - 1}{\lambda}, \quad \text{for } \lambda > 0 \]
\[ \log(x), \quad \text{for } \lambda = 0 \]

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
>>> 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)
>>> stats.probplot(xt, dist=stats.norm, plot=ax2)
>>> ax2.set_title('Probplot after Box-Cox transformation')
```

```python
>>> plt.show()
```
scipy.stats.boxcox_normmax(x, brack=(-2.0, 2.0), method='pearsonr')

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.
    - `'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
generate some data and determine optimal lmbda in various ways:
```
```python
>>> lmax_pearsonr = stats.boxcox_normmax(x)

>>> lmax_mle
7.177...
>>> lmax_pearsonr
7.916...
>>> stats.boxcox_normmax(x, method='all')
array([ 7.91667384,  7.17718692])

>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> stats.boxcox_normplot(x, -10, 10, plot=ax)
>>> ax.axvline(lmax_mle, color='r')
>>> ax.axvline(lmax_pearsonr, color='g', ls='--')

>>> plt.show()
```

scipy.stats.boxcox_llf(lmb, data)
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

5.34. Statistical functions (scipy.stats)
Notes

The Box-Cox log-likelihood function is defined here as

\[ llf = (\lambda - 1) \sum \left( \log(x_i) \right) - N/2 \log(\sum (y_i - \bar{y})^2 / N), \]

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)
>>> lmbdas = np.linspace(-2, 10)
>>> llf = np.zeros(lmbdas.shape, dtype=np.float)
>>> for ii, lmbda in enumerate(lmbdas):
...    llf[ii] = stats.boxcox_llf(lmbda, x)
```

Also find the optimal \( \lambda \) value with \texttt{boxcox}:

```python
>>> x_most_normal, lmbda_optimal = stats.boxcox(x)
```

Plot the log-likelihood as function of \( \lambda \). Add the optimal \( \lambda \) value 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 \texttt{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)
```

```python
>>> plt.show()
```
**scipy.stats.entropy** *(pk, 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 $S = -\sum(pk \times \log(pk))$, *axis=0*.

If *qk* is not None, then compute the Kullback-Leibler divergence $S = \sum(pk \times \log(pk / qk))$, *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.

### 5.34.5 Circular statistical functions

- **circmean** *(samples[, high, low, axis])*
  - Compute the circular mean for samples in a range.

- **circvar** *(samples[, high, low, axis])*
  - Compute the circular variance for samples assumed to be in a range.

- **circstd** *(samples[, high, low, axis])*
  - Compute the circular standard deviation for samples assumed to be in the range [low to high].

**scipy.stats.circmean** *(samples, high=6.283185307179586, low=0, axis=None)*

Compute the circular mean for samples in a range.

**Parameters**

- *samples*: array_like
  - Input array.
- *high*: float or int, optional
  - High boundary for circular mean range. Default is $2 \times \pi$.
- *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.

scipy.stats.circvar(samples, high=6.283185307179586, low=0, axis=None)
Compute the circular variance for samples assumed to be in a range

Parameters
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.

Notes
This uses a definition of circular variance that in the limit of small angles returns a number close to the ‘linear’ variance.

scipy.stats.circstd(samples, high=6.283185307179586, low=0, axis=None)
Compute the circular standard deviation for samples assumed to be in the range [low to high].

Parameters
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.

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.

5.34.6 Contingency table functions

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>chi2_contingency(observed[, correction, lambda_])</td>
<td>Chi-square test of independence of variables in a contingency table.</td>
</tr>
<tr>
<td>contingency.expected_freq(observed)</td>
<td>Compute the expected frequencies from a contingency table.</td>
</tr>
<tr>
<td>contingency.margins(a)</td>
<td>Return a list of the marginal sums of the array a.</td>
</tr>
<tr>
<td>fisher_exact(table[, alternative])</td>
<td>Performs a Fisher exact test on a 2x2 contingency table.</td>
</tr>
</tbody>
</table>

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 indepen-
dence of the observed frequencies in the contingency table \[ \text{observed} \]. The expected frequencies are computed based on the marginal sums under the assumption of independence; see \texttt{scipy.stats.contingency.expected_freq}. The number of degrees of freedom is (expressed using numpy functions and attributes):

\[
dof = \text{observed.size} - \text{sum(observed.shape)} + \text{observed.ndim} - 1
\]

**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 \[ \text{R305} \]. \texttt{lambda_} allows a statistic from the Cressie-Read power divergence family \[ \text{R306} \] to be used instead. See \texttt{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 \texttt{observed}
  The expected frequencies, based on the marginal sums of the table.

**See also:**

- \texttt{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 frequency in each cell is 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 \texttt{observed} is two or more. Applying the test to a one-dimensional table will always result in \texttt{expected} equal to \texttt{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 \texttt{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 \texttt{stats.chisquare}. That is, if one calls:

\[
\text{chi2, p, dof, ex} = \text{chi2_contingency}(%s, correction=False)
\]

then the following is true:

\[
(\text{chi2}, \text{p}) = \text{stats.chisquare}(\text{obs.ravel()}, \text{f_exp=ex.ravel()},
\text{ddof=obs.size} - 1 - \text{dof})
\]

The \texttt{lambda_} argument was added in version 0.13.0 of \texttt{scipy}.
References

[R304], [R305], [R306]

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],
      [11, 16]],
     ...
    [[[11, 12],
      [15, 16]],
     ...
    [[[23, 15],
      [30, 22]],
     ...
    [[[14, 17],
      [15, 16]]]])
>>> chi2_contingency(obs)
(8.7584514426741897,
 0.64417725029295503,
 11,
  array([[[ 14.15462386, 14.15462386],
          [ 16.49423111, 16.49423111]],
       [[ 11.2461395 , 11.2461395 ],
          [ 13.10500554, 13.10500554]],
       [[ 19.5591166 , 19.5591166 ],
          [ 22.79202844, 22.79202844]],
       [[ 15.54012004, 15.54012004],
          [ 18.10873492, 18.10873492]])))
```

**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

**Parameters**

- **observed** : array_like
  
The table of observed frequencies. (While this function can handle a 1-D
  
  **Returns**

- **expected** : ndarray of float64
  
  Generally observed is at least 2-D.)
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.],
       [ 13.,  18.,  24.]])
```

```python
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` : list of ndarrays

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
>>> a = np.arange(12).reshape(2, 6)
>>> a
array([[ 0,  1,  2,  3,  4,  5],
       [ 6,  7,  8,  9, 10, 11]])
>>> m0, m1 = margins(a)
>>> m0
array([[15],
       [51]])
>>> m1
array([[ 6,  8, 10, 12, 14, 16]])
```

```python
>>> b = np.arange(24).reshape(2,3,4)
>>> m0, m1, m2 = margins(b)
>>> m0
array([[ 66],
       [[210]])
>>> m1
array([[ 60,  92, 124],
       [124]])
>>> m2
array([[60, 66, 72, 78]])
```

```python
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.

5.34.7 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>Returns the shape parameter that maximizes the probability plot correlation coefficient for the given data to a one-parameter family of distributions.</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[, params, dist, fit, plot])</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>
</tbody>
</table>

`scipy.stats.ppcc_max(x, brack=(0.0, 1.0), dist='tukeylambda')`
Returns the shape parameter that maximizes the probability plot correlation coefficient for the given data to a one-parameter family of distributions.

See also `ppcc_plot`

`scipy.stats.ppcc_plot(x, a, b, dist='tukeylambda', plot=None, N=80)`
Calculate 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**

- **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
  Number of points on the horizontal axis (equally distributed from `a` to `b`).

- **ppcc**: ndarray
  The shape values for which ppcc was calculated.

**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)
>>> stats.probplot(x, plot=ax1)
>>> stats.boxcox_normplot(x, -5, 5, plot=ax2)
>>> stats.ppcc_plot(x, -5, 5, plot=ax3)
>>> ax3.vlines(-0.7, 0, 1, colors='r', label='Expected shape value')
>>> plt.show()
```
SciPy Reference Guide, Release 0.16.0

scipy.stats.probplot(x, sparams=(), dist='norm', fit=True, plot=None)

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
- 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('figname.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

\[
0.5**(1/n), \quad \text{for } i = n
\]
\[
(i - 0.3175) / (n + 0.365), \quad \text{for } i = 2, \ldots, n-1
\]
\[
1 - 0.5**(1/n), \quad \text{for } i = 1
\]

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:

```python
tax1 = plt.subplot(221)
tax1 = plt.subplot(222)
tax1 = plt.subplot(223)
tax1 = plt.subplot(224)
```

A t distribution with larger degrees of freedom:

```python
A mixture of two normal distributions with broadcasting:

```python
A standard normal distribution:

```python
Produce a new figure with a loggamma distribution, using the dist and sparams keywords:

```python
Show the results with Matplotlib:

```python
```
The `scipy.stats.boxcox_normplot` function computes parameters for a Box-Cox normality plot, optionally showing 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.
- **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.

See also:

probplot, boxcox, boxcox_normmax, boxcox_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.

Examples

```python
>>> from scipy import stats
>>> import matplotlib.pyplot as plt

Generate some non-normally distributed data, and create a Box-Cox plot:

```python
>>> x = stats.loggamma.rvs(5, size=500) + 5
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> stats.boxcox_normplot(x, -20, 20, plot=ax)

Determine and plot the optimal lmbda to transform x and plot it in the same plot:

```python
>>> _, maxlog = stats.boxcox(x)
>>> ax.axvline(maxlog, color='r')
```

```python
>>> plt.show()
```
5.34.8 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.

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>argstoaarray(*args)</td>
<td>Constructs a 2D array from a group of sequences.</td>
</tr>
<tr>
<td>betai(a, b, x)</td>
<td>Returns the incomplete beta function.</td>
</tr>
<tr>
<td>chisquare(f_obs[, f_exp, ddof, axis])</td>
<td>Calculates a one-way chi square test.</td>
</tr>
<tr>
<td>count_tied_groups(x[, use_missing])</td>
<td>Counts the number of tied values.</td>
</tr>
<tr>
<td>describe(a[, axis, ddof])</td>
<td>Computes several descriptive statistics of the passed array.</td>
</tr>
<tr>
<td>f_oneway(*args)</td>
<td>Performs a 1-way ANOVA, returning an F-value and probability given an array of input data.</td>
</tr>
<tr>
<td>f_value_wilks_lambda(ER, EF, dfnum, dfden, a, b)</td>
<td>Calculation of Wilks lambda F-statistic for multivariate data, per Maxwell &amp; Delaney p.657.</td>
</tr>
<tr>
<td>find_repeats(arr)</td>
<td>Finds repeats in arr and return a tuple (repeats, repeat_count).</td>
</tr>
<tr>
<td>friedmanchisquare(*args)</td>
<td>Friedman Chi-Square is a non-parametric, one-way within-subjects ANOVA.</td>
</tr>
<tr>
<td>kendalltau(x, y[, use_ties, use_missing])</td>
<td>Computes Kendall’s rank correlation tau on two variables x and y.</td>
</tr>
<tr>
<td>kendalltau_seasonal(x)</td>
<td>Computes a multivariate Kendall’s rank correlation tau, for seasonal data.</td>
</tr>
<tr>
<td>kruskalwallis(*args)</td>
<td>Computes the Kruskal-Wallis H-test for independent samples.</td>
</tr>
<tr>
<td>ks_twosamp(data1, data2[, alternative])</td>
<td>Computes the Kolmogorov-Smirnov test on two samples.</td>
</tr>
<tr>
<td>kurtosis(a[, axis, fisher, bias])</td>
<td>Computes the kurtosis (Fisher or Pearson) of a dataset.</td>
</tr>
<tr>
<td>kurtosistest(a[, axis])</td>
<td>Tests whether a dataset has normal kurtosis.</td>
</tr>
<tr>
<td>linregress(*args)</td>
<td>Calculates the linear regression line.</td>
</tr>
<tr>
<td>mannwhitneyu(x, y[, use_continuity])</td>
<td>Computes the Mann-Whitney statistic.</td>
</tr>
<tr>
<td>plotting_positions(data[, alpha, beta])</td>
<td>Returns plotting positions (or empirical percentile points) for the data.</td>
</tr>
<tr>
<td>mode(a[, axis])</td>
<td>Returns an array of the modal value in the passed array.</td>
</tr>
<tr>
<td>moment(a[, moment, axis])</td>
<td>Calculates the nth moment about the mean for a sample.</td>
</tr>
<tr>
<td>mquantiles(a[, prob, alphap, betap, axis, limit])</td>
<td>Computes empirical quantiles for a data array.</td>
</tr>
<tr>
<td>msign(x)</td>
<td>Returns the sign of x, or 0 if x is masked.</td>
</tr>
<tr>
<td>normaltest(a[, axis])</td>
<td>Tests whether a sample differs from a normal distribution.</td>
</tr>
<tr>
<td>obrientransform(*args)</td>
<td>Performs a transform on input data (any number of columns).</td>
</tr>
<tr>
<td>pearsonr(x, y)</td>
<td>Calculates a Pearson correlation coefficient and the p-value for testing non-correlation.</td>
</tr>
<tr>
<td>plotting_positions(data[, alpha, beta])</td>
<td>Returns plotting positions (or empirical percentile points) for the data.</td>
</tr>
<tr>
<td>pointbiserialr(x, y)</td>
<td>Calculates a point biserial correlation coefficient and the associated p-value.</td>
</tr>
<tr>
<td>rankdata(a[, axis, use_missing])</td>
<td>Returns the rank (also known as order statistics) of each data point along the given axis.</td>
</tr>
<tr>
<td>scoreatpercentile(data, per[, limit, ...])</td>
<td>Calculates the score at the given ‘per’ percentile of the sequence a.</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>signaltonoise(*args, **kwds)</td>
<td>signaltonoise is deprecated!</td>
</tr>
<tr>
<td>skew(a[, axis, bias])</td>
<td>Computes the skewness of a data set.</td>
</tr>
<tr>
<td>skewtest(*args, axis)</td>
<td>Tests whether the skew is different from the normal distribution.</td>
</tr>
<tr>
<td>spearmanr(x, y[, use_ties])</td>
<td>Calculates a Spearman rank-order correlation coefficient and the p-value.</td>
</tr>
<tr>
<td>theilslopes(y[, x, alpha])</td>
<td>Computes the Theil-Sen estimator for a set of points (x, y).</td>
</tr>
<tr>
<td>threshold(a[, threshmin, threshmax, newval])</td>
<td>Clip array to a given value.</td>
</tr>
<tr>
<td>tmax(a, upperlimit[, axis, inclusive])</td>
<td>Compute the trimmed maximum.</td>
</tr>
<tr>
<td>tmean(a[, limits, inclusive])</td>
<td>Compute the trimmed mean.</td>
</tr>
<tr>
<td>tmin(a[, lowerlimit, axis, inclusive])</td>
<td>Compute the trimmed minimum.</td>
</tr>
<tr>
<td>trim(a[, limits, inclusive, relative, axis])</td>
<td>Trims an array by masking the data outside some given limits.</td>
</tr>
<tr>
<td>trimboth(data[, proportiontocut, inclusive, ...])</td>
<td>Trims the smallest and largest data values.</td>
</tr>
<tr>
<td>trimmed_stde(a[, limits, inclusive, axis])</td>
<td>Returns the standard error of the trimmed mean along the given axis.</td>
</tr>
</tbody>
</table>
Table 5.267 – continued from previous page

- **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.
- **tsem** *(a[, limits, inclusive])* Computes the trimmed standard error of the mean.
- **ttest_onesamp** *(a, popmean[, axis])* Calculates the T-test for the mean of ONE group of scores.
- **ttest_ind** *(a, b[, axis])* Calculates the T-test for the means of TWO INDEPENDENT samples of scores.
- **ttest_onesamp** *(a, popmean[, axis])* Calculates the T-test for the mean of ONE group of scores.
- **ttest_rel** *(a, b[, axis])* Calculates the T-test on TWO RELATED samples of scores, a and b.
- **tvar** *(a[, limits, inclusive])* Computes the trimmed variance
- **variation** *(a[, axis])* Computes the coefficient of variation, the ratio of the biased standard deviation to the mean.
- **winsorize** *(a[, limits, inclusive, inplace, axis])* Returns a Winsorized version of the input array.
- **zmap** *(scores, compare[, axis, ddof])* Calculates the relative z-scores.
- **zscore** *(a[, axis, ddof])* Calculates the z score of each value in the sample, relative to the sample

```python
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**

- **args** : sequences

**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.

```python
scipy.stats.mstats.betai(a, b, x)
```
Returns the incomplete beta function.

\[
I_x(a,b) = \frac{1}{B(a,b)} \int_0^x t^{a-1}(1-t)^{b-1} \, dt
\]

where *a*, *b* > 0 and \( B(a,b) = \frac{G(a)G(b)}{G(a+b)} \) where *G(a)* is the gamma function of *a*.

The standard broadcasting rules apply to *a*, *b*, and *x*.

**Parameters**

- **a** : array_like or float > 0
- **b** : array_like or float > 0
- **x** : array_like or float

**Returns**

- **betai** : ndarray

Incomplete beta function.

```python
scipy.stats.mstats.chisquare(f_obs, f_exp=None, ddof=0, axis=0)
```
Calculates 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.

5.34. Statistical functions (scipy.stats) 1495
axis : int or None, optional
The axis of the broadcast result of \(f_{\text{obs}}\) and \(f_{\exp}\) along which to apply
the test. If axis is None, all values in \(f_{\text{obs}}\) 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 \(f_{\text{obs}}\)
  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

[R336], [R337]

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, 0.84914503608460956)
```

With \(f_{\exp}\) 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_obs` and `f_exp` are also broadcast. In the following, `f_obs` has shape (6,) and `f_exp` has shape (2, 6), so the result of broadcasting `f_obs` and `f_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.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, 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.describe(a, axis=0, ddof=0)`

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

**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
>>> ma = np.ma.array(range(6), mask=[0, 0, 0, 1, 1, 1])
>>> describe(ma)
(array(3),
 (0, 2),
 1.0,
1.0,
masked_array(data = 0.0,
   mask = False,
fill_value = 1e+20)
, -1.5)
```

**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.

- **statistic**: float
  - The computed F-value of the test.
- **pvalue**: float
  - The associated p-value from the F-distribution.

**scipy.stats.mstats.f_value_wilks_lambda(ER, EF, dfnum, dfden, a, b)**
Calculation of Wilks lambda F-statistic for multivariate data, per Maxwell & Delaney p.657.

**scipy.stats.mstats.find_repeats(arr)**
Find repeats in arr and return a tuple (repeats, repeat_count). 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.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.

```python
scipy.stats.mstats.kendalltau(x, y, use_ties=True, use_missing=False)
```

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)

**Returns**

- **correlation**: float
  
  Kendall tau

- **pvalue**: float
  
  Approximate 2-side p-value.

```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.

```python
scipy.stats.mstats.kruskalwallis(*args)
```

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.

**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**

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**

[R338]

```python
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.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.
    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

[R339]

scipy.stats.mstats.kurtosistest(a, axis=0)
Tests 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 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

Valid only for n>20. The Z-score is set to 0 for bad entries.

scipy.stats.mstats.linregress(*args)
Calculate a regression line
This computes a 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.

- `stderr : float`
  
  Standard error of the estimate

**Notes**

Missing values are considered pair-wise: if a value is missing in `x`, the corresponding value in `y` is masked.

**Examples**

```python
>>> from scipy import stats
>>> x = np.random.random(10)
>>> y = np.random.random(10)
>>> slope, intercept, r_value, p_value, std_err = stats.linregress(x, y)

# To get coefficient of determination (r_squared)

>>> print("r-squared: ", r_value**2)
r-squared: 0.15286643777
```

**scipy.stats.mstats.mannwhitneyu** *(x, y, use_continuity=True)*

Computes the Mann-Whitney statistic

Missing values in `x` and/or `y` are discarded.

**Parameters**

- `x : sequence`
  
  Input

- `y : sequence`
  
  Input

- `use_continuity : {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.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)
*(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)
*(0,0): $p(k) = (k-1)/n$, piecewise linear function (R, type 5)
*(1/3,1/3): $p(k) = (k-1)/(n+1)$, 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): $p(k) = (k-3/8)/(n+1/4)$, Blom. The resulting quantile estimates are approximately unbiased if $x$ is normally distributed (R type 9)
*(.4,.4): approximately quantile unbiased (Cunnane)
*(.3175,.3175): 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.

```python
scipy.stats.mstats.mode(a, axis=0)
```
Returns an array of the modal (most common) value in the passed array.
If there is more than one such value, only the first 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, 8, 4],
...                [5, 3, 0, 5],
...                [4, 7, 5, 9]])
```
```python
>>> 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:
```python
>>> stats.mode(a, axis=None)
(array([3]), array([3]))
```

```python
scipy.stats.mstats.moment(a, moment=1, axis=0)
```
Calculates the nth moment about the mean for a sample.
Generally used to calculate coefficients of skewness and kurtosis.

**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.

**scipy.stats.mstats.mquantiles**

- `a` : array_like
- `prob` : array_like, optional
- `alphap` : float, optional
- `betap` : float, optional
- `axis` : int, optional
- `limit` : tuple, optional

Computes empirical quantiles for a data array.

Samples quantile are defined by $Q(p) = (1-gamma) \times x[j] + gamma \times x[j+1]$, where $x[j]$ is the $j$-th order statistic, and gamma is a function of $j = \text{floor}(n \times p + m), m = \alpha p + p \times (1 - \alpha - \beta)$ and $g = n \times p + m - j$.

Reinterpreting the above equations to compare to R lead to the equation: $p(k) = (k - \alpha)/n$.

**Typical values of (alphap,betap) are:**

- (0,1): $p(k) = k/n$: linear interpolation of cdf (R type 4)
- (0.5,0.5): $p(k) = (k - 1/2)/n$: piecewise linear function (R type 5)
- (0.0): $p(k) = k/(n+1)$: (R type 6)
- (1,0): $p(k) = (k-1)/(n-1)$: mode[F(x[k])]. (R type 7, R default)
- (1/3,1/3): $p(k) = (k-1/3)/(n+1/3)$: 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): $p(k) = (k-3/8)/(n+1/4)$: Blom. The resulting quantile estimates are approximately unbiased if x is normally distributed (R type 9)
- (0.4,0.4): approximately quantile unbiased (Cunnane)
- (0.35,0.35): 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

[R340], [R341]

Examples

```python
>>> from scipy.stats.mstats import mquantiles
>>> a = np.array([6., 47., 49., 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.]])
>>> mquantiles(data, axis=0, limit=(0, 50))
array([[ 19.2 , 14.6 , 1.45],
[ 40.0, 37.5 , 2.5 ],
[ 42.8 , 40.05, 3.55]])
```

```python
>>> data[:, 2] = -999.
>>> mquantiles(data, axis=0, limit=(0, 50))
masked_array(data =
[[19.2 14.6 --]
[40.0 37.5 --]
[42.8 40.05 --]],
mask =
[[False False True]
[False False True]
[False False True]],
fill_value = 1e+20)
```

scipy.stats.mstats.msign(x)

Returns the sign of x, or 0 if x is masked.

scipy.stats.mstats.normaltest(a, axis=0)

Tests 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 [R342], [R343] test that combines skew and kurtosis to produce an omnibus test of normality.

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.

**References**

[R342], [R343]

`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.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 coefficient 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.

**References**

http://www.statsoft.com/textbook/glosp.html#Pearson%20Correlation

`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 (1−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)
- `(0,5): 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(0) = 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)
\begin{itemize}
\item \((3/8,3/8)\): \( p(k) = (k-3/8)/(n+1/4) \), Blom. The resulting quantile estimates are approximately unbiased if \( x \) is normally distributed (R type 9)
\item \((.4,.4)\) : approximately quantile unbiased (Cunnane)
\item \((.35,.35)\): APL, used with PWM
\item \((.3175, .3175)\): used in scipy.stats.probplot
\end{itemize}

### 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.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.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

**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)
>>> 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.mstats.signaltonoise** *(args, **kwds)*

**signaltonoise** is deprecated! mstats.signaltonoise is deprecated in scipy 0.16.0

Calculates the signal-to-noise ratio, as the ratio of the mean over standard deviation along the given axis.

**Parameters**

- **data**: sequence
  - Input data
**skew**

Computes the skewness of a data set.

For normally distributed data, the skewness should be about 0. A skewness value > 0 means that there is more weight in the left 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  
  - `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**

[R344]

**skewtest**

Tests 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**  
- `a`: array  
  - `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**

The sample size must be at least 8.

**spearmanr**

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 an exact linear 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`: array_like  
  - The length of `x` must be > 2.
y : array_like
    The length of y must be > 2.

use_ties : bool, optional
    Whether the correction for ties should be computed.

Returns

correlation : float
    Spearman correlation coefficient

pvalue : float
    2-tailed p-value.

References


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.

Notes

The implementation of theilslopes follows [R345]. The intercept is not defined in [R345], and here it
is defined as median(y) - medslope*median(x), which is given in [R347]. 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 [R345].

References

[R345], [R346], [R347]

Examples

>>> 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()
```

```python
scipy.stats.mstats.threshold(a, threshmin=None, threshmax=None, newval=0)
```

Clip array to a given value.

Similar to `numpy.clip()`, except that values less than `threshmin` or greater than `threshmax` are replaced by `newval`, instead of by `threshmin` and `threshmax` respectively.

**Parameters**
- `a` : ndarray
  Input data
- `threshmin` : {None, float}, optional
  Lower threshold. If None, set to the minimum value.
- `threshmax` : {None, float}, optional
  Upper threshold. If None, set to the maximum value.
- `newval` : {0, float}, optional

**Returns**
- `threshold` : ndarray
  Value outside the thresholds.

  Returns `a`, with values less than `threshmin` and values greater `threshmax` replaced with `newval`.
scipy.stats.mstats.tmax(a, upperlimit, 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

scipy.stats.mstats.tmean(a, limits=None, inclusive=(True, True))
Compute the trimmed mean.

This function finds the arithmetic mean 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 (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).

**Returns**
- `tmean` : float

scipy.stats.mstats.tmin(a, lowerlimit=None, axis=0, inclusive=True)
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.

**Returns**
- `tmin` : float

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 \( n \times \text{limits}[0] \) th smallest data and the \( n \times \text{limits}[1] \) th largest data are masked, and the total number of unmasked data after trimming is \( n \times (1. - \text{sum(limits)}) \). 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
>>> z = [ 1, 2, 3, 4, 5, 6, 7, 8, 9,10]
>>> trim(z,(3,8))
[--,--, 3, 4, 5, 6, 7, 8,--,--]
>>> trim(z,(0.1,0.2),relative=True)
[--, 2, 3, 4, 5, 6, 7, 8,--,--]
```

```python
scipy.stats.mstats.trim(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.

```python
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 \((1 - 2 \times \text{proportiontocut}) \times n\). 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.

```python
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 \( n \times \text{limits}[0] \) and the values larger than \( n \times \text{limits}[1] \) are masked, and the total number of unmasked data after trimming is \( n \times (1.-\text{sum(limits)}) \). In each case, the value of one limit can be set to None to indicate an open interval. If \( \text{limits} \) 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

**Returns**
- **trimmed_stde** : scalar or ndarray

```python
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 \( n \times \text{limits}[0] \)th smallest data and the \( n \times \text{limits}[1] \)th largest data are masked, and the total number of unmasked data after trimming is \( n \times (1.-\text{sum(limits)}) \). 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.

```python
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 $(1 - \text{proportiontocut}) \times n$. 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.

Returns
trimtail : ndarray
Returned array of same shape as data with masked tail values.

scipy.stats.mstats.tsem(a, limits=None, inclusive=(True, True))
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).

Returns
tsem : float

Notes
tsem uses unbiased sample standard deviation, i.e. it uses a correction factor $n / (n - 1)$.

scipy.stats.mstats.ttest_onesamp(a, popmean, axis=0)
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 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
**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]))

```python
>>> 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, 1.49986458e-04]))

```python
>>> stats.ttest_1samp(rvs.T,[5.0,0.0],axis=1)
(array([-0.68014479, 4.11038784]), array([ 4.99613833e-01, 1.49986458e-04]))

```python
>>> 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.mstats.ttest_ind(a, b, axis=0)`

Calculates 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 [R348]. If False, perform Welch’s t-test, which does not assume equal population variance [R349]. .. versionadded:: 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**

[R348], [R349]
Examples

```python
>>> from scipy import stats
>>> np.random.seed(12345678)

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)
(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, 0.64145827413436174)
>>> 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)
(-0.9982539442782481, 0.3182832709103896)
>>> stats.ttest_ind(rvs1, rvs4, equal_var = False)
(-0.69712570584654099, 0.48716927725402048)
```

T-test with different means, variance, and n:
```
>>> rvs5 = stats.norm.rvs(loc=8, scale=20, size=100)
>>> stats.ttest_ind(rvs1, rvs5)
(-1.4679669854490653, 0.14263895620529152)
>>> stats.ttest_ind(rvs1, rvs5, equal_var = False)
(-0.94365973617132992, 0.3474170334794122)
```

scipy.stats.mstats.ttest_onesamp(a, popmean, axis=0)
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 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

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, -0.04323899]), array([ 4.9961383e-01, 1.49986458e-04]))

>>> stats.ttest_1samp(rvs.T,[5.0,0.0],axis=1)
(array([ 2.77025808, 4.11038784]), array([ 4.99613833e-01, 9.65686743e-01]))

```

```python
scipy.stats.mstats.ttest_rel(a, b, axis=0)
Calculates 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.

**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,

**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**

http://en.wikipedia.org/wiki/T-test#Dependent_t-test
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.mstats.tvar(a, limits=None, inclusive=(True, True))

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).

**Returns**

- **tvar**: float
  Trimmed variance.

**Notes**

tvar computes the unbiased sample variance, i.e. it uses a correction factor \( n / (n - 1) \).

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.

**References**

[R350]

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 \((n*\text{limits}[0])\)th smallest data and the \((n*\text{limits}[1])\)th largest data are masked, and 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.

inclusive : {(True, True) tuple}, optional
Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (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.

```python
scipy.stats.mstats.zmap(scores, compare, axis=0, ddof=0)
```
Calculates the relative z-scores.

Returns 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 asarray 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([-1.00000000, 0.00000000, 0.35355339, 0.70710678])
```

```python
scipy.stats.mstats.zscore(a, axis=0, ddof=0)
```
Calculates 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, 1.07259584, 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 ]])
```

### 5.34.9 Univariate and multivariate kernel density estimation (scipy.stats.kde)

**gaussian_kde**(dataset[, bw_method])
   Representation of a kernel-density estimate using Gaussian kernels.

**class scipy.stats.gaussian_kde**(dataset, bw_method=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.

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 [R322], [R323] for reviews. gaussian_kde uses a rule of thumb, the default is Scott's Rule. Scott's Rule [R320], implemented as scotts_factor, is:

\[ n^{-(1/(d+4))}, \]

with \( n \) the number of data points and \( d \) the number of dimensions. Silverman's Rule [R321], implemented as silverman_factor, is:

\[ (n \times (d + 2) / 4.)^{(-1. / (d + 4))}. \]

Good general descriptions of kernel density estimation can be found in [R320] and [R321], the mathematics for this multi-dimensional implementation can be found in [R320].

References

[R320], [R321], [R322], [R323]

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)
>>> ax.set_xlim([xmin, xmax])
>>> ax.set_ylim([ymin, ymax])
>>> plt.show()
```

### Attributes

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dataset</td>
<td>(ndarray) The dataset with which <code>gaussian_kde</code> was initialized.</td>
</tr>
<tr>
<td>d</td>
<td>(int) Number of dimensions.</td>
</tr>
<tr>
<td>n</td>
<td>(int) Number of datapoints.</td>
</tr>
<tr>
<td>factor</td>
<td>(float) The bandwidth factor, obtained from <code>kde.covariance_factor</code>, with which the covariance matrix is multiplied.</td>
</tr>
<tr>
<td>covariance</td>
<td>(ndarray) The covariance matrix of dataset, scaled by the calculated bandwidth (<code>kde.factor</code>).</td>
</tr>
<tr>
<td>inv_cov</td>
<td>(ndarray) The inverse of <code>covariance</code>.</td>
</tr>
</tbody>
</table>

### Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>evaluate</code></td>
<td>Evaluate the estimated pdf on a set of points.</td>
</tr>
<tr>
<td><code>__call__</code></td>
<td>Evaluate the estimated pdf on a set of points.</td>
</tr>
<tr>
<td><code>integrate_gaussian</code></td>
<td>Multiply estimated density by a multivariate Gaussian and integrate over the whole space.</td>
</tr>
<tr>
<td><code>integrate_box_1d</code></td>
<td>Computes the integral of a 1D pdf between two bounds.</td>
</tr>
<tr>
<td><code>integrate_box</code></td>
<td>Computes the integral of a pdf over a rectangular interval.</td>
</tr>
<tr>
<td><code>integrate_kde</code></td>
<td>Computes the integral of the product of this kernel density estimate with another.</td>
</tr>
<tr>
<td><code>pdf</code></td>
<td>Evaluate the estimated pdf on a provided set of points.</td>
</tr>
<tr>
<td><code>logpdf</code></td>
<td>Evaluate the log of the estimated pdf on a provided set of points.</td>
</tr>
<tr>
<td><code>resample</code></td>
<td>Randomly sample a dataset from the estimated pdf.</td>
</tr>
<tr>
<td><code>set_bandwidth</code></td>
<td>Compute the estimator bandwidth with given method.</td>
</tr>
<tr>
<td><code>covariance_factor</code></td>
<td>Computes the coefficient (<code>kde.factor</code>) that multiplies the data covariance matrix.</td>
</tr>
</tbody>
</table>
gaussian_kde.evaluate(points)
Evaluate the estimated pdf on a set of points.

Parameters points: (# of dimensions, # of points)-array
Alternatively, a (# of dimensions,) vector can be passed in and treated
as a single point.

Returns values: (# 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.

gaussian_kde.__call__(points)
Evaluate the estimated pdf on a set of points.

Parameters points: (# of dimensions, # of points)-array
Alternatively, a (# of dimensions,) vector can be passed in and treated
as a single point.

Returns values: (# 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.

gaussian_kde.integrate_gaussian(mean, cov)
Multiply estimated density by a multivariate Gaussian and integrate over the whole space.

Parameters mean : array_like
A 1-D array, specifying the mean of the Gaussian.

cov : array_like
A 2-D array, specifying the covariance matrix of the Gaussian.

Returns result : scalar
The value of the integral.

Raises ValueError:
If the mean or covariance of the input Gaussian differs from the
KDE’s dimensionality.

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.

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 maximum number of points to use for integration.

The result of the integral.

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.

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.

gaussian_kde.logpdf(x)  
Evaluate the log of the estimated pdf on a provided set of points.

Notes  
See gaussian_kde.evaluate for more details; this method simply returns np.log(gaussian_kde.evaluate(x)).

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 underlying dataset.

Returns: resample : (self.d, size) ndarray  
The sampled dataset.

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()
```

```
Data points (rescaled)
Scott (default)
Silverman
Const (1/3 * Silverman)
```

```
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.
```

For many more stat related functions install the software R and the interface package rpy.

### 5.35 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.

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>argstoarray(*args)</code></td>
<td>Constructs a 2D array from a group of sequences.</td>
</tr>
<tr>
<td><code>betai(a, b, x)</code></td>
<td>Returns the incomplete beta function.</td>
</tr>
<tr>
<td><code>chisquare(f_obs[, f_exp, ddof, axis])</code></td>
<td>Calculates a one-way chi square test.</td>
</tr>
<tr>
<td><code>count_tied_groups(x[, use_missing])</code></td>
<td>Counts the number of tied values.</td>
</tr>
<tr>
<td><code>describe(a[, axis, ddof])</code></td>
<td>Computes several descriptive statistics of the passed array.</td>
</tr>
<tr>
<td><code>f_oneway(*args)</code></td>
<td>Performs a 1-way ANOVA, returning an F-value and probability given an array of one-way data.</td>
</tr>
<tr>
<td><code>f_value_wilks_lambda(ER, EF, dfnum, dfden, a, b)</code></td>
<td>Calculation of Wilks lambda F-statistic for multivariate data, per Maxwell &amp; Delaney p.657.</td>
</tr>
<tr>
<td><code>find_repeats(arr)</code></td>
<td>Find repeats in arr and return a tuple (repeats, repeat_count).</td>
</tr>
<tr>
<td><code>friedmanchisquare(*args)</code></td>
<td>Friedman Chi-Square is a non-parametric, one-way within-subjects ANOVA.</td>
</tr>
<tr>
<td><code>kendalltau(x, y[, use_ties, use_missing])</code></td>
<td>Computes Kendall’s rank correlation tau on two variables x and y.</td>
</tr>
</tbody>
</table>

5.35. Statistical functions for masked arrays (scipy.stats.mstats) 1525
### Table 5.270 – continued from previous page

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>kendalltau_seasonal(x)</code></td>
<td>Computes a multivariate Kendall’s rank correlation tau, for seasonal data.</td>
</tr>
<tr>
<td><code>kruskalwallis(*args)</code></td>
<td>Computes the Kruskal-Wallis H-test for independent samples.</td>
</tr>
<tr>
<td><code>ks_twosamp(data1, data2[, alternative])</code></td>
<td>Computes the Kolmogorov-Smirnovo test on two samples.</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>kurtosistest(a[, axis])</code></td>
<td>Tests whether a dataset has normal kurtosis.</td>
</tr>
<tr>
<td><code>linregress(*args)</code></td>
<td>Calculate a regression line.</td>
</tr>
<tr>
<td><code>mannwhitneyu(x, y[, use_continuity])</code></td>
<td>Computes the Mann-Whitney statistic</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>mode(a[, axis])</code></td>
<td>Returns an array of the modal (most common) value in the passed array.</td>
</tr>
<tr>
<td><code>moment(a[, moment, axis])</code></td>
<td>Calculates the nth moment about the mean for a sample.</td>
</tr>
<tr>
<td><code>mquantiles(a[, prob, alphap, betap, axis, limit])</code></td>
<td>Computes empirical quantiles for a data array.</td>
</tr>
<tr>
<td><code>msign(x)</code></td>
<td>Returns the sign of x, or 0 if x is masked.</td>
</tr>
<tr>
<td><code>normaltest(*args)</code></td>
<td>Tests whether a sample differs from a normal distribution.</td>
</tr>
<tr>
<td><code>obrientransform(*args)</code></td>
<td>Computes a transform on input data (any number of columns).</td>
</tr>
<tr>
<td><code>pearsonr(x, y)</code></td>
<td>Calculates a Pearson correlation coefficient and the p-value for testing no</td>
</tr>
<tr>
<td></td>
<td>correlation.</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>pointbiserialr(x, y)</code></td>
<td>Computes a point biserial correlation coefficient and the associated p-value for testing non-correlation.</td>
</tr>
<tr>
<td><code>rankdata(data[, axis, use_missing])</code></td>
<td>Returns the rank (also known as order statistics) of each data point along a given axis.</td>
</tr>
<tr>
<td><code>scoreatpercentile(data, per[, limit, ...])</code></td>
<td>Calculate the score at the given 'per' percentile of the sequence a.</td>
</tr>
<tr>
<td><code>sem(a[, axis, ddof])</code></td>
<td>Calculates the standard error of the mean of the input array.</td>
</tr>
<tr>
<td><code>signaltonoise(*args, **kwds)</code></td>
<td><code>signaltonoise</code> is deprecated!</td>
</tr>
<tr>
<td><code>skew(a[, axis, bias])</code></td>
<td>Computes the skewness of a data set.</td>
</tr>
<tr>
<td><code>skewtest(a[, axis])</code></td>
<td>Tests whether the skew is different from the normal distribution.</td>
</tr>
<tr>
<td><code>spearmanr(x, y[, use_ties])</code></td>
<td>Calculates a Spearman rank-order correlation coefficient and the p-value for testing non-correlation.</td>
</tr>
<tr>
<td><code>theilslopes(y[, x, alpha])</code></td>
<td>Computes the Theil-Sen estimator for a set of points (x, y).</td>
</tr>
<tr>
<td><code>threshold(a[, threshmin, threshmax, newval])</code></td>
<td>Clip array to a given value.</td>
</tr>
<tr>
<td><code>tmax(a, upperlimit[, axis, inclusive])</code></td>
<td>Compute the trimmed maximum</td>
</tr>
<tr>
<td><code>tmean(a[, limits, inclusive])</code></td>
<td>Compute the trimmed mean.</td>
</tr>
<tr>
<td><code>tmin(a[, lowerlimit, axis, inclusive])</code></td>
<td>Compute the trimmed minimum</td>
</tr>
<tr>
<td><code>trim(a[, limits, inclusive, axis])</code></td>
<td>Trims an array by masking the data outside some given limits.</td>
</tr>
<tr>
<td><code>trimboth(data[, proportiontocut, inclusive, ...])</code></td>
<td>Trims the smallest and largest data values.</td>
</tr>
<tr>
<td><code>trimmed_stde(a[, limits, inclusive, axis])</code></td>
<td>Returns the standard error of the trimmed mean along the given axis.</td>
</tr>
<tr>
<td><code>trimr(a[, limits, inclusive, axis])</code></td>
<td>Trims an array by masking some proportion of the data on each end.</td>
</tr>
<tr>
<td><code>trimtail(data[, proportiontocut, tail, ...])</code></td>
<td>Trims the data by masking values from one tail.</td>
</tr>
<tr>
<td><code>tsem(a[, limits, inclusive])</code></td>
<td>Computes the trimmed standard error of the mean.</td>
</tr>
<tr>
<td><code>tttest_onesamp(a, popmean[, axis])</code></td>
<td>Calculates the T-test for the mean of ONE group of scores.</td>
</tr>
</tbody>
</table>
| `tttest_ind(a, b[, axis])`       | Calculates the T-test for the means of TWO INDEPENDENT samples of.
| `tttest_onesamp(a, popmean[, axis])` | Calculates the T-test for the mean of ONE group of scores.                |
| `tttest_rel(a, b[, axis])`       | Calculates the T-test on TWO RELATED samples of scores, a and b.           |
| `tvar(a[, limits, inclusive])`   | Computes the trimmed variance.                                             |
| `variation(a[, axis])`           | Computes the coefficient of variation, the ratio of the biased standard deviation to the mean. |
| `winsorize(a[, limits, inclusive, inplace, axis])` | Returns a Winsorized version of the input array.                          |
| `zmap(scores, compare[, axis, ddof])` | Calculates the relative z-scores.                                          |
| `zscore(a[, axis, ddof])`        | Calculates the z score of each value in the sample, relative to the sample mean. |

### 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**

- **args**: sequences
SciPy Reference Guide, Release 0.16.0

**Returns**

argstoaarray : 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.betai(a, b, x)

Returns the incomplete beta function.

\[ I_x(a,b) = \frac{1}{B(a,b)} \int_0^x t^{a-1}(1-t)^{b-1} \, dt \]

where a,b > 0 and B(a,b) = G(a)*G(b)/(G(a+b)) where G(a) is the gamma function of a.

The standard broadcasting rules apply to a, b, and x.

**Parameters**

- a : array_like or float > 0
- b : array_like or float > 0
- x : array_like or float

**Returns**

- betai : ndarray
  
  x will be clipped to be no greater than 1.0.

scipy.stats.mstats.chisquare(f_obs, f_exp=None, ddof=0, axis=0)

Calculates 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 chi-square, in which case this test is not appropriate.

References
[R336], [R337]

Examples
When just f_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, 0.84914503608460956)
```

With f_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_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)
```

ddof is the change to make to the default degrees of freedom.

```python
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=1)
(2.0, 0.73575888238467)
```

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, 0.57240674]))
```

f_obs and f_exp are also broadcast. In the following, f_obs has shape (6,) and f_exp has shape (2, 6), so the result of broadcasting f_obs and f_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.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, 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.describe \((a, axis=0, ddof=0)\)
 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

**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
>>> ma = np.ma.array(range(6), mask=[0, 0, 0, 1, 1, 1])

>>> describe(ma)
(array(3),
 (0, 2),
 1.0,
)```
1.0,
mask = False,
fill_value = 1e+20)
,
-1.5)

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.f_value_wilks_lambda(ER, EF, dfnum, dfden, a, b)
Calculation of Wilks lambda F-statistic for multivariate data, per Maxwell & Delaney p.657.

scipy.stats.mstats.find_repeats(arr)
Find repeats in arr and return a tuple (repeats, repeat_count). 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.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.kendalltau(x, y, use_ties=True, use_missing=False)
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)

Returns
correlation : float
Kendall tau

**pvalue**: float

Approximate 2-side p-value.

```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.

```python
scipy.stats.mstats.kruskalwallis(*args)
```

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.

**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**

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**

[R338]

```python
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.

```python
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`.
- **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

[R339]

scipy.stats.mstats.kurtosistest(\(a, axis=0\))

Tests 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 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

Valid only for n>20. The Z-score is set to 0 for bad entries.

scipy.stats.mstats.linregress(*args)

Calculate a regression line

This computes a 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.
- **stderr**: float
  - Standard error of the estimate
Notes
Missing values are considered pair-wise: if a value is missing in x, the corresponding value in y is masked.

Examples
>>> from scipy import stats
>>> x = np.random.random(10)
>>> y = np.random.random(10)
>>> slope, intercept, r_value, p_value, std_err = stats.linregress(x, y)

# To get coefficient of determination (r_squared)

>>> print("r-squared:", r_value**2)
r-squared: 0.15286643777

scipy.stats.mstats.mannwhitneyu(x, y, use_continuity=True)
Computes the Mann-Whitney statistic
Missing values in x and/or y are discarded.

Parameters  
x: sequence
  Input
y: sequence
  Input
use_continuity: {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.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.mode (a, axis=0)
Returns an array of the modal (most common) value in the passed array.

If there is more than one such value, only the first 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

>>> a = np.array([[6, 8, 3, 0],
... [3, 2, 1, 7],
... [8, 1, 8, 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:

>>> stats.mode(a, axis=None)
(array([3]), array([3]))

scipy.stats.mstats.moment (a, moment=1, axis=0)
Calculates the nth moment about the mean for a sample.

Generally used to calculate coefficients of skewness and kurtosis.

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.

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)
- $(1,1)$: $p(k) = (k-1)/(n-1)$: mode[$F(x[k])$]. (R type 7, R default)
- $(1/3,1/3)$: $p(k) = (k-1/3)/(n+1/3)$: Then $p(k) \sim$ 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

**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**

[R340], [R341]

**Examples**

```python
>>> from scipy.stats.mstats import mquantiles
>>> a = np.array([6.0, 47.0, 49.0, 15.0, 42.0, 41.0, 7.0, 39.0, 43.0, 40.0, 36.0])
>>> 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.]]
```

```python
>>> mquantiles(data, axis=0, limit=(0, 50))
array([[ 19.2,  14.6,  1.45],
       [ 40.0,  37.5,  2.5 ],
       [ 42.8,  40.05,  3.55]])
```

```python
>>> data[:, 2] = -999.
```

```python
>>> mquantiles(data, axis=0, limit=(0, 50))
masked_array(data =
             [[ 19.2 14.6 --]
              [40.0 37.5 --]
              [42.8 40.05 --]],
          mask =
             [[False False True]
              [False False True]
              [False False True]],
          fill_value = 1e+20)
```

```python
scipy.stats.mstats.msign(x)
```

Returns the sign of x, or 0 if x is masked.

```python
scipy.stats.mstats.normaltest(a, axis=0)
```

Tests 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 [R342], [R343] test that combines skew and kurtosis to produce an omnibus test of normality.

**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.

**References**

[R342], [R343]

```python
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.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

**Returns**
- \(\text{pearsonr}\) : float
  Pearson’s correlation coefficient, 2-tailed p-value.

**References**
http://www.statsoft.com/textbook/glosp.html#Pearson%20Correlation

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* \((1-\alpha)/(n+1-\alpha-\beta)\), *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 \(p(k) \sim \text{median}[F(x[k])]\). The resulting quantile estimates are approximately median-unbiased regardless of the distribution of \(x\). (R type 8)
- \((3/8,3/8)\) : \(p(k) = (k-3/8)/(n+1/4)\), 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**
- \(\text{data}\) : 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**
- \(\text{positions}\) : MaskedArray
  The calculated plotting positions.
scipy.stats.mstats.pointbiserialr(x, y)
Calculates a point biserial correlation coefficient and the associated 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
Missing values are considered pair-wise: if a value is missing in x, the corresponding value in y is masked.

References
http://en.wikipedia.org/wiki/Point-biserial_correlation_coefficient

Examples
>>> from scipy import stats
>>> a = np.array([0, 0, 0, 1, 1, 1, 1])
>>> b = np.arange(7)
>>> stats.pointbiserialr(a, b)
(0.8660254037844386, 0.011724811003954652)
>>> stats.pearsonr(a, b)
(0.86602540378443871, 0.011724811003954626)
>>> np.corrcoef(a, b)
array([[ 1.00000000, 0.8660254],
       [ 0.8660254 , 1.0000000]])

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.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
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)
>>> 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.mstats.signaltonoise(*args, **kwds)

`signaltonoise` is deprecated! mstats.signaltonoise is deprecated in scipy 0.16.0

Calculates the signal-to-noise ratio, as the ratio of the mean over standard deviation along the given axis.

Parameters

- **data**: sequence
  Input data
- **axis**: int or None, optional
  Axis along which to compute. If None, the computation is performed on a flat version of the array.

scipy.stats.mstats.skew(a, axis=0, bias=True)

Computes the skewness of a data set.

For normally distributed data, the skewness should be about 0. A skewness value > 0 means that there is more weight in the left 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

[R344]

scipy.stats.mstats.skewtest (a, axis=0)

Tests 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

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

The sample size must be at least 8.

scipy.stats.mstats.spearmanr (x, y, use_ties=True)

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 an exact linear 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 : array_like

The length of x must be > 2.

y : array_like

The length of y must be > 2.

use_ties : bool, optional

Whether the correction for ties should be computed.

Returns

correlation : float

Spearman correlation coefficient

pvalue : float

2-tailed p-value.

References


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.

**Notes**

The implementation of theilslopes follows [R345]. The intercept is not defined in [R345], and here it is defined as median(y) - medslope*median(x), which is given in [R347]. 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 [R345].

**References**

[R345], [R346], [R347]

**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-')
```
```python
>>> ax.plot(x, lsq_res[1] + lsq_res[0] * x, 'g-')
>>> plt.show()
```

---

**scipy.stats.mstats.threshold** *(a, threshmin=None, threshmax=None, newval=0)*

Clip array to a given value.

Similar to numpy.clip(), except that values less than `threshmin` or greater than `threshmax` are replaced by `newval`, instead of by `threshmin` and `threshmax` respectively.

**Parameters**

- **a**: ndarray
  - Input data
- **threshmin**: {None, float}, optional
  - Lower threshold. If None, set to the minimum value.
- **threshmax**: {None, float}, optional
  - Upper threshold. If None, set to the maximum value.
- **newval**: {0, float}, optional
  - Value outside the thresholds.

**Returns**

- **threshold**: ndarray
  - Returns `a`, with values less then `threshmin` and values greater `threshmax` replaced with `newval`.

---

**scipy.stats.mstats.tmax** *(a, upperlimit, 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
  - Trimmed maximum value.
**scipy.stats.mstats.tmean**

Compute the trimmed mean.

This function finds the arithmetic mean 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 (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).

**Returns**
- **tmean**: float

**scipy.stats.mstats.tmin**

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.

**Returns**
- **tmin**: float

**scipy.stats.mstats.trim**

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. 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).

---

5.35. Statistical functions for masked arrays (**scipy.stats.mstats**) 1543
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

>>> z = [ 1, 2, 3, 4, 5, 6, 7, 8, 9,10]
>>> trim(z,(3,8))
[--,--, 3, 4, 5, 6, 7, 8,--,--]
>>> trim(z,(0.1,0.2),relative=True)
[--, 2, 3, 4, 5, 6, 7, 8,--,--]

scipy.stats.mstats.trim(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.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.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 $n \times (1.-\text{sum}({\text{limits}}))$. 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.trim(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 $n\times\text{limits[0]}$th smallest data and the $n\times\text{limits[1]}$th largest data are masked, and the total number of unmasked data after trimming is $n\times(1.-\text{sum}({\text{limits}}))$. 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(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 $(1 - \text{proportiontocut}) \times n$. 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.

Returns
trimtail : ndarray
    Returned array of same shape as data with masked tail values.

scipy.stats.mstats.tsem(a, limits=None, inclusive=(True, True))
    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).

Returns
tsem : float

Notes
tsem uses unbiased sample standard deviation, i.e. it uses a correction factor \( n / (n - 1) \).

scipy.stats.mstats.ttest_onesamp(a, popmean, axis=0)
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, \( \text{popmean} \).

Parameters

\( a \) : array_like
    sample observation

\( \text{popmean} \) : 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

Returns

\( \text{statistic} \) : float or array
    t-statistic

\( \text{pvalue} \) : float or array
    two-tailed p-value

Examples

>>> 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.

>>> 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.

>>> stats.ttest_1samp(rvs,[5.0,0.0])
(array([-0.68014479, 4.11038784]), array([ 4.99613833e-01, 1.49986458e-04]))

>>> stats.ttest_1samp(rvs.T,[5.0,0.0],axis=1)
(array([-0.68014479, 4.11038784]), array([ 4.99613833e-01, 1.49986458e-04]))

>>> stats.ttest_1samp(rvs,[[5.0],[0.0]])
scipy.stats.mstats.ttest_ind(a, b, axis=0)

Calculates 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 [R348]. If False, perform Welch’s t-test, which does not assume equal population variance [R349].

**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**

[R348], [R349]

**Examples**

```python
>>> from scipy import stats

>>> np.random.seed(12345678)

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)
(0.26833823296239279, 0.78849443369564776)
```  
```python
>>> stats.ttest_ind(rvs1, rvs2, equal_var = False)
(0.26833823296239279, 0.78849452749500748)
```  
```

**ttest_ind** underestimates p for unequal variances:

```python
>>> rvs3 = stats.norm.rvs(loc=5, scale=20, size=500)
>>> stats.ttest_ind(rvs1, rvs3)
(-0.46580283298287162, 0.64145827413436174)
```  
```python
>>> stats.ttest_ind(rvs1, rvs3, equal_var = False)
(-0.46580283298287162, 0.64149646246569292)
```
When \( n_1 \neq n_2 \), the equal variance t-statistic is no longer equal to the unequal variance t-statistic:

```python
>>> rvs4 = stats.norm.rvs(loc=5, scale=20, size=100)
>>> stats.ttest_ind(rvs1, rvs4)
(-0.9988253944782481, 0.3182832709103896)
>>> stats.ttest_ind(rvs1, rvs4, equal_var=False)
(-0.69712570584654099, 0.48716927725402048)
```

T-test with different means, variance, and \( n \):

```python
>>> rvs5 = stats.norm.rvs(loc=8, scale=20, size=100)
>>> stats.ttest_ind(rvs1, rvs5)
(-1.4679669854490653, 0.14263895620529152)
>>> stats.ttest_ind(rvs1, rvs5, equal_var=False)
(-0.94365973617132992, 0.34744170334794122)
```

**scipy.stats.mstats.ttest_onesamp**\((a, \text{popmean}, \text{axis}=0)\)

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, \( \text{popmean} \).

**Parameters**

- \( a \) : array_like
  sample observation
- \( \text{popmean} \) : 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
- \( \text{axis} \) : int or None, optional
  Axis along which to compute test. If None, compute over the whole array

**Returns**

- \( \text{statistic} \) : float or array
  t-statistic
- \( \text{pvalue} \) : 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, 1.49986458e-04]))
>>> stats.ttest_1samp(rvs.T, [5.0, 0.0], axis=1)
(array([-0.68014479, 4.11038784]), array([4.99613833e-01, 1.49986458e-04]))
>>> stats.ttest_1samp(rvs, [[5.0], [0.0]])
```
scipy.stats.mstats.ttest_rel(a, b, axis=0)

Calculates 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.

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

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

http://en.wikipedia.org/wiki/T-test#Dependent_t-test

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)
```

```python
>>> 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.mstats.tvar(a, limits=None, inclusive=(True, True))

Compute 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

---

5.35. Statistical functions for masked arrays (scipy.stats.mstats) 1549
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).

Returns tvar : float
Trimmed variance.

Notes
tvar computes the unbiased sample variance, i.e. it uses a correction factor \( n / (n - 1) \).

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.

References

[R350]

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 rounded (True) or truncated (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(scores, compare, axis=0, ddof=0)
Calculates the relative z-scores.

Returns 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])
```

Calculates the z score of each value in the sample, relative to the sample mean and standard deviation.

```python
scipy.stats.mstats.zscore(a, axis=0, ddof=0)
```

**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:
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 ]])

5.36 C/C++ integration (scipy.weave)

Warning: This documentation is work-in-progress and unorganized.

5.36.1 C/C++ integration

NOTE: this module is deprecated and will be removed from Scipy before the 1.0 release – use the standalone weave package (‘https://github.com/scipy/weave’) instead.

inline – a function for including C/C++ code within Python
blitz – a function for compiling Numeric expressions to C++

ext_tools – a module that helps construct C/C++ extension modules.
accelerate – a module that inline accelerates Python functions

Note: On Linux one needs to have the Python development headers installed in order to be able to compile things with the weave module. Since this is a runtime dependency these headers (typically in a pythonX.Y-dev package) are not always installed when installing scipy.

```
scipy.weave.inline(code[, arg_names, local_dict, ...])  Inline C/C++ code within Python scripts.
blitz(expr[, local_dict, global_dict, ...])
```

```
Parameters
code : string
```
A string of valid C++ code. It should not specify a return statement. Instead
it should assign results that need to be returned to Python in the return_val.

arg_names : [str], optional
A list of Python variable names that should be transferred from Python into
the C/C++ code. It defaults to an empty string.

local_dict : dict, optional
If specified, it is a dictionary of values that should be used as the local scope
for the C/C++ code. If local_dict is not specified the local dictionary of the
calling function is used.

global_dict : dict, optional
If specified, it is a dictionary of values that should be used as the global
scope for the C/C++ code. If global_dict is not specified, the global dictio-
nary of the calling function is used.

force : {0, 1}, optional
If 1, the C++ code is compiled every time inline is called. This is really only
useful for debugging, and probably only useful if your editing support_code
a lot.

compiler : str, optional
The name of compiler to use when compiling. On windows, it understands
’msvc’ and ‘gcc’ as well as all the compiler names understood by distutils.
On Unix, it’ll only understand the values understood by distutils. (I should
add ‘gcc’ though to this).

On windows, the compiler defaults to the Microsoft C++ compiler. If this
isn’t available, it looks for mingw32 (the gcc compiler).

On Unix, it’ll probably use the same compiler that was used when compil-
ing Python. Cygwin’s behavior should be similar.

verbose : {0,1,2}, optional
Specifies how much information is printed during the compile phase of in-
lining code. 0 is silent (except on windows with msvc where it still prints
some garbage). 1 informs you when compiling starts, finishes, and how
long it took. 2 prints out the command lines for the compilation process
and can be useful if your having problems getting code to work. Its handy
for finding the name of the .cpp file if you need to examine it. verbose has
no effect if the compilation isn’t necessary.

support_code : str, optional
A string of valid C++ code declaring extra code that might be needed by
your compiled function. This could be declarations of functions, classes, or
structures.

headers : [str], optional
A list of strings specifying header files to use when compiling the code.
The list might look like ["<vector>" ,"my_header"] . Note that
the header strings need to be in a form than can be pasted at the end of a
#include statement in the C++ code.

customize : base_info.custom_info, optional
An alternative way to specify support_code, headers, etc. needed by the
function. See scipy.weave.base_info for more details. (not sure
this’ll be used much).

type_converters : [type converters], optional
These guys are what convert Python data types to C/C++ data types. If
you’d like to use a different set of type conversions than the default, specify
them here. Look in the type conversions section of the main documentation
for examples.

auto_downcast : {1,0}, optional
This only affects functions that have numpy arrays as input variables. Setting this to 1 will cause all floating point values to be cast as float instead of double if all the Numeric arrays are of type float. If even one of the arrays has type double or double complex, all variables maintain their standard types.

**newarr_converter** : int, optional
Unused.

**Other Parameters**

Relevant :mod:`distutils` keywords. These are duplicated from Greg Ward’s :class:`distutils.extension.Extension` class for convenience:

- **sources** : [string]
  List of source filenames, relative to the distribution root (where the setup script lives), in Unix form (slash-separated) for portability. Source files may be C, C++, SWIG (.i), platform-specific resource files, or whatever else is recognized by the “build_ext” command as source for a Python extension.

  **Note:** The module_path file is always appended to the front of this list

- **include_dirs** : [string]
  List of directories to search for C/C++ header files (in Unix form for portability).

- **define_macros** : [(name, value)]
  List of macros to define; each macro is defined using a 2-tuple, where ‘value’ is either the string to define it to or None to define it without a particular value (equivalent of “#define FOO” in source or -DFOO on Unix C compiler command line).

- **undef_macros** : [string]
  List of macros to undefine explicitly.

- **library_dirs** : [string]
  List of directories to search for C/C++ libraries at link time.

- **libraries** : [string]
  List of library names (not filenames or paths) to link against.

- **runtime_library_dirs** : [string]
  List of directories to search for C/C++ libraries at run time (for shared extensions, this is when the extension is loaded).

- **extra_objects** : [string]
  List of extra files to link with (e.g. object files not implied by ‘sources’, static libraries that must be explicitly specified, binary resource files, etc.)

- **extra_compile_args** : [string]
  Any extra platform- and compiler-specific information to use when compiling the source files in ‘sources’. For platforms and compilers where “command line” makes sense, this is typically a list of command-line arguments, but for other platforms it could be anything.

- **extra_link_args** : [string]
  Any extra platform- and compiler-specific information to use when linking object files together to create the extension (or to create a new static Python interpreter). Similar interpretation as for ‘extra_compile_args’.

- **export_symbols** : [string]
  List of symbols to be exported from a shared extension. Not used on all platforms, and not generally necessary for Python extensions, which typically export exactly one symbol: “init” + extension_name.

- **swig_opts** : [string]
  Any extra options to pass to SWIG if a source file has the .i extension.

- **depends** : [string]
  List of files that the extension depends on.
language : string
Extension language (i.e. “c”, “c++”, “objc”). Will be detected from the source extensions if not provided.

See also:

distutils.extension.Extension
Describes additional parameters.

scipy.weave.blitz (expr, local_dict=None, global_dict=None, check_size=1, verbose=0, **kw)

Functions

assign_variable_types(variables[...,])
downcast(var_specs) Cast python scalars down to most common type of arrays used.
format_error_msg(errors)
generate_file_name(module_name, module_location)
generate_module(module_string, module_file) generate the source code file. Only overwrite
indent(st, spaces)

Classes

ext_function(name, code_block, args[...])
ext_function_from_specs(name, code_block, ...)
ext_module(name[, compiler])
BIBLIOGRAPHY


[AMG] PyAMG (algebraic multigrid preconditioners/solvers) http://code.google.com/p/pyamg/


[R46] Python package regulargrid by Johannes Buchner, see https://pypi.python.org/pypi регулярная сетка


Bibliography


SciPy Reference Guide, Release 0.16.0


Bibliography 1569


[R340] R statistical software: http://www.r-project.org/


[R340] R statistical software: http://www.r-project.org/


S
scipy.cluster, 267
scipy.cluster.hierarchy, 271
scipy.cluster.vq, 267
scipy.constants, 286
scipy.fftpack, 302
scipy.fftpack.convolve, 316
scipy.integrate, 317
scipy.interpolate, 337
scipy.io, 407
scipy.io.arff, 414
scipy.io.netcdf, 415
scipy.io.wavfile, 413
scipy.linalg, 419
scipy.linalg.blas, 478
scipy.linalg.cython_blas, 592
scipy.linalg.cython_lapack, 596
scipy.linalg.interpolative, 633
scipy.linalg.lapack, 513
scipy.misc, 642
scipy.ndimage, 654
scipy.ndimage.filters, 654
scipy.ndimage.fourier, 666
scipy.ndimage.interpolation, 668
scipy.ndimage.measurements, 673
scipy.ndimage.morphology, 685
scipy.odr, 709
scipy.optimize, 718
scipy.optimize.nonlin, 799
scipy.signal, 801
scipy.sparse, 948
scipy.sparse.csgraph, 1081
scipy.sparse.linalg, 1051
scipy.spatial, 1092
scipy.spatial.distance, 1128
scipy.special, 1143
scipy.stats, 1200
scipy.stats.mstats, 1525
scipy.weave, 1552
scipy.weave.ext_tools, 1555
Symbols

__call__() (scipy.interpolate.Akima1DInterpolator method), 348
__call__() (scipy.interpolate.BPoly method), 354
__call__() (scipy.interpolate.BarycentricInterpolator method), 340
__call__() (scipy.interpolate.BivariateSpline method), 395
__call__() (scipy.interpolate.CloughTocher2DInterpolator method), 360
__call__() (scipy.interpolate.InterpolatedUnivariateSpline method), 374
__call__() (scipy.interpolate.KroghInterpolator method), 341
__call__() (scipy.interpolate.LSQBivariateSpline method), 401
__call__() (scipy.interpolate.LSQSphereBivariateSpline method), 403
__call__() (scipy.interpolate.LSQUnivariateSpline method), 379
__call__() (scipy.interpolate.LinearNDInterpolator method), 359
__call__() (scipy.interpolate.NearestNDInterpolator method), 359
__call__() (scipy.interpolate.PPoly method), 351
__call__() (scipy.interpolate.PchipInterpolator method), 345
__call__() (scipy.interpolate.PiecewisePolynomial method), 343
__call__() (scipy.interpolate.Rbf method), 361
__call__() (scipy.interpolate.RectBivariateSpline method), 366, 389
__call__() (scipy.interpolate.RectSphereBivariateSpline method), 393
__call__() (scipy.interpolate.RegularGridInterpolator method), 365
__call__() (scipy.interpolate.SmoothBivariateSpline method), 396
__call__() (scipy.interpolate.SmoothSphereBivariateSpline method), 399
__call__() (scipy.interpolate.UnivariateSpline method), 369
__call__() (scipy.interpolate.interp1d method), 339
__call__() (scipy.interpolate.interp2d method), 363
__call__() (scipy.optimize.LbfgsInvHessProduct method), 798
__call__() (scipy.sparse.linalg.LinearOperator method), 1019, 1053
__call__() (scipy.stats.gaussian_kde method), 1523
__call__() (scipy.stats.rv_continuous method), 1208
__call__() (scipy.stats.rv_discrete method), 1217

A
A (scipy.signal.lti attribute), 860
A (scipy.signal.StateSpace attribute), 863
A (scipy.signal.TransferFunction attribute), 866
A (scipy.signal.ZerosPolesGain attribute), 868
abcd_normalize() (in module scipy.signal), 842
add_points() (scipy.spatial.ConvexHull method), 1122
add_points() (scipy.spatial.Delaunay method), 1119
add_points() (scipy.spatial.Voronoi method), 1124
add_xi() (scipy.interpolate.BarycentricInterpolator method), 340
adjoint() (scipy.optimize.LbfgsInvHessProduct method), 798
adjoint() (scipy.sparse.linalg.LinearOperator method), 1019, 1053
affine_transform() (in module scipy.ndimage.interpolation), 669
agm() (in module scipy.special), 1192
ai_zeros() (in module scipy.special), 1144
airy (in module scipy.special), 1144
airy_e (in module scipy.special), 1144
Akima1DInterpolator (class in scipy.interpolate), 348
alpha (in module scipy.stats), 1218
anderson() (in module scipy.optimize), 784
anderson() (in module scipy.stats), 1472
anderson_ksamp() (in module scipy.stats), 1473
anglit (in module scipy.stats), 1220
ansari() (in module scipy.stats), 1471
antiderivative() (scipy.interpolate.Akima1DInterpolator method), 349
antiderivative() (scipy.interpolate.BPoly method), 355
antiderivative() (scipy.interpolate.InterpolatedUnivariateSpline method), 374
antiderivative() (scipy.interpolate.LSQUnivariateSpline method), 379
antiderivative() (scipy.interpolate.PchipInterpolator method), 345
antiderivative() (scipy.interpolate.PPoly method), 351
antiderivative() (scipy.interpolate.UnivariateSpline method), 370
append() (scipy.interpolate.PiecewisePolynomial method), 343
approx_fprime() (in module scipy.optimize), 793
approximate_taylor_polynomial() (in module scipy.interpolate), 406
arcsin() (scipy.sparse.bsr_matrix method), 952
arcsin() (scipy.sparse.coo_matrix method), 960
arcsin() (scipy.sparse.csc_matrix method), 967
arcsin() (scipy.sparse.csr_matrix method), 975
arcsine (in module scipy.stats), 1222
arcsinh() (scipy.sparse.bsr_matrix method), 952
arcsinh() (scipy.sparse.coo_matrix method), 960
arcsinh() (scipy.sparse.csc_matrix method), 967
arcsinh() (scipy.sparse.csr_matrix method), 975
arcsinh() (scipy.sparse.dia_matrix method), 982
arctan() (scipy.sparse.bsr_matrix method), 952
arctan() (scipy.sparse.coo_matrix method), 960
arctan() (scipy.sparse.csc_matrix method), 967
arctan() (scipy.sparse.csr_matrix method), 975
arctan() (scipy.sparse.dia_matrix method), 982
arctanh() (scipy.sparse.bsr_matrix method), 952
arctanh() (scipy.sparse.coo_matrix method), 960
arctanh() (scipy.sparse.csc_matrix method), 967
arctanh() (scipy.sparse.csr_matrix method), 975
arctanh() (scipy.sparse.dia_matrix method), 982
argrelextrema() (in module scipy.signal), 934
argrelmax() (in module scipy.signal), 933
argrelmin() (in module scipy.signal), 933
argstoarray() (in module scipy.stats.mstats), 1495, 1526
ArpackError, 1046, 1079
ArpackNoConvergence, 1046, 1079
ascent() (in module scipy.misc), 643
asformat() (scipy.sparse.bsr_matrix method), 952
asformat() (scipy.sparse.coo_matrix method), 960
asformat() (scipy.sparse.csc_matrix method), 967
asformat() (scipy.sparse.csr_matrix method), 975
asformat() (scipy.sparse.dia_matrix method), 982
asformat() (scipy.sparse.dok_matrix method), 988
asformat() (scipy.sparse.lil_matrix method), 994
astype() (scipy.sparse.bsr_matrix method), 952
astype() (scipy.sparse.coo_matrix method), 960
astype() (scipy.sparse.csc_matrix method), 967
astype() (scipy.sparse.csr_matrix method), 975
astype() (scipy.sparse.dia_matrix method), 982
astype() (scipy.sparse.dok_matrix method), 988
astype() (scipy.sparse.lil_matrix method), 994
average() (in module scipy.cluster.hierarchy), 276
B
B (scipy.signal.lti attribute), 860
B (scipy.signal.StateSpace attribute), 863
B (scipy.signal.TransferFunction attribute), 866
B (scipy.signal.ZerosPolesGain attribute), 868
band_stop_obj() (in module scipy.signal), 842
barthann() (in module scipy.signal), 894
bartlett() (in module scipy.signal), 895
bartlett() (in module scipy.stats), 1471
barycentric_interpolate() (in module scipy.interpolate), 345
BarycentricInterpolator (class in scipy.interpolate), 339
basinhopping() (in module scipy.optimize), 752
bayes_mvs() (in module scipy.stats), 1445
bdtr (in module scipy.special), 1155
bdtrc (in module scipy.special), 1156
bdtri (in module scipy.special), 1156
bdtrik (in module scipy.special), 1156
bdtrin (in module scipy.special), 1156
bei (in module scipy.special), 1190
bei_zeros() (in module scipy.special), 1190
beip (in module scipy.special), 1190
beip_zeros() (in module scipy.special), 1190
bellman_ford() (in module scipy.sparse.csgraph), 1010, 1085
ber (in module scipy.special), 1190
ber_zeros() (in module scipy.special), 1190
beroulli (in module scipy.stats), 1399
beroulli() (in module scipy.special), 1193
berp (in module scipy.special), 1190
berp_zeros() (in module scipy.special), 1190
bessel() (in module scipy.signal), 856
besselap() (in module scipy.signal), 842
besselpoly (in module scipy.special), 1152
beta (in module scipy.special), 1170
beta (in module scipy.stats), 1224
betal() (in module scipy.stats.mstats), 1495, 1527
betainc (in module scipy.special), 1170
betaincinv (in module scipy.special), 1170
betaincinv (in module scipy.special), 1170
betaincinv (in module scipy.special), 1170
betaincinv (in module scipy.special), 1170
betaprime (in module scipy.stats), 1226
bi_zeros() (in module scipy.special), 1144
bicgstb() (in module scipy.sparse.linalg), 1024, 1058
bilinear() (in module scipy.signal), 825
binary_closing() (in module scipy.ndimage.morphology), 685
binary_dilation() (in module scipy.ndimage.morphology), 687
binary_erosion() (in module scipy.ndimage.morphology), 688
binary_fill_holes() (in module scipy.ndimage.morphology), 690
binary_hit_or_miss() (in module scipy.ndimage.morphology), 691
binary_opening() (in module scipy.ndimage.morphology), 692
binary_propagation() (in module scipy.ndimage.morphology), 693
binned_statistic() (in module scipy.stats), 1439
binned_statistic_2d() (in module scipy.stats), 1442
binned_statistic_dd() (in module scipy.stats), 1443
binom (in module scipy.special), 1193
binom (in module scipy.stats), 1401
binom_test() (in module scipy.stats), 1474
bisect() (in module scipy.optimize), 749
bisect() (in module scipy.optimize), 766
bisplev() (in module scipy.interpolate), 405
bisplrep() (in module scipy.interpolate), 404
BivariateSpline (class in scipy.interpolate), 394
black_tophat() (in module scipy.ndimage.morphology), 695
blackman() (in module scipy.signal), 897
blackmanharris() (in module scipy.signal), 899
blitz() (in module scipy.weave), 1555
block_diag() (in module scipy.sparse.linalg), 1024, 1058
block_diag() (in module scipy.sparse), 1000
block_diag() (in module scipy.sparse.csr_matrix), 1002
bode() (in module scipy.signal), 875
bode() (scipy.signal.lti attribute), 860
bode() (scipy.signal.StateSpace attribute), 863
bode() (scipy.signal.TransferFunction attribute), 866
bode() (scipy.signal.ZerosPolesGain attribute), 868
butter() (in module scipy.signal), 843
butter() (in module scipy.signal), 844
butterd() (in module scipy.signal), 845
byte_scale() (in module scipy.misc), 644
C
C (scipy.signal.lti attribute), 860
C (scipy.signal.StateSpace attribute), 863
C (scipy.signal.TransferFunction attribute), 866
C (scipy.signal.ZerosPolesGain attribute), 868
C2F() (in module scipy.constants), 300
C2K() (in module scipy.constants), 299
canberra() (in module scipy.spatial.distance), 1109, 1137
cascade() (in module scipy.signal), 928
cauchy (in module scipy.stats), 1232
cayce (in module scipy.sparse.linalg.blas), 480
cbtr (in module scipy.signal), 1198
cce_diff() (in module scipy.fftpack), 314
ccopy (in module scipy.sparse.linalg.blas), 480
cdf() (scipy.stats.rv_continuous method), 1203
cdf() (scipy.stats.rv_discrete method), 1213
cdist() (in module scipy.spatial.distance), 1103, 1131
cdot() (in module scipy.sparse.linalg.blas), 481
cdotu() (in module scipy.sparse.linalg.blas), 481
ceil() (scipy.sparse.bsr_matrix method), 952
ceil() (scipy.sparse.coo_matrix method), 960
ceil() (scipy.sparse.csc_matrix method), 968
ceil() (scipy.sparse.csr_matrix method), 975
cel1() (scipy.sparse.dia_matrix method), 982
center_of_mass() (in module scipy.ndimage.measurements), 674
central_diff_weights() (in module scipy.misc), 644
centroid() (in module scipy.cluster.hierarchy), 276
cg() (in module scipy.sparse.linalg), 1025, 1059
cgbsv (in module scipy.sparse.linalg), 519
Index 1579
diagonal() (scipy.sparse.csc_matrix method), 968
diagonal() (scipy.sparse.csr_matrix method), 976
diagonal() (scipy.sparse.dia_matrix method), 983
diagonal() (scipy.sparse.dok_matrix method), 988
diagonal() (scipy.sparse.lil_matrix method), 994
diags() (in module scipy.sparse), 998
diagsvd() (in module scipy.linalg), 441
diff() (in module scipy.spatial.distance), 1111, 1139
diff() (scipy.sparse.csr_matrix method), 976
diff() (scipy.sparse.dia_matrix method), 983
diff() (scipy.sparse.dok_matrix method), 988
diff() (scipy.sparse.lil_matrix method), 994
differential_evolution() (in module scipy.optimize), 746, 758
digamma (in module scipy.special), 1171
dijkstra() (in module scipy.sparse.csgraph), 1008, 1084
dimpulse() (in module scipy.signal), 877
diric() (in module scipy.special), 1193
dirichlet (in module scipy.stats), 1394
distance_matrix() (in module scipy.spatial), 1126
distance_transform_bf() (in module scipy.ndimage.morphology), 696
distance_transform_cdt() (in module scipy.ndimage.morphology), 697
distance_transform_edt() (in module scipy.ndimage.morphology), 697
dlarmch (in module scipy.linalg.lapack), 582
dlange (in module scipy.linalg.lapack), 591
dlaplace (in module scipy.stats), 1405
dlarf (in module scipy.linalg.lapack), 560
dlarfg (in module scipy.linalg.lapack), 562
dlartg (in module scipy.linalg.lapack), 562
dlasd4 (in module scipy.linalg.lapack), 563
dlswp (in module scipy.linalg.lapack), 564
dlauum (in module scipy.linalg.lapack), 565
dlscal (in module scipy.linalg.blas), 484
dok_matrix (class in scipy.sparse), 986
dorghr (in module scipy.linalg.lapack), 583
dorgqr (in module scipy.linalg.lapack), 584
dormqr (in module scipy.linalg.lapack), 584
dot() (scipy.optimize.LbfgsInvHessProduct method), 798
dot() (scipy.sparse.bsr_matrix method), 953
dot() (scipy.sparse.coo_matrix method), 960
dot() (scipy.sparse.csc_matrix method), 968
dot() (scipy.sparse.csr_matrix method), 976
dot() (scipy.sparse.dia_matrix method), 983
dot() (scipy.sparse.dok_matrix method), 988
dot() (scipy.sparse.lil_matrix method), 994
dot() (scipy.sparse.linalg.LinearOperator method), 1019, 1053
dpbsv (in module scipy.linalg.lapack), 566
dpbtrs (in module scipy.linalg.lapack), 567
dpsov (in module scipy.linalg.lapack), 568
dpotf (in module scipy.linalg.lapack), 570
dpotri (in module scipy.linalg.lapack), 571
dpotrs (in module scipy.linalg.lapack), 572
dptsv (in module scipy.linalg.lapack), 581
drot (in module scipy.linalg.blas), 484
drotg (in module scipy.linalg.blas), 485
drotm (in module scipy.linalg.blas), 485
drotmg (in module scipy.linalg.blas), 485
dsbenv (in module scipy.linalg.lapack), 585
dsbvdx (in module scipy.linalg.lapack), 586
dscal (in module scipy.linalg.lapack), 485
dst() (in module scipy.fftpack), 309
dstep() (in module scipy.signal), 878
dswap (in module scipy.linalg.blas), 486
dsyev (in module scipy.linalg.lapack), 587
dsyevd (in module scipy.linalg.lapack), 588
dsyevr (in module scipy.linalg.lapack), 588
dsygv (in module scipy.linalg.lapack), 589
dsygvd (in module scipy.linalg.lapack), 590
dsygdx (in module scipy.linalg.lapack), 591
dsymm (in module scipy.linalg.blas), 509
dsymv (in module scipy.linalg.blas), 499
dyr (in module scipy.linalg.blas), 499
dyr2 (in module scipy.linalg.blas), 500
dyr2k (in module scipy.linalg.blas), 509
dsyrk (in module scipy.linalg.blas), 509
dtrmv (in module scipy.linalg.blas), 499
dtrsv (in module scipy.linalg.blas), 574
dtrtri (in module scipy.linalg.lapack), 575
dtrtrs (in module scipy.linalg.lapack), 576
dweibull (in module scipy.stats), 1242
dzasum (in module scipy.linalg.blas), 486
dznrm2 (in module scipy.linalg.blas), 486

eig() (in module scipy.linalg), 432
eig_banded() (in module scipy.linalg), 435
eigh() (in module scipy.linalg), 433
eigs() (in module scipy.linalg), 1035, 1068
eighsh () (in module scipy.linalg), 1037, 1070
eigvals() (in module scipy.linalg), 432
eigvals_banded() (in module scipy.linalg), 436
eigvalsh() (in module scipy.linalg), 434
eigvalsh() (in module scipy.linalg), 434
eliminate_zeros() (scipy.sparse.bsr_matrix method), 953
eliminate_zeros() (scipy.sparse.csc_matrix method), 968
eliminate_zeros() (scipy.sparse.csr_matrix method), 976
ellip() (in module scipy.signal), 853
ellip_harm() (in module scipy.special), 1177
ellip_harm_2() (in module scipy.special), 1178
ellip_normal() (in module scipy.special), 1179
ellipap() (in module scipy.signal), 843
ellipe() (in module scipy.special), 1146
ellipeinc() (in module scipy.special), 1147
ellipj() (in module scipy.special), 1145
get_window() (in module scipy.signal), 893
getcol() (scipy.sparse.bsr_matrix method), 953
getcol() (scipy.sparse.coo_matrix method), 961
getcol() (scipy.sparse.cs_matrix method), 969
getcol() (scipy.sparse.cs_matrix method), 976
getcol() (scipy.sparse.dia_matrix method), 983
getcol() (scipy.sparse.dok_matrix method), 989
getcol() (scipy.sparse.lil_matrix method), 994
getdata() (scipy.sparse.bsr_matrix method), 953
getdata() (scipy.sparse.coo_matrix method), 961
getdata() (scipy.sparse.csc_matrix method), 969
getdata() (scipy.sparse.csr_matrix method), 977
getdata() (scipy.sparse.dia_matrix method), 983
getdata() (scipy.sparse.dok_matrix method), 989
getdata() (scipy.sparse.lil_matrix method), 994
getH() (scipy.sparse.bsr_matrix method), 953
getH() (scipy.sparse.coo_matrix method), 961
getH() (scipy.sparse.csc_matrix method), 969
getH() (scipy.sparse.csr_matrix method), 976
geth() (scipy.sparse.dia_matrix method), 983
getH() (scipy.sparse.dok_matrix method), 989
getH() (scipy.sparse.lil_matrix method), 994
getmaxprint() (scipy.sparse.bsr_matrix method), 953
getmaxprint() (scipy.sparse.coo_matrix method), 961
getmaxprint() (scipy.sparse.csc_matrix method), 969
getmaxprint() (scipy.sparse.csr_matrix method), 977
getmaxprint() (scipy.sparse.dia_matrix method), 983
getmaxprint() (scipy.sparse.dok_matrix method), 989
getmaxprint() (scipy.sparse.lil_matrix method), 994
getnnz() (scipy.sparse.bsr_matrix method), 953
getnnz() (scipy.sparse.coo_matrix method), 961
getnnz() (scipy.sparse.csc_matrix method), 969
getnnz() (scipy.sparse.csr_matrix method), 977
getnnz() (scipy.sparse.dia_matrix method), 983
getnnz() (scipy.sparse.dok_matrix method), 989
getnnz() (scipy.sparse.lil_matrix method), 994
getrow() (scipy.sparse.bsr_matrix method), 953
getrow() (scipy.sparse.coo_matrix method), 961
getrow() (scipy.sparse.csc_matrix method), 969
getrow() (scipy.sparse.csr_matrix method), 977
getrow() (scipy.sparse.dok_matrix method), 983
getrow() (scipy.sparse.lil_matrix method), 994
getrowview() (scipy.sparse.lil_matrix method), 995
getValue() (scipy.io.netcdf.netcdf_variable method), 418
gilbrat (in module scipy.stats), 1288
gmean() (in module scipy.stats), 1426
gmres() (in module scipy.sparse.linalg), 1027, 1060
golden() (in module scipy.optimize), 749
gomperzt (in module scipy.stats), 1290
grey_closing() (in module scipy.ndimage.morphology), 701
grey_dilation() (in module scipy.ndimage.morphology), 701
grey_erosion() (in module scipy.ndimage.morphology), 703
grey_opening() (in module scipy.ndimage.morphology), 704
griddata() (in module scipy.interpolate), 356
group_delay() (in module scipy.signal), 831
gumbel_l (in module scipy.stats), 1294

gumbel_r (in module scipy.stats), 1292

H

H (scipy.optimize.LbfsInvHessProduct attribute), 797
h1vp() (in module scipy.special), 1153
h2vp() (in module scipy.special), 1153
hadamard() (in module scipy.linalg), 470
halfcauchy (in module scipy.stats), 1296
halfgennorm (in module scipy.stats), 1302
halflogistic (in module scipy.stats), 1298
halfnorm (in module scipy.stats), 1300
hamming() (in module scipy.signal), 914
hamming() (in module scipy.spatial.distance), 1111, 1139
hankel() (in module scipy.linalg), 471
hankel1 (in module scipy.special), 1148
hankel1e (in module scipy.special), 1148
hankel2 (in module scipy.special), 1149
hankel2e (in module scipy.special), 1149
hann() (in module scipy.signal), 916
has_key() (scipy.optimize.OptimizeResult method), 724
has_key() (scipy.sparse.bsr_matrix method), 989
has_key() (scipy.sparse.coo_matrix method), 989
has_key() (scipy.sparse.csc_matrix method), 966
has_key() (scipy.sparse.csr_matrix method), 973

helmert() (in module scipy.linalg), 471
hermite() (in module scipy.special), 1182
hermitenorm() (in module scipy.special), 1182
hessenberg() (in module scipy.linalg), 456
hilbert() (in module scipy.fftpack), 312
hilbert() (in module scipy.linalg), 472
hilbert() (in module scipy.signal), 822
hilbert2() (in module scipy.signal), 823

histogram() (in module scipy.ndimage.measurements), 676

histogram() (in module scipy.stats), 1436
histogram2() (in module scipy.stats), 1435
hmean() (in module scipy.stats), 1427
hstack() (in module scipy.sparse), 1003
huber (in module scipy.special), 1168
hyp0f1() (in module scipy.special), 1183
hyp1f1() (in module scipy.special), 1182
hyp1f2() (in module scipy.special), 1183
hyp2f0 (in module scipy.special), 1183
hyp2f1 (in module scipy.special), 1182
hyp3f0 (in module scipy.special), 1183
hypergeom (in module scipy.stats), 1409
hyperu (in module scipy.special), 1183
hypsecant (in module scipy.stats), 1304

i0 (in module scipy.special), 1151
i0e (in module scipy.special), 1151
i1 (in module scipy.special), 1151
i1e (in module scipy.special), 1151
icamax (in module scipy.linalg.blas), 486
id_to_svd() (in module scipy.linalg.interpolative), 636
idmax (in module scipy.linalg.blas), 487
idct() (in module scipy.fftpack), 308
identity() (in module scipy.sparse), 997
ifft() (in module scipy.fft), 304
ifft2() (in module scipy.fft), 304
ifftn() (in module scipy.fftpack), 305
iirfilter() (in module scipy.signal), 833
ihilbert() (in module scipy.signal), 834
imfiter() (in module scipy.misc), 648
impulse() (in module scipy.signal), 872
interp() (scipy.signal.lti method), 862
interpolate() (scipy.signal.lti method), 865
interp1d (class in scipy.interpolate), 337
interp2d (class in scipy.interpolate), 361
integrate() (scipy.integrate.complex_ode method), 335
integral() (scipy.interpolate.UnivariateSpline method), 397
integral() (scipy.interpolate.UnivariateSpline method), 371
integrate() (scipy.interpolate.ode method), 336
integral() (scipy.interpolate.BPoly method), 355
integral() (scipy.interpolate.PPoly method), 351
integrate_box() (scipy.stats.gaussian_kde method), 1523
integrate_box_1d() (scipy.stats.gaussian_kde method), 1523
integrate_gaussian() (scipy.stats.gaussian_kde method), 1523
interpn() (in module scipy.interpolate), 363
InterpolatedUnivariateSpline (class in scipy.interpolate), 372
interval() (scipy.stats.rv_continuous method), 1207
interval() (scipy.stats.rv_discrete method), 1216
inver() (in module scipy.linalg), 419
inv() (in module scipy.sparse.linalg), 1021, 1054
invgamma (in module scipy.stats), 1306
invgamma (in module scipy.stats), 1308
invhilbert() (in module scipy.linalg), 472
invpascal() (in module scipy.linalg), 474
invres() (in module scipy.signal), 840
invresz() (in module scipy.signal), 841
inweibull (in module scipy.stats), 1310
inweibulliu (in module scipy.stats), 1397
ihfft() (in module scipy.fft), 306
is_isomorphic() (in module scipy.cluster.hierarchy), 285
is_leaf() (scipy.cluster.hierarchy.ClusterNode method), 283
is_monotonic() (in module scipy.cluster.hierarchy), 285
is_valid_dm() (in module scipy.spatial.distance), 1108, 1136
is_valid_dm() (in module scipy.spatial.distance), 1108, 1136
is_valid_im() (in module scipy.cluster.hierarchy), 284
is_valid_linkage() (in module scipy.cluster.hierarchy), 285
is_valid_y() (in module scipy.spatial.distance), 1108, 1136
is_valid_y() (in module scipy.spatial.distance), 1108, 1136
issparse() (in module scipy.sparse), 1005
issparse() (in module scipy.sparse), 1005
isspmatrix() (in module scipy.sparse), 1005
isspmatrix() (in module scipy.sparse), 1005
isspmatrix_bsr() (in module scipy.sparse), 1005
isspmatrix_bsr() (in module scipy.sparse), 1005
isspmatrix_coo() (in module scipy.sparse), 1005
isspmatrix_csc() (in module scipy.sparse), 1005
isspmatrix_csr() (in module scipy.sparse), 1005

1586  Index
<table>
<thead>
<tr>
<th>Function/Method</th>
<th>Module/Package</th>
<th>Pages</th>
</tr>
</thead>
<tbody>
<tr>
<td>laguerre()</td>
<td>scipy.special</td>
<td>1182</td>
</tr>
<tr>
<td>lambda2nu()</td>
<td>scipy.constants</td>
<td>302</td>
</tr>
<tr>
<td>lambertw()</td>
<td>scipy.special</td>
<td>1196</td>
</tr>
<tr>
<td>laplace()</td>
<td>scipy.stats</td>
<td>1320</td>
</tr>
<tr>
<td>laplace()</td>
<td>scipy.ndimage.filters</td>
<td>661</td>
</tr>
<tr>
<td>laplacian()</td>
<td>scipy.sparse.csgraph</td>
<td>1006, 1082</td>
</tr>
<tr>
<td>leaders()</td>
<td>scipy.cluster.hierarchy</td>
<td>273</td>
</tr>
<tr>
<td>leafsize</td>
<td>scipy.spatial.cKDTree</td>
<td>1098</td>
</tr>
<tr>
<td>leastsq()</td>
<td>scipy.optimize</td>
<td>750</td>
</tr>
<tr>
<td>leaves_list()</td>
<td>scipy.cluster.hierarchy</td>
<td>284</td>
</tr>
<tr>
<td>legendre()</td>
<td>scipy.special</td>
<td>1181</td>
</tr>
<tr>
<td>lena()</td>
<td>scipy.misc</td>
<td>651</td>
</tr>
<tr>
<td>leslie()</td>
<td>scipy.linalg</td>
<td>473</td>
</tr>
<tr>
<td>levene()</td>
<td>scipy.stats</td>
<td>1471</td>
</tr>
<tr>
<td>lfilter()</td>
<td>scipy.signal</td>
<td>813</td>
</tr>
<tr>
<td>lfilter_zi()</td>
<td>scipy.signal</td>
<td>814</td>
</tr>
<tr>
<td>lfilter()</td>
<td>scipy.signal</td>
<td>814</td>
</tr>
<tr>
<td>lgmres()</td>
<td>scipy.sparse.linalg</td>
<td>1028, 1062</td>
</tr>
<tr>
<td>lift_points()</td>
<td>scipy.spatial.Delaunay</td>
<td>1120</td>
</tr>
<tr>
<td>lil_matrix</td>
<td>scipy.sparse</td>
<td>992</td>
</tr>
<tr>
<td>line_search()</td>
<td>scipy.optimize</td>
<td>795</td>
</tr>
<tr>
<td>linearmixing()</td>
<td>scipy.optimize</td>
<td>786</td>
</tr>
<tr>
<td>LinearNDInterpolator()</td>
<td>scipy.interpolate</td>
<td>358</td>
</tr>
<tr>
<td>LinearOperator()</td>
<td>scipy.sparse.linalg</td>
<td>1018, 1051</td>
</tr>
<tr>
<td>linkage()</td>
<td>scipy.cluster.hierarchy</td>
<td>274</td>
</tr>
<tr>
<td>linprog()</td>
<td>scipy.optimize</td>
<td>788</td>
</tr>
<tr>
<td>linregress()</td>
<td>scipy.stats</td>
<td>1454</td>
</tr>
<tr>
<td>linregress()</td>
<td>scipy.stats.mstats</td>
<td>1500, 1532</td>
</tr>
<tr>
<td>lmbdat()</td>
<td>scipy.optimize</td>
<td>1149</td>
</tr>
<tr>
<td>loadarff()</td>
<td>scipy.io.arff</td>
<td>414</td>
</tr>
<tr>
<td>loadmat()</td>
<td>scipy.io.arff</td>
<td>407</td>
</tr>
<tr>
<td>lobpcg()</td>
<td>scipy.sparse.linalg</td>
<td>1039, 1073</td>
</tr>
<tr>
<td>log1p()</td>
<td>scipy.sparse.linalg</td>
<td>1199</td>
</tr>
<tr>
<td>log1p()</td>
<td>scipy.sparse.bsr_matrix</td>
<td>954</td>
</tr>
<tr>
<td>log1p()</td>
<td>scipy.sparse.coo_matrix</td>
<td>961</td>
</tr>
<tr>
<td>log1p()</td>
<td>scipy.sparse.csc_matrix</td>
<td>969</td>
</tr>
<tr>
<td>log1p()</td>
<td>scipy.sparse.csr_matrix</td>
<td>977</td>
</tr>
<tr>
<td>log1p()</td>
<td>scipy.sparse.dia_matrix</td>
<td>983</td>
</tr>
<tr>
<td>log_ndtr()</td>
<td>scipy.special</td>
<td>983</td>
</tr>
<tr>
<td>logcdf()</td>
<td>scipy.stats</td>
<td>1164</td>
</tr>
<tr>
<td>logcdf()</td>
<td>scipy.stats RV continuous method</td>
<td>1204</td>
</tr>
<tr>
<td>loggamma()</td>
<td>scipy.stats</td>
<td>1213</td>
</tr>
<tr>
<td>logit()</td>
<td>scipy.stats</td>
<td>1322</td>
</tr>
<tr>
<td>loglaplace()</td>
<td>scipy.stats</td>
<td>1165</td>
</tr>
<tr>
<td>logm()</td>
<td>scipy.linalg</td>
<td>1326</td>
</tr>
<tr>
<td>lognorm()</td>
<td>scipy.stats</td>
<td>458</td>
</tr>
<tr>
<td>logpdf()</td>
<td>scipy.stats gaussian_kde</td>
<td>1328</td>
</tr>
<tr>
<td>logpdf()</td>
<td>scipy.stats RV continuous method</td>
<td>1524</td>
</tr>
<tr>
<td>logpmf()</td>
<td>scipy.stats RV discrete method</td>
<td>1203</td>
</tr>
<tr>
<td>logser()</td>
<td>scipy.stats</td>
<td>1411</td>
</tr>
<tr>
<td>logsf()</td>
<td>scipy.stats RV continuous method</td>
<td>1204</td>
</tr>
<tr>
<td>logsf()</td>
<td>scipy.stats RV discrete method</td>
<td>1213</td>
</tr>
<tr>
<td>logsumexp()</td>
<td>scipy.misc</td>
<td>652</td>
</tr>
<tr>
<td>lomax()</td>
<td>scipy.stats</td>
<td>1330</td>
</tr>
<tr>
<td>lombscargle()</td>
<td>scipy.signal</td>
<td>946</td>
</tr>
<tr>
<td>lp2bp()</td>
<td>scipy.signal</td>
<td>843</td>
</tr>
<tr>
<td>lp2bs()</td>
<td>scipy.signal</td>
<td>843</td>
</tr>
<tr>
<td>lp2hp()</td>
<td>scipy.signal</td>
<td>844</td>
</tr>
<tr>
<td>lp2lp()</td>
<td>scipy.signal</td>
<td>844</td>
</tr>
<tr>
<td>lpmn()</td>
<td>scipy.special</td>
<td>1176</td>
</tr>
<tr>
<td>lpmv()</td>
<td>scipy.special</td>
<td>1174</td>
</tr>
<tr>
<td>lqn()</td>
<td>scipy.special</td>
<td>1176</td>
</tr>
<tr>
<td>lqmn()</td>
<td>scipy.special</td>
<td>1177</td>
</tr>
<tr>
<td>lsim()</td>
<td>scipy.signal</td>
<td>871</td>
</tr>
<tr>
<td>lsim2()</td>
<td>scipy.signal</td>
<td>872</td>
</tr>
<tr>
<td>lsmr()</td>
<td>scipy.sparse.linalg</td>
<td>1033, 1067</td>
</tr>
<tr>
<td>LSQBivariateSpline()</td>
<td>scipy.interpolate</td>
<td>400</td>
</tr>
<tr>
<td>lsq()</td>
<td>scipy.sparse.linalg</td>
<td>1031, 1065</td>
</tr>
<tr>
<td>LSQSphereBivariateSpline()</td>
<td>scipy.interpolate</td>
<td>402</td>
</tr>
<tr>
<td>LSQUnivariateSpline()</td>
<td>scipy.interpolate</td>
<td>376</td>
</tr>
<tr>
<td>lstsq()</td>
<td>scipy.linalg</td>
<td>427</td>
</tr>
<tr>
<td>lti()</td>
<td>scipy.signal</td>
<td>859</td>
</tr>
<tr>
<td>lu()</td>
<td>scipy.sparse.linalg</td>
<td>438</td>
</tr>
<tr>
<td>lu_factor()</td>
<td>scipy.sparse.linalg</td>
<td>438</td>
</tr>
<tr>
<td>lu_solve()</td>
<td>scipy.sparse.linalg</td>
<td>439</td>
</tr>
</tbody>
</table>

**Index**

- m (scipy.spatial.cKDTree attribute), 1098
- mahalanobis() (scipy.spatial.distance), 1112, 1140
- mannwhitneyu() (scipy.stats), 1466
- manswhitneyu() (scipy.stats.mstats), 1501, 1533
- map_coordinates() (scipy.ndimage.interpolation), 670
- margins() (scipy.stats.contingency), 1487
- matching() (scipy.spatial.distance), 1112, 1140
- mathieua (scipy.special), 1184
- mathieub (scipy.special), 1184
- mathieuc (scipy.special), 1185
- mathieu_even_coef() (scipy.special), 1185
- mathieu_modcem1 (scipy.special), 1188
- mathieu_modcem2 (scipy.special), 1186
- mathieu_modsem1 (scipy.special), 1186
- mathieu_modsem2 (scipy.special), 1186
- mathieuodd_coef() (scipy.special), 1185
- mathieusem (scipy.special), 1185
- matmat() (scipy.optimize.LbfgsInvHessProduct method), 798
- matmat() (scipy.sparse.bsr_matrix method), 954
- matmat() (scipy.sparse.linalg.LinearOperator method), 1019, 1053
- matvec() (scipy.optimize.LbfgsInvHessProduct method), 798

1588
Index

1589
n (scipy.spatial.cKDTree attribute), 1098
nakagami (in module scipy.stats), 1336
nanmean() (in module scipy.stats), 1433
nanmedian() (in module scipy.stats), 1434
nanstd() (in module scipy.stats), 1433
nbdtr (in module scipy.special), 1159
nbdtrc (in module scipy.special), 1159
nbdtrik (in module scipy.special), 1159
nbinom (in module scipy.stats), 1413
ncf (in module scipy.stats), 1340
ncfdr (in module scipy.special), 1160
ncfdrifd (in module scipy.special), 1161
ncfdtrif (in module scipy.special), 1161
ncfdtrifd (in module scipy.special), 1161
ncfdtric (in module scipy.special), 1161
ncfdtrinc (in module scipy.special), 1161
nct (in module scipy.stats), 1342
nctdtr (in module scipy.special), 1161
nctdtrid (in module scipy.special), 1163
nctdtric (in module scipy.special), 1163
nctdtrinc (in module scipy.special), 1163
nx2 (in module scipy.stats), 1338
ndt (in module scipy.stats), 1164
ndtr (in module scipy.special), 1165
NearestNDInterpolator (class in scipy.interpolate), 359
netcdf_file (class in scipy.io.netcdf), 415
netcdf_variable (class in scipy.io.netcdf), 417
newton() (in module scipy.optimize), 767
newton_krylov() (in module scipy.optimize), 783
nnlf() (scipy.stats.rv_continuous method), 1209
nnls() (in module scipy.optimize), 752
nnz (scipy.sparse.coo_matrix attribute), 958
nnz (scipy.sparse.csc_matrix attribute), 965
nnz (scipy.sparse.csr_matrix attribute), 973
nnz (scipy.sparse.dia_matrix attribute), 980
nnz (scipy.sparse.lil_matrix attribute), 993
nnz (scipy.sparse.linalg.SuperLU attribute), 1045, 1078
nonzero() (scipy.sparse.bsr_matrix method), 954
nonzero() (scipy.sparse.coo_matrix method), 962
nonzero() (scipy.sparse.csc_matrix method), 969
nonzero() (scipy.sparse.csr_matrix method), 977
nonzero() (scipy.sparse.dia_matrix method), 984
nonzero() (scipy.sparse.dok_matrix method), 990
nonzero() (scipy.sparse.lil_matrix method), 995
norm (in module scipy.stats), 1344
norm() (in module scipy.linalg), 426
normalize() (in module scipy.signal), 844
normaltest() (in module scipy.stats), 1429
normaltest() (in module scipy.stats.mstats), 1504, 1536
nquad() (in module scipy.integrate), 323
nrtrim (in module scipy.special), 1163
nrtrisd (in module scipy.special), 1163
nu2lambda() (in module scipy.constants), 302
num (scipy.signal.lti attribute), 860
num (scipy.signal.StateSpace attribute), 863
num (scipy.signal.TransferFunction attribute), 866
num (scipy.signal.ZerosPolesGain attribute), 869
num_obs_dm() (in module scipy.spatial.distance), 1108, 1136
num_obs_linkage() (in module scipy.cluster.hierarchy), 286
num_obs_y() (in module scipy.spatial.distance), 1109, 1137
nutall() (in module scipy.signal), 920
obl_ang1 (in module scipy.special), 1187
obl_ang1_c (in module scipy.special), 1189
obl_c (in module scipy.special), 1188
obl_c_seq() (in module scipy.special), 1188
obl_rad1 (in module scipy.special), 1187
obl_rad1_c (in module scipy.special), 1189
obl_rad2 (in module scipy.special), 1187
obl_rad2_c (in module scipy.special), 1189
obrientransform() (in module scipy.stats), 1444
obrientransform() (in module scipy.stats.mstats), 1505, 1536
ode (class in scipy.integrate), 333
odeint() (in module scipy.integrate), 331
ODR (class in scipy.odr), 712
odr() (in module scipy.odr), 716
odr_error, 716
odr_stop, 716
onenormest() (in module scipy.sparse.linalg), 1022, 1056
OptimizeResult (class in scipy.optimize), 723
order_filter() (in module scipy.signal), 811
orth() (in module scipy.linalg), 441
orthogonal_procrustes() (in module scipy.linalg), 431
Output (class in scipy.odr), 715
output() (scipy.signal.lti method), 862
output() (scipy.signal.StateSpace method), 865
output() (scipy.signal.TransferFunction method), 867
output() (scipy.signal.ZerosPolesGain method), 870
pade() (in module scipy.misc), 653
pareto (in module scipy.stats), 1346
parzen() (in module scipy.signal), 922
pascal() (in module scipy.linalg), 473
pbd_seq() (in module scipy.special), 1184
pbv (in module scipy.special), 1183
pbv_seq() (in module scipy.special), 1184
pbv_seq() (module scipy.special), 1184
pchip_interpolate() (in module scipy.interpolate), 347
rad2deg() (scipy.sparse.bsr_matrix method), 954
rad2deg() (scipy.sparse.coo_matrix method), 962
rad2deg() (scipy.sparse.csc_matrix method), 970
rad2deg() (scipy.sparse.csr_matrix method), 978
rad2deg() (scipy.sparse.dia_matrix method), 984
radian (in module scipy.special), 1199
rand() (in module scipy.linalg.interpolative), 638
rand() (in module scipy.sparse), 1004
randint (in module scipy.stats), 1419
random_state (scipy.stats.rv_continuous attribute), 1202
random_state (scipy.stats.rv_discrete attribute), 1211
rank_filter() (in module scipy.ndimage.filters), 665
rankdata() (in module scipy.sparse.stats), 1467
rankdata() (in module scipy.stats.mstats), 1506, 1538
ranksums() (in module scipy.stats), 1468
rayleigh (in module scipy.stats), 1361
Rbf (class in scipy.interpolate), 360
r dist (in module scipy.odr), 710
recipinvgauss (in module scipy.stats), 1365
reciprocal (in module scipy.stats), 1359
reconstruct_interp_matrix() (in module scipy.linalg.interpolative), 635
reconstruct_matrix_from_id() (in module scipy.linalg.interpolative), 635
reconstruct_skel_matrix() (in module scipy.linalg.interpolative), 636
RectBivariateSpline (class in scipy.interpolate), 365, 388
RectSphereBivariateSpline (class in scipy.interpolate), 390
RegularGridInterpolator (class in scipy.interpolate), 364
rel_entr (in module scipy.special), 1167
rfftfreq() (in module scipy.fft), 316
rfftfreq() (in module scipy.fft) (in module scipy.fft), 305
rfft() (in module scipy.fft), 316
rfftfreq() (in module scipy.fft), 316
rgamma (in module scipy.special), 1171
ricatti_jnt() (in module scipy.special), 1153
ricatti_ynt() (in module scipy.special), 1153
rice (in module scipy.stats), 1363
ricker() (in module scipy.signal), 929
ridder() (in module scipy.optimize), 765
rint() (scipy.sparse.bsr_matrix method), 955
rint() (scipy.sparse.coo_matrix method), 962
rint() (scipy.sparse.csc_matrix method), 970
rint() (scipy.sparse.csr_matrix method), 978
rint() (scipy.sparse.dia_matrix method), 984
rmatvec() (scipy.optimize.LbfgsInvHessProduct method), 798
rmatvec() (scipy.sparse.linalg.LinearOperator method), 1020, 1053
rogerstanimoto() (in module scipy.spatial.distance), 1113, 1141
romb() (in module scipy.integrate), 330
romb() (in module scipy.integrate), 326
root() (in module scipy.optimize), 768
roots() (scipy.interpolate.Akima1DInterpolator method), 349
roots() (scipy.interpolate.InterpolatedUnivariateSpline method), 376
roots() (scipy.interpolate.LSQUnivariateSpline method), 381
roots() (scipy.interpolate.PPoly method), 352
roots() (scipy.interpolate.UnivariateSpline method), 372
roten() (in module scipy.optimize), 761
roten() (in module scipy.optimize), 761
roten() (in module scipy.optimize), 761
rotate() (in module scipy.ndimage.interpolation), 671
round (in module scipy.special), 1199
rqq() (in module scipy.linalg), 453
rsf2csf() (in module scipy.linalg), 456
run() (scipy.odr.ODR method), 714
russellrao() (in module scipy.spatial.distance), 1113, 1141
rv_continuous (class in scipy.stats), 1200
rv_continuous (class in scipy.stats), 1200
r discrete (class in scipy.stats), 1209
r vs() (scipy.stats.rv_continuous method), 1203
r vs() (scipy.stats.rv_discrete method), 1212
S
sasum (in module scipy.linalg.blas), 487
savemat() (in module scipy.io), 408
savewrite() (in module scipy.signal), 836
savewrite() (in module scipy.signal), 818
sawtooth() (in module scipy.signal), 890
savexy (in module scipy.linalg.blas), 488
sgeev (in module scipy.linalg.lapack), 526
sgeev_lwork (in module scipy.linalg.lapack), 527
sgehrd (in module scipy.linalg.lapack), 530
sgehrd_lwork (in module scipy.linalg.lapack), 531
sgehsd (in module scipy.linalg.lapack), 534
sgels (in module scipy.linalg.lapack), 536
sgels_lwork (in module scipy.linalg.lapack), 537
sgelsy (in module scipy.linalg.lapack), 538
sgemm (in module scipy.linalg.blas), 510
sgemv (in module scipy.linalg.blas), 500
sgeqp3 (in module scipy.linalg.lapack), 539
sgeqr (in module scipy.linalg.lapack), 540
sger (in module scipy.linalg.lapack), 501
sgesdd (in module scipy.linalg.lapack), 544
sgesv (in module scipy.linalg.lapack), 544
sgetrf (in module scipy.linalg.lapack), 546
sgetri (in module scipy.linalg.lapack), 546
sgetrs (in module scipy.linalg.lapack), 547
sh_chebyt() (in module scipy.special), 1182
sh_chebyu() (in module scipy.special), 1182
sh_jacobi() (in module scipy.special), 1182
sh_legendre() (in module scipy.special), 1182
shape (scipy.sparse.linalg.SuperLU attribute), 1045, 1078
shapiro() (in module scipy.stats), 1472
shichi (in module scipy.special), 1182
shift() (in module scipy.fftpack), 314
shift() (in module scipy.ndimage.interpolation), 672
shortest_path() (in module scipy.sparse.csgraph), 1007, 1082
show_options() (in module scipy.optimize), 796
sign() (scipy.sparse.bsr_matrix method), 955
sign() (scipy.sparse.coo_matrix method), 962
sign() (scipy.sparse.csc_matrix method), 978
sign() (scipy.sparse.csr_matrix method), 984
sin() (scipy.sparse.dia_matrix method), 984
sindg (in module scipy.special), 1199
single() (in module scipy.cluster.hierarchy), 275
sinh() (scipy.sparse.bsr_matrix method), 955
sinh() (scipy.sparse.coo_matrix method), 962
sinh() (scipy.sparse.csc_matrix method), 970
sinh() (scipy.sparse.csr_matrix method), 978
sinh() (scipy.sparse.dia_matrix method), 985
sinhm() (in module scipy.linalg), 460
sinm() (in module scipy.linalg), 459
skellam (in module scipy.stats), 1421
skew() (in module scipy.stats), 1429
skew() (in module scipy.stats.mstats), 1508, 1539
skewtest() (in module scipy.stats), 1429
skewtest() (in module scipy.stats.mstats), 1508, 1540
slamch (in module scipy.linalg.lapack), 582
slange (in module scipy.linalg.lapack), 591
slarf (in module scipy.linalg.lapack), 560
slarfg (in module scipy.linalg.lapack), 561
slartg (in module scipy.linalg.lapack), 562
slasd4 (in module scipy.linalg.lapack), 563
slaswp (in module scipy.linalg.lapack), 563
slauum (in module scipy.linalg.lapack), 565
slepian() (in module scipy.signal), 923
smirnov (in module scipy.stats), 1165
smirnov (in module scipy.stats), 1165
SmoothBivariateSpline (class in scipy.interpolate), 396
SmoothSphereBivariateSpline (class in scipy.interpolate), 397
snrm2 (in module scipy.linalg.blas), 489
sobel() (in module scipy.ndimage.filters), 665
sokalmichener() (in module scipy.spatial.distance), 1114, 1142
sokalsneath() (in module scipy.spatial.distance), 1114, 1142
solve() (in module scipy.linalg), 420
solve() (scipy.sparse.linalg.SuperLU method), 1045, 1079
solve_banded() (in module scipy.linalg), 421
solve_circulant() (in module scipy.linalg), 422
solve_continuous_are() (in module scipy.linalg), 465
solve_discrete_are() (in module scipy.linalg), 466
solve_discrete_lyapunov() (in module scipy.linalg), 466
solve_lyapunov() (in module scipy.linalg), 467
solve_sylvester() (in module scipy.linalg), 424
solve_triangular() (in module scipy.linalg), 424
solve_banded() (in module scipy.linalg), 421
sorghr (in module scipy.linalg.lapack), 582
sorghr (in module scipy.linalg.lapack), 583
sorgqr (in module scipy.linalg.lapack), 584
sormqr (in module scipy.linalg.lapack), 584
sort_indices() (scipy.sparse.bsr_matrix method), 955
sort_indices() (scipy.sparse.csc_matrix method), 970
sort_indices() (scipy.sparse.csr_matrix method), 978

1594 Index
sum() (in module scipy.ndimage.measurements), 683
sum() (scipy.sparse.bsr_matrix method), 955
sum() (scipy.sparse.coo_matrix method), 963
sum() (scipy.sparse.csc_matrix method), 971
sum() (scipy.sparse.csr_matrix method), 978
sum() (scipy.sparse.dia_matrix method), 985
sum() (scipy.sparse.dok_matrix method), 990
sum() (scipy.sparse.lil_matrix method), 995
sum_duplicates() (scipy.sparse.bsr_matrix method), 955
sum_duplicates() (scipy.sparse.coo_matrix method), 963
sum_duplicates() (scipy.sparse.csc_matrix method), 971
sum_duplicates() (scipy.sparse.csr_matrix method), 979
SuperLU (class in scipy.sparse.linalg), 1043, 1077
svd() (in module scipy.linalg), 439
svd() (in module scipy.linalg.interpolative), 637
svds() (in module scipy.sparse.linalg), 1041, 1075
sweep_poly() (in module scipy.signal), 440
symiorder1() (in module scipy.signal), 892
symiorder2() (in module scipy.signal), 812
t (in module scipy.optimize.LbfgsInvHessProduct attribute), 797
tan() (scipy.sparse.bsr_matrix method), 955
tan() (scipy.sparse.coo_matrix method), 963
tan() (scipy.sparse.csc_matrix method), 971
tan() (scipy.sparse.csr_matrix method), 979
tan() (scipy.sparse.dia_matrix method), 985
tandg (in module scipy.special), 1199
tanh() (scipy.sparse.bsr_matrix method), 956
tanh() (scipy.sparse.coo_matrix method), 963
tanh() (scipy.sparse.csc_matrix method), 971
tanh() (scipy.sparse.csr_matrix method), 979
tanh() (scipy.sparse.dia_matrix method), 985
tanhm() (in module scipy.linalg), 461
tanm() (in module scipy.linalg), 459
tf2ss() (in module scipy.signal), 879
tf2ss() (in module scipy.signal), 879
tf2zpk() (in module scipy.signal), 878
theilslopes() (in module scipy.stats), 1455
theilslopes() (in module scipy.stats.mstats), 1509, 1540
threshold() (in module scipy.stats), 1449
threshold() (in module scipy.stats.mstats), 1510, 1542
tiecorrect() (in module scipy.stats), 1467
tilbert() (in module scipy.fftpack), 311
tklmbda (in module scipy.special), 1165
tmax() (in module scipy.stats), 1432
tmax() (in module scipy.stats.mstats), 1510, 1542
tmean() (in module scipy.stats), 1431
rmean() (in module scipy.stats.mstats), 1511, 1542
tmin() (in module scipy.stats), 1431
rmin() (in module scipy.stats.mstats), 1511, 1543
to_nlab_linkage() (in module scipy.cluster.hierarchy), 279
to_ss() (scipy.signal.StateSpace method), 865
to_ss() (scipy.signal.TransfereFunction method), 868
to_zpk() (scipy.signal.StateSpace method), 865
to_zpk() (scipy.signal.TransfereFunction method), 868
### Z
- `z` (in module `scipy.linalg.blas`), 491
- `zaxpy` (in module `scipy.linalg.blas`), 491
- `zcopy` (in module `scipy.linalg.blas`), 491
- `zdcte` (in module `scipy.linalg.blas`), 492
- `zdote` (in module `scipy.linalg.blas`), 492
- `zdrot` (in module `scipy.linalg.blas`), 492
- `zscal` (in module `scipy.linalg.blas`), 493
- `zeros` (in module `scipy.signal.lti`), 860
- `zeros` (in module `scipy.signal.StateSpace`), 863
- `zeros` (in module `scipy.signal.TransferFunction`), 866
- `zeros` (in module `scipy.signal.ZerosPolesGain`), 869
- `ZerosPolesGain` (in module `scipy.signal`), 868
- `zeta` (in module `scipy.special`), 1198
- `zetac` (in module `scipy.special`), 1198
- `zgbsv` (in module `scipy.linalg.lapack`), 519
- `zgbtrf` (in module `scipy.linalg.lapack`), 520
- `zgbtrs` (in module `scipy.linalg.lapack`), 522
- `zgebal` (in module `scipy.linalg.lapack`), 523
- `zgees` (in module `scipy.linalg.lapack`), 525
- `zgeev` (in module `scipy.linalg.lapack`), 527
- `zgeev_lwork` (in module `scipy.linalg.lapack`), 528
- `zgegv` (in module `scipy.linalg.lapack`), 529
- `zgehrd` (in module `scipy.linalg.lapack`), 531
- `zgehrd_lwork` (in module `scipy.linalg.lapack`), 532
- `zgelsd` (in module `scipy.linalg.lapack`), 535
- `zgelsd_lwork` (in module `scipy.linalg.lapack`), 537
- `zgelss` (in module `scipy.linalg.lapack`), 533
- `zgelss_lwork` (in module `scipy.linalg.lapack`), 534
- `zgelsy` (in module `scipy.linalg.lapack`), 538
- `zgelsy_lwork` (in module `scipy.linalg.lapack`), 539
- `zgemm` (in module `scipy.linalg.blas`), 511
- `zgemv` (in module `scipy.linalg.blas`), 503
- `zgeqpf3` (in module `scipy.linalg.lapack`), 540
- `zgeqrf` (in module `scipy.linalg.lapack`), 541
- `zgev` (in module `scipy.linalg.lapack`), 503
- `zgerf` (in module `scipy.linalg.lapack`), 542
- `zgerc` (in module `scipy.linalg.blas`), 503
- `zgerq` (in module `scipy.linalg.lapack`), 543
- `zgesdd` (in module `scipy.linalg.lapack`), 543
- `zgesdd_lwork` (in module `scipy.linalg.lapack`), 544
- `zgesv` (in module `scipy.linalg.lapack`), 545
- `zgetrf` (in module `scipy.linalg.lapack`), 546
- `zgetri` (in module `scipy.linalg.lapack`), 547
- `zgetri_lwork` (in module `scipy.linalg.lapack`), 547
- `zgetrs` (in module `scipy.linalg.lapack`), 548
- `zgges` (in module `scipy.linalg.lapack`), 551
- `zggev` (in module `scipy.linalg.lapack`), 553
- `zgtsv` (in module `scipy.linalg.lapack`), 581
- `zhbevd` (in module `scipy.linalg.lapack`), 554
- `zhbevx` (in module `scipy.linalg.lapack`), 555
- `zheev` (in module `scipy.linalg.lapack`), 556
- `zheevd` (in module `scipy.linalg.lapack`), 557
- `zheevr` (in module `scipy.linalg.lapack`), 557
- `zhegvd` (in module `scipy.linalg.lapack`), 559

### W
- `wald` (in module `scipy.stats`), 1383
- `ward` (in module `scipy.cluster.hierarchy`), 277
- `watershed_ift` (in module `scipy.ndimage.measurements`), 684
- `weibull_max` (in module `scipy.stats`), 1387
- `weibull_min` (in module `scipy.stats`), 1385
- `weighted` (in module `scipy.cluster.hierarchy`), 276
- `welch` (in module `scipy.signal`), 937
- `white_tophat` (in module `scipy.ndimage.morphology`), 708
- `whiten` (in module `scipy.cluster.vq`), 267
- `who` (in module `scipy.misc`), 653
- `whosmat` (in module `scipy.io`), 409
- `wiener` (in module `scipy.signal`), 812
- `wilcoxon` (in module `scipy.stats`), 1468
- `winsorize` (in module `scipy.stats.mstats`), 1518, 1550
- `wishart` (in module `scipy.stats`), 1395
- `wminkowski` (in module `scipy.spatial.distance`), 1114, 1142
- `wofz` (in module `scipy.stats`), 1173
- `wrapcauchy` (in module `scipy.stats`), 1389
- `write` (in module `scipy.io.wavfile`), 414
- `write_record` (in module `scipy.io.FortranFile`), 413

### X
- `xlog1py` (in module `scipy.special`), 1199
- `xlogy` (in module `scipy.special`), 1199

### Y
- `y0` (in module `scipy.special`), 1151
- `y0_zeros` (in module `scipy.special`), 1150
- `y1` (in module `scipy.special`), 1151
- `y1_zeros` (in module `scipy.special`), 1150
- `y1p_zeros` (in module `scipy.special`), 1150
- `yn` (in module `scipy.special`), 1147
- `yn_zeros` (in module `scipy.special`), 1150
- `ynp_zeros` (in module `scipy.special`), 1150
- `yule` (in module `scipy.spatial.distance`), 1115, 1143
- `yv` (in module `scipy.special`), 1148
- `yve` (in module `scipy.special`), 1148
- `yvp` (in module `scipy.special`), 1153
zhegvx (in module scipy.linalg.lapack), 560
zhemm (in module scipy.linalg.blas), 511
zhemv (in module scipy.linalg.blas), 504
zher (in module scipy.linalg.blas), 505
zher2 (in module scipy.linalg.blas), 505
zher2k (in module scipy.linalg.blas), 512
zherk (in module scipy.linalg.blas), 512
zipf (in module scipy.stats), 1423
zlanhe (in module scipy.linalg.lapack), 592
zlarf (in module scipy.linalg.lapack), 561
zlarfg (in module scipy.linalg.lapack), 562
zlarft (in module scipy.linalg.lapack), 563
zlaswp (in module scipy.linalg.lapack), 564
zlaum (in module scipy.linalg.lapack), 565
zmap() (in module scipy.stats), 1447
zmap() (in module scipy.stats.mstats), 1519, 1550
zoom() (in module scipy.ndimage.interpolation), 673
zpbsv (in module scipy.linalg.lapack), 566
zpbtrf (in module scipy.linalg.lapack), 568
zpbtrs (in module scipy.linalg.lapack), 569
zpk2sos() (in module scipy.signal), 880
zpk2ss() (in module scipy.signal), 882
zpk2tf() (in module scipy.signal), 880
zposv (in module scipy.linalg.lapack), 570
zpotrf (in module scipy.linalg.lapack), 571
zpotri (in module scipy.linalg.lapack), 572
zptsv (in module scipy.linalg.lapack), 582
zrot (in module scipy.linalg.lapack), 573
zrotg (in module scipy.linalg.lapack), 493
zscal (in module scipy.linalg.blas), 493
zscore() (in module scipy.stats), 1448
zscore() (in module scipy.stats.mstats), 1519, 1551
zswap (in module scipy.linalg.blas), 494
zsyr (in module scipy.linalg.blas), 512
zsyr2k (in module scipy.linalg.blas), 513
zsyrk (in module scipy.linalg.blas), 512
ztrmv (in module scipy.linalg.blas), 504
ztrsv (in module scipy.linalg.blas), 512
ztrtrs (in module scipy.linalg.lapack), 577
zunghr (in module scipy.linalg.lapack), 577
zungqr (in module scipy.linalg.lapack), 578
zungrq (in module scipy.linalg.lapack), 579
zunmqr (in module scipy.linalg.lapack), 579