SciPy Reference Guide

Release 0.8.dev

Written by the SciPy community

February 11, 2010

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Release
0.8.dev

Date
February 11, 2010

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

CHAPTER

ONE

SCIPY TUTORIAL

1.1 Introduction

Contents

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

The additional power of using SciPy within Python, however, is that a powerful programming language is also available for use in developing sophisticated programs and specialized applications. Scientific applications written in 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 document provides a tutorial for the first-time user of SciPy to help get started with some of the features available in this powerful package. It is assumed that the user has already installed the package. Some general Python facility is also assumed such as could be acquired by working through the Tutorial in the Python distribution. 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:

```
>>> import numpy as np
>>> import scipy as sp
>>> 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:

Subpackage	Description
cluster	Clustering algorithms
constants	Physical and mathematical constants
fftpack	Fast Fourier Transform routines
integrate	Integration and ordinary differential equation solvers
interpolate	Interpolation and smoothing splines
io	Input and Output
linalg	Linear algebra
maxentropy	Maximum entropy methods
ndimage	N-dimensional image processing
odr	Orthogonal distance regression
optimize	Optimization and root-finding routines
signal	Signal processing
sparse	Sparse matrices and associated routines
spatial	Spatial data structures and algorithms
special	Special functions
stats	Statistical distributions and functions
weave	C/C++ integration

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

```
>>> 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 HTML and PDF versions of their documentation available at http://docs.scipy.org/, which currently details 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 also provides the facility of documentation strings. The functions and classes available in SciPy use this method for on-line documentation. There are two methods for reading these messages and getting help. Python provides the 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. Running the command help with an object as the argument displays the calling signature, and the documentation string of the object.

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 scipy-specific help system is also available under the command sp.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 sp.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:

```
>>> sp.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)
      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, {fopt, iter, funcalls, warnflag})

  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 fval 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 in Numpy (and top-level scipy)

Contents

1.2.1 Interaction with Numpy

To begin with, all of the Numpy functions have been subsumed into the `scipy` namespace so that all of those functions are available without additionally importing Numpy. In addition, the universal functions (addition, subtraction, division) have been altered to not raise exceptions if floating-point errors are encountered; instead, NaN's and Inf's are returned in the arrays. To assist in detection of these events, several functions (`sp.isnan`, `sp.isfinite`, `sp.isinf`) are available.

Finally, some of the basic functions like log, sqrt, and inverse trig functions have been modified to return complex numbers instead of NaN's where appropriate (*i.e.* `sp.sqrt(-1)` returns `1j`).

1.2.2 Top-level scipy routines

The purpose of the top level of scipy is to collect general-purpose routines that the other sub-packages can use and to provide a simple replacement for Numpy. Anytime you might think to import Numpy, you can import scipy instead and remove yourself from direct dependence on Numpy. These routines are divided into several files for organizational purposes, but they are all available under the numpy namespace (and the scipy namespace). There are routines for type handling and type checking, shape and matrix manipulation, polynomial processing, and other useful functions. 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.

Type handling

Note the difference between `sp.iscomplex`/`sp.isreal` and `sp.iscomplexobj`/`sp.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 `sp.real` and `sp.imag` . These functions succeed for anything that can be turned into

a Numpy array. Consider also the function `sp.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 `sp.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 `sp.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, `sp.cast['f'](d)` returns an array of `sp.float32` from *d*. This function is also useful as an easy way to get a scalar of a certain type:

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

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 `sp.mgrid` , `sp.ogrid` , `sp.r_` , and `sp.c_` for quickly constructing arrays.

One familiar with Matlab may complain that it is difficult to construct arrays from the interactive session with Python. Suppose, for example that one wants to construct an array that begins with 3 followed by 5 zeros and then contains 10 numbers spanning the range -1 to 1 (inclusive on both ends). Before SciPy, you would need to enter something like the following

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

With the `r_` command one can enter this as

```
>>> 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:

```
>>> 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.    ],
        [ 1.6667,  1.6667,  1.6667,  1.6667],
        [ 3.3333,  3.3333,  3.3333,  3.3333],
        [ 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:

```
>>> p = poly1d([3,4,5])
>>> print p
   2
3 x + 4 x + 5
>>> print p*p
   4      3      2
9 x + 24 x + 46 x + 40 x + 25
>>> print p.integ(k=6)
 3     2
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:

```
>>> 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

```
>>> vec_addsubtract = vectorize(addsubtract)
```

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

```
>>> 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`.

Other useful functions

There are several other functions in the scipy_base package including most of the other functions that are also in the Numpy package. The reason for duplicating these functions is to allow SciPy to potentially alter their original interface and make it easier for users to know how to get access to functions

```
>>> from scipy import *
```

Functions which should be mentioned are `mod(x,y)` which can replace `x % y` when it is desired that the result take the sign of y instead of x . Also included is `fix` which always rounds to the nearest integer towards zero. For doing phase processing, the functions `angle`, and `unwrap` are also 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 new 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

```
>>> x = r_[-2:3]
>>> x
array([-2, -1,  0,  1,  2])
>>> select([x > 3, x >= 0],[0,x+2])
array([0, 0, 2, 3, 4])
```

1.2.3 Common functions

Some functions depend on sub-packages of SciPy but should be available from the top-level of SciPy due to their common use. These are functions that might have been placed in scipy_base except for their dependence on other sub-packages of SciPy. 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. The functions `rand` and `randn` are used so often that they warranted a place at the top level. There are convenience functions for the interactive use: `disp` (similar to print), and `who` (returns a list of defined variables and memory consumption–upper bounded). Another function returns a common image used in image processing: `lena`.

Finally, two functions are provided that are useful for approximating derivatives of functions using discrete-differences. The function `central_diff_weights` returns weighting coefficients for an equally-spaced N-point approximation to the derivative of order o. These weights must be multiplied by the function corresponding to these points and the results added to obtain the derivative approximation. This function is intended for use when only samples of the function are avaiable. When the function is an object that can be handed to a routine and evaluated, the function `derivative` can be used to automatically evaluate the object at the correct points to obtain an N-point approximation to the o-th derivative at a given point.

1.3 Special functions (`scipy.special`)

The main feature of the `scipy.special` package is the definition of numerous special functions of mathematical physics. Available functions include airy, elliptic, bessel, gamma, beta, hypergeometric, parabolic cylinder, mathieu, spheroidal wave, struve, and kelvin. There are also some low-level stats functions that are not intended for general use as an easier interface to these functions is provided by the `stats` module. Most of these functions can take array arguments and return array results following the same broadcasting rules as other math functions in Numerical Python. Many of these functions also accept complex numbers as input. For a complete list of the available functions with a one-line description type `>>> help(special)`. Each function also has its own documentation accessible using help. If you don't see a function you need, consider writing it and contributing it to the library. You can write the function in either C, Fortran, or Python. Look in the source code of the library for examples of each of these kinds of functions.

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:

```
>>> help(integrate)
 Methods for Integrating Functions given function object.

   quad          -- General purpose integration.
   dblquad       -- General purpose double integration.
   tplquad       -- General purpose triple integration.
   fixed_quad    -- Integrate func(x) using Gaussian quadrature of order n.
   quadrature    -- Integrate with given tolerance using Gaussian quadrature.
   romberg       -- Integrate func using Romberg integration.

 Methods for Integrating Functions given fixed samples.

   trapz         -- Use trapezoidal rule to compute integral from samples.
   cumtrapz      -- Use trapezoidal rule to cumulatively compute integral.
   simps         -- Use Simpson's rule to compute integral from samples.
   romb          -- Use Romberg Integration to compute integral from
```

```
                    (2**k + 1) evenly-spaced samples.

   See the special module's orthogonal polynomials (special) for Gaussian
      quadrature roots and weights for other weighting factors and regions.

 Interface to numerical integrators of ODE systems.

   odeint        -- General integration of ordinary differential equations.
   ode           -- Integrate ODE using VODE and ZVODE routines.
```

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 $\pm\infty$ ($\pm$ inf) to indicate infinite limits. For example, suppose you wish to integrate a bessel function jv(2.5,x) along the interval $[0, 4.5]$.

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

This could be computed using quad:

```
>>> 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

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

where

$$\mathrm{Si}(x) = \int_0^x \sin\left(\frac{\pi}{2}t^2\right) dt.$$

is the Fresnel sine integral. Note that the numerically-computed integral is within 1.04×10^{-11} of the exact result — well below the reported error bound.

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

$$E_n(x) = \int_1^\infty \frac{e^{-xt}}{t^n}\, dt.$$

is desired (and the fact that this integral can be computed as special.expn(n,x) is forgotten). The functionality of the function special.expn can be replicated by defining a new function vec_expint based on the routine quad:

```
>>> 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 quad argument (though the error bound may underestimate the error due to possible numerical error in the integrand from the use of `quad`). The integral in this case is

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

```
>>> result = quad(lambda x: expint(3, x), 0, inf)
>>> print result
(0.33333333324560266, 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 `quad`. The mechanics of this for double and triple integration have been wrapped up into the functions `dblquad` and `tplquad`. The function, `dblquad` performs double integration. Use the help function to be sure that the arguments are defined in the correct order. In addition, the limits on all inner integrals are actually functions which can be constant functions. An example of using double integration to compute several values of I_n is shown below:

```
>>> 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)
```

1.4.2 Gaussian quadrature (integrate.gauss_quadtol)

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`).

1.4.3 Integrating using samples

There are three functions for computing integrals given only samples: `trapz` , `simps`, and `romb` . The first two functions use Newton-Coates formulas of order 1 and 2 respectively to perform integration. These two functions can handle, non-equally-spaced samples. 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.

If the samples are equally-spaced and the number of samples available is $2^k + 1$ for some integer k, then Romberg 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. (A different interface to Romberg integration useful when the function can be provided is also available as `romberg`).

1.4.4 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:

$$\frac{d\mathbf{y}}{dt} = \mathbf{f}\left(\mathbf{y}, t\right),$$

given initial conditions $\mathbf{y}\left(0\right) = y_0$, where $\mathbf{y}$ is a length N vector and $\mathbf{f}$ is a mapping from $\mathcal{R}^N$ to $\mathcal{R}^N$. A higher-order ordinary differential equation can always be reduced to a differential equation of this type by introducing intermediate derivatives into the $\mathbf{y}$ 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 $w\left(0\right) = \frac{1}{\sqrt[3]{3^2}\Gamma\left(\frac{2}{3}\right)}$ and $\frac{dw}{dz}\Big|_{z=0} = -\frac{1}{\sqrt[3]{3}\Gamma\left(\frac{1}{3}\right)}$. It is known that the solution to this differential equation with these boundary conditions is the Airy function

$$w = \mathrm{Ai}\left(z\right),$$

which gives a means to check the integrator using `special.airy`.

First, convert this ODE into standard form by setting $\mathbf{y} = \left[\frac{dw}{dz}, w\right]$ and $t = z$. Thus, the differential equation becomes

$$\frac{d\mathbf{y}}{dt} = \begin{bmatrix} ty_1 \\ y_0 \end{bmatrix} = \begin{bmatrix} 0 & t \\ 1 & 0 \end{bmatrix} \begin{bmatrix} y_0 \\ y_1 \end{bmatrix} = \begin{bmatrix} 0 & t \\ 1 & 0 \end{bmatrix} \mathbf{y}.$$

In other words,

$$\mathbf{f}\left(\mathbf{y}, t\right) = \mathbf{A}\left(t\right)\mathbf{y}.$$

As an interesting reminder, if $\mathbf{A}(t)$ commutes with $\int_0^t \mathbf{A}(\tau)\, d\tau$ under matrix multiplication, then this linear differential equation has an exact solution using the matrix exponential:

$$\mathbf{y}(t) = \exp\left(\int_0^t \mathbf{A}(\tau)\, d\tau\right) \mathbf{y}(0),$$

However, in this case, $\mathbf{A}(t)$ 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 $\mathbf{y}$) of the function, $\mathbf{f}(\mathbf{y}, t)$.

```
>>> 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]

>>> print y2[:36:6,1]
[ 0.355028  0.339511  0.324067  0.308763  0.293658  0.278806]
```

1.5 Optimization (optimize)

There are several classical optimization algorithms provided by SciPy in the `scipy.optimize` package. An overview of the module is available using `help` (or `pydoc.help`):

```
from scipy import optimize
>>> info(optimize)
Optimization Tools
==================

 A collection of general-purpose optimization routines.

   fmin        --  Nelder-Mead Simplex algorithm
                     (uses only function calls)
   fmin_powell --  Powell's (modified) level set method (uses only
                     function calls)
   fmin_cg     --  Non-linear (Polak-Ribiere) conjugate gradient algorithm
                     (can use function and gradient).
   fmin_bfgs   --  Quasi-Newton method (Broydon-Fletcher-Goldfarb-Shanno);
                     (can use function and gradient)
   fmin_ncg    --  Line-search Newton Conjugate Gradient (can use
                     function, gradient and Hessian).
   leastsq     --  Minimize the sum of squares of M equations in
                     N unknowns given a starting estimate.


  Constrained Optimizers (multivariate)

   fmin_l_bfgs_b -- Zhu, Byrd, and Nocedal's L-BFGS-B constrained optimizer
                      (if you use this please quote their papers -- see help)

   fmin_tnc      -- Truncated Newton Code originally written by Stephen Nash and
                      adapted to C by Jean-Sebastien Roy.

   fmin_cobyla   -- Constrained Optimization BY Linear Approximation


  Global Optimizers

   anneal      --  Simulated Annealing
   brute       --  Brute force searching optimizer


  Scalar function minimizers

   fminbound   --  Bounded minimization of a scalar function.
   brent       --  1-D function minimization using Brent method.
   golden      --  1-D function minimization using Golden Section method
   bracket     --  Bracket a minimum (given two starting points)


 Also a collection of general-purpose root-finding routines.

   fsolve      --  Non-linear multi-variable equation solver.


  Scalar function solvers

   brentq      --  quadratic interpolation Brent method
   brenth      --  Brent method (modified by Harris with hyperbolic
                     extrapolation)
   ridder      --  Ridder's method
   bisect      --  Bisection method
   newton      --  Secant method or Newton's method
   fixed_point --  Single-variable fixed-point solver.
```



```
 A collection of general-purpose nonlinear multidimensional solvers.

   broyden1            --  Broyden's first method - is a quasi-Newton-Raphson
```

The first four algorithms are unconstrained minimization algorithms (fmin: Nelder-Mead simplex, fmin_bfgs: BFGS, fmin_ncg: Newton Conjugate Gradient, and leastsq: Levenburg-Marquardt). The last algorithm actually finds the roots of a general function of possibly many variables. It is included in the optimization package because at the (non-boundary) extreme points of a function, the gradient is equal to zero.

1.5.1 Nelder-Mead Simplex algorithm (fmin)

The simplex algorithm is probably the simplest way to minimize a fairly well-behaved function. The simplex algorithm 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. To demonstrate the minimization function consider the problem of minimizing the Rosenbrock function of N variables:

$$f(\mathbf{x}) = \sum_{i=1}^{N-1} 100\left(x_i - x_{i-1}^2\right)^2 + \left(1 - x_{i-1}\right)^2.$$

The minimum value of this function is 0 which is achieved when $x_i = 1$. This minimum can be found using the fmin routine as shown in the example below:

```
>>> from scipy.optimize import fmin
>>> def rosen(x):
...     """The Rosenbrock function"""
...     return sum(100.0*(x[1:]-x[:-1]**2.0)**2.0 + (1-x[:-1])**2.0)

>>> x0 = [1.3, 0.7, 0.8, 1.9, 1.2]
>>> xopt = fmin(rosen, x0, xtol=1e-8)
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 339
         Function evaluations: 571

>>> print xopt
[ 1.  1.  1.  1.  1.]
```

Another optimization algorithm that needs only function calls to find the minimum is Powell's method available as fmin_powell.

1.5.2 Broyden-Fletcher-Goldfarb-Shanno algorithm (fmin_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:

$$\begin{aligned}\frac{\partial f}{\partial x_j} &= \sum_{i=1}^{N} 200\left(x_i - x_{i-1}^2\right)\left(\delta_{i,j} - 2x_{i-1}\delta_{i-1,j}\right) - 2\left(1 - x_{i-1}\right)\delta_{i-1,j}. \\ &= 200\left(x_j - x_{j-1}^2\right) - 400x_j\left(x_{j+1} - x_j^2\right) - 2\left(1 - x_j\right).\end{aligned}$$

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

$$\begin{aligned}\frac{\partial f}{\partial x_0} &= -400x_0\left(x_1 - x_0^2\right) - 2\left(1 - x_0\right), \\ \frac{\partial f}{\partial x_{N-1}} &= 200\left(x_{N-1} - x_{N-2}^2\right).\end{aligned}$$

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 = 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
```

The calling signature for the BFGS minimization algorithm is similar to `fmin` with the addition of the *fprime* argument. An example usage of `fmin_bfgs` is shown in the following example which minimizes the Rosenbrock function.

```
>>> from scipy.optimize import fmin_bfgs


>>> x0 = [1.3, 0.7, 0.8, 1.9, 1.2]
>>> xopt = fmin_bfgs(rosen, x0, fprime=rosen_der)
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 53
         Function evaluations: 65
         Gradient evaluations: 65
>>> print xopt
[ 1.  1.  1.  1.  1.]
```

1.5.3 Newton-Conjugate-Gradient (`fmin_ncg`)

The method which requires the fewest function calls and is therefore often the fastest method to minimize functions of many variables is `fmin_ncg`. 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:

$$f(\mathbf{x}) \approx f(\mathbf{x}_0) + \nabla f(\mathbf{x}_0) \cdot (\mathbf{x} - \mathbf{x}_0) + \frac{1}{2}(\mathbf{x} - \mathbf{x}_0)^T \mathbf{H}(\mathbf{x}_0)(\mathbf{x} - \mathbf{x}_0).$$

where $\mathbf{H}(\mathbf{x}_0)$ 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

$$\mathbf{x}_{\text{opt}} = \mathbf{x}_0 - \mathbf{H}^{-1}\nabla f.$$

The inverse of the Hessian is evaluted 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 NewtonCG method, a function which computes the Hessian must be provided. The Hessian matrix itself does not need to be constructed, only a vector which is the product of the Hessian with an arbitrary vector needs to be available to the minimization routine. As a result, the user can provide either a function to compute the Hessian matrix, or a function to compute the product of the Hessian with an arbitrary vector.

Full Hessian example:

The Hessian of the Rosenbrock function is

$$\begin{aligned} H_{ij} = \frac{\partial^2 f}{\partial x_i \partial x_j} &= 200(\delta_{i,j} - 2x_{i-1}\delta_{i-1,j}) - 400x_i(\delta_{i+1,j} - 2x_i\delta_{i,j}) - 400\delta_{i,j}\left(x_{i+1} - x_i^2\right) + 2\delta_{i,j}, \\ &= \left(202 + 1200x_i^2 - 400x_{i+1}\right)\delta_{i,j} - 400x_i\delta_{i+1,j} - 400x_{i-1}\delta_{i-1,j}, \end{aligned}$$

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

$$\begin{aligned}
\frac{\partial^2 f}{\partial x_0^2} &= 1200x_0^2 - 400x_1 + 2, \\
\frac{\partial^2 f}{\partial x_0 \partial x_1} = \frac{\partial^2 f}{\partial x_1 \partial x_0} &= -400x_0, \\
\frac{\partial^2 f}{\partial x_{N-1} \partial x_{N-2}} = \frac{\partial^2 f}{\partial x_{N-2} \partial x_{N-1}} &= -400x_{N-2}, \\
\frac{\partial^2 f}{\partial x_{N-1}^2} &= 200.
\end{aligned}$$

For example, the Hessian when $N = 5$ is

$$\mathbf{H} = \begin{bmatrix}
1200x_0^2 - 400x_1 + 2 & -400x_0 & 0 & 0 & 0 \\
-400x_0 & 202 + 1200x_1^2 - 400x_2 & -400x_1 & 0 & 0 \\
0 & -400x_1 & 202 + 1200x_2^2 - 400x_3 & -400x_2 & 0 \\
0 & & -400x_2 & 202 + 1200x_3^2 - 400x_4 & -400x_3 \\
0 & 0 & 0 & -400x_3 & 200
\end{bmatrix}.$$

The code which computes this Hessian along with the code to minimize the function using `fmin_ncg` is shown in the following example:

```
>>> from scipy.optimize import fmin_ncg
>>> def rosen_hess(x):
...     x = asarray(x)
...     H = diag(-400*x[:-1],1) - diag(400*x[:-1],-1)
...     diagonal = zeros_like(x)
...     diagonal[0] = 1200*x[0]-400*x[1]+2
...     diagonal[-1] = 200
...     diagonal[1:-1] = 202 + 1200*x[1:-1]**2 - 400*x[2:]
...     H = H + diag(diagonal)
...     return H

>>> x0 = [1.3, 0.7, 0.8, 1.9, 1.2]
>>> xopt = fmin_ncg(rosen, x0, rosen_der, fhess=rosen_hess, avextol=1e-8)
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 23
         Function evaluations: 26
         Gradient evaluations: 23
         Hessian evaluations: 23
>>> print xopt
[ 1.  1.  1.  1.  1.]
```

Hessian product example:

For larger minimization problems, storing the entire Hessian matrix can consume considerable time and memory. The Newton-CG algorithm only needs the product of the Hessian times an arbitrary vector. As a result, the user can supply code to compute this product rather than the full Hessian by setting the *fhess_p* keyword to the desired function. The *fhess_p* function should take the minimization vector as the first argument and the arbitrary vector as the second argument. Any extra arguments passed to the function to be minimized will also be passed to this function. 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 $\mathbf{p}$ is the arbitrary vector, then $\mathbf{H}(\mathbf{x})\mathbf{p}$ has elements:

$$\mathbf{H}(\mathbf{x})\mathbf{p} = \begin{bmatrix} \left(1200x_0^2 - 400x_1 + 2\right)p_0 - 400x_0p_1 \\ \vdots \\ -400x_{i-1}p_{i-1} + \left(202 + 1200x_i^2 - 400x_{i+1}\right)p_i - 400x_ip_{i+1} \\ \vdots \\ -400x_{N-2}p_{N-2} + 200p_{N-1} \end{bmatrix}.$$

Code which makes use of the *fhess_p* keyword to minimize the Rosenbrock function using `fmin_ncg` follows:

```
>>> from scipy.optimize import fmin_ncg
>>> def rosen_hess_p(x,p):
...     x = asarray(x)
...     Hp = zeros_like(x)
...     Hp[0] = (1200*x[0]**2 - 400*x[1] + 2)*p[0] - 400*x[0]*p[1]
...     Hp[1:-1] = -400*x[:-2]*p[:-2]+(202+1200*x[1:-1]**2-400*x[2:])*p[1:-1] \
...                -400*x[1:-1]*p[2:]
...     Hp[-1] = -400*x[-2]*p[-2] + 200*p[-1]
...     return Hp


>>> x0 = [1.3, 0.7, 0.8, 1.9, 1.2]
>>> xopt = fmin_ncg(rosen, x0, rosen_der, fhess_p=rosen_hess_p, avextol=1e-8)
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 22
         Function evaluations: 25
         Gradient evaluations: 22
         Hessian evaluations: 54
>>> print xopt
[ 1.  1.  1.  1.  1.]
```

1.5.4 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 $\{\mathbf{x}_i, \mathbf{y}_i\}$ to a known model, $\mathbf{y} = \mathbf{f}(\mathbf{x}, \mathbf{p})$ where $\mathbf{p}$ 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

$$e_i(\mathbf{p}, \mathbf{y}_i, \mathbf{x}_i) = \|\mathbf{y}_i - \mathbf{f}(\mathbf{x}_i, \mathbf{p})\|.$$

An objective function to pass to any of the previous minization algorithms to obtain a least-squares fit is.

$$J(\mathbf{p}) = \sum_{i=0}^{N-1} e_i^2(\mathbf{p}).$$

The `leastsq` algorithm performs this squaring and summing of the residuals automatically. It takes as an input argument the vector function $\mathbf{e}(\mathbf{p})$ and returns the value of $\mathbf{p}$ which minimizes $J(\mathbf{p}) = \mathbf{e}^T\mathbf{e}$ 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

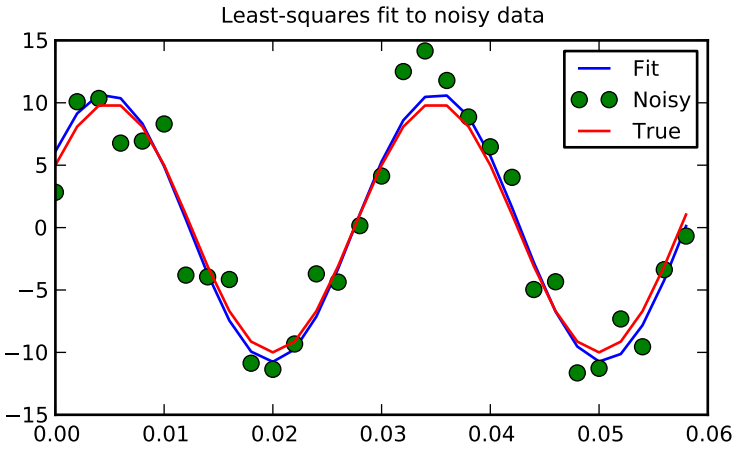
$$y_i = A\sin(2\pi kx_i + \theta)$$

where the parameters A, k , and θ 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:

```
>>> from numpy import *
>>> 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]

>>> from scipy.optimize import leastsq
>>> plsq = leastsq(residuals, p0, args=(y_meas, x))
>>> print plsq[0]
[ 10.9437  33.3605   0.5834]

>>> print array([A, k, theta])
[ 10.      33.3333   0.5236]

>>> import matplotlib.pyplot as plt
>>> plt.plot(x,peval(x,plsq[0]),x,y_meas,'o',x,y_true)
>>> plt.title('Least-squares fit to noisy data')
>>> plt.legend(['Fit', 'Noisy', 'True'])
>>> plt.show()
```



1.5.5 Sequential Least-square fitting with constraints (`fmin_slsqp`)

This module implements the Sequential Least SQuares Programming optimization algorithm (SLSQP).

$$
\begin{aligned}
&\min F(x) \\
&\text{subject to} \quad C_j(X) = 0, \quad j = 1, ..., \text{MEQ} \\
&\qquad\qquad\quad C_j(x) \geq 0, \quad j = \text{MEQ}+1, ..., M \\
&\qquad\qquad\quad XL \leq x \leq XU, \quad I = 1, ..., N.
\end{aligned}
$$

The following script shows examples for how constraints can be specified.

```
"""
This script tests fmin_slsqp using Example 14.4 from Numerical Methods for
Engineers by Steven Chapra and Raymond Canale.  This example maximizes the
function f(x) = 2*x*y + 2*x - x**2 - 2*y**2, which has a maximum at x=2,y=1.
"""

from scipy.optimize import fmin_slsqp
from numpy import array, asfarray, finfo,ones, sqrt, zeros


def testfunc(d,*args):
    """
    Arguments:
    d     - A list of two elements, where d[0] represents x and
            d[1] represents y in the following equation.
    sign - A multiplier for f.  Since we want to optimize it, and the scipy
           optimizers can only minimize functions, we need to multiply it by
           -1 to achieve the desired solution
    Returns:
    2*x*y + 2*x - x**2 - 2*y**2

    """
    try:
        sign = args[0]
```

```
    except:
        sign = 1.0
    x = d[0]
    y = d[1]
    return sign*(2*x*y + 2*x - x**2 - 2*y**2)

def testfunc_deriv(d,*args):
    """ This is the derivative of testfunc, returning a numpy array
    representing df/dx and df/dy

    """
    try:
        sign = args[0]
    except:
        sign = 1.0
    x = d[0]
    y = d[1]
    dfdx = sign*(-2*x + 2*y + 2)
    dfdy = sign*(2*x - 4*y)
    return array([ dfdx, dfdy ],float)


from time import time

print '\n\n'

print "Unbounded optimization. Derivatives approximated."
t0 = time()
x = fmin_slsqp(testfunc, [-1.0,1.0], args=(-1.0,), iprint=2, full_output=1)
print "Elapsed time:", 1000*(time()-t0), "ms"
print "Results",x
print "\n\n"

print "Unbounded optimization.  Derivatives provided."
t0 = time()
x = fmin_slsqp(testfunc, [-1.0,1.0], args=(-1.0,), iprint=2, full_output=1)
print "Elapsed time:", 1000*(time()-t0), "ms"
print "Results",x
print "\n\n"

print "Bound optimization.  Derivatives approximated."
t0 = time()
x = fmin_slsqp(testfunc, [-1.0,1.0], args=(-1.0,),
               eqcons=[lambda x, y: x[0]-x[1] ], iprint=2, full_output=1)
print "Elapsed time:", 1000*(time()-t0), "ms"
print "Results",x
print "\n\n"

print "Bound optimization (equality constraints).  Derivatives provided."
t0 = time()
x = fmin_slsqp(testfunc, [-1.0,1.0], fprime=testfunc_deriv, args=(-1.0,),
               eqcons=[lambda x, y: x[0]-x[1] ], iprint=2, full_output=1)
print "Elapsed time:", 1000*(time()-t0), "ms"
print "Results",x
print "\n\n"

print "Bound optimization (equality and inequality constraints)."
print "Derivatives provided."
```

```
t0 = time()
x = fmin_slsqp(testfunc,[-1.0,1.0], fprime=testfunc_deriv, args=(-1.0,),
               eqcons=[lambda x, y: x[0]-x[1] ],
               ieqcons=[lambda x, y: x[0]-.5], iprint=2, full_output=1)
print "Elapsed time:", 1000*(time()-t0), "ms"
print "Results",x
print "\n\n"


def test_eqcons(d,*args):
    try:
        sign = args[0]
    except:
        sign = 1.0
    x = d[0]
    y = d[1]
    return array([ x**3-y ])


def test_ieqcons(d,*args):
    try:
        sign = args[0]
    except:
        sign = 1.0
    x = d[0]
    y = d[1]
    return array([ y-1 ])

print "Bound optimization (equality and inequality constraints)."
print "Derivatives provided via functions."
t0 = time()
x = fmin_slsqp(testfunc, [-1.0,1.0], fprime=testfunc_deriv, args=(-1.0,),
               f_eqcons=test_eqcons, f_ieqcons=test_ieqcons,
               iprint=2, full_output=1)
print "Elapsed time:", 1000*(time()-t0), "ms"
print "Results",x
print "\n\n"


def test_fprime_eqcons(d,*args):
    try:
        sign = args[0]
    except:
        sign = 1.0
    x = d[0]
    y = d[1]
    return array([ 3.0*(x**2.0), -1.0 ])


def test_fprime_ieqcons(d,*args):
    try:
        sign = args[0]
    except:
        sign = 1.0
    x = d[0]
    y = d[1]
    return array([ 0.0, 1.0 ])
```

```
print "Bound optimization (equality and inequality constraints)."
print "Derivatives provided via functions."
print "Constraint jacobians provided via functions"
t0 = time()
x = fmin_slsqp(testfunc,[-1.0,1.0], fprime=testfunc_deriv, args=(-1.0,),
               f_eqcons=test_eqcons, f_ieqcons=test_ieqcons,
               fprime_eqcons=test_fprime_eqcons,
               fprime_ieqcons=test_fprime_ieqcons, iprint=2, full_output=1)
print "Elapsed time:", 1000*(time()-t0), "ms"
print "Results",x
print "\n\n"
```

1.5.6 Scalar function minimizers

Often only the minimum of a scalar function is needed (a scalar function is one that takes a scalar as input and returns a scalar output). In these circumstances, other optimization techniques have been developed that can work faster.

Unconstrained minimization (`brent`)

There are actually two methods that can be used to minimize a scalar function (`brent` and `golden`), but `golden` is included only for academic purposes and should rarely be used. The brent method uses Brent's algorithm for locating a minimum. Optimally a bracket 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).

Bounded minimization (`fminbound`)

Thus far all of the minimization routines described have been unconstrained minimization routines. Very often, however, there are constraints that can be placed on the solution space before minimization occurs. The `fminbound` function 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.

For example, to find the minimum of $J_1(x)$ near $x = 5$, `fminbound` can be called using the interval $[4, 7]$ as a constraint. The result is $x_{\min} = 5.3314$:

```
>>> from scipy.special import j1
>>> from scipy.optimize import fminbound
>>> xmin = fminbound(j1, 4, 7)
>>> print xmin
5.33144184241
```

1.5.7 Root finding

Sets of equations

To find the roots of a polynomial, the command `roots` is useful. To find a root of a set of non-linear equations, the command `fsolve` is needed. For example, the following example finds the roots of the single-variable transcendental equation

$$x + 2\cos(x) = 0,$$

and the set of non-linear equations

$$\begin{aligned} x_0 \cos(x_1) &= 4, \\ x_0 x_1 - x_1 &= 5. \end{aligned}$$

The results are $x = -1.0299$ and $x_0 = 6.5041$, $x_1 = 0.9084$.

```
>>> def func(x):
...     return x + 2*cos(x)

>>> def func2(x):
...     out = [x[0]*cos(x[1]) - 4]
...     out.append(x[1]*x[0] - x[1] - 5)
...     return out

>>> from scipy.optimize import fsolve
>>> x0 = fsolve(func, 0.3)
>>> print x0
-1.02986652932

>>> x02 = fsolve(func2, [1, 1])
>>> print x02
[ 6.50409711  0.90841421]
```

Scalar function root finding

If one has a single-variable equation, there are four different root finder algorithms that can be tried. Each of these root finding algorithms requires the endpoints of an interval where a root is suspected (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.

1.6 Interpolation (`scipy.interpolate`)

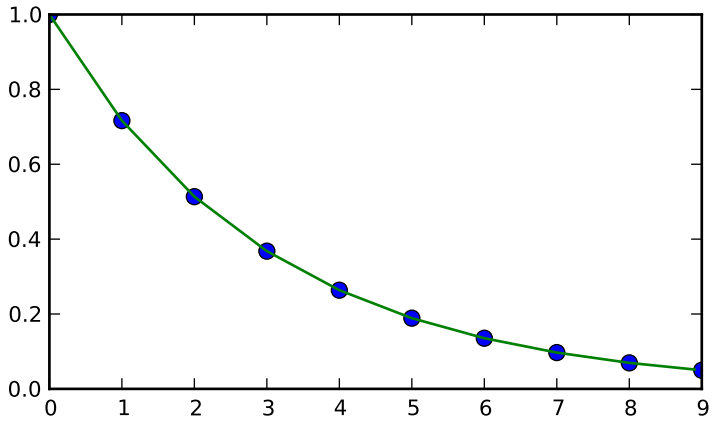
Contents

There are two general interpolation facilities available in SciPy. The first facility is an interpolation class which performs linear 1-dimensional interpolation. The second facility is based on the FORTRAN library FITPACK and provides functions for 1- and 2-dimensional (smoothed) cubic-spline interpolation.

1.6.1 Linear 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 by treated like a function which interpolates between known data values to obtain unknown values (it also has a docstring for help). Behavior at the boundary can be specified at instantiation time. The following example demonstrates it's use.

```
>>> import numpy as np
>>> 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)
>>> import matplotlib.pyplot as plt
>>> plt.plot(x,y,'o',xnew,f(xnew),'-')
```



1.6.2 Spline interpolation in 1-d (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 was 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 keword 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** $\mathbf{s} = 0$ **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`, `splade`) 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.

```
>>> 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
>>>     return out
>>>
>>> yint = integ(xnew,tck)
>>> plt.figure()
```

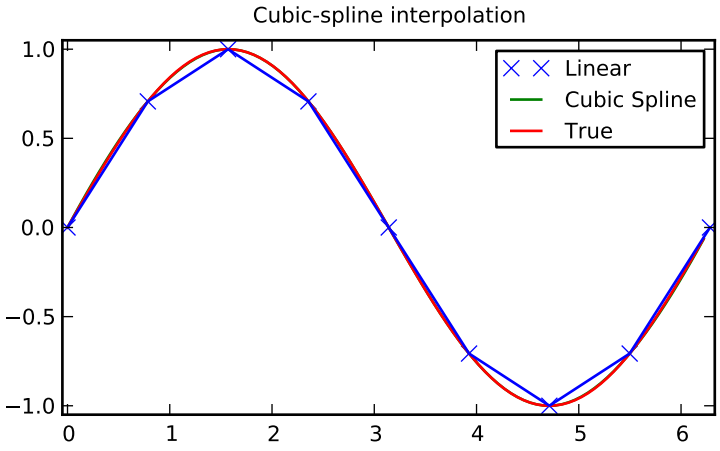
```
>>> plt.plot(xnew,yint,xnew,-np.cos(xnew),'--')
>>> plt.legend(['Cubic Spline', 'True'])
>>> plt.axis([-0.05,6.33,-1.05,1.05])
>>> plt.title('Integral estimation from spline')
>>> plt.show()
```

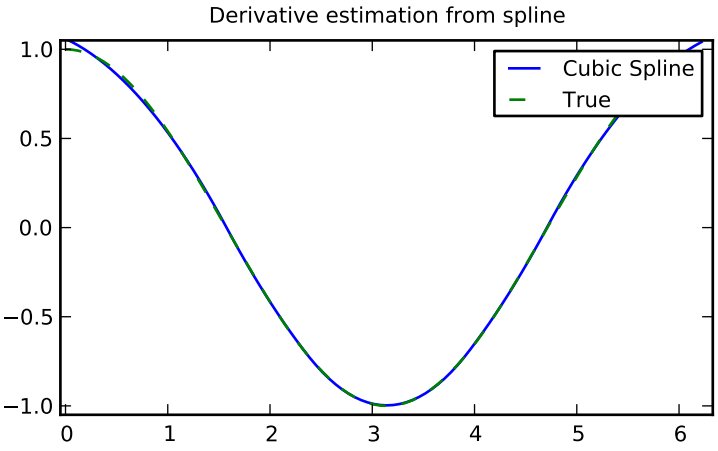
Roots of spline

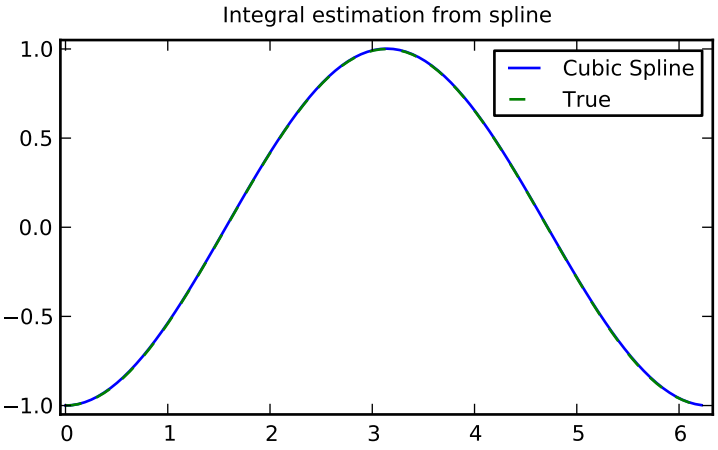
```
>>> print interpolate.sproot(tck)
[ 0.      3.1416]
```

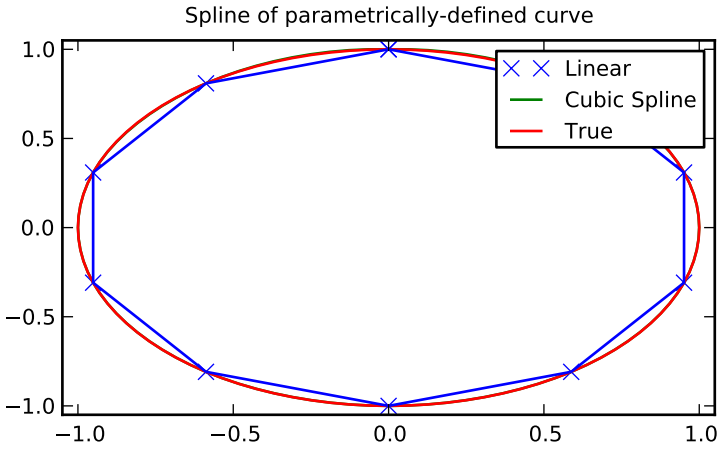
Parametric spline

```
>>> 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()
```




Derivative estimation from spline
Cubic Spline
True
1.0
0.5
0.0
−0.5
−1.0
0
1
2
3
4
5
6


Integral estimation from spline
Cubic Spline
True
1.0
0.5
0.0
−0.5
−1.0
0
1
2
3
4
5
6



1.6.3 Two-dimensional spline representation (`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 SciPy 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`.

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

Define function over sparse 20x20 grid

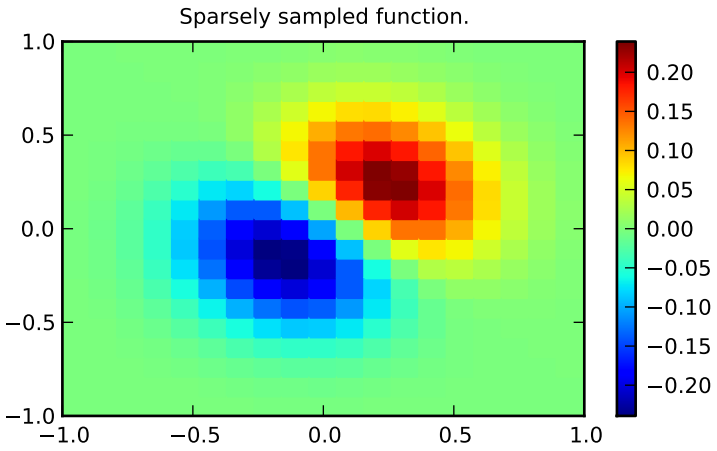
```
>>> x,y = np.mgrid[-1:1:20j,-1:1:20j]
>>> z = (x+y)*np.exp(-6.0*(x*x+y*y))
```

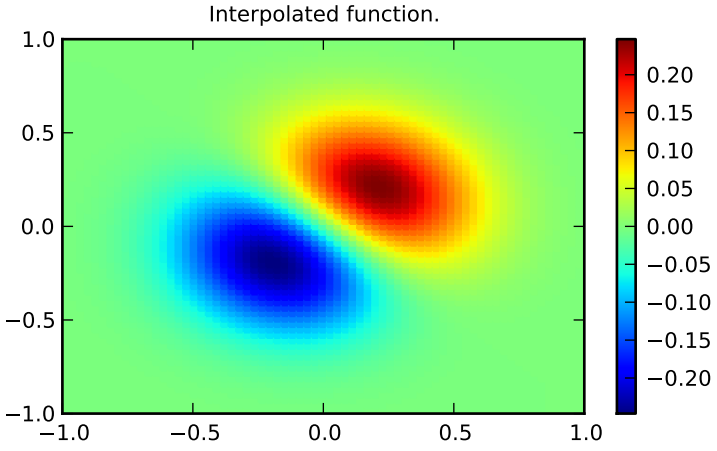
```
>>> plt.figure()
>>> plt.pcolor(x,y,z)
>>> plt.colorbar()
>>> plt.title("Sparsely sampled function.")
>>> plt.show()
```

Interpolate function over new 70x70 grid

```
>>> 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()
```





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.

2-d Example

This example shows how to interpolate scattered 2d data.

1.7 Signal Processing (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.

1.7.1 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 Δx , then the B-spline approximation to a 1-dimensional function is the finite-basis expansion.

$$y\left(x\right) \approx \sum_{j} c_{j} \beta^{o}\left(\frac{x}{\Delta x} - j\right).$$

In two dimensions with knot-spacing Δx and Δy , the function representation is

$$z\left(x,y\right) \approx \sum_{j}\sum_{k} c_{jk} \beta^{o}\left(\frac{x}{\Delta x} - j\right) \beta^{o}\left(\frac{y}{\Delta y} - k\right).$$

In these expressions, $\beta^{o}\left(\cdot\right)$ 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

$$y''\left(x\right) = \frac{1}{\Delta x^{2}} \sum_{j} c_{j} \beta^{o\prime\prime}\left(\frac{x}{\Delta x} - j\right).$$

Using the property of B-splines that

$$\frac{d^{2}\beta^{o}\left(w\right)}{dw^{2}} = \beta^{o-2}\left(w+1\right) - 2\beta^{o-2}\left(w\right) + \beta^{o-2}\left(w-1\right)$$

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,

$$\begin{aligned}\Delta x^2\, y'(x)|_{x=n\Delta x} &= \sum_j c_j\delta_{n-j+1} - 2c_j\delta_{n-j} + c_j\delta_{n-j-1},\\ &= c_{n+1} - 2c_n + c_{n-1}.\end{aligned}$$

Thus, the second-derivative signal can be easily calculated from the spline fit. if desired, smoothing splines can be found to make the second-derivative less sensitive to random-errors.

The savvy reader will have already noticed that the data samples are related to the knot coefficients via a convolution operator, so that simple convolution with the sampled B-spline function recovers the original data from the spline coefficients. The output of convolutions can change depending on how boundaries are handled (this becomes increasingly more important as the number of dimensions in the data- set increases). The algorithms relating to B-splines in the signal- processing sub package assume mirror-symmetric boundary conditions. Thus, spline coefficients are computed based on that assumption, and data-samples can be recovered exactly from the spline coefficients by assuming them to be mirror-symmetric also.

Currently the package provides functions for determining second- and third-order cubic spline coefficients from equally spaced samples in one- and two-dimensions (`signal.qspline1d`, `signal.qspline2d`, `signal.cspline1d`, `signal.cspline2d`). The package also supplies a function (`signal.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 $\sigma_o = (o+1)/12$:

$$\beta^o(x) \approx \frac{1}{\sqrt{2\pi\sigma_o^2}}\exp\left(-\frac{x^2}{2\sigma_o}\right).$$

A function to compute this Gaussian for arbitrary x and o is also available (`signal.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 `lena`. The command `signal.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 `signal.convolve2d` which convolves arbitrary two-dimensional filters and allows for choosing mirror-symmetric boundary conditions.

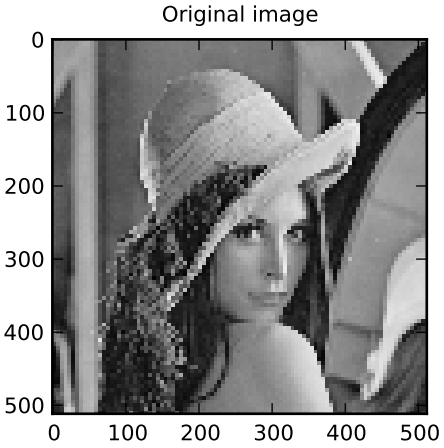
```
>>> from numpy import *
>>> from scipy import signal, misc
>>> import matplotlib.pyplot as plt


>>> image = misc.lena().astype(float32)
>>> derfilt = array([1.0,-2,1.0],float32)
>>> ck = signal.cspline2d(image,8.0)
>>> deriv = signal.sepfir2d(ck, derfilt, [1]) + \
>>>         signal.sepfir2d(ck, [1], derfilt)
```

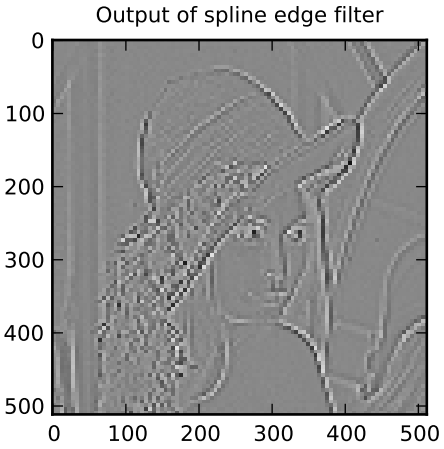
Alternatively we could have done:

```
laplacian = array([[0,1,0],[1,-4,1],[0,1,0]],float32)
deriv2 = signal.convolve2d(ck,laplacian,mode='same',boundary='symm')
```

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

```
>>> plt.figure()
>>> plt.imshow(deriv)
>>> plt.gray()
>>> plt.title('Output of spline edge filter')
>>> plt.show()
```





1.7.2 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 512×512 image with this method would require multiplication of a $512^2 x 512^2$ 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

$$\begin{aligned}
y[0] &= x[0]\, h[0] \\
y[1] &= x[0]\, h[1] + x[1]\, h[0] \\
y[2] &= x[0]\, h[2] + x[1]\, h[1] + x[2]\, h[0] \\
&\vdots \\
y[M] &= x[0]\, h[M] + x[1]\, h[M-1] + \cdots + x[M]\, h[0] \\
y[M+1] &= x[1]\, h[M] + x[2]\, h[M-1] + \cdots + x[M+1]\, h[0] \\
&\vdots \\
y[K] &= x[K-M]\, h[M] + \cdots + x[K]\, h[0] \\
y[K+1] &= x[K+1-M]\, h[M] + \cdots + x[K]\, h[1] \\
&\vdots \\
y[K+M-1] &= x[K-1]\, h[M] + x[K]\, h[M-1] \\
y[K+M] &= x[K]\, h[M].
\end{aligned}$$

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 `signal.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 largest 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.

This same function `signal.convolve` can actually take N -dimensional arrays as inputs and will return the N -dimensional convolution of the two arrays. The same input flags are available for that case as well.

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

$$\begin{aligned}
w[-K] &= y[K]\, x[0] \\
w[-K+1] &= y[K-1]\, x[0] + y[K]\, x[1] \\
&\vdots \\
w[M-K] &= y[K-M]\, x[0] + y[K-M+1]\, x[1] + \cdots + y[K]\, x[M] \\
w[M-K+1] &= y[K-M-1]\, x[0] + \cdots + y[K-1]\, x[M] \\
&\vdots \\
w[-1] &= y[1]\, x[0] + y[2]\, x[1] + \cdots + y[M+1]\, x[M] \\
w[0] &= y[0]\, x[0] + y[1]\, x[1] + \cdots + y[M]\, x[M] \\
w[1] &= y[0]\, x[1] + y[1]\, x[2] + \cdots + y[M-1]\, x[M] \\
w[2] &= y[0]\, x[2] + y[1]\, x[3] + \cdots + y[M-2]\, x[M] \\
&\vdots \\
w[M-1] &= y[0]\, x[M-1] + y[1]\, x[M] \\
w[M] &= y[0]\, x[M].
\end{aligned}$$

The SciPy function `signal.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 $w\left[-K+\left\lfloor\frac{M-1}{2}\right\rfloor\right]$ ('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 `signal.correlate` can also take arbitrary N -dimensional arrays as input and return the N -dimensional convolution of the two arrays on output.

When $N = 2$, `signal.correlate` and/or `signal.convolve` can be used to construct arbitrary image filters to perform actions such as blurring, enhancing, and edge-detection for an image.

Convolution is mainly used for filtering when one of the signals is much smaller than the other ($K \gg M$), otherwise linear filtering is more easily accomplished in the frequency domain (see Fourier Transforms).

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 it's 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 then 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 $a_0 = 1$).

$$\begin{aligned}
y[n] &= b_0 x[n] + z_0[n-1] \\
z_0[n] &= b_1 x[n] + z_1[n-1] - a_1 y[n] \\
z_1[n] &= b_2 x[n] + z_2[n-1] - a_2 y[n] \\
&\vdots \quad \vdots \quad \vdots \\
z_{K-2}[n] &= b_{K-1} x[n] + z_{K-1}[n-1] - a_{K-1} y[n] \\
z_{K-1}[n] &= b_K x[n] - a_K y[n],
\end{aligned}$$

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 `signal.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 $0 \leq m < K$,

$$z_m[n] = \sum_{p=0}^{K-m-1} \left(b_{m+p+1} x[n-p] - a_{m+p+1} y[n-p] \right).$$

Using this formula we can find the intial condition vector $z_0[-1]$ to $z_{K-1}[-1]$ given initial conditions on y (and x). The command `signal.lfiltic` performs this function.

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 `signal.medfilt` . A specialized version that works only for two-dimensional arrays is available as `signal.medfilt2d` .

Order Filter

A median filter is a specific example of a more general class of filters called order filters. To compute the output at a particular pixel, all order filters use the array values in a region surrounding that pixel. These array values are sorted and then one of them is selected as the output value. For the median filter, the sample median of the list of array values is used as the output. A general order filter allows the user to select which of the sorted values will be used as the output. So, for example one could choose to pick the maximum in the list or the minimum. The order filter takes an additional argument besides the input array and the region mask that specifies which of the elements in the sorted list of neighbor array values should be used as the output. The command to perform an order filter is `signal.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

$$y = \begin{cases} \frac{\sigma^2}{\sigma_x^2} m_x + \left(1 - \frac{\sigma^2}{\sigma_x^2}\right) x & \sigma_x^2 \geq \sigma^2, \\ m_x & \sigma_x^2 < \sigma^2. \end{cases}$$

Where m_x is the local estimate of the mean and σ_x^2 is the local estimate of the variance. The window for these estimates is an optional input parameter (default is 3×3). The parameter σ^2 is a threshold noise parameter. If σ 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.

1.8 Linear Algebra

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. There is a matrix class defined in Numpy, which you can initialize with an appropriate Numpy array in order to get objects for which multiplication is matrix-multiplication instead of the default, element-by-element multiplication.

1.8.1 Matrix Class

The matrix class is initialized with the SciPy command `mat` which is just convenient short-hand for `matrix`. If you are going to be doing a lot of matrix-math, it is convenient to convert arrays into matrices using this command. One advantage of using the `mat` command is that you can enter two-dimensional matrices using MATLAB-like syntax with commas or spaces separating columns and semicolons separting rows as long as the matrix is placed in a string passed to `mat` .

1.8.2 Basic routines

Finding Inverse

The inverse of a matrix $\mathbf{A}$ is the matrix $\mathbf{B}$ such that $\mathbf{AB} = \mathbf{I}$ where $\mathbf{I}$ is the identity matrix consisting of ones down the main diagonal. Usually $\mathbf{B}$ is denoted $\mathbf{B} = \mathbf{A}^{-1}$. 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

$$\mathbf{A} = \begin{bmatrix} 1 & 3 & 5 \\ 2 & 5 & 1 \\ 2 & 3 & 8 \end{bmatrix}$$

then

$$\mathbf{A^{-1}} = \frac{\mathbf{1}}{\mathbf{25}} \begin{bmatrix} -37 & 9 & 22 \\ 14 & 2 & -9 \\ 4 & -3 & 1 \end{bmatrix} = \begin{bmatrix} -1.48 & 0.36 & 0.88 \\ 0.56 & 0.08 & -0.36 \\ 0.16 & -0.12 & 0.04 \end{bmatrix}.$$

The following example demonstrates this computation in SciPy

```
>>> A = mat('[1 3 5; 2 5 1; 2 3 8]')
>>> A
matrix([[1, 3, 5],
        [2, 5, 1],
        [2, 3, 8]])
>>> A.I
matrix([[-1.48,  0.36,  0.88],
        [ 0.56,  0.08, -0.36],
        [ 0.16, -0.12,  0.04]])
>>> from scipy import linalg
>>> linalg.inv(A)
array([[-1.48,  0.36,  0.88],
       [ 0.56,  0.08, -0.36],
       [ 0.16, -0.12,  0.04]])
```

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 symmetrix matrix is offered which can speed up the processing when applicable. As an example, suppose it is desired to solve the following simultaneous equations:

$$\begin{aligned} x + 3y + 5z &= 10 \\ 2x + 5y + z &= 8 \\ 2x + 3y + 8z &= 3 \end{aligned}$$

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:

```
>>> A = mat('[1 3 5; 2 5 1; 2 3 8]')
>>> b = mat('[10;8;3]')
>>> A.I*b
matrix([[-9.28],
        [ 5.16],
        [ 0.76]])
>>> linalg.solve(A,b)
array([[-9.28],
       [ 5.16],
       [ 0.76]])
```

Finding Determinant

The determinant of a square matrix $\mathbf{A}$ is often denoted $|\mathbf{A}|$ and is a quantity often used in linear algebra. Suppose a_{ij} are the elements of the matrix $\mathbf{A}$ and let $M_{ij} = |\mathbf{A}_{ij}|$ be the determinant of the matrix left by removing the i^{th} row and j^{th} column from $\mathbf{A}$. Then for any row i,

$$|\mathbf{A}| = \sum_j (-1)^{i+j} a_{ij} M_{ij}.$$

This is a recursive way to define the determinant where the base case is defined by accepting that the determinant of a 1×1 matrix is the only matrix element. In SciPy the determinant can be calculated with `linalg.det` . For example, the determinant of

$$\mathbf{A} = \begin{bmatrix} 1 & 3 & 5 \\ 2 & 5 & 1 \\ 2 & 3 & 8 \end{bmatrix}$$

is

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

In SciPy this is computed as shown in this example:

```
>>> A = mat('[1 3 5; 2 5 1; 2 3 8]')
>>> linalg.det(A)
-25.000000000000004
```

Computing norms

Matrix and vector norms can also be computed with SciPy. A wide range of norm definitions are available using different parameters to the order argument of `linalg.norm` . This function takes a rank-1 (vectors) or a rank-2 (matrices) array and an optional order argument (default is 2). Based on these inputs a vector or matrix norm of the requested order is computed.

For vector *x* , the order parameter can be any real number including `inf` or `-inf`. The computed norm is

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

For matrix $\mathbf{A}$ the only valid values for norm are $\pm 2, \pm 1, \pm$ inf, and 'fro' (or 'f') Thus,

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

where σ_i are the singular values of $\mathbf{A}$.

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 $\mathbf{x}_i$ through a set of coefficients c_j and model functions $f_j\left(\mathbf{x}_i\right)$ via the model

$$y_i = \sum_j c_j f_j\left(\mathbf{x}_i\right) + \epsilon_i$$

where ϵ_i represents uncertainty in the data. The strategy of least squares is to pick the coefficients c_j to minimize

$$J\left(\mathbf{c}\right) = \sum_i \left| y_i - \sum_j c_j f_j\left(x_i\right) \right|^2 .$$

Theoretically, a global minimum will occur when

$$\frac{\partial J}{\partial c_n^*} = 0 = \sum_i \left(y_i - \sum_j c_j f_j\left(x_i\right) \right) \left(-f_n^*\left(x_i\right)\right)$$

or

$$\begin{aligned} \sum_j c_j \sum_i f_j\left(x_i\right) f_n^*\left(x_i\right) &= \sum_i y_i f_n^*\left(x_i\right) \\ \mathbf{A}^H\mathbf{A}\mathbf{c} &= \mathbf{A}^H\mathbf{y} \end{aligned}$$

where

$$\left\{\mathbf{A}\right\}_{ij} = f_j\left(x_i\right).$$

When $\mathbf{A^H A}$ is invertible, then

$$\mathbf{c} = \left(\mathbf{A}^H\mathbf{A}\right)^{-1}\mathbf{A}^H\mathbf{y} = \mathbf{A}^\dagger\mathbf{y}$$

where $\mathbf{A}^\dagger$ is called the pseudo-inverse of $\mathbf{A}$. Notice that using this definition of $\mathbf{A}$ the model can be written

$$\mathbf{y} = \mathbf{A}\mathbf{c} + \boldsymbol{\epsilon}.$$

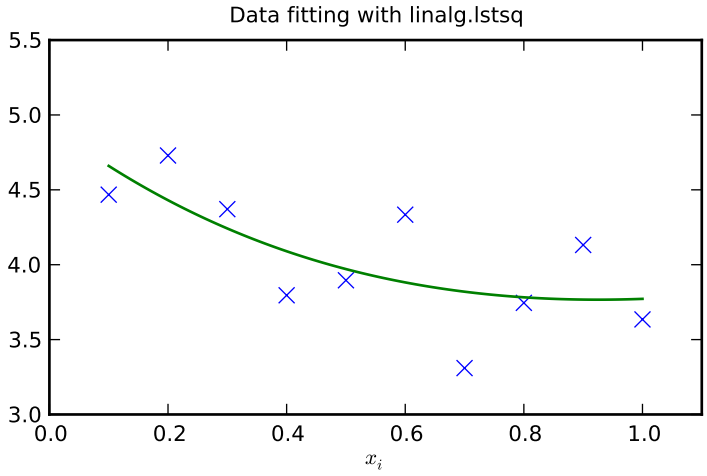
The command `linalg.lstsq` will solve the linear least squares problem for $\mathbf{c}$ given $\mathbf{A}$ and $\mathbf{y}$. In addition `linalg.pinv` or `linalg.pinv2` (uses a different method based on singular value decomposition) will find $\mathbf{A}^\dagger$ given $\mathbf{A}$.

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 $x_i = 0.1i$ 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.

```
>>> from numpy import *
>>> from scipy import linalg
>>> import matplotlib.pyplot as plt

>>> c1,c2= 5.0,2.0
>>> i = r_[1:11]
>>> xi = 0.1*i
>>> yi = c1*exp(-xi)+c2*xi
>>> zi = yi + 0.05*max(yi)*random.randn(len(yi))

>>> A = c_[exp(-xi)[:,newaxis],xi[:,newaxis]]
>>> c,resid,rank,sigma = linalg.lstsq(A,zi)

>>> xi2 = r_[0.1:1.0:100j]
>>> yi2 = c[0]*exp(-xi2) + c[1]*xi2

>>> plt.plot(xi,zi,'x',xi2,yi2)
>>> plt.axis([0,1.1,3.0,5.5])
>>> plt.xlabel('$x_i$')
>>> plt.title('Data fitting with linalg.lstsq')
>>> plt.show()
```



Generalized inverse

The generalized inverse is calculated using the command `linalg.pinv` or `linalg.pinv2`. These two commands differ in how they compute the generalized inverse. The first uses the linalg.lstsq algorithm while the second uses singular value decomposition. Let $\mathbf{A}$ be an $M \times N$ matrix, then if $M > N$ the generalized inverse is

$$\mathbf{A}^{\dagger} = \left(\mathbf{A}^H \mathbf{A}\right)^{-1} \mathbf{A}^H$$

while if $M < N$ matrix the generalized inverse is

$$\mathbf{A}^{\#} = \mathbf{A}^H \left(\mathbf{A}\mathbf{A}^H\right)^{-1}.$$

In both cases for $M = N$, then

$$\mathbf{A}^{\dagger} = \mathbf{A}^{\#} = \mathbf{A}^{-1}$$

as long as $\mathbf{A}$ is invertible.

1.8.3 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 $\mathbf{A}$ scalars λ and corresponding vectors $\mathbf{v}$ such that

$$\mathbf{A}\mathbf{v} = \lambda\mathbf{v}.$$

For an $N \times N$ matrix, there are N (not necessarily distinct) eigenvalues — roots of the (characteristic) polynomial

$$|\mathbf{A} - \lambda\mathbf{I}| = 0.$$

The eigenvectors, $\mathbf{v}$, are also sometimes called right eigenvectors to distinguish them from another set of left eigenvectors that satisfy

$$\mathbf{v}_L^H\mathbf{A} = \lambda\mathbf{v}_L^H$$

or

$$\mathbf{A}^H\mathbf{v}_L = \lambda^*\mathbf{v}_L.$$

With it's default optional arguments, the command `linalg.eig` returns λ and $\mathbf{v}$. However, it can also return $\mathbf{v}_L$ and just λ by itself (`linalg.eigvals` returns just λ as well).

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

$$\begin{aligned}\mathbf{A}\mathbf{v} &= \lambda\mathbf{B}\mathbf{v}\\ \mathbf{A}^H\mathbf{v}_L &= \lambda^*\mathbf{B}^H\mathbf{v}_L\end{aligned}$$

for square matrices $\mathbf{A}$ and $\mathbf{B}$. The standard eigenvalue problem is an example of the general eigenvalue problem for $\mathbf{B} = \mathbf{I}$. When a generalized eigenvalue problem can be solved, then it provides a decomposition of $\mathbf{A}$ as

$$\mathbf{A} = \mathbf{B}\mathbf{V}\mathbf{\Lambda}\mathbf{V}^{-1}$$

where $\mathbf{V}$ is the collection of eigenvectors into columns and $\mathbf{\Lambda}$ 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 $\|\mathbf{v}\|^2 = \sum_i v_i^2 = 1$.

As an example, consider finding the eigenvalues and eigenvectors of the matrix

$$\mathbf{A} = \begin{bmatrix} 1 & 5 & 2 \\ 2 & 4 & 1 \\ 3 & 6 & 2 \end{bmatrix}.$$

The characteristic polynomial is

$$\begin{aligned}|\mathbf{A} - \lambda\mathbf{I}| &= (1-\lambda)\left[(4-\lambda)(2-\lambda) - 6\right] - \\ &\quad 5\left[2(2-\lambda) - 3\right] + 2\left[12 - 3(4-\lambda)\right] \\ &= -\lambda^3 + 7\lambda^2 + 8\lambda - 3.\end{aligned}$$

The roots of this polynomial are the eigenvalues of $\mathbf{A}$:

$$\begin{aligned}\lambda_1 &= 7.9579\\ \lambda_2 &= -1.2577\\ \lambda_3 &= 0.2997.\end{aligned}$$

The eigenvectors corresponding to each eigenvalue can be found using the original equation. The eigenvectors associated with these eigenvalues can then be found.

```
>>> from scipy import linalg
>>> A = mat('[1 5 2; 2 4 1; 3 6 2]')
>>> la,v = linalg.eig(A)
>>> l1,l2,l3 = la
>>> print l1, l2, l3
(7.95791620491+0j) (-1.25766470568+0j) (0.299748500767+0j)


>>> print v[:,0]
[-0.5297175  -0.44941741 -0.71932146]
>>> print v[:,1]
[-0.90730751  0.28662547  0.30763439]
>>> print v[:,2]
[ 0.28380519 -0.39012063  0.87593408]
>>> print sum(abs(v**2),axis=0)
[ 1.  1.  1.]


>>> v1 = mat(v[:,0]).T
>>> print max(ravel(abs(A*v1-l1*v1)))
8.881784197e-16
```

Singular value decomposition

Singular Value Decompostion (SVD) can be thought of as an extension of the eigenvalue problem to matrices that are not square. Let $\mathbf{A}$ be an $M \times N$ matrix with M and N arbitrary. The matrices $\mathbf{A}^H\mathbf{A}$ and $\mathbf{A}\mathbf{A}^H$ are square hermitian matrices [1] of size $N \times N$ and $M \times M$ respectively. It is known that the eigenvalues of square hermitian matrices are real and non-negative. In addtion, there are at most $\min(M, N)$ identical non-zero eigenvalues of $\mathbf{A}^H\mathbf{A}$ and $\mathbf{A}\mathbf{A}^H$. Define these positive eigenvalues as σ_i^2. The square-root of these are called singular values of $\mathbf{A}$. The eigenvectors of $\mathbf{A}^H\mathbf{A}$ are collected by columns into an $N \times N$ unitary [2] matrix $\mathbf{V}$ while the eigenvectors of $\mathbf{A}\mathbf{A}^H$ are collected by columns in the unitary matrix $\mathbf{U}$, the singular values are collected in an $M \times N$ zero matrix $\mathbf{\Sigma}$ with main diagonal entries set to the singular values. Then

$$\mathbf{A} = \mathbf{U}\mathbf{\Sigma}\mathbf{V}^H$$

is the singular-value decomposition of $\mathbf{A}$. Every matrix has a singular value decomposition. Sometimes, the singular values are called the spectrum of $\mathbf{A}$. The command `linalg.svd` will return $\mathbf{U}$, $\mathbf{V}^H$, and σ_i as an array of the singular values. To obtain the matrix $\mathbf{\Sigma}$ use `linalg.diagsvd`. The following example illustrates the use of `linalg.svd`.

```
>>> A = mat('[1 3 2; 1 2 3]')
>>> M,N = A.shape
>>> U,s,Vh = linalg.svd(A)
>>> Sig = mat(linalg.diagsvd(s,M,N))
>>> U, Vh = mat(U), mat(Vh)
```

[1] A hermitian matrix $\mathbf{D}$ satisfies $\mathbf{D}^H = \mathbf{D}$.
[2] A unitary matrix $\mathbf{D}$ satisfies $\mathbf{D}^H\mathbf{D} = \mathbf{I} = \mathbf{D}\mathbf{D}^H$ so that $\mathbf{D}^{-1} = \mathbf{D}^H$.

```
>>> print U
[[-0.70710678 -0.70710678]
 [-0.70710678  0.70710678]]
>>> print Sig
[[ 5.19615242  0.          0.        ]
 [ 0.          1.          0.        ]]
>>> print Vh
[[ -2.72165527e-01  -6.80413817e-01  -6.80413817e-01]
 [ -6.18652536e-16  -7.07106781e-01   7.07106781e-01]
 [ -9.62250449e-01   1.92450090e-01   1.92450090e-01]]

>>> print A
[[1 3 2]
 [1 2 3]]
>>> print U*Sig*Vh
[[ 1.  3.  2.]
 [ 1.  2.  3.]]
```

LU decomposition

The LU decompostion finds a representation for the $M \times N$ matrix $\mathbf{A}$ as

$$\mathbf{A} = \mathbf{PLU}$$

where $\mathbf{P}$ is an $M \times M$ permutation matrix (a permutation of the rows of the identity matrix), $\mathbf{L}$ is in $M \times K$ lower triangular or trapezoidal matrix ($K = \min(M, N)$) with unit-diagonal, and $\mathbf{U}$ 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

$$\mathbf{A}\mathbf{x}_i = \mathbf{b}_i$$

for many different $\mathbf{b}_i$. The LU decomposition allows this to be written as

$$\mathbf{PLU}\mathbf{x}_i = \mathbf{b}_i.$$

Because $\mathbf{L}$ is lower-triangular, the equation can be solved for $\mathbf{U}\mathbf{x}_i$ and finally $\mathbf{x}_i$ very rapidly using forward- and back-substitution. An initial time spent factoring $\mathbf{A}$ 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 $\mathbf{A} = \mathbf{A}^H$ and $\mathbf{x}^H\mathbf{A}\mathbf{x} \geq 0$ for all $\mathbf{x}$, then decompositions of $\mathbf{A}$ can be found so that

$$\begin{aligned} \mathbf{A} &= \mathbf{U}^H\mathbf{U} \\ \mathbf{A} &= \mathbf{L}\mathbf{L}^H \end{aligned}$$

where $\mathbf{L}$ is lower-triangular and $\mathbf{U}$ is upper triangular. Notice that $\mathbf{L} = \mathbf{U}^H$. The command `linagl.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 $\mathbf{Q}$ and an $M \times N$ upper-trapezoidal matrix $\mathbf{R}$ such that

$$\mathbf{A} = \mathbf{QR}.$$

Notice that if the SVD of $\mathbf{A}$ is known then the QR decomposition can be found

$$\mathbf{A} = \mathbf{U\Sigma V}^H = \mathbf{QR}$$

implies that $\mathbf{Q} = \mathbf{U}$ and $\mathbf{R} = \mathbf{\Sigma V}^H$. Note, however, that in SciPy independent algorithms are used to find QR and SVD decompositions. The command for QR decomposition is `linalg.qr` .

Schur decomposition

For a square $N \times N$ matrix, $\mathbf{A}$, the Schur decomposition finds (not-necessarily unique) matrices $\mathbf{T}$ and $\mathbf{Z}$ such that

$$\mathbf{A} = \mathbf{ZTZ}^H$$

where $\mathbf{Z}$ is a unitary matrix and $\mathbf{T}$ 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 $\mathbf{T}$ and $\mathbf{Z}$ are real-valued when $\mathbf{A}$ is real-valued. When $\mathbf{A}$ is a real-valued matrix the real schur form is only quasi-upper triangular because 2×2 blocks extrude from the main diagonal corresponding to any complex- valued eigenvalues. The command `linalg.schur` finds the Schur decomposition while the command `linalg.rsf2csf` converts $\mathbf{T}$ and $\mathbf{Z}$ 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:

```
>>> 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   1.33226763e-15   8.88178420e-16]
```

```
 [  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]
 [  2.88899660e-15   8.44927041e-15   9.77322008e-15]
 [  3.11291538e-15   1.15463228e-14   1.15464861e-14]]
>>> print abs(A-Z2*T2*Z2.H) # same
[[  3.34058710e-16   8.88611201e-16   4.18773089e-18]
 [  1.48694940e-16   8.95109973e-16   8.92966151e-16]
 [  1.33228956e-15   1.33582317e-15   3.55373104e-15]]
```

1.8.4 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 $\mathbf{A}$ as

$$f(\mathbf{A}) = \sum_{k=0}^{\infty} \frac{f^{(k)}(0)}{k!} \mathbf{A}^k.$$

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

$$e^{\mathbf{A}} = \sum_{k=0}^{\infty} \frac{1}{k!} \mathbf{A}^k.$$

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 $\mathbf{A}$:

$$\mathbf{A} = \mathbf{V}\mathbf{\Lambda}\mathbf{V}^{-1}$$

and note that

$$e^{\mathbf{A}} = \mathbf{V}e^{\mathbf{\Lambda}}\mathbf{V}^{-1}$$

where the matrix exponential of the diagonal matrix $\mathbf{\Lambda}$ 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.

$$\mathbf{A} \equiv \exp(\log(\mathbf{A})).$$

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

$$\begin{aligned}\sin(\mathbf{A}) &= \frac{e^{j\mathbf{A}} - e^{-j\mathbf{A}}}{2j} \\ \cos(\mathbf{A}) &= \frac{e^{j\mathbf{A}} + e^{-j\mathbf{A}}}{2}.\end{aligned}$$

The tangent is

$$\tan(x) = \frac{\sin(x)}{\cos(x)} = [\cos(x)]^{-1}\sin(x)$$

and so the matrix tangent is defined as

$$[\cos(\mathbf{A})]^{-1}\sin(\mathbf{A}).$$

Hyperbolic trigonometric functions

The hyperbolic trigonemetric functions sinh , cosh , and tanh can also be defined for matrices using the familiar definitions:

$$\begin{aligned}\sinh(\mathbf{A}) &= \frac{e^{\mathbf{A}} - e^{-\mathbf{A}}}{2} \\ \cosh(\mathbf{A}) &= \frac{e^{\mathbf{A}} + e^{-\mathbf{A}}}{2} \\ \tanh(\mathbf{A}) &= [\cosh(\mathbf{A})]^{-1}\sinh(\mathbf{A}).\end{aligned}$$

These matrix functions can be found using `linalg.sinhm`, `linalg.coshm` , and `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 `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.

```
>>> from scipy import special, random, linalg
>>> A = random.rand(3,3)
>>> B = linalg.funm(A,lambda x: special.jv(0,x))
>>> print A
[[ 0.72578091  0.34105276  0.79570345]
 [ 0.65767207  0.73855618  0.541453  ]
 [ 0.78397086  0.68043507  0.4837898 ]]
>>> print B
[[ 0.72599893 -0.20545711 -0.22721101]
 [-0.27426769  0.77255139 -0.23422637]
 [-0.27612103 -0.21754832  0.7556849 ]]
>>> print linalg.eigvals(A)
[ 1.91262611+0.j  0.21846476+0.j -0.18296399+0.j]
>>> print special.jv(0, linalg.eigvals(A))
[ 0.27448286+0.j  0.98810383+0.j  0.99164854+0.j]
>>> print linalg.eigvals(B)
[ 0.27448286+0.j  0.98810383+0.j  0.99164854+0.j]
```

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

1.9 Statistics

1.9.1 Introduction

SciPy has a tremendous number of basic statistics routines with more 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 had using `info(stats)`.

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 and 10 discrete random variables have been implemented using these classes. The list of the random variables available is in the docstring for the stats sub-package.

Note: The following is work in progress

1.9.2 Distributions

First some imports

```
>>> import numpy as np
>>> from scipy import stats
>>> import warnings
>>> warnings.simplefilter('ignore', DeprecationWarning)
```

We can obtain the list of available distribution through introspection:

```
>>> 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
```

Distributions can be used in one of two ways, either by passing all distribution parameters to each method call or by freezing the parameters for the instance of the distribution. As an example, we can get the median of the distribution by using the percent point function, ppf, which is the inverse of the cdf:

```
>>> print stats.nct.ppf(0.5, 10, 2.5)
2.56880722561
>>> my_nct = stats.nct(10, 2.5)
>>> print my_nct.ppf(0.5)
2.56880722561
```

`help(stats.nct)` prints the complete docstring of the distribution. Instead we can print just some basic information:

```
>>> print stats.nct.extradoc #contains the distribution specific docs
Non-central Student T distribution

                                  df**(df/2) * gamma(df+1)
nct.pdf(x,df,nc) = --------------------------------------------------
                   2**df*exp(nc**2/2)*(df+x**2)**(df/2) * gamma(df/2)
for df > 0, nc > 0.


>>> print 'number of arguments: %d, shape parameters: %s'% (stats.nct.numargs,
...                                                         stats.nct.shapes)
number of arguments: 2, shape parameters: df,nc
>>> print 'bounds of distribution lower: %s, upper: %s' % (stats.nct.a,
...                                                        stats.nct.b)
bounds of distribution lower: -1.#INF, upper: 1.#INF
```

We can list all methods and properties of the distribution with `dir(stats.nct)`. Some of the methods are private methods, that are not named as such, i.e. no leading underscore, for example veccdf or xa and xb are for internal calculation. The main methods we can see when we list the methods of the frozen distribution:

```
>>> print dir(my_nct) #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']
```

The main public methods 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

The main additional methods of the not frozen distribution are related to the estimation of distrition parameters:

- **fit: maximum likelihood estimation of distribution parameters, including location**
  and scale
- est_loc_scale: estimation of location and scale when shape parameters are given
- nnlf: negative log likelihood function

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 location is the mean and scale is the standard deviation. The standardized distribution for a random variable *x* is obtained through `(x - loc) / scale`.

Discrete distribution have most of the same basic methods, however pdf is replaced the probability mass function *pmf*, no estimation methods, such as fit, are available, and scale is not a valid keyword parameter. The location parameter, keyword *loc* can be used to shift the distribution.

The basic methods, pdf, cdf, sf, ppf, and isf are vectorized with `np.vectorize`, and the usual numpy broadcasting is applied. For example, we can calculate the critical values for the upper tail of the t distribution for different probabilites and degrees of freedom.

```
>>> 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 is for 11 d.o.f., i.e. this is the same as

```
>>> stats.t.isf([0.1, 0.05, 0.01], 10)
array([ 1.37218364,  1.81246112,  2.76376946])
>>> stats.t.isf([0.1, 0.05, 0.01], 11)
array([ 1.36343032,  1.79588482,  2.71807918])
```

If both, probabilities and degrees of freedom have the same array shape, then element wise matching is used. As an example, we can obtain the 10% tail for 10 d.o.f., the 5% tail for 11 d.o.f. and the 1% tail for 12 d.o.f. by

```
>>> stats.t.isf([0.1, 0.05, 0.01], [10, 11, 12])
array([ 1.37218364,  1.79588482,  2.68099799])
```

Performance and Remaining Issues

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, 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 are used if the distribution does not specify any explicit calculation. To define a distribution, only one of pdf or cdf is necessary, all other methods can be derived using numeric integration and root finding. 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.

The distributions in scipy.stats have recently been corrected and improved and gained a considerable test suite, however a few issues remain:

- skew and kurtosis, 3rd and 4th moments and entropy are not thoroughly tested and some coarse testing indicates that there are still some incorrect results left.
- 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.

The next example shows how to build our own discrete distribution, and more examples for the usage of the distributions are shown below together with the statistical tests.

Example: discrete distribution rv_discrete

In the following we use stats.rv_discrete to generate a discrete distribution that has the probabilites of the truncated normal for the intervalls centered around the integers.

```
>>> 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
>>> grid = grid[:-1]
>>> probs = np.diff(stats.truncnorm.cdf(gridlimitsnorm, -normbound, normbound))
>>> gridint = grid
>>> normdiscrete = stats.rv_discrete(values = (gridint,
...              np.round(probs, decimals=7)), name='normdiscrete')
```

From the docstring of rv_discrete:

> "You can construct an aribtrary discrete rv where P{X=xk} = pk by passing to the rv_discrete initialization method (through the values= keyword) a tuple of sequences (xk, pk) which describes only those values of X (xk) that occur with nonzero probability (pk)."

There are some requirements for this distribution to work. The keyword *name* is required. The support points of the distribution xk have to be integers. Also, I needed to limit the number of decimals. If the last two requirements are not satisfied an exception may be raised or the resulting numbers may be incorrect.

After defining the distribution, we obtain access to all methods of discrete distributions.

```
>>> print 'mean = %6.4f, variance = %6.4f, skew = %6.4f, kurtosis = %6.4f'% \
...       normdiscrete.stats(moments =  'mvsk')
mean = -0.0000, variance = 6.3302, skew = 0.0000, kurtosis = -0.0076


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

Generate a random sample and compare observed frequencies with probabilities

```
>>> n_sample = 500
>>> np.random.seed(87655678) # fix the seed for replicability
>>> 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
[[ -1.00000000e+01   0.00000000e+00   2.95019349e-02]
 [ -9.00000000e+00   0.00000000e+00   1.32294142e-01]
 [ -8.00000000e+00   0.00000000e+00   5.06497902e-01]
 [ -7.00000000e+00   2.00000000e+00   1.65568919e+00]
 [ -6.00000000e+00   1.00000000e+00   4.62125309e+00]
 [ -5.00000000e+00   9.00000000e+00   1.10137298e+01]
 [ -4.00000000e+00   2.60000000e+01   2.24137683e+01]
 [ -3.00000000e+00   3.70000000e+01   3.89503370e+01]
 [ -2.00000000e+00   5.10000000e+01   5.78004747e+01]
 [ -1.00000000e+00   7.10000000e+01   7.32455414e+01]
 [  0.00000000e+00   7.40000000e+01   7.92618251e+01]
 [  1.00000000e+00   8.90000000e+01   7.32455414e+01]
 [  2.00000000e+00   5.50000000e+01   5.78004747e+01]
 [  3.00000000e+00   5.00000000e+01   3.89503370e+01]
 [  4.00000000e+00   1.70000000e+01   2.24137683e+01]
 [  5.00000000e+00   1.10000000e+01   1.10137298e+01]
```

```
[  6.00000000e+00   4.00000000e+00   4.62125309e+00]
[  7.00000000e+00   3.00000000e+00   1.65568919e+00]
[  8.00000000e+00   0.00000000e+00   5.06497902e-01]
[  9.00000000e+00   0.00000000e+00   1.32294142e-01]
[  1.00000000e+01   0.00000000e+00   2.95019349e-02]]
```

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.

```
>>> 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)
chisquare for normdiscrete: chi2 = 12.466 pvalue = 0.4090
```

The pvalue in this case is high, so we can be quite confident that our random sample was actually generated by the distribution.

1.9.3 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:

```
>>> 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=100 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.

```
>>> print x.max(), x.min()  # equivalent to np.max(x), np.min(x)
5.26327732981 -3.78975572422
>>> 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?

```
>>> m, v, s, k = stats.t.stats(10, moments='mvsk')
>>> n, (smin, smax), sm, sv, ss, sk = stats.describe(x)
```

```
>>> print 'distribution:',
distribution:
>>> 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 'sample:      ',
sample:
>>> 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 statistcally significant way from the theoretical expectation.

```
>>> 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 ttest also directly without using the provided function, which should give us the same answer, and so it does:

```
>>> tt = (sm-m)/np.sqrt(sv/float(n))  # t-statistic for mean
>>> pval = stats.t.sf(np.abs(tt), n-1)*2  # two-sided pvalue = Prob(abs(t)>tt)
>>> print 't-statistic = %6.3f pvalue = %6.4f' % (tt, pval)
t-statistic =  0.391 pvalue = 0.6955
```

The Kolmogorov-Smirnov test can be used to test the hypothesis that the sample comes from the standard t-distribution

```
>>> 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%.

```
>>> print 'KS-statistic D = %6.3f pvalue = %6.4f' % stats.kstest(x,'norm')
KS-statistic D =  0.028 pvalue = 0.3949
```

However, the standard normal distribution has a variance of 1, while our sample has a variance of 1.29. If we standardize our sample and test it against the normal distribution, then the p-value is again large enough that we cannot reject the hypothesis that the sample came form the normal distribution.

```
>>> d, pval = stats.kstest((x-x.mean())/x.std(), 'norm')
>>> print 'KS-statistic D = %6.3f pvalue = %6.4f' % (d, pval)
KS-statistic D =  0.032 pvalue = 0.2402
```

Note: The Kolmogorov-Smirnov test assumes that we test against a distribution with given parameters, since in the last case we estimated mean and variance, this assumption is violated, and the distribution of the test statistic on which the p-value is based, is not correct.

Tails of the distribution

Finally, we can check the upper tail of the distribution. We can use the percent point function ppf, which is the inverse of the cdf function, to obtain the critical values, or, more directly, we can use the inverse of the survival function

```
>>> crit01, crit05, crit10 = stats.t.ppf([1-0.01, 1-0.05, 1-0.10], 10)
>>> print 'critical values from ppf at 1%, 5% and 10% %8.4f %8.4f %8.4f'% (crit01, crit05, cr
critical values from ppf at 1%, 5% and 10%   2.7638   1.8125   1.3722
>>> print 'critical values from isf at 1%, 5% and 10% %8.4f %8.4f %8.4f'% tuple(stats.t.isf(
critical values from isf at 1%, 5% and 10%   2.7638   1.8125   1.3722


>>> freq01 = np.sum(x>crit01) / float(n) * 100
>>> freq05 = np.sum(x>crit05) / float(n) * 100
>>> freq10 = np.sum(x>crit10) / float(n) * 100
>>> print 'sample %-frequency at 1%, 5% and 10% tail %8.4f %8.4f %8.4f'% (freq01, freq05, fr
sample %-frequency at 1%, 5% and 10% tail   1.4000   5.8000  10.5000
```

In all three cases, our sample has more weight in the top tail than the underlying distribution. We can briefly check a larger sample to see if we get a closer match. In this case the empirical frequency is quite close to the theoretical probability, but if we repeat this several times the fluctuations are still pretty large.

```
>>> freq05l = np.sum(stats.t.rvs(10, size=10000) > crit05) / 10000.0 * 100
>>> print 'larger sample %-frequency at 5% tail %8.4f'% freq05l
larger sample %-frequency at 5% tail   4.8000
```

We can also compare it with the tail of the normal distribution, which has less weight in the tails:

```
>>> print 'tail prob. of normal at 1%, 5% and 10% %8.4f %8.4f %8.4f'% \
...       tuple(stats.norm.sf([crit01, crit05, crit10])*100)
tail prob. of normal at 1%, 5% and 10%   0.2857   3.4957   8.5003
```

The chisquare test can be used to test, whether for a finite number of bins, the observed frequencies differ significantly from the probabilites of the hypothesized distribution.

```
>>> quantiles = [0.0, 0.01, 0.05, 0.1, 1-0.10, 1-0.05, 1-0.01, 1.0]
>>> crit = stats.t.ppf(quantiles, 10)
>>> print crit
[       -Inf -2.76376946 -1.81246112 -1.37218364  1.37218364  1.81246112
  2.76376946         Inf]
>>> n_sample = x.size
>>> freqcount = np.histogram(x, bins=crit)[0]
>>> tprob = np.diff(quantiles)
>>> nprob = np.diff(stats.norm.cdf(crit))
>>> tch, tpval = stats.chisquare(freqcount, tprob*n_sample)
>>> nch, npval = stats.chisquare(freqcount, nprob*n_sample)
>>> print 'chisquare for t:      chi2 = %6.3f pvalue = %6.4f' % (tch, tpval)
chisquare for t:      chi2 =  2.300 pvalue = 0.8901
>>> print 'chisquare for normal: chi2 = %6.3f pvalue = %6.4f' % (nch, npval)
chisquare for normal: chi2 = 64.605 pvalue = 0.0000
```

We see that the standard normal distribution is clearly rejected while the standard t-distribution cannot be rejected. Since the variance of our sample differs from both standard distribution, we can again redo the test taking the estimate for scale and location into account.

The fit method of the distributions can be used to estimate the parameters of the distribution, and the test is repeated using probabilites of the estimated distribution.

```
>>> tdof, tloc, tscale = stats.t.fit(x)
>>> nloc, nscale = stats.norm.fit(x)
>>> tprob = np.diff(stats.t.cdf(crit, tdof, loc=tloc, scale=tscale))
>>> nprob = np.diff(stats.norm.cdf(crit, loc=nloc, scale=nscale))
>>> tch, tpval = stats.chisquare(freqcount, tprob*n_sample)
>>> nch, npval = stats.chisquare(freqcount, nprob*n_sample)
>>> print 'chisquare for t:      chi2 = %6.3f pvalue = %6.4f' % (tch, tpval)
chisquare for t:      chi2 =  1.577 pvalue = 0.9542
>>> print 'chisquare for normal: chi2 = %6.3f pvalue = %6.4f' % (nch, npval)
chisquare for normal: chi2 = 11.084 pvalue = 0.0858
```

Taking account of the estimated parameters, we can still reject the hypothesis that our sample came from a normal distribution (at the 5% level), but again, with a p-value of 0.95, we cannot reject the t distribution.

Special tests for normal distributions

Since the normal distribution is the most common distribution in statistics, there are several additional functions available to test whether a sample could have been drawn from a normal distribution

First we can test if skew and kurtosis of our sample differ significantly from those of a normal distribution:

```
>>> print 'normal skewtest teststat = %6.3f pvalue = %6.4f' % stats.skewtest(x)
normal skewtest teststat =  2.785 pvalue = 0.0054
>>> print 'normal kurtosistest teststat = %6.3f pvalue = %6.4f' % stats.kurtosistest(x)
normal kurtosistest teststat =  4.757 pvalue = 0.0000
```

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:

```
>>> 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:

```
>>> 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.

1.9.4 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:

```
>>> 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:

```
>>> 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

```
>>> 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)
```

1.10 Multi-dimensional image processing (ndimage)

1.10.1 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 multi-dimensional 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.

1.10.2 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:

```
>>> print correlate(arange(10), [1, 2.5])
[ 0  2  6  9 13 16 20 23 27 30]
>>> print correlate(arange(10), [1, 2.5], output = Float64)
[  0.    2.5   6.    9.5  13.   16.5  20.   23.5  27.   30.5]
```

Note: In previous versions of `scipy.ndimage`, some functions accepted the *output_type* argument to achieve the same effect. This argument is still supported, but its use will generate an deprecation warning. In a future version all instances of this argument will be removed. The preferred way to specify an output type, is by using the *output* argument, either by specifying an output array of the desired type, or by specifying the type of the output that is to be returned.

1.10.3 Filter functions

The functions described in this section all perform some type of spatial filtering of the 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:

```
>>> footprint = array([[0,1,0],[1,1,1],[0,1,0]])
>>> print footprint
[[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:

```
>>> a = [0, 0, 0, 1, 0, 0, 0]
>>> correlate1d(a, [1, 1, 1])
[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:

```
>>> a = [0, 0, 0, 1, 0, 0, 0]
>>> print correlate1d(a, [1, 1, 1], origin = -1)
[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:

```
>>> a = [0, 0, 1, 1, 1, 0, 0]
>>> print correlate1d(a, [-1, 1])              ## backward difference
[ 0  0  1  0  0 -1  0]
>>> print correlate1d(a, [-1, 1], origin = -1) ## forward difference
[ 0  1  0  0 -1  0  0]
```

We could also have calculated the forward difference as follows:

```
>>> print correlate1d(a, [0, -1, 1])
[ 0  1  0  0 -1  0  0]
```

however, using the origin parameter instead of a larger kernel is more efficient. For multi-dimensional kernels *origin* can be a number, in which case the origin is assumed to be equal along all axes, or a sequence giving the origin along each axis.

Since the output elements are a function of elements in the neighborhood of the input elements, the borders of the array need to be dealt with appropriately by providing the values outside the borders. This is done by assuming that the arrays are extended beyond their boundaries according certain boundary conditions. In the functions described below, the boundary conditions can be selected using the *mode* parameter which must be a string with the name of the boundary condition. Following boundary conditions are currently supported:

"nearest"	Use the value at the boundary	[1 2 3]->[1 1 2 3 3]
"wrap"	Periodically replicate the array	[1 2 3]->[3 1 2 3 1]
"reflect"	Reflect the array at the boundary	[1 2 3]->[1 1 2 3 3]
"constant"	Use a constant value, default is 0.0	[1 2 3]->[0 1 2 3 0]

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 multi-dimensional 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 multi-dimensional 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 multi-dimensional 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 multi-dimensional 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 multi-dimensional 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 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 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 multi-dimensional 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 multi-dimensional 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 multi-dimensional rank filter. The *rank* may be less then 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 multi-dimensional percentile filter. The *percentile* may be less then 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 multi-dimensional 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:

```
>>> 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
>>> print generic_laplace(a, d2)
[[ 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:

```
>>> 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
>>> print generic_laplace(a, d2, extra_arguments = ([1, -2, 1],))
[[ 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:

```
>>> print generic_laplace(a, d2, extra_keywords = {'weights': [1, -2, 1]})
[[ 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:

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

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

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

For example, the `sobel` function fits the required signature:

```
>>> a = zeros((5, 5))
>>> a[2, 2] = 1
>>> print generic_gradient_magnitude(a, sobel)
[[0 0 0 0 0]
 [0 1 2 1 0]
 [0 2 0 2 0]
 [0 1 2 1 0]
 [0 0 0 0 0]]
```

See the documentation of `generic_laplace` for examples of using the *extra_arguments* and *extra_keywords* arguments.

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

The function gaussian_gradient_magnitude calculates the gradient magnitude using gaussian_filter to calculate the first derivatives. The standard-deviations of the Gaussian filter along each axis are passed through the parameter *sigma* as a sequence or numbers. If *sigma* is not a sequence but a single number, the standard deviation of the filter is equal along all directions.

Generic filter functions

To implement filter functions, generic functions can be used that accept a callable object that implements the filtering operation. The iteration over the input and output arrays is handled by these generic functions, along with such details as the implementation of the boundary conditions. Only a callable object implementing a callback function that does the actual filtering work must be provided. The callback function can also be written in C and passed using a PyCObject (see *Extending ndimage in C* for more information).

The generic_filter1d function implements a generic one-dimensional filter function, where the actual filtering operation must be supplied as a python function (or other callable object). The generic_filter1d function iterates over the lines of an array and calls function at each line. The arguments that are passed to function are one-dimensional arrays of the tFloat64 type. The first contains the values of the current line. It is extended at the beginning end the end, according to the *filter_size* and *origin* arguments. The second array should be modified in-place to provide the output values of the line. For example consider a correlation along one dimension:

```
>>> a = arange(12, shape = (3,4))
>>> print correlate1d(a, [1, 2, 3])
[[ 3  8 14 17]
 [27 32 38 41]
 [51 56 62 65]]
```

The same operation can be implemented using generic_filter1d as follows:

```
>>> def fnc(iline, oline):
...     oline[...] = iline[:-2] + 2 * iline[1:-1] + 3 * iline[2:]
...
>>> print generic_filter1d(a, fnc, 3)
[[ 3  8 14 17]
 [27 32 38 41]
 [51 56 62 65]]
```

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:

```
>>> def fnc(iline, oline, a, b):
...     oline[...] = iline[:-2] + a * iline[1:-1] + b * iline[2:]
...
>>> print generic_filter1d(a, fnc, 3, extra_arguments = (2, 3))
[[ 3  8 14 17]
```

```
 [27 32 38 41]
 [51 56 62 65]]
```

or

```
>>> print generic_filter1d(a, fnc, 3, extra_keywords = {'a':2, 'b':3})
[[ 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:

```
>>> a = arange(12, shape = (3,4))
>>> print correlate(a, [[1, 0], [0, 3]])
[[ 0  3  7 11]
 [12 15 19 23]
 [28 31 35 39]]
```

The same operation can be implemented using *generic_filter* as follows:

```
>>> def fnc(buffer):
...     return (buffer * array([1, 3])).sum()
...
>>> print generic_filter(a, fnc, footprint = [[1, 0], [0, 1]])
[[ 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:

```
>>> def fnc(buffer, weights):
...     weights = asarray(weights)
...     return (buffer * weights).sum()
...
>>> print generic_filter(a, fnc, footprint = [[1, 0], [0, 1]], extra_arguments = ([1, 3],))
[[ 0  3  7 11]
 [12 15 19 23]
 [28 31 35 39]]
```

or

```
>>> print generic_filter(a, fnc, footprint = [[1, 0], [0, 1]], extra_keywords= {'weights': [1, 3
[[ 0  3  7 11]
 [12 15 19 23]
 [28 31 35 39]]
```

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 `generic_filter`, but additionally prints the current coordinates:

```
>>> a = arange(12, shape = (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))
>>> print generic_filter(a, fnc.filter, footprint = [[1, 0], [0, 1]])
[0, 0]
[0, 1]
[0, 2]
[0, 3]
[1, 0]
[1, 1]
[1, 2]
[1, 3]
[2, 0]
[2, 1]
[2, 2]
[2, 3]
[[ 0  3  7 11]
 [12 15 19 23]
 [28 31 35 39]]
```

For the `generic_filter1d` function the same approach works, except that this function does not iterate over the axis that is being filtered. The example for `generic_filter1d` then becomes this:

```
>>> a = arange(12, shape = (3,4))
>>>
>>> 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))
>>> print generic_filter1d(a, fnc.filter, 3)
[0, 0]
[1, 0]
[2, 0]
[[ 3  8 14 17]
 [27 32 38 41]
 [51 56 62 65]]
```

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 multi-dimensional 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 multi-dimensional 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 multi-dimensional 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 multi-dimensional Fourier transform of a 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.

1.10.4 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 then 1 and less than 6.

The `spline_filter` function calculates a multi-dimensional spline filter.

Note: 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, 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 multi-dimensional 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:

```
>>> a = arange(12, shape=(4,3), type = Float64)
>>> def shift_func(output_coordinates):
...     return (output_coordinates[0] - 0.5, output_coordinates[1] - 0.5)
...
>>> print geometric_transform(a, shift_func)
[[ 0.      0.      0.    ]
 [ 0.      1.3625  2.7375]
```

```
 [ 0.      4.8125  6.1875]
 [ 0.      8.2625  9.6375]]
```

Optionally extra arguments can be defined and passed to the filter function. The *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:

```
>>> def shift_func(output_coordinates, s0, s1):
...     return (output_coordinates[0] - s0, output_coordinates[1] - s1)
...
>>> print geometric_transform(a, shift_func, extra_arguments = (0.5, 0.5))
[[ 0.      0.      0.    ]
 [ 0.      1.3625  2.7375]
 [ 0.      4.8125  6.1875]
 [ 0.      8.2625  9.6375]]
```

or

```
>>> print geometric_transform(a, shift_func, extra_keywords = {'s0': 0.5, 's1': 0.5})
[[ 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):

```
>>> a = arange(12, shape=(4,3), type = numarray.Float64)
>>> print a
[[  0.   1.   2.]
 [  3.   4.   5.]
 [  6.   7.   8.]
 [  9.  10.  11.]]
>>> print map_coordinates(a, [[0.5, 2], [0.5, 1]])
[ 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.

1.10.5 Morphology

Binary morphology

Binary morphology (need something to put here).

The generate_binary_structure functions generates a binary structuring element for use in binary morphology operations. The *rank* of the structure must be provided. The size of the structure that is returned is equal to three in each direction. The value of each element is equal to one if the square of the Euclidean distance from the element to the center is less or equal to *connectivity*. For instance, two dimensional 4-connected and 8-connected structures are generated as follows:

```
>>> print generate_binary_structure(2, 1)
[[0 1 0]
 [1 1 1]
 [0 1 0]]
>>> print generate_binary_structure(2, 2)
[[1 1 1]
 [1 1 1]
 [1 1 1]]
```

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:

```
>>> 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]])
>>> print a
[[1 0 0 0 0]
 [1 1 0 1 0]
 [0 0 1 1 0]
 [0 0 0 0 0]]
```

```
>>> print binary_dilation(zeros(a.shape), struct, -1, a, border_value=1)
[[1 0 0 0 0]
 [1 1 0 0 0]
 [0 0 0 0 0]
 [0 0 0 0 0]]
```

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:

```
>>> struct = generate_binary_structure(2, 1)
>>> print struct
[[0 1 0]
 [1 1 1]
 [0 1 0]]
>>> print iterate_structure(struct, 2)
[[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]]
```

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:

```
>>> print iterate_structure(struct, 2, -1)
(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]], type=Bool), [-2, -2])
```

Other morphology operations can be defined in terms of erosion and d 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*.

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 multi-dimensional grey- scale erosion.

The grey_dilation function calculates a multi-dimensional 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.

1.10.6 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 basics of the algorithm used to implement this function is described in: G. Borgefors, "Distance transformations in arbitrary dimensions.", Computer Vision, Graphics, and Image Processing, 27:321-345, 1984.

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 algorithm used to implement this function is described in: C. R. Maurer, Jr., R. Qi, and V. Raghavan, "A linear time algorithm for computing exact euclidean distance transforms of binary images in arbitrary dimensions. IEEE Trans. PAMI 25, 265-270, 2003.

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.

1.10.7 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:

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

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 = [[0, 1, 0], [1,1,1], [0,1,0]]
>>> print label(a, s)
(array([[0, 1, 1, 0, 0, 0],
       [0, 1, 1, 0, 2, 0],
       [0, 0, 0, 2, 2, 2],
       [0, 0, 0, 0, 2, 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]]
>>> print label(a, s)[0]
[[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])
>>> print l
[1 0 2 0 3]
>>> l = where(l != 2, l, 0)
>>> print l
[1 0 0 0 3]
>>> print label(l)[0]
[1 0 0 0 2]
```

Note: The structuring element used by `label` is assumed to be symmetric.

There is a large number of other approaches for segmentation, for instance from an estimation of the borders of the objects that can be obtained for instance by derivative filters. One such an approach is watershed segmentation. The function `watershed_ift` generates an array where each object is assigned a unique label, from an array that localizes the object borders, generated for instance by a gradient magnitude filter. It uses an array containing initial markers for the objects:

The `watershed_ift` function applies a watershed from markers algorithm, using an Iterative Forest Transform, as described in: P. Felkel, R. Wegenkittl, and M. Bruckschwaiger, "Implementation and Complexity of the Watershed-from-Markers Algorithm Computed as a Minimal Cost Forest.", Eurographics 2001, pp. C:26-35.

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],
...                [0, 1, 1, 1, 1, 1, 0],
...                [0, 1, 0, 0, 0, 1, 0],
...                [0, 1, 0, 0, 0, 1, 0],
...                [0, 1, 0, 0, 0, 1, 0],
...                [0, 1, 1, 1, 1, 1, 0],
...                [0, 0, 0, 0, 0, 0, 0]], numarray.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, 2, 0, 0, 0],
...                  [0, 0, 0, 0, 0, 0, 0],
...                  [0, 0, 0, 0, 0, 0, 0],
...                  [0, 0, 0, 0, 0, 0, 0]], numarray.Int8)
>>> print watershed_ift(input, markers)
[[1 1 1 1 1 1 1]
 [1 1 2 2 2 1 1]
 [1 2 2 2 2 2 1]
 [1 2 2 2 2 2 1]
 [1 2 2 2 2 2 1]
 [1 1 2 2 2 1 1]
 [1 1 1 1 1 1 1]]
```

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:

```
>>> 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]], numarray.Int8)
>>> print watershed_ift(input, markers)
[[1 1 1 1 1 1 1]
 [1 1 1 1 1 1 1]
 [1 1 2 2 2 1 1]
 [1 1 2 2 2 1 1]
 [1 1 2 2 2 1 1]
 [1 1 1 1 1 1 1]
 [1 1 1 1 1 1 1]]
```

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:

```
>>> 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]], numarray.Int8)
>>> print watershed_ift(input, markers)
[[-1 -1 -1 -1 -1 -1 -1]
 [-1 -1  2  2  2 -1 -1]
 [-1  2  2  2  2  2 -1]
 [-1  2  2  2  2  2 -1]
 [-1  2  2  2  2  2 -1]
 [-1 -1  2  2  2 -1 -1]
 [-1 -1 -1 -1 -1 -1 -1]]
```

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:

```
>>> print watershed_ift(input, markers,
...                     structure = [[1,1,1], [1,1,1], [1,1,1]])
[[-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]]
```

Note: The implementation of `watershed_ift` limits the data types of the input to `UInt8` and `UInt16`.

1.10.8 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:

```
>>> 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]])
>>> l, n = label(a)
>>> f = find_objects(l)
>>> print a[f[0]]
[[1 1]
 [1 1]]
>>> print a[f[1]]
[[0 1 0]
 [1 1 1]
 [0 1 0]]
```

`find_objects` returns slices for all objects, unless the *max_label* parameter is larger then 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:

```
>>> print 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:

```
>>> image = arange(4*6,shape=(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:

```
>>> print 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:

```
>>> print sum(image, labels, 2)
80.0
```

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

```
>>> print sum(image[slices[1]], labels[slices[1]], 2)
80.0
```

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:

```
>>> print sum(image, labels, [0, 2])
[178.0, 80.0]
```

The measurement functions described below all support the *index* parameter to indicate which object(s) should be measured. The default value of *index* is None. This indicates that all elements where the label is larger than zero should be treated as a single object and measured. Thus, in this case the *labels* array is treated as a mask defined by the elements that are larger than zero. If *index* is a number or a sequence of numbers it gives the labels of the objects that are measured. If *index* is a sequence, a list of the results is returned. Functions that return more than one result, return their result as a tuple if *index* is a single number, or as a tuple of lists, if *index* is a sequence.

The `sum` function calculates the sum of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation.

The `mean` function calculates the mean of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation.

The `variance` function calculates the variance of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation.

The `standard_deviation` function calculates the standard deviation of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation.

The `minimum` function calculates the minimum of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation.

The `maximum` function calculates the maximum of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation.

The `minimum_position` function calculates the position of the minimum of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation.

The `maximum_position` function calculates the position of the maximum of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation.

The `extrema` function calculates the minimum, the maximum, and their positions, of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is None, all elements with a non-zero label value are treated as a single object. If *label* is None, all elements of *input* are used in the calculation. The result is a tuple giving the minimum, the maximum, the position of the minimum and the postition 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`.

1.10.9 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:

```
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:

```
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:

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

To use these functions, an extension module is built:

```
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:

```
>>> import example
>>> array = arange(12, shape=(4,3), type = Float64)
>>> fnc = example.shift_function(0.5)
>>> print geometric_transform(array, fnc)
[[ 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 acccept a C callback function and gives the prototype of the callback function.

1.10.10 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.

1.11 File IO (`scipy.io`)

See Also:

numpy-reference.routines.io (in numpy)

1.11.1 Matlab files

`loadmat`(file_name, **kwargs[, mdict, appendmat])	Load Matlab(tm) file
`savemat`(file_name, mdict[, appendmat, ...])	Save a dictionary of names and arrays into the MATLAB-style .mat file.

Getting started:

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

If you are using IPython, try tab completing on `sio`. You'll find:

```
sio.loadmat
sio.savemat
```

These are the high-level functions you will most likely use. You'll also find:

```
sio.matlab
```

This is the package from which `loadmat` and `savemat` are imported. Within `sio.matlab`, you will find the `mio` module - containing 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 / load functions. Start Octave (`octave` at the command line for me):

```
octave:1> a = 1:12
a =

   1   2   3   4   5   6   7   8   9  10  11  12

octave:2> a = reshape(a, [1 3 4])
a =

ans(:,:,1) =

   1   2   3

ans(:,:,2) =

   4   5   6

ans(:,:,3) =

   7   8   9

ans(:,:,4) =

   10   11   12



octave:3> save -6 octave_a.mat a % Matlab 6 compatible
octave:4> ls octave_a.mat
octave_a.mat
```

Now, to Python:

```
>>> mat_contents = sio.loadmat('octave_a.mat')
/home/mb312/usr/local/lib/python2.5/site-packages/scipy/io/Matlab/mio.py:84: FutureWarning: Using str
  return MatFile5Reader(byte_stream, **kwargs)
>>> print mat_contents
{'a': array([[[  1.,   4.,   7.,  10.],
        [  2.,   5.,   8.,  11.],
        [  3.,   6.,   9.,  12.]]]), '__version__': '1.0', '__header__': 'MATLAB 5.0 MAT-file, writte
>>> oct_a = mat_contents['a']
>>> print oct_a
[[[  1.   4.   7.  10.]
  [  2.   5.   8.  11.]
  [  3.   6.   9.  12.]]]
>>> print oct_a.shape
(1, 3, 4)
```

We'll get to the deprecation warning in a second. Now let's try the other way round:

```
>>> import numpy as np
>>> vect = np.arange(10)
>>> print vect.shape
(10,)
>>> sio.savemat('np_vector.mat', {'vect':vect})
/home/mb312/usr/local/lib/python2.5/site-packages/scipy/io/Matlab/mio.py:165: FutureWarning: Using or
  oned_as=oned_as)
```

Then back to Octave:

```
octave:5> load np_vector.mat
octave:6> vect
vect =

  0
  1
  2
  3
  4
  5
  6
  7
  8
  9

octave:7> size(vect)
ans =

   10    1
```

Note the deprecation warning. The `oned_as` keyword determines the way in which one-dimensional vectors are stored. In the future, this will default to `row` instead of `column`:

```
>>> sio.savemat('np_vector.mat', {'vect':vect}, oned_as='row')
```

We can load this in Octave or Matlab:

```
octave:8> load np_vector.mat
octave:9> vect
vect =

  0  1  2  3  4  5  6  7  8  9

octave:10> size(vect)
ans =

    1   10
```

Matlab structs

Matlab structs are a little bit like Python dicts, except the field names must be strings. Any Matlab object can be a value of a field. As for all objects in Matlab, structs are in fact arrays of structs, where a single struct is an array of shape (1, 1).

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

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

We can load this in Python:

```
>>> mat_contents = sio.loadmat('octave_struct.mat')
>>> print mat_contents
{'my_struct': array([[<scipy.io.matlab.mio5.mat_struct object at 0x26421d0>]], dtype=object), '__vers
>>> oct_struct = mat_contents['my_struct']
>>> print oct_struct.shape
(1, 1)
>>> val = oct_struct[0,0]
>>> print val
<scipy.io.Matlab.mio5.mat_struct object at 0x2ade950>
>>> print val.field1
[[ 1.]]
>>> print val.field2
[[ 2.]]
```

In this version of Scipy (0.7.1), Matlab structs come back as custom objects, called `mat_struct`, with attributes named for the fields in the structure. Note also:

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

and:

```
octave:13> size(my_struct)
ans =

   1   1
```

So, in Matlab, the struct array must be at least 2D, and we replicate that when we read into Scipy. If you want all length 1 dimensions squeezed out, try this:

```
>>> mat_contents = sio.loadmat('octave_struct.mat', 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'
>>> print oct_struct
<scipy.io.Matlab.mio5.mat_struct object at 0x2aded90>
>>> print oct_struct.field1
1.0
```

Saving struct arrays can be done in various ways. One simple method is to use dicts:

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

loaded as:

```
octave:21> load saved_struct
octave:22> a_dict
a_dict =
{
  field2 = a string
  field1 =  0.50000
}
```

Further up, you'll remember this deprecation warning:

```
>>> mat_contents = sio.loadmat('octave_a.mat')
/home/mb312/usr/local/lib/python2.5/site-packages/scipy/io/Matlab/mio.py:84: FutureWarning: Using str
  return MatFile5Reader(byte_stream, **kwargs)
```

The way that the reader returns struct arrays will soon change. Like this:

```
>>> mat_contents = sio.loadmat('octave_struct.mat', struct_as_record=True)
>>> oct_struct = mat_contents['my_struct']
>>> val = oct_struct[0,0]
>>> print val
([[1.0]], [[2.0]])
>>> print val.dtype
[('field1', '|O8'), ('field2', '|O8')]
```

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)
>>> print arr
[(0.0, '') (0.0, '')]
>>> 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
[[ 1.]]
>>> 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'
>>> print obj_arr
[1 a string]
>>> 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
}
```

1.11.2 Matrix Market files

mminfo(source)	Queries the contents of the Matrix Market file 'filename' to
mmread(source)	Reads the contents of a Matrix Market file 'filename' into a matrix.
mmwrite(target, a[, comment, field, precision])	Writes the sparse or dense matrix A to a Matrix Market formatted file.

1.11.3 Other

save_as_module([file_name, data])	Save the dictionary "data" into

1.11.4 Wav sound files (scipy.io.wavfile)

read(file)	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

1.11.5 Arff files (scipy.io.arff)

Module to read arff files (weka format).

arff is a simple file format which support numerical, string and data values. It supports sparse data too.

See http://weka.sourceforge.net/wekadoc/index.php/en:ARFF_(3.4.6) for more details about arff format and available datasets.

`loadarff`(filename)	Read an arff file.

1.11.6 Netcdf (`scipy.io.netcdf`)

`netcdf_file`(filename[, mode, mmap, version])	A `netcdf_file` object has two standard attributes: `dimensions` and `variables`.

Allows reading of NetCDF files (version of pupynere package)

1.12 Weave

1.12.1 Outline

Contents

1.12.2 Introduction

The scipy.weave (below just weave) package provides tools for including C/C++ code within in 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 convertable 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 check out the sources using svn co http://svn.scipy.org/svn/scipy/trunk/Lib/weave weave and install as 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.

1.12.3 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.

1.12.4 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. setup.py file to simplify installation.

1.12.5 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
```

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?

1.12.6 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 1.1: inline and ext_tools

Algorithm	Speed up
binary search	1.50
fibonacci (recursive)	82.10
fibonacci (loop)	9.17
return None	0.14
map	1.20
dictionary sort	2.54
vector quantization	37.40

Table 1.2: blitz – double precision

Algorithm	Speed up
a = b + c 512x512	3.05
a = b + c + d 512x512	4.59
5 pt avg. filter, 2D Image 512x512	9.01
Electromagnetics (FDTD) 100x100x100	8.61

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.

1.12.7 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()`:

```
>>> 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 speed up can be worth while – anywhwere 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 supress the first time the code executes:

```
>>> weave.inline(r'printf("%d\n",a);',['a'])
sc_e013937dbc8c647ac62438874e5795131.cpp
   Creating library C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp
   \Release\sc_e013937dbc8c647ac62438874e5795131.lib and
   object C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\sc_e013937dbc8c647ac62438874e
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` preceeding 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?

```
>>> 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.

```
>>> 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')
AssertError...
```

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 cor the char* version.

```
>>> 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::`.

```
>>> 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 beacuse `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()`.

```
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 cheack 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 in 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:

```
C:\home\ej\wrk\scipy\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 decompisition 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):
    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);
    """ % NumPy_type
    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 simplier 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.

```
#C:\home\ej\wrk\scipy\weave\examples> python cast_copy_transpose.py
# Cast/Copy/Transposing (150,150)array 1 times
#  speed in python: 0.870999932289
#  speed in c: 0.25
#  speed up: 3.48
#  inplace transpose c: 0.129999995232
#  speed up: 6.70
```

wxPython

`inline` knows how to handle wxPython objects. Thats 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))
    te = dc.GetTextExtent("Hello World")
    dc.DrawText("Hello World", 60, 65)

    dc.SetPen(wxPen(wxNamedColour('VIOLET'), 4))
    dc.DrawLine(5, 65+te[1], 60+te[0], 65+te[1])
    ...
```

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. Thats 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.

```
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. If local_dict is not specified the local dictionary of the calling function is used. 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. If global_dict is not specified the global dictionary of the calling function is used. 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 understoof 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. defualt 0. Speficies 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 specifiy 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.

```
>>> from weave import inline
>>> a = 'string'
>>> code = """
...         int l = a.length();
...         return_val = Py::new_reference_to(Py::Int(l));
...         """
>>> inline(code,['a'])
 sc_86e98826b65b047ffd2cd5f479c627f12.cpp
Creating
   library C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\sc_86e98826b65b047ffd2cd5f4
and object C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\sc_86e98826b65b047ff
d2cd5f479c627f12.exp
6
>>> inline(code,['a'])
6
```

When `inline` is first run, you'll notice that pause and some trash printed to the screen. The "trash" is acutually part of the compilers output that distutils does not supress. The name of the extension file, `sc_bighonkingnumber.cpp`, is generated from the md5 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.

```
>>> 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:

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

Everytime, 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:

```
>>>inline(code,['a'],compiler='gcc',verbose=2,force=1)
running build_ext
building 'sc_86e98826b65b047ffd2cd5f479c627f13' extension
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_86e98826b65b047ffd2cd5f479c627f13.cpp
-o C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\sc_86e98826b65b04ffd2cd5f479c627f13
skipping C:\home\ej\wrk\scipy\weave\CXX\cxxextensions.c
(C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\cxxextensions.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_86e98826b65b047ffd2cd5f479c6
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_86e98826b65b047ffd2cd5f479c627f13
C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\sc_86e98826b65b047ffd2cd5f479c627f13.de
-sC:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\sc_86e98826b65b047ffd2cd5f479c627f13
C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\cxxextensions.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\indirectpythoninterface.o
C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\temp\Release\cxx_extensions.o -LC:\Python21\libs
-lpython21 -o
C:\DOCUME~1\eric\LOCALS~1\Temp\python21_compiled\sc_86e98826b65b047ffd2cd5f479c627f13.pyd
15
```

That's quite a bit of output. `verbose=1` just prints the compile time.

```
>>>inline(code,['a'],compiler='gcc',verbose=1,force=1)
Compiling code...
finished compiling (sec):  6.00800001621
15
```

Note: I've only used the `compiler` option for switching between 'msvc' and 'gcc' on windows. It may have use on Unix also, but I don't know yet.

The `support_code` argument is likely to be used a lot. It allows you to specify extra code fragments such as function, structure or class definitions that you want to use in the `code` string. Note that changes to `support_code` do *not* force a recompile. The catalog only relies on `code` (for performance reasons) to determine whether recompiling is necessary. So, if you make a change to support_code, you'll need to alter `code` in some way or use the `force` argument to get the code to recompile. I usually just add some inocuous whitespace to the end of one of the lines in `code` somewhere. Here's an example of defining a separate method for calculating the string length:

```
>>> from weave import inline
>>> a = 'a longer string'
>>> support_code = """
...                 PyObject* length(Py::String a)
...                 {
...                     int l = a.length();
...                     return Py::new_reference_to(Py::Int(l));
...                 }
...                 """
>>> inline("return_val = length(a);",['a'],
...        support_code = support_code)
15
```

`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 there default type, set `auto_downcast` to 0.

Returning Values

Python variables in the local and global scope transfer seemlessly 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:

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

Instead you get:

```
>>> 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.

```
>>> 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:

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

# C version.
def c_multi_return():
    code =  """
              py::tuple results(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 then 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/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` truely 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 md5 signature of the code snippet and saved to a location specified by the PYTHONCOM-

PILED 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:

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

And here is the extension function generated by `inline`:

```
static PyObject* compiled_func(PyObject*self, PyObject* args)
{
    py::object return_val;
    int exception_occured = 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.

```
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);
}


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);
}

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";
    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 interagation (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 "unkown 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 withing 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 straight forward, but there are subtlties 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 1.3: Default Data Type Conversions

Python	C++
int	int
float	double
complex	std::complex
string	py::string
list	py::list
dict	py::dict
tuple	py::tuple
file	FILE*
callable	py::object
instance	py::object
numpy.ndarray	PyArrayObject*
wxXXX	wxXXX*

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 currenlty 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 convserion 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 demostrate 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:

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

The argument conversion code inserted for `a` is:

```
/* 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:

```
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:

```
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);
}

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,

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

The argument conversion code inserted for `a` is:

```
/* 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 has the following form:

```
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);
}

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);
}

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);
}

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,

```
>>> a = open("bob",'w')
>>> inline("",['a'])
```

The argument conversion code is:

```
/* 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*:

```
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

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

Its 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

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

You might try:

```
>>> 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:

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

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:

```
>>> 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.

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

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

```
/* 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.

```
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;
}

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 generate C++ code needed to convert from Python to C++ types for a specific variable.

When

```
>>> 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 everytime 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 persisent 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 everytime 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 manor using standard Python shelves.

Early on, there was a question as to whether md5 check sums 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 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 shelve 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 environement 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:

```
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.

1.12.8 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:

```
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`:

```
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 arguements, 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. Futher, 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 most be compiled again. This does not overwrite the previously compiled function – both of them are saved and available for exectution.

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

Method Run Time (seconds) Standard NumPy 0.46349 blitz (1st time compiling) 78.95526 blitz (subsequent calls) 0.05843 (factor of 8 speedup)

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 snuff. 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 mathematic operators except for the ** power operator. The built-in trigonmetric, 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 temprorary 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.  ,   25.       ,   31.25     ,   32.8125   , 0. ],
       [   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.,   25.,   25.,   25.,    0.],
       [   0.,    0.,    0.,    0.,    0.],
       [   0.,    0.,    0.,    0.,    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 compuationally 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 * b + c * d
```

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

```
temp1 = 1.2 * b
temp2 = c * d
a = temp1 + temp2
```

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 * 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:

```
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 straight forward to write. (take a peak in 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 Jermey Hylton's parser module and Travis Oliphant's NumPy module. On the compiled language side, Todd Veldhuizen's blitz++ array library, written in C++ (shhhh. 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.

```
>>> 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',
    ['expr_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', '']]
```

Despite its looks, with some tools developed by Jermey H., its 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:

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

In Blitz it is as follows:

```
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 declaraions 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[:-1] -> b(Range(0,Nb[0]-1-1))
```

This approach fails, however, when the top index is calculated from other values. In the following scenario, if `i+j` evaluates to a negative value, the compiled code will produce incorrect results and could even core- dump. Right now, all calculated indices are assumed to be positive.

```
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
[                -> (
]                -> )
_stp             -> 1
```

`_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 name spaces are maintained in the C++ code to lessen the likelyhood 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 coersion

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:

```
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 savespace 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:

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

In this example,

```
>>> 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 decern 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 comptible 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 it 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 (ie. 50x50x50), the overhead is negligible compared to evaluating the actual expression. For small arrays (ie. 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.

1.12.9 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 convereted to C from these.

A Simple Example

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

```
# 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()`,

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

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:

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

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

```
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.

```
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 md5 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 md5 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

`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:

```
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.

1.12.10 Customizing Type Conversions – Type Factories

not written

1.12.11 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

RELEASE NOTES

2.1 SciPy 0.7.0 Release Notes

Contents

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.

2.1.1 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.

2.1.2 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.

2.1.3 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:

```
>>> 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.

2.1.4 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.

2.1.5 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.

2.1.6 Sparse Matrices

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

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

Several new sparse matrix construction functions were added:

- `sparse.kron` : sparse Kronecker product
- `sparse.bmat` : sparse version of `numpy.bmat`
- `sparse.vstack` : sparse version of `numpy.vstack`
- `sparse.hstack` : sparse version of `numpy.hstack`

Extraction of submatrices and nonzero values have been added:

- `sparse.tril` : extract lower triangle
- `sparse.triu` : extract upper triangle
- `sparse.find` : nonzero values and their indices

`csr_matrix` and `csc_matrix` now support slicing and fancy indexing (e.g., `A[1:3, 4:7]` and `A[[3,2,6,8],:]`). Conversions among all sparse formats are now possible:

- using member functions such as `.tocsr()` and `.tolil()`
- using the `.asformat()` member function, e.g. `A.asformat('csr')`
- using constructors `A = lil_matrix([[1,2]]); B = csr_matrix(A)`

All sparse constructors now accept dense matrices and lists of lists. For example:

- `A = csr_matrix( rand(3,3) )` and `B = lil_matrix( [[1,2],[3,4]] )`

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

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

2.1.7 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.

2.1.8 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

2.1.9 New Hierarchical Clustering module

This module adds new hierarchical clustering functionality to the `scipy.cluster` package. The function interfaces are similar to the functions provided MATLAB(TM)'s Statistics Toolbox to help facilitate easier migration to

the NumPy/SciPy framework. Linkage methods implemented include single, complete, average, weighted, centroid, median, and ward.

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

2.1.10 New Spatial package

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

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

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

2.1.11 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.

2.1.12 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.

2.1.13 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.

2.1.14 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).

2.1.15 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.

2.1.16 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.

2.1.17 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.

2.1.18 Known problems

Here are known problems with scipy 0.7.0:

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

CHAPTER

THREE

REFERENCE

3.1 Clustering package (`scipy.cluster`)

3.1.1 Hierarchical clustering (`scipy.cluster.hierarchy`)

Warning: This documentation is work-in-progress and unorganized.

Function Reference

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.

Function	*Description*
fcluster	forms flat clusters from hierarchical clusters.
fclusterdata	forms flat clusters directly from data.
leaders	singleton root nodes for flat cluster.

These are routines for agglomerative clustering.

Function	*Description*
linkage	agglomeratively clusters original observations.
single	the single/min/nearest algorithm. (alias)
complete	the complete/max/farthest algorithm. (alias)
average	the average/UPGMA algorithm. (alias)
weighted	the weighted/WPGMA algorithm. (alias)
centroid	the centroid/UPGMC algorithm. (alias)
median	the median/WPGMC algorithm. (alias)
ward	the Ward/incremental algorithm. (alias)

These routines compute statistics on hierarchies.

Function	*Description*
cophenet	computes the cophenetic distance between leaves.
from_mlab_linkage	converts a linkage produced by MATLAB(TM).
inconsistent	the inconsistency coefficients for cluster.
maxinconsts	the maximum inconsistency coefficient for each cluster.
maxdists	the maximum distance for each cluster.
maxRstat	the maximum specific statistic for each cluster.
to_mlab_linkage	converts a linkage to one MATLAB(TM) can understand.

Routines for visualizing flat clusters.

Function	*Description*
dendrogram	visualizes linkages (requires matplotlib).

These are data structures and routines for representing hierarchies as tree objects.

Function	*Description*
ClusterNode	represents cluster nodes in a cluster hierarchy.
leaves_list	a left-to-right traversal of the leaves.
to_tree	represents a linkage matrix as a tree object.

These are predicates for checking the validity of linkage and inconsistency matrices as well as for checking isomorphism of two flat cluster assignments.

Function	*Description*
is_valid_im	checks for a valid inconsistency matrix.
is_valid_linkage	checks for a valid hierarchical clustering.
is_isomorphic	checks if two flat clusterings are isomorphic.
is_monotonic	checks if a linkage is monotonic.
correspond	checks whether a condensed distance matrix corresponds with a linkage
num_obs_linkage	the number of observations corresponding to a linkage matrix.

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References

Copyright Notice

class `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.

Seealso

- to_tree: for converting a linkage matrix `Z` into a tree object.

Methods

`get_count`()	The number of leaf nodes (original observations) belonging to the cluster node nd.
`get_id`()	The identifier of the target node.
`get_left`()	Returns a reference to the left child tree object.
`get_right`()	Returns a reference to the right child tree object.
`is_leaf`()	Returns True iff the target node is a leaf.
`pre_order`([func])	Performs preorder traversal without recursive function calls.

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

c
[int] The number of leaf nodes below the target node.

get_id()
The identifier of the target node. For $0 \leq i < n$, i corresponds to original observation i. For $n \leq i < 2n-1$, i corresponds to non-singleton cluster formed at iteration $i-n$.

Returns

id
[int] The identifier of the target node.

get_left()
Returns a reference to the left child tree object. If the node is a leaf, None is returned.

Returns

left
[ClusterNode] The left child of the target node.

get_right()
Returns a reference to the right child tree object. If the node is a leaf, None is returned.

Returns

right
[ClusterNode] The left child of the target node.

is_leaf()
Returns True iff the target node is a leaf.

Returns

leafness
[bool] True if the target node is a leaf node.

pre_order(*func=<function <lambda> at 0x14e64320>*)
Performs preorder 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.

average(*y*)

Performs average/UPGMA linkage on the condensed distance matrix `y`. 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.

Seealso

- linkage: for advanced creation of hierarchical clusterings.

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

Q

[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 a m by n array.

Returns

Z

[ndarray] A linkage matrix containing the hierarchical clustering. See the `linkage` function documentation for more information on its structure.

Seealso

- linkage: for advanced creation of hierarchical clusterings.

complete(*y*)

Performs complete complete/max/farthest point linkage on the condensed distance matrix `y`. 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.

cophenet(*Z, Y=None*)

Calculates the cophenetic distances between each observation in the hierarchical clustering defined by the linkage `Z`.

Suppose `p` and `q` are original observations in disjoint clusters `s` and `t`, respectively and `s` and `t` are joined by a direct parent cluster `u`. The cophenetic distance between observations `i` and `j` is simply the distance between clusters `s` and `t`.

Parameters

- 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, {d}) - c : ndarray

The cophentic 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.

correspond(*Z, Y*)

Checks if a linkage matrix `Z` and condensed distance matrix `Y` could possibly correspond to one another.

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.

Arguments

- **Z**
  [ndarray] The linkage matrix to check for correspondance.
- **Y**
  [ndarray] The condensed distance matrix to check for correspondance.

Returns

- **b**
  [bool] A boolean indicating whether the linkage matrix and distance matrix could possibly correspond to one another.

dendrogram(*Z, p=30, truncate_mode=None, color_threshold=None, get_leaves=True, orientation='top', labels=None, count_sort=False, distance_sort=False, show_leaf_counts=True, no_plot=False, no_labels=False, color_list=None, leaf_font_size=None, leaf_rotation=None, leaf_label_func=None, no_leaves=False, show_contracted=False, link_color_func=None*)

Plots the hiearchical clustering defined by the linkage Z 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.

Arguments

- 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`.
- truncate_mode : string 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 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.
- p : int The `p` parameter for `truncate_mode`.

'

- color_threshold : double 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 Includes a list `R['leaves']=H` in the result dictionary. For each i, `H[i] == j`, cluster node j appears in the i th position in the left-to-right traversal of the leaves, where $j < 2n-1$ and $i < n$.
- orientation : string The direction to plot the dendrogram, which can be any of the following strings
  - 'top': plots the root at the top, and plot descendent

    links going downwards. (default).
  - 'bottom': plots the root at the bottom, and plot descendent

    links going upwards.

– 'left': plots the root at the left, and plot descendent

links going right.

– 'right': plots the root at the right, and plot descendent

links going left.

- labels : ndarray By default `labels` is `None` so the index of the original observation is used to label the leaf nodes.

  Otherwise, this is an n -sized list (or tuple). The `labels[i]` value is the text to put under the i th leaf node only if it corresponds to an original observation and not a non-singleton cluster.

- count_sort : string/bool For each node n, the order (visually, from left-to-right) n's two descendent links are plotted is determined by this parameter, which can be any of the following values:

  – False: nothing is done.

  – 'ascending'/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 : string/bool For each node n, the order (visually, from left-to-right) n's two descendent links are plotted is determined by this parameter, which can be any of the following values:

  – False: nothing is done.

  – 'ascending'/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

  When `True`, leaf nodes representing $k > 1$ original observation are labeled with the number of observations they contain in parentheses.

- no_plot : bool 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 When `True`, no labels appear next to the leaf nodes in the rendering of the dendrogram.

- leaf_label_rotation : double

  Specifies the angle (in degrees) to rotate the leaf labels. When unspecified, the rotation based on the number of nodes in the dendrogram. (Default=0)

- leaf_font_size : int 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

  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:

```
# First define the leaf label function.
def llf(id):
    if id < n:
        return str(id)
    else:
        return '[%d %d %1.2f]' % (id, count, R[n-id,3])

# The text for the leaf nodes is going to be big so force
# a rotation of 90 degrees.
dendrogram(Z, leaf_label_func=llf, leaf_rotation=90)
```

- show_contracted : bool When `True` the heights of non-singleton nodes contracted into a leaf node are plotted as crosses along the link connecting that leaf node. This really is only useful when truncation is used (see `truncate_mode` parameter).
- link_color_func : lambda/function When a callable function, 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:

  ```
  dendrogram(Z, link_color_func=lambda k: colors[k])
  ```

  colors the direct links below each untruncated non-singleton node `k` using `colors[k]`.

  Returns

  - R : dict A dictionary of data structures computed to render the dendrogram. Its has the following keys:
    - 'icoords': a list of lists `[I1, I2, ..., Ip]` where

      `Ik` is a list of 4 independent variable coordinates corresponding to the line that represents the k'th link painted.

    - 'dcoords': a list of lists `[I2, I2, ..., Ip]` where

      `Ik` is a list of 4 independent variable coordinates corresponding to the line that represents the k'th link painted.

    - 'ivl': a list of labels corresponding to the leaf nodes.

    - 'leaves': for each i, `H[i] == j`, cluster node

      j appears in the i th position in the left-to-right traversal of the leaves, where $j < 2n - 1$ and $i < n$. If j is less than n, the i th leaf node corresponds to an original observation. Otherwise, it corresponds to a non-singleton cluster.

fcluster(*Z, t, criterion='inconsistent', depth=2, R=None, monocrit=None*)

Forms flat clusters from the hierarchical clustering defined by the linkage matrix `Z`. The threshold `t` is a required parameter.

Arguments

- Z : ndarray The hierarchical clustering encoded with the matrix returned by the `linkage` function.
- t : double The threshold to apply when forming flat clusters.
- criterion : string (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

    decendents have an inconsistent value less than or equal to `t` then all its leaf descendents belong to the same flat cluster. When no non-singleton cluster meets this criterion, every node is assigned to its own cluster. (Default)
  - 'distance': Forms flat clusters so that the original

    observations in each flat cluster have no greater a cophenetic distance than `t`.
  - 'maxclust': Finds a minimum threshold `r` so that

    the cophenetic distance between any two original observations in the same flat cluster is no more than `r` and no more than `t` flat clusters are formed.
  - 'monocrit': Forms a flat cluster from a cluster node c

    with index i when `monocrit[j] <= 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 = maxRstat(Z, R, 3)
    cluster(Z, t=0.8, criterion='monocrit', monocrit=MR)
    ```
  - 'maxclust_monocrit': Forms a flat cluster from a

    non-singleton cluster node `c` when `monocrit[i] <= r` for all cluster indices `i` below and including `c`. `r` is minimized such that no more than `t` flat clusters are formed. monocrit must be monotonic. For example, to minimize the threshold t on maximum inconsistency values so that no more than 3 flat clusters are formed, do:

    MI = maxinconsts(Z, R) cluster(Z, t=3, criterion='maxclust_monocrit', monocrit=MI)
- depth : int (optional) The maximum depth to perform the inconsistency calculation. It has no meaning for the other criteria. (default=2)
- R : ndarray (optional) The inconsistency matrix to use for the 'inconsistent' criterion. This matrix is computed if not provided.
- monocrit : ndarray (optional) A `(n-1)` numpy vector of doubles. `monocrit[i]` is the statistics upon which non-singleton `i` is thresholded. The monocrit vector must be monotonic, i.e. given a node `c` with index `i`, for all node indices j corresponding to nodes below `c`, `monocrit[i] >= monocrit[j]`.

Returns

- **T**

  [ndarray] A vector of length `n`. `T[i]` is the flat cluster number to which original observation `i` belongs.

fclusterdata(*X, t, criterion='inconsistent', metric='euclidean', depth=2, method='single', R=None*)

```
T = fclusterdata(X, t)
```

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 numpy array `T` of length `n` is returned. `T[i]` is the index of the flat cluster to which the original observation `i` belongs.

Arguments

- X : ndarray `n` by `m` data matrix with `n` observations in `m` dimensions.
- t : double The threshold to apply when forming flat clusters.
- criterion : string Specifies the criterion for forming flat clusters. Valid values are 'inconsistent', 'distance', or 'maxclust' cluster formation algorithms. See `fcluster` for descriptions.
- method : string The linkage method to use (single, complete, average, weighted, median centroid, ward). See `linkage` for more information.
- metric : string The distance metric for calculating pairwise distances. See distance.pdist for descriptions and linkage to verify compatibility with the linkage method.
- t : double The cut-off threshold for the cluster function or the maximum number of clusters (criterion='maxclust').
- depth : int The maximum depth for the inconsistency calculation. See `inconsistent` for more information.
- R : ndarray The inconsistency matrix. It will be computed if necessary if it is not passed.

Returns

- T : 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 MATLAB(TM) clusterdata function.

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] is 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.

Arguments

- **Z**
  [ndarray] A linkage matrix generated by MATLAB(TM)

Returns

- **ZS**
  [ndarray] A linkage matrix compatible with this library.

inconsistent(*Z, d=2*)
Calculates inconsistency statistics on a linkage.

Note: This function behaves similarly to the MATLAB(TM) inconsistent function.

Parameters

- **d**
  [int] The number of links up to `d` levels below each non-singleton cluster
- **Z**
  [ndarray] The $(n-1)$ by 4 matrix encoding the linkage (hierarchical clustering). See `linkage` documentation for more information on its form.

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,

$$\frac{\mathtt{Z}[\mathtt{i},2] - \mathtt{R}[\mathtt{i},0]}{R[i,1]}.$$

is_isomorphic(*T1, T2*)
Determines if two different cluster assignments `T1` and `T2` are equivalent.

Arguments

- T1 : ndarray An assignment of singleton cluster ids to flat cluster ids.
- T2 : ndarray An assignment of singleton cluster ids to flat cluster ids.

Returns

- b : boolean Whether the flat cluster assignments `T1` and `T2` are equivalent.

is_monotonic(*Z*)
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.

Arguments

- Z : ndarray The linkage matrix to check for monotonicity.

Returns

- b : bool A boolean indicating whether the linkage is monotonic.

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 $n-1$.

Arguments

- R : ndarray The inconsistency matrix to check for validity.
- warning : bool When `True`, issues a Python warning if the linkage matrix passed is invalid.
- throw : bool When `True`, throws a Python exception if the linkage matrix passed is invalid.
- name : string This string refers to the variable name of the invalid linkage matrix.

Returns

- b : bool True iff the inconsistency matrix is valid.

is_valid_linkage(*Z, warning=False, throw=False, name=None*)

Checks the validity of a linkage matrix. A linkage matrix is valid if it is a two dimensional nd-array (type double) with n rows and 4 columns. The first two columns must contain indices between 0 and $2n-1$. For a given row `i`, $0 \leq \texttt{Z}[\texttt{i},\texttt{0}] \leq i+n-1$ 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.)

Arguments

- warning : bool When `True`, issues a Python warning if the linkage matrix passed is invalid.
- throw : bool When `True`, throws a Python exception if the linkage matrix passed is invalid.
- name : string This string refers to the variable name of the invalid linkage matrix.

Returns

- **b**
  [bool] True iff the inconsistency matrix is valid.

leaders(*Z, T*)

(L, M) = leaders(Z, T):

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 descendent 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.

Arguments

- **Z**

  [ndarray] The hierarchical clustering encoded as a matrix. See `linkage` for more information.

- **T**

  [ndarray] The flat cluster assignment vector.

Returns

(L, M)

- **L**

  [ndarray] The leader linkage node id's stored as a k-element 1D 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 1D 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.

leaves_list(*Z*)

Returns a list of leaf node ids (corresponding to observation vector index) as they appear in the tree from left to right. Z is a linkage matrix.

Arguments

- **Z**

  [ndarray] The hierarchical clustering encoded as a matrix. See `linkage` for more information.

Returns

- **L**

  [ndarray] The list of leaf node ids.

linkage(*y, method='single', metric='euclidean'*)

Performs hierarchical/agglomerative clustering on the

condensed distance matrix y. y must be a $\binom{n}{2}$ sized vector where n is the number of original observations paired in the distance matrix. The behavior of this function is very similar to the MATLAB(TM) 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

$$d(u,v) = \sum_{ij} \frac{d(u[i], v[j])}{(|u| * |v|)}$$

  for all points i and j where $|u|$ and $|v|$ are the cardinalities of clusters u and v, respectively. This is also called the UPGMA algorithm. This is called UPGMA.

- method='weighted' assigns

$$d(u,v) = (dist(s,v) + dist(t,v))/2$$

  where cluster u was formed with cluster s and t and v is a remaining cluster in the forest. (also called WPGMA)

- method='centroid' assigns

$$dist(s,t) = ||c_s - c_t||_2$$

  where c_s and c_t are the centroids of clusters s and t, respectively. When two clusters s and t are combined into a new cluster u, the new centroid is computed over all the original objects in clusters s and t. The distance then becomes the Euclidean distance between the centroid of u and the centroid of a remaining cluster v in the forest. This is also known as the UPGMC algorithm.

- method='median' assigns math:*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(TM) 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**
  [string] The linkage algorithm to use. See the `Linkage Methods` section below for full descriptions.
- **metric**
  [string] The distance metric to use. See the `distance.pdist` function for a list of valid distance metrics.

Returns

- **Z**
  [ndarray] The hierarchical clustering encoded as a linkage matrix.

maxRstat (*Z, R, i*)

Returns the maximum statistic for each non-singleton cluster and its descendents.

Arguments

- **Z**
  [ndarray] The hierarchical clustering encoded as a matrix. See `linkage` for more information.
- **R**
  [ndarray] 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`.

maxdists(*Z*)

Returns the maximum distance between any cluster for each non-singleton cluster.

Arguments

- **Z**
  [ndarray] The hierarchical clustering encoded as a matrix. See `linkage` for more information.

Returns

- MD : 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.

maxinconsts(*Z, R*)

Returns the maximum inconsistency coefficient for each non-singleton cluster and its descendents.

Arguments

- **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.

median(*y*)

Performs median/WPGMC linkage. See `linkage` for more information on the return structure and algorithm.

The following are common calling conventions:

1. `Z = median(y)`

   Performs median/WPGMC linkage on the condensed distance matrix `y`. See `linkage` for more information on the return structure and algorithm.

2. `Z = median(X)`

   Performs median/WPGMC linkage on the observation matrix `X` using Euclidean distance as the distance metric. See linkage for more information on the return structure and algorithm.

Parameters

Q
[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 a m by n array.

Returns

- **Z**
  [ndarray] The hierarchical clustering encoded as a linkage matrix.

Seealso

- linkage: for advanced creation of hierarchical clusterings.

num_obs_linkage(*Z*)
Returns the number of original observations of the linkage matrix passed.

Arguments

- **Z**
  [ndarray] The linkage matrix on which to perform the operation.

Returns

- **n**
  [int] The number of original observations in the linkage.

set_link_color_palette(*palette*)
Changes the list of matplotlib color codes to use when coloring links with the dendrogram color_threshold feature.

Arguments

- palette : 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.

single(*y*)
Performs single/min/nearest linkage on the condensed distance matrix `y`. 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] The linkage matrix.

Seealso

- linkage: for advanced creation of hierarchical clusterings.

to_mlab_linkage(*Z*)
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.

Arguments

- **Z**
  [ndarray] A linkage matrix generated by this library.

Returns

- **ZM**
  [ndarray] A linkage matrix compatible with MATLAB(TM)'s hierarchical clustering functions.

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).
- r : bool 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.

ward(*y*)

Performs Ward's linkage on a condensed or redundant distance matrix. See linkage for more information on the return structure and algorithm.

The following are common calling conventions:

1. `Z = ward(y)` Performs Ward's linkage on the condensed distance matrix `Z`. See linkage for more information on the return structure and algorithm.
2. `Z = ward(X)` Performs Ward's 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

Q
[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 a m by n array.

Returns

- **Z**
  [ndarray] The hierarchical clustering encoded as a linkage matrix.

Seealso

- linkage: for advanced creation of hierarchical clusterings.

weighted(*y*)
Performs weighted/WPGMA linkage on the condensed distance matrix y. 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.

Seealso

- linkage: for advanced creation of hierarchical clusterings.

3.1.2 K-means clustering and vector quantization (scipy.cluster.vq)

K-means Clustering and Vector Quantization Module

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.

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. Common variants of k-means try to minimize distortion, which is defined as the sum of the 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 often used as a stopping criterion: when the change is lower than a threshold, the k-means algorithm is not making sufficient progress and terminates.

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.

For 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.

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.

whiten(obs) –
Normalize a group of observations so each feature has unit variance.

vq(obs,code_book) –
Calculate code book membership of a set of observation vectors.

kmeans(obs,k_or_guess,iter=20,thresh=1e-5) –
Clusters a set of observation vectors. Learns centroids with the k-means algorithm, trying to minimize distortion. A code book is generated that can be used to quantize vectors.

kmeans2 –
A different implementation of k-means with more methods for initializing centroids. Uses maximum number of iterations as opposed to a distortion threshold as its stopping criterion.

whiten (*obs*)
Normalize a group of observations on a per feature basis.

Before running k-means, it is beneficial to rescale each feature dimension of the observation set with whitening. Each feature is divided by its standard deviation across all observations to give it unit variance.

Parameters

obs
[ndarray] Each row of the array is an observation. The columns are the features seen during each observation.

```
      #    f0    f1    f2
obs = [[  1.,   1.,   1.],  #o0
       [  2.,   2.,   2.],  #o1
       [  3.,   3.,   3.],  #o2
       [  4.,   4.,   4.]]) #o3
```

XXX perhaps should have an axis variable here.

Returns

result
[ndarray] Contains the values in obs scaled by the standard devation of each column.

Examples

```
>>> from numpy import array
>>> from scipy.cluster.vq import whiten
>>> features  = array([[  1.9,2.3,1.7],
...                    [  1.5,2.5,2.2],
...                    [  0.8,0.6,1.7,]])
```

```
>>> whiten(features)
array([[ 3.41250074,  2.20300046,  5.88897275],
       [ 2.69407953,  2.39456571,  7.62102355],
       [ 1.43684242,  0.57469577,  5.88897275]])
```

vq(*obs, code_book*)

Vector Quantization: assign 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 acheived 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 NxM 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.

```
                #   f0    f1    f2   f3
code_book = [[  1.,   2.,   3.,   4.],  #c0
             [  1.,   2.,   3.,   4.],  #c1
             [  1.,   2.,   3.,   4.]]) #c2
```

Returns

code
[ndarray] A length N array holding the code book index for each observation.

dist
[ndarray] The distortion (distance) between the observation and its nearest code.

Notes

This currently forces 32-bit math precision for speed. Anyone know of a situation where this undermines the accuracy of the algorithm?

Examples

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

kmeans(*obs, k_or_guess, iter=20, thresh=1.0000000000000001e-05*)

Performs k-means on a set of observation vectors forming k

clusters. This yields a code book mapping centroids to codes and vice versa. 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.

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] 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 paramter. This parameter does not represent the number of iterations of the k-means algorithm.

thresh

[float] Terminates the k-means algorithm if the change in distortion since the last k-means iteration is less than thresh.

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.

Seealso

- 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

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

kmeans2 (*data, k, iter=10, thresh=1.0000000000000001e-05, minit='random', missing='warn'*)

Classify a set of observations into k clusters using the k-means
algorithm.

The algorithm attempts to minimize the Euclidian distance between observations and centroids. Several initialization methods are included.

Parameters

data
[ndarray] A M by N array of M observations in N dimensions or a length M array of M one-dimensional observations.

k
[int or ndarray] The number of clusters to form as well as the number of centroids to generate. If minit initialization string is 'matrix', or if a ndarray is given instead, it is interpreted as initial cluster to use instead.

iter
[int] Number of iterations of the k-means algrithm to run. Note that this differs in meaning from the iters parameter to the kmeans function.

thresh
[float] (not used yet).

minit
[string] 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.

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.

3.1.3 Vector Quantization / Kmeans

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. Development of self-organizing maps (SOM) and other approaches is underway.

3.1.4 Hierarchical Clustering

The hierarchy module provides functions for hierarchical and agglomerative clustering. Its features include generating hierarchical clusters from distance matrices, computing distance matrices from observation vectors, calculating statistics on clusters, cutting linkages to generate flat clusters, and visualizing clusters with dendrograms.

3.1.5 Distance Computation

The distance module provides functions for computing distances between pairs of vectors from a set of observation vectors.

3.2 Constants (`scipy.constants`)

Physical and mathematical constants and units.

3.2.1 Mathematical constants

`pi`	Pi
`golden`	Golden ratio

3.2.2 Physical constants

c	speed of light in vacuum
mu_0	the magnetic constant μ_0
epsilon_0	the electric constant (vacuum permittivity), ϵ_0
h	the Planck constant h
hbar	$\hbar = h/(2\pi)$
G	Newtonian constant of gravitation
g	standard acceleration of gravity
e	elementary charge
R	molar gas constant
alpha	fine-structure constant
N_A	Avogadro constant
k	Boltzmann constant
sigma	Stefan-Boltzmann constant σ
Wien	Wien displacement law constant
Rydberg	Rydberg constant
m_e	electron mass
m_p	proton mass
m_n	neutron mass

3.2.3 Constants database

In addition to the above variables containing physical constants, `scipy.constants` also contains a database of additional physical constants.

value(key)	Value in physical_constants indexed by key
unit(key)	Unit in physical_constants indexed by key
precision(key)	Relative precision in physical_constants indexed by key
find(sub)	Return list of codata.physical_constant keys containing a given string

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

```
>>> from scipy.constants import codata
>>> codata.value('elementary charge')
1.60217653e-019
```

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

```
>>> from scipy.constants import codata
>>> codata.unit(u'proton mass')
'kg'
```

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

```
>>> from scipy.constants import codata
>>> codata.precision(u'proton mass')
1.7338050694080732e-007
```

find(*sub*)
Return list of codata.physical_constant keys containing a given string

Parameters
sub : str or unicode

Sub-string to search keys for

Returns
keys : list

List of keys containing *sub*

See Also:

codata
Contains the description of *physical_constants*, which, as a dictionary literal object, does not itself possess a docstring.

physical_constants
Dictionary of physical constants, of the format `physical_constants[name] = (value, unit, uncertainty)`.

Available constants:

```
alpha particle mass
alpha particle mass energy equivalent
alpha particle mass energy equivalent in MeV
alpha particle mass in u
alpha particle molar mass
alpha particle-electron mass ratio
alpha particle-proton mass ratio
Angstrom star
atomic mass constant
atomic mass constant energy equivalent
atomic mass constant energy equivalent in MeV
atomic mass unit-electron volt relationship
atomic mass unit-hartree relationship
atomic mass unit-hertz relationship
atomic mass unit-inverse meter relationship
atomic mass unit-joule relationship
atomic mass unit-kelvin relationship
atomic mass unit-kilogram relationship
atomic unit of 1st hyperpolarizablity
atomic unit of 2nd hyperpolarizablity
atomic unit of action
atomic unit of charge
atomic unit of charge density
atomic unit of current
atomic unit of electric dipole moment
atomic unit of electric field
atomic unit of electric field gradient
atomic unit of electric polarizablity
atomic unit of electric potential
atomic unit of electric quadrupole moment
atomic unit of energy
atomic unit of force
atomic unit of length
atomic unit of magnetic dipole moment
atomic unit of magnetic flux density
atomic unit of magnetizability
atomic unit of mass
atomic unit of momentum
atomic unit of permittivity
atomic unit of time
```

Continued on next page

Table 3.1 – continued from previous page

atomic unit of velocity	
Avogadro constant	
Bohr magneton	
Bohr magneton in eV/T	
Bohr magneton in Hz/T	
Bohr magneton in inverse meters per tesla	
Bohr magneton in K/T	
Bohr radius	
Boltzmann constant	
Boltzmann constant in eV/K	
Boltzmann constant in Hz/K	
Boltzmann constant in inverse meters per kelvin	
characteristic impedance of vacuum	
classical electron radius	
Compton wavelength	
Compton wavelength over 2 pi	
conductance quantum	
conventional value of Josephson constant	
conventional value of von Klitzing constant	
Cu x unit	
deuteron magnetic moment	
deuteron magnetic moment to Bohr magneton ratio	
deuteron magnetic moment to nuclear magneton ratio	
deuteron mass	
deuteron mass energy equivalent	
deuteron mass energy equivalent in MeV	
deuteron mass in u	
deuteron molar mass	
deuteron rms charge radius	
deuteron-electron magnetic moment ratio	
deuteron-electron mass ratio	
deuteron-neutron magnetic moment ratio	
deuteron-proton magnetic moment ratio	
deuteron-proton mass ratio	
electric constant	
electron charge to mass quotient	
electron g factor	
electron gyromagnetic ratio	
electron gyromagnetic ratio over 2 pi	
electron magnetic moment	
electron magnetic moment anomaly	
electron magnetic moment to Bohr magneton ratio	
electron magnetic moment to nuclear magneton ratio	
electron mass	
electron mass energy equivalent	
electron mass energy equivalent in MeV	
electron mass in u	
electron molar mass	
electron to alpha particle mass ratio	
electron to shielded helion magnetic moment ratio	
electron to shielded proton magnetic moment ratio	
electron volt	

Continued on next page

Table 3.1 – continued from previous page

electron volt-atomic mass unit relationship	
electron volt-hartree relationship	
electron volt-hertz relationship	
electron volt-inverse meter relationship	
electron volt-joule relationship	
electron volt-kelvin relationship	
electron volt-kilogram relationship	
electron-deuteron magnetic moment ratio	
electron-deuteron mass ratio	
electron-muon magnetic moment ratio	
electron-muon mass ratio	
electron-neutron magnetic moment ratio	
electron-neutron mass ratio	
electron-proton magnetic moment ratio	
electron-proton mass ratio	
electron-tau mass ratio	
elementary charge	
elementary charge over h	
Faraday constant	
Faraday constant for conventional electric current	
Fermi coupling constant	
fine-structure constant	
first radiation constant	
first radiation constant for spectral radiance	
Hartree energy	
Hartree energy in eV	
hartree-atomic mass unit relationship	
hartree-electron volt relationship	
hartree-hertz relationship	
hartree-inverse meter relationship	
hartree-joule relationship	
hartree-kelvin relationship	
hartree-kilogram relationship	
helion mass	
helion mass energy equivalent	
helion mass energy equivalent in MeV	
helion mass in u	
helion molar mass	
helion-electron mass ratio	
helion-proton mass ratio	
hertz-atomic mass unit relationship	
hertz-electron volt relationship	
hertz-hartree relationship	
hertz-inverse meter relationship	
hertz-joule relationship	
hertz-kelvin relationship	
hertz-kilogram relationship	
inverse fine-structure constant	
inverse meter-atomic mass unit relationship	
inverse meter-electron volt relationship	
inverse meter-hartree relationship	
inverse meter-hertz relationship	

Continued on next page

Table 3.1 – continued from previous page

inverse meter-joule relationship	
inverse meter-kelvin relationship	
inverse meter-kilogram relationship	
inverse of conductance quantum	
Josephson constant	
joule-atomic mass unit relationship	
joule-electron volt relationship	
joule-hartree relationship	
joule-hertz relationship	
joule-inverse meter relationship	
joule-kelvin relationship	
joule-kilogram relationship	
kelvin-atomic mass unit relationship	
kelvin-electron volt relationship	
kelvin-hartree relationship	
kelvin-hertz relationship	
kelvin-inverse meter relationship	
kelvin-joule relationship	
kelvin-kilogram relationship	
kilogram-atomic mass unit relationship	
kilogram-electron volt relationship	
kilogram-hartree relationship	
kilogram-hertz relationship	
kilogram-inverse meter relationship	
kilogram-joule relationship	
kilogram-kelvin relationship	
lattice parameter of silicon	
Loschmidt constant (273.15 K, 101.325 kPa)	
magnetic constant	
magnetic flux quantum	
Mo x unit	
molar gas constant	
molar mass constant	
molar mass of carbon-12	
molar Planck constant	
molar Planck constant times c	
molar volume of ideal gas (273.15 K, 100 kPa)	
molar volume of ideal gas (273.15 K, 101.325 kPa)	
molar volume of silicon	
muon Compton wavelength	
muon Compton wavelength over 2 pi	
muon g factor	
muon magnetic moment	
muon magnetic moment anomaly	
muon magnetic moment to Bohr magneton ratio	
muon magnetic moment to nuclear magneton ratio	
muon mass	
muon mass energy equivalent	
muon mass energy equivalent in MeV	
muon mass in u	
muon molar mass	
muon-electron mass ratio	

Continued on next page

Table 3.1 – continued from previous page

muon-neutron mass ratio
muon-proton magnetic moment ratio
muon-proton mass ratio
muon-tau mass ratio
natural unit of action
natural unit of action in eV s
natural unit of energy
natural unit of energy in MeV
natural unit of length
natural unit of mass
natural unit of momentum
natural unit of momentum in MeV/c
natural unit of time
natural unit of velocity
neutron Compton wavelength
neutron Compton wavelength over 2 pi
neutron g factor
neutron gyromagnetic ratio
neutron gyromagnetic ratio over 2 pi
neutron magnetic moment
neutron magnetic moment to Bohr magneton ratio
neutron magnetic moment to nuclear magneton ratio
neutron mass
neutron mass energy equivalent
neutron mass energy equivalent in MeV
neutron mass in u
neutron molar mass
neutron to shielded proton magnetic moment ratio
neutron-electron magnetic moment ratio
neutron-electron mass ratio
neutron-muon mass ratio
neutron-proton magnetic moment ratio
neutron-proton mass ratio
neutron-tau mass ratio
Newtonian constant of gravitation
Newtonian constant of gravitation over h-bar c
nuclear magneton
nuclear magneton in eV/T
nuclear magneton in inverse meters per tesla
nuclear magneton in K/T
nuclear magneton in MHz/T
Planck constant
Planck constant in eV s
Planck constant over 2 pi
Planck constant over 2 pi in eV s
Planck constant over 2 pi times c in MeV fm
Planck length
Planck mass
Planck temperature
Planck time
proton charge to mass quotient
proton Compton wavelength

Continued on next page

Table 3.1 – continued from previous page

proton Compton wavelength over 2 pi	
proton g factor	
proton gyromagnetic ratio	
proton gyromagnetic ratio over 2 pi	
proton magnetic moment	
proton magnetic moment to Bohr magneton ratio	
proton magnetic moment to nuclear magneton ratio	
proton magnetic shielding correction	
proton mass	
proton mass energy equivalent	
proton mass energy equivalent in MeV	
proton mass in u	
proton molar mass	
proton rms charge radius	
proton-electron mass ratio	
proton-muon mass ratio	
proton-neutron magnetic moment ratio	
proton-neutron mass ratio	
proton-tau mass ratio	
quantum of circulation	
quantum of circulation times 2	
Rydberg constant	
Rydberg constant times c in Hz	
Rydberg constant times hc in eV	
Rydberg constant times hc in J	
Sackur-Tetrode constant (1 K, 100 kPa)	
Sackur-Tetrode constant (1 K, 101.325 kPa)	
second radiation constant	
shielded helion gyromagnetic ratio	
shielded helion gyromagnetic ratio over 2 pi	
shielded helion magnetic moment	
shielded helion magnetic moment to Bohr magneton ratio	
shielded helion magnetic moment to nuclear magneton ratio	
shielded helion to proton magnetic moment ratio	
shielded helion to shielded proton magnetic moment ratio	
shielded proton gyromagnetic ratio	
shielded proton gyromagnetic ratio over 2 pi	
shielded proton magnetic moment	
shielded proton magnetic moment to Bohr magneton ratio	
shielded proton magnetic moment to nuclear magneton ratio	
speed of light in vacuum	
standard acceleration of gravity	
standard atmosphere	
Stefan-Boltzmann constant	
tau Compton wavelength	
tau Compton wavelength over 2 pi	
tau mass	
tau mass energy equivalent	
tau mass energy equivalent in MeV	
tau mass in u	
tau molar mass	
tau-electron mass ratio	

Continued on next page

Table 3.1 – continued from previous page

tau-muon mass ratio	
tau-neutron mass ratio	
tau-proton mass ratio	
Thomson cross section	
unified atomic mass unit	
von Klitzing constant	
weak mixing angle	
Wien displacement law constant	
{220} lattice spacing of silicon	

3.2.4 Unit prefixes

SI

yotta	10^{24}
zetta	10^{21}
exa	10^{18}
peta	10^{15}
tera	10^{12}
giga	10^{9}
mega	10^{6}
kilo	10^{3}
hecto	10^{2}
deka	10^{1}
deci	10^{-1}
centi	10^{-2}
milli	10^{-3}
micro	10^{-6}
nano	10^{-9}
pico	10^{-12}
femto	10^{-15}
atto	10^{-18}
zepto	10^{-21}

Binary

kibi	2^{10}
mebi	2^{20}
gibi	2^{30}
tebi	2^{40}
pebi	2^{50}
exbi	2^{60}
zebi	2^{70}
yobi	2^{80}

3.2.5 Units

Weight

gram	10^{-3} kg
metric_ton	10^{3} kg
grain	one grain in kg
lb	one pound (avoirdupous) in kg
oz	one ounce in kg
stone	one stone in kg
grain	one grain in kg
long_ton	one long ton in kg
short_ton	one short ton in kg
troy_ounce	one Troy ounce in kg
troy_pound	one Troy pound in kg
carat	one carat in kg
m_u	atomic mass constant (in kg)

Angle

degree	degree in radians
arcmin	arc minute in radians
arcsec	arc second in radians

Time

minute	one minute in seconds
hour	one hour in seconds
day	one day in seconds
week	one week in seconds
year	one year (365 days) in seconds
Julian_year	one Julian year (365.25 days) in seconds

Length

inch	one inch in meters
foot	one foot in meters
yard	one yard in meters
mile	one mile in meters
mil	one mil in meters
pt	one point in meters
survey_foot	one survey foot in meters
survey_mile	one survey mile in meters
nautical_mile	one nautical mile in meters
fermi	one Fermi in meters
angstrom	one Ångström in meters
micron	one micron in meters
au	one astronomical unit in meters
light_year	one light year in meters
parsec	one parsec in meters

Pressure

atm	standard atmosphere in pascals
bar	one bar in pascals
torr	one torr (mmHg) in pascals
psi	one psi in pascals

Area

hectare	one hectare in square meters
acre	one acre in square meters

Volume

liter	one liter in cubic meters
gallon	one gallon (US) in cubic meters
gallon_imp	one gallon (UK) in cubic meters
fluid_ounce	one fluid ounce (US) in cubic meters
fluid_ounce_imp	one fluid ounce (UK) in cubic meters
bbl	one barrel in cubic meters

Speed

kmh	kilometers per hour in meters per second
mph	miles per hour in meters per second
mach	one Mach (approx., at 15 °C, 1 atm) in meters per second
knot	one knot in meters per second

Temperature

zero_Celsius	zero of Celsius scale in Kelvin
degree_Fahrenheit	one Fahrenheit (only differences) in Kelvins

C2K(C)	Convert Celsius to Kelvin
K2C(K)	Convert Kelvin to Celsius
F2C(F)	Convert Fahrenheit to Celsius
C2F(C)	Convert Celsius to Fahrenheit
F2K(F)	Convert Fahrenheit to Kelvin
K2F(K)	Convert Kelvin to Fahrenheit

C2K(*C*)

Convert Celsius to Kelvin

Parameters

C : float-like scalar or array-like

Celsius temperature(s) to be converted

Returns

K : float or a numpy array of floats, corresponding to type of Parameters

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

```
>>> 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 : float-like scalar or array-like

Kelvin temperature(s) to be converted

Returns

C : float or a numpy array of floats, corresponding to type of Parameters

Equivalent Celsius temperature(s)

Notes

Computes $C = K - zero\_Celsius$ where $zero\_Celsius = 273.15$, i.e., (the absolute value of) temperature "absolute zero" as measured in Celsius.

Examples

```
>>> from scipy.constants.constants import K2C
>>> K2C(np.array([233.15, 313.15]))
array([-40.,  40.])
```

F2C(*F*)

Convert Fahrenheit to Celsius

Parameters

F : float-like scalar or array-like

Fahrenheit temperature(s) to be converted

Returns

C : float or a numpy array of floats, corresponding to type of Parameters

Equivalent Celsius temperature(s)

Notes

Computes $C = (F - 32) / 1.8$

Examples

```
>>> from scipy.constants.constants import F2C
>>> F2C(np.array([-40, 40.0]))
array([-40.        ,   4.44444444])
```

C2F(*C*)

Convert Celsius to Fahrenheit

Parameters

C : float-like scalar or array-like

Celsius temperature(s) to be converted

Returns

F : float or a numpy array of floats, corresponding to type of Parameters

Equivalent Fahrenheit temperature(s)

Notes

Computes *F = 1.8 * C + 32*

Examples

```
>>> from scipy.constants.constants import C2F
>>> C2F(np.array([-40, 40.0]))
array([ -40.,  104.])
```

F2K(*F*)

Convert Fahrenheit to Kelvin

Parameters

F : float-like scalar or array-like

Fahrenheit temperature(s) to be converted

Returns

K : float or a numpy array of floats, corresponding to type of Parameters

Equivalent Kelvin temperature(s)

Notes

Computes *K = (F - 32)/1.8 + zero_Celsius* where *zero_Celsius* = 273.15, i.e., (the absolute value of) temperature "absolute zero" as measured in Celsius.

Examples

```
>>> from scipy.constants.constants import F2K
>>> F2K(np.array([-40, 104]))
array([ 233.15,  313.15])
```

K2F(*K*)

Convert Kelvin to Fahrenheit

Parameters

K : float-like scalar or array-like

Kelvin temperature(s) to be converted

Returns

F : float or a numpy array of floats, corresponding to type of Parameters

Equivalent Fahrenheit temperature(s)

Notes

Computes *F = 1.8 * (K - zero_Celsius) + 32* where *zero_Celsius* = 273.15, i.e., (the absolute value of) temperature "absolute zero" as measured in Celsius.

Examples

```
>>> from scipy.constants.constants import K2F
>>> K2F(np.array([233.15,  313.15]))
array([ -40.,  104.])
```

Energy

eV	one electron volt in Joules
calorie	one calorie (thermochemical) in Joules
calorie_IT	one calorie (International Steam Table calorie, 1956) in Joules
erg	one erg in Joules
Btu	one British thermal unit (International Steam Table) in Joules
Btu_th	one British thermal unit (thermochemical) in Joules
ton_TNT	one ton of TNT in Joules

Power

hp	one horsepower in watts

Force

dyn	one dyne in watts
lbf	one pound force in watts
kgf	one kilogram force in watts

Optics

lambda2nu(**lambda_**)	Convert wavelength to optical frequency
nu2lambda(nu)	Convert optical frequency to wavelength.

lambda2nu(*lambda_*)

Convert wavelength to optical frequency

Parameters

lambda : float-like scalar or array-like

Wavelength(s) to be converted

Returns

nu : float or a numpy array of floats, corresponding to type of Parameters

Equivalent optical frequency(ies)

Notes

Computes $\nu = c/\lambda$ where c = 299792458.0, i.e., the (vacuum) speed of light in meters/second.

Examples

```
>>> from scipy.constants.constants import lambda2nu
>>> lambda2nu(np.array((1, speed_of_light)))
array([  2.99792458e+08,   1.00000000e+00])
```

nu2lambda(*nu*)
Convert optical frequency to wavelength.

Parameters
nu : float-like scalar or array-like

Optical frequency(ies) to be converted

Returns
lambda : float or a numpy array of floats, corresp. to type of Parameters

Equivalent wavelength(s)

Notes

Computes $\lambda = c/\nu$ where c = 299792458.0, i.e., the (vacuum) speed of light in meters/second.

Examples

```
>>> from scipy.constants.constants import nu2lambda
>>> nu2lambda(np.array((1, speed_of_light)))
array([  2.99792458e+08,   1.00000000e+00])
```

3.3 Fourier transforms (scipy.fftpack)

3.3.1 Fast Fourier transforms

fft(x[, n, axis, overwrite_x])	Return discrete Fourier transform of arbitrary type sequence x.
ifft(x[, n, axis, overwrite_x])	ifft(x, n=None, axis=-1, overwrite_x=0) -> y
fftn(x[, shape, axes, overwrite_x])	fftn(x, shape=None, axes=None, overwrite_x=0) -> y
ifftn(x[, shape, axes, overwrite_x])	ifftn(x, s=None, axes=None, overwrite_x=0) -> y
fft2(x[, shape, axes, overwrite_x])	2-D discrete Fourier transform.
ifft2(x[, shape, axes, overwrite_x])	ifft2(x, shape=None, axes=(-2,-1), overwrite_x=0) -> y
rfft(x[, n, axis, overwrite_x])	rfft(x, n=None, axis=-1, overwrite_x=0) -> y
irfft(x[, n, axis, overwrite_x])	irfft(x, n=None, axis=-1, overwrite_x=0) -> y

fft(*x, n=None, axis=-1, overwrite_x=0*)
Return discrete Fourier transform of arbitrary type sequence x.

Parameters
x : array-like

array to fourier transform.

n : int, optional

Length of the Fourier transform. If n<x.shape[axis], x is truncated. If n>x.shape[axis], x is zero-padded. (Default n=x.shape[axis]).

axis : int, optional

Axis along which the fft's are computed. (default=-1)

overwrite_x : bool, optional

If True the contents of x can be destroyed. (default=False)

Returns
z : complex ndarray

with the elements:
[y(0),y(1),..,y(n/2-1),y(-n/2),...,y(-1)] if n is even [y(0),y(1),..,y((n-1)/2),y(-(n-1)/2),...,y(-1)] if n is odd

where
y(j) = sum[k=0..n-1] x[k] * exp(-sqrt(-1)*j*k* 2*pi/n), j = 0..n-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 = fft(a, n), then A[0] contains the zero-frequency term, A[1:n/2+1] contains the positive-frequency terms, and A[n/2+1:] contains the negative-frequency terms, in order of decreasingly negative frequency. So for an 8-point transform, the frequencies of the result are [0, 1, 2, 3, 4, -3, -2, -1].

This is most efficient for n a power of two.

Examples

```
>>> x = np.arange(5)
>>> np.all(np.abs(x-fft(ifft(x))<1.e-15) #within numerical accuracy.
True
```

ifft(*x, n=None, axis=-1, overwrite_x=0*)
ifft(x, n=None, axis=-1, overwrite_x=0) -> y

Return inverse discrete Fourier transform of arbitrary type sequence x.

The returned complex array contains
[y(0),y(1),...,y(n-1)]

where
y(j) = 1/n sum[k=0..n-1] x[k] * exp(sqrt(-1)*j*k* 2*pi/n)

Optional input: see fft.__doc__

fftn(*x, shape=None, axes=None, overwrite_x=0*)
fftn(x, shape=None, axes=None, overwrite_x=0) -> y

Return multi-dimensional discrete Fourier transform of arbitrary type sequence x.

The returned array contains

y[j_1,..,j_d] = sum[k_1=0..n_1-1, ..., k_d=0..n_d-1]
x[k_1,..,k_d] * prod[i=1..d] exp(-sqrt(-1)*2*pi/n_i * j_i * k_i)

where d = len(x.shape) and n = x.shape. Note that y[..., -j_i, ...] = y[..., n_i-j_i, ...].conjugate().

Optional input:

shape
Defines the shape of the Fourier transform. If shape is not specified then

shape=take(x.shape,axes,axis=0). If shape[i]>x.shape[i] then the i-th dimension is padded with zeros. If shape[i]<x.shape[i], then the i-th dimension is truncated to desired length shape[i].

axes
The transform is applied along the given axes of the input array (or the newly constructed array if shape argument was used).

overwrite_x
If set to true, the contents of x can be destroyed.

Notes:
y == fftn(ifftn(y)) within numerical accuracy.

ifftn (*x, shape=None, axes=None, overwrite_x=0*)
ifftn(x, s=None, axes=None, overwrite_x=0) -> y

Return inverse multi-dimensional discrete Fourier transform of arbitrary type sequence x.

The returned array contains

y[j_1,..,j_d] = 1/p * sum[k_1=0..n_1-1, ..., k_d=0..n_d-1]
x[k_1,..,k_d] * prod[i=1..d] exp(sqrt(-1)*2*pi/n_i * j_i * k_i)

where d = len(x.shape), n = x.shape, and p = prod[i=1..d] n_i.

Optional input: see fftn.__doc__

fft2 (*x, shape=None, axes=(-2, -1), overwrite_x=0*)
2-D discrete Fourier transform.

Return the two-dimensional discrete Fourier transform of the 2-D argument *x*.

See Also:

fftn
for detailed information.

ifft2 (*x, shape=None, axes=(-2, -1), overwrite_x=0*)
ifft2(x, shape=None, axes=(-2,-1), overwrite_x=0) -> y

Return inverse two-dimensional discrete Fourier transform of arbitrary type sequence x.

See ifftn.__doc__ for more information.

rfft (*x, n=None, axis=-1, overwrite_x=0*)
rfft(x, n=None, axis=-1, overwrite_x=0) -> y

Return discrete Fourier transform of real sequence x.

The returned real arrays contains
[y(0),Re(y(1)),Im(y(1)),...,Re(y(n/2))] if n is even [y(0),Re(y(1)),Im(y(1)),...,Re(y(n/2)),Im(y(n/2))] if n is odd

where
y(j) = sum[k=0..n-1] x[k] * exp(-sqrt(-1)*j*k* 2*pi/n) j = 0..n-1

Note that y(-j) = y(n-j).conjugate().

Optional input:

n
Defines the length of the Fourier transform. If n is not specified then n=x.shape[axis] is set. If n<x.shape[axis], x is truncated. If n>x.shape[axis], x is zero-padded.

axis
The transform is applied along the given axis of the input array (or the newly constructed array if n argument was used).

overwrite_x
If set to true, the contents of x can be destroyed.

Notes:
y == rfft(irfft(y)) within numerical accuracy.

irfft (*x, n=None, axis=-1, overwrite_x=0*)
irfft(x, n=None, axis=-1, overwrite_x=0) -> y

Return inverse discrete Fourier transform of real sequence x. The contents of x is interpreted as the output of rfft(..) function.

The returned real array contains
[y(0),y(1),...,y(n-1)]

where for n is even

y(j) = 1/n (sum[k=1..n/2-1] (x[2*k-1]+sqrt(-1)*x[2*k])

- exp(sqrt(-1)*j*k* 2*pi/n)
- c.c. + x[0] + (-1)**(j) x[n-1])

and for n is odd

y(j) = 1/n (sum[k=1..(n-1)/2] (x[2*k-1]+sqrt(-1)*x[2*k])

- exp(sqrt(-1)*j*k* 2*pi/n)
- c.c. + x[0])

c.c. denotes complex conjugate of preceeding expression.

Optional input: see rfft.__doc__

3.3.2 Differential and pseudo-differential operators

diff(x[, order, period, _cache])	diff(x, order=1, period=2*pi) -> y
tilbert(x, h[, period, _cache])	tilbert(x, h, period=2*pi) -> y
itilbert(x, h[, period, _cache])	itilbert(x, h, period=2*pi) -> y
hilbert(x[, _cache])	hilbert(x) -> y
ihilbert(x)	ihilbert(x) -> y
cs_diff(x, a, b[, period, _cache])	cs_diff(x, a, b, period=2*pi) -> y
sc_diff(x, a, b[, period, _cache])	sc_diff(x, a, b, period=2*pi) -> y
ss_diff(x, a, b[, period, _cache])	ss_diff(x, a, b, period=2*pi) -> y
cc_diff(x, a, b[, period, _cache])	cc_diff(x, a, b, period=2*pi) -> y
shift(x, a[, period, _cache])	shift(x, a, period=2*pi) -> y

diff (*x, order=1, period=None, _cache={}*)
diff(x, order=1, period=2*pi) -> y

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 = pow(sqrt(-1)*j*2*pi/period, order) * x_j y_0 = 0 if order is not 0.

Optional input:

order
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
The assumed period of the sequence. Default is 2*pi.

Notes:

If sum(x,axis=0)=0 then
diff(diff(x,k),-k)==x (within numerical accuracy)

For odd order and even len(x), the Nyquist mode is taken zero.

tilbert(*x, h, period=None, _cache={}*)
tilbert(x, h, period=2*pi) -> y

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

Input:

h
Defines the parameter of the Tilbert transform.

period
The assumed period of the sequence. Default period is 2*pi.

Notes:

If sum(x,axis=0)==0 and n=len(x) is odd then
tilbert(itilbert(x)) == x

If 2*pi*h/period is approximately 10 or larger then numerically
tilbert == hilbert

(theoretically oo-Tilbert == Hilbert). For even len(x), the Nyquist mode of x is taken zero.

itilbert(*x, h, period=None, _cache={}*)
itilbert(x, h, period=2*pi) -> y

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)*tanh(j*h*2*pi/period) * x_j y_0 = 0

Optional input: see tilbert.__doc__

hilbert(*x, _cache={}*)
hilbert(x) -> y

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)*sign(j) * x_j y_0 = 0

Notes:

If sum(x,axis=0)==0 then
hilbert(ihilbert(x)) == x

For even len(x), the Nyquist mode of x is taken zero.

ihilbert(*x*)
ihilbert(x) -> y

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

y_j = -sqrt(-1)*sign(j) * x_j y_0 = 0

cs_diff(*x, a, b, period=None, _cache={}*)
cs_diff(x, a, b, period=2*pi) -> y

Return (a,b)-cosh/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 = -sqrt(-1)*cosh(j*a*2*pi/period)/sinh(j*b*2*pi/period) * x_j y_0 = 0

Input:

a,b
Defines the parameters of the cosh/sinh pseudo-differential operator.

period
The period of the sequence. Default period is 2*pi.

Notes:
For even len(x), the Nyquist mode of x is taken zero.

sc_diff(*x, a, b, period=None, _cache={}*)
sc_diff(x, a, b, period=2*pi) -> y

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

Input:

a,b
Defines the parameters of the sinh/cosh pseudo-differential operator.

period
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 zero.

ss_diff (*x, a, b, period=None, _cache={}*)
ss_diff(x, a, b, period=2*pi) -> y

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

Input:

a,b
Defines the parameters of the sinh/sinh pseudo-differential operator.

period
The period of the sequence x. Default is 2*pi.

Notes:
ss_diff(ss_diff(x,a,b),b,a) == x

cc_diff (*x, a, b, period=None, _cache={}*)
cc_diff(x, a, b, period=2*pi) -> y

Return (a,b)-cosh/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 = cosh(j*a*2*pi/period)/cosh(j*b*2*pi/period) * x_j

Input:

a,b
Defines the parameters of the sinh/sinh pseudo-differential operator.

Optional input:

period
The period of the sequence x. Default is 2*pi.

Notes:
cc_diff(cc_diff(x,a,b),b,a) == x

shift (*x, a, period=None, _cache={}*)
shift(x, a, period=2*pi) -> y

Shift periodic sequence x by a: y(u) = x(u+a).

If x_j and y_j are Fourier coefficients of periodic functions x and y, respectively, then

y_j = exp(j*a*2*pi/period*sqrt(-1)) * x_f

Optional input:

period
The period of the sequences x and y. Default period is 2*pi.

3.3.3 Helper functions

fftshift(x[, axes])	Shift the zero-frequency component to the center of the spectrum.
ifftshift(x[, axes])	The inverse of fftshift.
dftfreq	
rfftfreq(n[, d])	rfftfreq(n, d=1.0) -> f

fftshift (*x, axes=None*)

Shift the zero-frequency component to the center of the spectrum.

This function swaps half-spaces for all axes listed (defaults to all). Note that `y[0]` is the Nyquist component only if `len(x)` is even.

Parameters

x : array_like

Input array.

axes : int or shape tuple, optional

Axes over which to shift. Default is None, which shifts all axes.

Returns

y : ndarray

The shifted array.

See Also:

ifftshift

The inverse of *fftshift*.

Examples

```
>>> 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.])
```

Shift the zero-frequency component only along the second axis:

```
>>> 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.]])
```

ifftshift (*x, axes=None*)

The inverse of fftshift.

Parameters

x : array_like

Input array.

axes : int or shape tuple, optional

Axes over which to calculate. Defaults to None, which shifts all axes.

Returns

y : ndarray

The shifted array.

See Also:

`fftshift`
Shift zero-frequency component to the center of the spectrum.

Examples

```
>>> 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.]])
```

rfftfreq(*n, d=1.0*)
rfftfreq(n, d=1.0) -> f

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

3.3.4 Convolutions (`scipy.fftpack.convolve`)

`convolve`	convolve - Function signature:
`convolve_z`	convolve_z - Function signature:
`init_convolution_kernel`	init_convolution_kernel - Function signature:
`destroy_convolve_cache`	destroy_convolve_cache - Function signature:

convolve

convolve - Function signature:
y = convolve(x,omega,[swap_real_imag,overwrite_x])

Required arguments:
x : input rank-1 array('d') with bounds (n) omega : input rank-1 array('d') with bounds (n)

Optional arguments:
overwrite_x := 0 input int swap_real_imag := 0 input int

Return objects:
y : rank-1 array('d') with bounds (n) and x storage

convolve_z

convolve_z - Function signature:
y = convolve_z(x,omega_real,omega_imag,[overwrite_x])

Required arguments:
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)

Optional arguments:
overwrite_x := 0 input int

Return objects:
y : rank-1 array('d') with bounds (n) and x storage

init_convolution_kernel

init_convolution_kernel - Function signature:
omega = init_convolution_kernel(n,kernel_func,[d,zero_nyquist,kernel_func_extra_args])

Required arguments:
n : input int kernel_func : call-back function

Optional arguments:
d := 0 input int kernel_func_extra_args := () input tuple zero_nyquist := d%2 input int

Return objects:
omega : rank-1 array('d') with bounds (n)

Call-back functions:
def kernel_func(k): return kernel_func Required arguments:

k : input int

Return objects:
kernel_func : float

destroy_convolve_cache
destroy_convolve_cache - Function signature: destroy_convolve_cache()

3.3.5 scipy.fftpack._fftpack

drfft	drfft - Function signature:
zfft	zfft - Function signature:
zrfft	zrfft - Function signature:
zfftnd	zfftnd - Function signature:
destroy_drfft_cache	destroy_drfft_cache - Function signature:
destroy_zfft_cache	destroy_zfft_cache - Function signature:
destroy_zfftnd_cache	destroy_zfftnd_cache - Function signature:

drfft

drfft - Function signature:
y = drfft(x,[n,direction,normalize,overwrite_x])

Required arguments:
x : input rank-1 array('d') with bounds (*)

Optional arguments:
overwrite_x := 0 input int n := size(x) input int direction := 1 input int normalize := (direction<0) input int

Return objects:
y : rank-1 array('d') with bounds (*) and x storage

zfft

zfft - Function signature:
y = zfft(x,[n,direction,normalize,overwrite_x])

Required arguments:
x : input rank-1 array('D') with bounds (*)

Optional arguments:
overwrite_x := 0 input int n := size(x) input int direction := 1 input int normalize := (direction<0) input int

Return objects:
y : rank-1 array('D') with bounds (*) and x storage

zrfft

zrfft - Function signature:
y = zrfft(x,[n,direction,normalize,overwrite_x])

Required arguments:
x : input rank-1 array('D') with bounds (*)

Optional arguments:
overwrite_x := 1 input int n := size(x) input int direction := 1 input int normalize := (direction<0) input int

Return objects:
y : rank-1 array('D') with bounds (*) and x storage

zfftnd

zfftnd - Function signature:
y = zfftnd(x,[s,direction,normalize,overwrite_x])

Required arguments:
x : input rank-1 array('D') with bounds (*)

Optional arguments:
overwrite_x := 0 input int s := old_shape(x,j++) input rank-1 array('i') with bounds (r) direction := 1 input int normalize := (direction<0) input int

Return objects:
y : rank-1 array('D') with bounds (*) and x storage

destroy_drfft_cache
destroy_drfft_cache - Function signature: destroy_drfft_cache()

destroy_zfft_cache
destroy_zfft_cache - Function signature: destroy_zfft_cache()

destroy_zfftnd_cache
destroy_zfftnd_cache - Function signature: destroy_zfftnd_cache()

3.4 Integration and ODEs (scipy.integrate)

3.4.1 Integrating functions, given function object

quad(func, a, b[, args, full_output, ...])	Compute a definite integral.
dblquad(func, a, b, gfun, hfun[, args, ...])	Compute the double integral of func2d(y,x) from x=a..b and y=gfun(x)..hfun(x).
tplquad(func, a, b, gfun, hfun, qfun, rfun)	Compute a triple (definite) integral.
fixed_quad(func, a, b[, args, n])	Compute a definite integral using fixed-order Gaussian quadrature.
quadrature(func, a, b[, args, tol, maxiter, ...])	Compute a definite integral using fixed-tolerance Gaussian quadrature.
romberg(function, a, b[, args, tol, show, ...])	Romberg integration of a callable function or method.

quad(*func, a, b, args=(), full_output=0, epsabs=1.4899999999999999e-08, epsrel=1.4899999999999999e-08, limit=50, points=None, weight=None, wvar=None, wopts=None, maxp1=50, limlst=50*)

Compute a definite integral.

Integrate func from a to b (possibly infinite interval) using a technique from the Fortran library QUADPACK.

Run scipy.integrate.quad_explain() for more information on the more esoteric inputs and outputs.

Parameters

func : function

a Python function or method to integrate.

a

[float] lower limit of integration (use -scipy.integrate.Inf for -infinity).

b

[float] upper limit of integration (use scipy.integrate.Inf for +infinity).

full_output :

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']

Examples

Calculate $\int_0^4 x^2 dx$ and compare with an analytic result

```
>>> x2 = lambda x: x**2
>>> quad(x,0.,4.)
(21.333333333333332, 2.368475785867003e-13)
>> print 4.**3/3
21.3333333333
```

Calculate $\int_0^\infty e^{-x} dx$

```
>>> invexp = lambda x: exp(-x)
>>> quad(invexp,0,inf)
(0.99999999999999989, 5.8426061711142159e-11)
```

See also:

dblquad, tplquad - double and triple integrals fixed_quad - fixed-order Gaussian quadrature quadrature - adaptive Gaussian quadrature odeint, ode - ODE integrators simps, trapz, romb - integrators for sampled data scipy.special - for coefficients and roots of orthogonal polynomials

dblquad (*func, a, b, gfun, hfun, args=(), epsabs=1.4899999999999999e-08, epsrel=1.4899999999999999e-08*)

Compute the double integral of func2d(y,x) from x=a..b and y=gfun(x)..hfun(x).

Parameters

func2d : function

a Python function or method of at least two variables: y must be the first argument and x the second argument.

(a,b)
[tuple] 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).

args :
extra arguments to pass to func2d.

epsabs
[float] absolute tolerance passed directly to the inner 1-D quadrature integration.

epsrel
[float] relative tolerance of the inner 1-D integrals.

Returns

y : float

the resultant integral.

abserr
[float] an estimate of the error.

See also: :

quad - single integral tplquad - triple integral fixed_quad - fixed-order Gaussian quadrature quadrature - adaptive Gaussian quadrature odeint, ode - ODE integrators simps, trapz, romb - integrators for sampled data scipy.special - for coefficients and roots of orthogonal polynomials

tplquad(*func, a, b, gfun, hfun, qfun, rfun, args=(), epsabs=1.4899999999999999e-08, epsrel=1.4899999999999999e-08*)

Compute a triple (definite) integral.

Return the triple integral of func3d(z, y,x) from x=a..b, y=gfun(x)..hfun(x), and z=qfun(x,y)..rfun(x,y)

Parameters

func3d : function

a Python function or method of at least three variables in the order (z, y, x).

(a,b)

[tuple] 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 :

extra arguments to pass to func3d.

epsabs

[float]

absolute tolerance passed directly to the innermost 1-D quadrature
integration.

epsrel

[float] relative tolerance of the innermost 1-D integrals.

Returns

y : float

the resultant integral.

abserr

[float] an estimate of the error.

See also: :

quad - single integral dblquad - double integral fixed_quad - fixed-order Gaussian quadrature quadrature - adaptive Gaussian quadrature odeint, ode - ODE integrators simps, trapz, romb - integrators for sampled data scipy.special - for coefficients and roots of orthogonal polynomials

fixed_quad (*func, a, b, args=(), n=5*)
Compute a definite integral using fixed-order Gaussian quadrature.

Description:

Integrate func from a to b using Gaussian quadrature of order n.

Inputs:

func – a Python function or method to integrate
(must accept vector inputs)

a – lower limit of integration b – upper limit of integration args – extra arguments to pass to function. n – order of quadrature integration.

Outputs: (val, None)

val – Gaussian quadrature approximation to the integral.

See also:

quad - adaptive quadrature using QUADPACK dblquad, tplquad - double and triple integrals romberg - adaptive Romberg quadrature quadrature - adaptive Gaussian quadrature romb, simps, trapz - integrators for sampled data cumtrapz - cumulative integration for sampled data ode, odeint - ODE integrators

quadrature (*func, a, b, args=(), tol=1.4899999999999999e-08, maxiter=50, vec_func=True*)
Compute a definite integral using fixed-tolerance Gaussian quadrature.

Description:

Integrate func from a to b using Gaussian quadrature with absolute tolerance tol.

Inputs:

func – a Python function or method to integrate. a – lower limit of integration. b – upper limit of integration. args – extra arguments to pass to function. tol – iteration stops when error between last two iterates is less than

tolerance.

maxiter – maximum number of iterations. vec_func – True or False if func handles arrays as arguments (is

a "vector" function). Default is True.

Outputs: (val, err)

val – Gaussian quadrature approximation (within tolerance) to integral. err – 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, tplquad - double and triple integrals romb, simps, trapz - integrators for sampled data cumtrapz - cumulative integration for sampled data ode, odeint - ODE integrators

romberg (*function, a, b, args=(), tol=1.48e-08, show=False, divmax=10, vec_func=False*)
Romberg integration of a callable function or method.

Returns the integral of *function* (a function of one variable) over the interval (*a*, *b*).

If *show* is 1, the triangular array of the intermediate results will be printed. If *vec_func* is True (default is False), then *function* is assumed to support vector arguments.

Parameters

function : callable

Function to be integrated.

a : float

Lower limit of integration.

b : float

Upper limit of integration.

Returns

results : float

Result of the integration.

See Also:

fixed_quad
Fixed-order Gaussian quadrature.

quad
Adaptive quadrature using QUADPACK.

dblquad, tplquad, romb, simps, trapz

cumtrapz
Cumulative integration for sampled data.

ode, odeint

References

[R1]

Examples

Integrate a gaussian from 0,1 and compare to the error function.

```
>>> from scipy.special import erf
>>> gaussian = lambda x: 1/np.sqrt(np.pi) * np.exp(-x**2)
>>> result = romberg(gaussian, 0, 1, show=True)
Romberg integration of <function vfunc at 0x101eceaa0> 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  0.421350
   16  0.062500  0.421215  0.421350  0.421350  0.421350  0.421350
   32  0.031250  0.421317  0.421350  0.421350  0.421350  0.421350  0.421350
```

The final result is 0.421350396475 after 33 function evaluations.

```
>>> print 2*result,erf(1)
0.84270079295 0.84270079295
```

3.4.2 Integrating functions, given fixed samples

trapz(y[, x, dx, axis])	Integrate along the given axis using the composite trapezoidal rule.
cumtrapz(y[, x, dx, axis])	Cumulatively integrate y(x) using samples along the given axis and the composite trapezoidal rule.
simps(y[, x, dx, axis, even])	Integrate y(x) using samples along the given axis and the composite
romb(y[, dx, axis, show])	Romberg integration using samples of a function

trapz (*y, x=None, dx=1.0, axis=-1*)

Integrate along the given axis using the composite trapezoidal rule.

Integrate *y* (*x*) along given axis.

Parameters

y : array_like

Input array to integrate.

x : array_like, optional

If *x* is None, then spacing between all *y* elements is *dx*.

dx : scalar, optional

If *x* is None, spacing given by *dx* is assumed. Default is 1.

axis : int, optional

Specify the axis.

Returns

out : float

Definite integral as approximated by trapezoidal rule.

See Also:

sum, cumsum

Notes

Image [R3] illustrates trapezoidal rule – y-axis locations of points will be taken from *y* array, by default x-axis distances between points will be 1.0, alternatively they can be provided with *x* array or with *dx* scalar. Return value will be equal to combined area under the red lines.

References

[R2], [R3]

Examples

```
>>> np.trapz([1,2,3])
4.0
>>> np.trapz([1,2,3], x=[4,6,8])
8.0
>>> np.trapz([1,2,3], dx=2)
8.0
>>> a = np.arange(6).reshape(2, 3)
>>> a
array([[0, 1, 2],
       [3, 4, 5]])
```

```
>>> np.trapz(a, axis=0)
array([ 1.5,  2.5,  3.5])
>>> np.trapz(a, axis=1)
array([ 2.,  8.])
```

cumtrapz (*y, x=None, dx=1.0, axis=-1*)

Cumulatively integrate y(x) using samples along the given axis and the composite trapezoidal rule. If x is None, spacing given by dx is assumed.

See also:

quad - adaptive quadrature using QUADPACK romberg - adaptive Romberg quadrature quadrature - adaptive Gaussian quadrature fixed_quad - fixed-order Gaussian quadrature dblquad, tplquad - double and triple integrals romb, trapz - integrators for sampled data cumtrapz - cumulative integration for sampled data ode, odeint - ODE integrators

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 as follows:

even='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

even='first': Use Simpson's rule for the first N-2 intervals with
a trapezoidal rule on the last interval.

even='last': Use Simpson's rule for the last N-2 intervals with a
trapezoidal rule on the first interval.

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.

See also:

quad - adaptive quadrature using QUADPACK romberg - adaptive Romberg quadrature quadrature - adaptive Gaussian quadrature fixed_quad - fixed-order Gaussian quadrature dblquad, tplquad - double and triple integrals romb, trapz - integrators for sampled data cumtrapz - cumulative integration for sampled data ode, odeint - ODE integrators

romb (*y, dx=1.0, axis=-1, show=False*)

Romberg integration using samples of a function

Inputs:

y - a vector of 2**k + 1 equally-spaced samples of a fucntion dx - the sample spacing. axis - the axis along which to integrate show - When y is a single 1-d array, then if this argument is True

print the table showing Richardson extrapolation from the samples.

Output: ret

ret - The integrated result for each axis.

See also:

quad - adaptive quadrature using QUADPACK romberg - adaptive Romberg quadrature quadrature - adaptive Gaussian quadrature fixed_quad - fixed-order Gaussian quadrature dblquad, tplquad - dou-

ble and triple integrals simps, trapz - integrators for sampled data cumtrapz - cumulative integration for sampled data ode, odeint - ODE integrators

See Also:

`scipy.special` for orthogonal polynomials (special) for Gaussian quadrature roots and weights for other weighting factors and regions.

3.4.3 Integrators of ODE systems

`odeint`(func, y0, t[, args, Dfun, col_deriv, ...])	Integrate a system of ordinary differential equations.
`ode`(f[, jac])	A generic interface class to numeric integrators.

odeint (*func, y0, t, args=(), Dfun=None, col_deriv=0, full_output=0, ml=None, mu=None, rtol=None, atol=None, tcrit=None, h0=0.0, hmax=0.0, hmin=0.0, ixpr=0, mxstep=0, mxhnil=0, mxordn=12, mxords=5, printmessg=0*)

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 = func(y,t0,...)
```

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

Extra arguments to pass to function.

Dfun : callable(y, t0, ...)

Gradient (Jacobian) of func.

col_deriv : boolean

True if Dfun defines derivatives down columns (faster), otherwise Dfun should define derivatives across rows.

full_output : boolean

True if to return a dictionary of optional outputs as the second output

printmessg : boolean

Whether to print the convergence message

Returns

y : array, shape (len(y0), len(t))

Array containing the value of y for each desired time in t, with the initial value y0 in the first row.

infodict : dict, only returned if full_output == True

Dictionary containing additional output information

key	meaning
'hu'	vector of step sizes successfully used for each time step.
'tcur'	vector with the value of t reached for each time step. (will always be at least as large as the input time
'tolsf'	vector of tolerance scale factors, greater than 1.0, computed when a request for too much accuracy w detected.
'tsw'	value of t at the time of the last method switch (given for each time step)
'nst'	cumulative number of time steps
'nfe'	cumulative number of function evaluations for each time step
'nje'	cumulative number of jacobian evaluations for each time step
'nqu'	a vector of method orders for each successful step.
'imxer'	index of the component of largest magnitude in the weighted local error vector (e / ewt) on an error return, -1 otherwise.
'lenrw'	the length of the double work array required.
'leniw'	the length of integer work array required.
'mused'	a vector of method indicators for each successful time step: 1: adams (nonstiff), 2: bdf (stiff)

See Also:

ode
a more object-oriented integrator based on VODE

quad
for finding the area under a curve

class ode (*f, jac=None*)
A generic interface class to numeric integrators.

See Also:

odeint
an integrator with a simpler interface based on lsoda from ODEPACK

quad
for finding the area under a curve

Examples

A problem to integrate and the corresponding jacobian:

```
>>> from scipy import eye
>>> 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:

```
>>> r = ode(f, jac).set_integrator('zvode', method='bdf', with_jacobian=True)
>>> 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:
>>>     r.integrate(r.t+dt)
>>>     print r.t, r.y
```

Methods

ode.integrate
ode.set_f_params
ode.set_initial_value
ode.set_integrator
ode.set_jac_params
ode.successful

3.5 Interpolation (scipy.interpolate)

3.5.1 Univariate interpolation

interp1d(x, y[, kind, axis, copy, ...])	Interpolate a 1D function.
BarycentricInterpolator(xi[, yi])	The interpolating polynomial for a set of points
KroghInterpolator(xi, yi)	The interpolating polynomial for a set of points
PiecewisePolynomial(xi, yi[, orders, direction])	Piecewise polynomial curve specified by points and derivatives
barycentric_interpolate(xi, yi, x)	Convenience function for polynomial interpolation
krogh_interpolate(xi, yi, x[, der])	Convenience function for polynomial interpolation.
piecewise_polynomial_interpolate(xi, yi, x)	Convenience function for piecewise polynomial interpolation

class interp1d(*x, y, kind='linear', axis=-1, copy=True, bounds_error=True, fill_value=nan*)

Interpolate a 1D function.

See Also:

splrep, splev, UnivariateSpline

class BarycentricInterpolator(*xi, yi=None*)

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.

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

add_xi(xi[, yi])	Add more x values to the set to be interpolated
set_yi(yi)	Update the y values to be interpolated

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 of length N1

The x coordinates of the points the polynomial should pass through

yi : array-like N1 by R or None

The y coordinates of the points the polynomial should pass through; if R>1 the polynomial is vector-valued. If None the y values will be supplied later. The yi should be specified if and only if the interpolator has y values specified.

set_yi (*yi*)
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 N by R

The y coordinates of the points the polynomial should pass through; if R>1 the polynomial is vector-valued. If None the y values will be supplied later.

class KroghInterpolator (*xi, yi*)
The interpolating polynomial for a set of points

Constructs a polynomial that passes through a given set of points, optionally with specified derivatives at those points. 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.

Be aware that the algorithms implemented here are not necessarily the most numerically stable known. Moreover, even in a world of exact computation, unless the x coordinates are chosen very carefully - Chebyshev zeros (e.g. cos(i*pi/n)) are a good choice - polynomial interpolation itself is a very ill-conditioned process due to the Runge phenomenon. In general, even with well-chosen x values, degrees higher than about thirty cause problems with numerical instability in this code.

Based on Krogh 1970, "Efficient Algorithms for Polynomial Interpolation and Numerical Differentiation"

Methods

derivative(x, der)	Evaluate one derivative of the polynomial at the point x
derivatives(x[, der])	Evaluate many derivatives of the polynomial at the point x

derivative (*x, der*)
Evaluate one derivative of the polynomial at the point x

Parameters
x : scalar or array-like of length N

Point or points at which to evaluate the derivatives

der : None or integer

Which derivative to extract. This number includes the function value as 0th derivative.

Returns :

——- :

d : array

If the interpolator's values are R-dimensional then the returned array will be N by R. If x is a scalar, the middle dimension will be dropped; if R is 1 then the last dimension will be dropped.

Notes

This is computed by evaluating all derivatives up to the desired one (using self.derivatives()) and then discarding the rest.

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 : scalar or array-like of length N

Point or points at which to evaluate the derivatives

der : None or integer

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 : array

If the interpolator's values are R-dimensional then the returned array will be der by N by R. If x is a scalar, the middle dimension will be dropped; if R is 1 then the last dimension will be dropped.

class PiecewisePolynomial (*xi, yi, orders=None, direction=None*)

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 very 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.

Methods

append(xi, yi[, order])	Append a single point with derivatives to the PiecewisePolynomial
derivative(x, der)	Evaluate a derivative of the piecewise polynomial
derivatives(x, der)	Evaluate a derivative of the piecewise polynomial
extend(xi, yi[, orders])	Extend the PiecewisePolynomial by a list of points

append (*xi, yi, order=None*)

Append a single point with derivatives to the PiecewisePolynomial

Parameters

xi : float

yi : array-like

yi is the list of derivatives known at xi

order : integer or None

a polynomial order, or instructions to use the highest possible order

derivative(*x, der*)

Evaluate a derivative of the piecewise polynomial

Parameters

x : scalar or array-like of length N

der : integer

which single derivative to extract

Returns

y : scalar or array-like of length R or length N or N by R

Notes

This currently computes (using self.derivatives()) all derivatives of the curve segment containing each x but returns only one.

derivatives(*x, der*)

Evaluate a derivative of the piecewise polynomial Parameters ———- x : scalar or array-like of length N der : integer

how many derivatives (including the function value as 0th derivative) to extract

Returns

y : array-like of shape der by R or der by N or der by N by R

extend(*xi, yi, orders=None*)

Extend the PiecewisePolynomial by a list of points

Parameters

xi : array-like of length N1

a sorted list of x-coordinates

yi : list of lists of length N1

yi[i] is the list of derivatives known at xi[i]

orders : list of integers, or integer

a list of polynomial orders, or a single universal order

direction : {None, 1, -1}

indicates whether the xi are increasing or decreasing +1 indicates increasing -1 indicates decreasing None indicates that it should be deduced from the first two xi

barycentric_interpolate(*xi, yi, x*)

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.

Based on Berrut and Trefethen 2004, "Barycentric Lagrange Interpolation".

Parameters

xi : array-like of length N

The x coordinates of the points the polynomial should pass through

yi : array-like N by R

The y coordinates of the points the polynomial should pass through; if R>1 the polynomial is vector-valued.

x : scalar or array-like of length M

Returns

y : scalar or array-like of length R or length M or M by R

The shape of y depends on the shape of x and whether the interpolator is vector-valued or scalar-valued.

Notes

Construction of the interpolation weights is a relatively slow process. If you want to call this many times with the same xi (but possibly varying yi or x) you should use the class BarycentricInterpolator. This is what this function uses internally.

krogh_interpolate(*xi, yi, x, der=0*)

Convenience function for polynomial interpolation.

Constructs a polynomial that passes through a given set of points, optionally with specified derivatives at those points. Evaluates the polynomial or some of 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.

Be aware that the algorithms implemented here are not necessarily the most numerically stable known. Moreover, even in a world of exact computation, unless the x coordinates are chosen very carefully - Chebyshev zeros (e.g. cos(i*pi/n)) are a good choice - polynomial interpolation itself is a very ill-conditioned process due to the Runge phenomenon. In general, even with well-chosen x values, degrees higher than about thirty cause problems with numerical instability in this code.

Based on Krogh 1970, "Efficient Algorithms for Polynomial Interpolation and Numerical Differentiation"

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.

Parameters

xi : array-like, length N

known x-coordinates

yi : array-like, N by R

known y-coordinates, interpreted as vectors of length R, or scalars if R=1

x : scalar or array-like of length N

Point or points at which to evaluate the derivatives

der : integer or list

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.

Returns :

——- :

d : array

If the interpolator's values are R-dimensional then the returned array will be the number of derivatives by N by R. If x is a scalar, the middle dimension will be dropped; if the yi are scalars then the last dimension will be dropped.

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).

piecewise_polynomial_interpolate(*xi, yi, x, orders=None, der=0*)

Convenience function for piecewise polynomial interpolation

Parameters

xi : array-like of length N

a sorted list of x-coordinates

yi : list of lists of length N

yi[i] is the list of derivatives known at xi[i]

x : scalar or array-like of length M

orders : list of integers, or integer

a list of polynomial orders, or a single universal order

der : integer

which single derivative to extract

Returns

y : scalar or array-like of length R or length M or M by R

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).

3.5.2 Multivariate interpolation

interp2d(x, y, z[, kind, copy, ...])	Interpolate over a 2D grid.
Rbf(*args)	A class for radial basis function approximation/interpolation of n-dimensional scattered data.

class interp2d(*x, y, z, kind='linear', copy=True, bounds_error=False, fill_value=nan*)

Interpolate over a 2D grid.

Parameters

x, y : 1D arrays

Arrays defining the coordinates of a 2D grid. If the points lie on a regular grid, *x* can specify the column coordinates and *y* the row coordinates, e.g.:

```
x = [0,1,2];  y = [0,3,7]
```

otherwise x and y must specify the full coordinates, i.e.:

```
x = [0,1,2,0,1,2,0,1,2];  y = [0,0,0,3,3,3,7,7,7]
```

If *x* and *y* are multi-dimensional, they are flattened before use.

z : 1D array

The values of the interpolated function on the grid points. If z is a multi-dimensional array, it is flattened before use.

kind : {'linear', 'cubic', 'quintic'}

The kind of interpolation to use.

copy : bool

If True, then data is copied, otherwise only a reference is held.

bounds_error : bool

If True, when interpolated values are requested outside of the domain of the input data, an error is raised. If False, then *fill_value* is used.

fill_value : number

If provided, the value to use for points outside of the interpolation domain. Defaults to NaN.

Raises

ValueError when inputs are invalid. :

See Also:

`bisplrep`, `bisplev`

`BivariateSpline`
a more recent wrapper of the FITPACK routines

class `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 (defult 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:

```
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

```
>>> rbfi = Rbf(x, y, z, d)  # radial basis function interpolator instance
>>> di = rbfi(xi, yi, zi)   # interpolated values
```

3.5.3 1-D Splines

UnivariateSpline(x, y[, w, bbox, k, s])	Univariate spline s(x) of degree k on the interval [xb,xe] calculated from a given set of data points (x,y).
InterpolatedUnivariateSpline(x, y[, w, bbox, k])	Interpolated univariate spline approximation.
LSQUnivariateSpline(x, y, t[, w, bbox, k])	Weighted least-squares univariate spline approximation.

class UnivariateSpline(*x, y, w=None, bbox=, [None, None], k=3, s=None*)

Univariate spline s(x) of degree k on the interval [xb,xe] calculated from a given set of data points (x,y).

Can include least-squares fitting.

See Also:

splrep, splev, sproot, spint, spalde

BivariateSpline

A similar class for bivariate spline interpolation

Methods

`__call__`(x[, nu])	Evaluate spline (or its nu-th derivative) at positions x.
`get_knots`()	Return the positions of (boundary and interior)
`get_coeffs`()	Return spline coefficients.
`get_residual`()	Return weighted sum of squared residuals of the spline
`integral`(a, b)	Return definite integral of the spline between two
`derivatives`(x)	Return all derivatives of the spline at the point x.
`roots`()	Return the zeros of the spline.
`set_smoothing_factor`(s)	Continue spline computation with the given smoothing

__call__ (*x, nu=None*)
Evaluate spline (or its nu-th derivative) at positions x. Note: x can be unordered but the evaluation is more efficient if x is (partially) ordered.

get_knots ()
Return the positions of (boundary and interior) knots of the spline.

get_coeffs ()
Return spline coefficients.

get_residual ()
Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(y[i]-s(x[i])))**2,axis=0)

integral (*a, b*)
Return definite integral of the spline between two given points.

derivatives (*x*)
Return all derivatives of the spline at the point x.

roots ()
Return the zeros of the spline.

Restriction: only cubic splines are supported by fitpack.

set_smoothing_factor (*s*)
Continue spline computation with the given smoothing factor s and with the knots found at the last call.

class InterpolatedUnivariateSpline (*x, y, w=None, bbox=, [None, None], k=3*)
Interpolated univariate spline approximation. Identical to UnivariateSpline with less error checking.

Methods

`derivatives`(x)	Return all derivatives of the spline at the point x.
`get_coeffs`()	Return spline coefficients.
`get_knots`()	Return the positions of (boundary and interior)
`get_residual`()	Return weighted sum of squared residuals of the spline
`integral`(a, b)	Return definite integral of the spline between two
`roots`()	Return the zeros of the spline.
`set_smoothing_factor`(s)	Continue spline computation with the given smoothing

derivatives (*x*)
Return all derivatives of the spline at the point x.

get_coeffs ()
Return spline coefficients.

get_knots ()
Return the positions of (boundary and interior) knots of the spline.

get_residual()
Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(y[i]-s(x[i])))**2,axis=0)

integral(*a, b*)
Return definite integral of the spline between two given points.

roots()
Return the zeros of the spline.

Restriction: only cubic splines are supported by fitpack.

set_smoothing_factor(*s*)
Continue spline computation with the given smoothing factor s and with the knots found at the last call.

class LSQUnivariateSpline(*x, y, t, w=None, bbox=, [None, None], k=3*)
Weighted least-squares univariate spline approximation. Appears to be identical to UnivariateSpline with more error checking.

Methods

derivatives(x)	Return all derivatives of the spline at the point x.
get_coeffs()	Return spline coefficients.
get_knots()	Return the positions of (boundary and interior)
get_residual()	Return weighted sum of squared residuals of the spline
integral(a, b)	Return definite integral of the spline between two
roots()	Return the zeros of the spline.
set_smoothing_factor(s)	Continue spline computation with the given smoothing

derivatives(*x*)
Return all derivatives of the spline at the point x.

get_coeffs()
Return spline coefficients.

get_knots()
Return the positions of (boundary and interior) knots of the spline.

get_residual()
Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(y[i]-s(x[i])))**2,axis=0)

integral(*a, b*)
Return definite integral of the spline between two given points.

roots()
Return the zeros of the spline.

Restriction: only cubic splines are supported by fitpack.

set_smoothing_factor(*s*)
Continue spline computation with the given smoothing factor s and with the knots found at the last call.

The above univariate spline classes have the following methods:

UnivariateSpline.__call__(x[, nu])	Evaluate spline (or its nu-th derivative) at positions x.
UnivariateSpline.derivatives(x)	Return all derivatives of the spline at the point x.
UnivariateSpline.integral(a, b)	Return definite integral of the spline between two
UnivariateSpline.roots()	Return the zeros of the spline.
UnivariateSpline.get_coeffs()	Return spline coefficients.
UnivariateSpline.get_knots()	Return the positions of (boundary and interior)
UnivariateSpline.get_residual()	Return weighted sum of squared residuals of the spline
UnivariateSpline.set_smoothing_factor(s)	Continue spline computation with the given smoothing

__call__(*x, nu=None*)
Evaluate spline (or its nu-th derivative) at positions x. Note: x can be unordered but the evaluation is more efficient if x is (partially) ordered.

derivatives(*x*)
Return all derivatives of the spline at the point x.

integral(*a, b*)
Return definite integral of the spline between two given points.

roots()
Return the zeros of the spline.

Restriction: only cubic splines are supported by fitpack.

get_coeffs()
Return spline coefficients.

get_knots()
Return the positions of (boundary and interior) knots of the spline.

get_residual()
Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(y[i]-s(x[i])))**2,axis=0)

set_smoothing_factor(*s*)
Continue spline computation with the given smoothing factor s and with the knots found at the last call.

Low-level interface to FITPACK functions:

splrep(x, y[, w, xb, xe, k, task, s, t, ...])	Find the B-spline representation of 1-D curve.
splprep(x[, w, u, ub, ue, k, task, s, t, ...])	Find the B-spline representation of an N-dimensional curve.
splev(x, tck[, der])	Evaulate a B-spline and its derivatives.
splint(a, b, tck[, full_output])	Evaluate the definite integral of a B-spline.
sproot(tck[, mest])	Find the roots of a cubic B-spline.
spalde(x, tck)	Evaluate all derivatives of a B-spline.
bisplrep(x, y, z[, w, xb, xe, yb, ye, kx, ...])	Find a bivariate B-spline representation of a surface.
bisplev(x, y, tck[, dx, dy])	Evaluate a bivariate B-spline and its derivatives.

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.

Description:

Given the set of data points (x[i], y[i]) determine a smooth spline approximation of degree k on the interval xb <= x <= xe. The coefficients, c, and the knot points, t, are returned. Uses the FORTRAN routine curfit from FITPACK.

Inputs:

x, y – The data points defining a curve y = f(x). w – 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 – The interval to fit. If None, these default to x[0] and x[-1]
respectively.

k – 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 – 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 an used internally)

If task=-1 find the weighted least square spline for
a given set of knots, t. These should be interior knots as knots on the ends will be added automatically.

s – 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 – The knots needed for task=-1. If given then task is automatically
set to -1.

full_output – If non-zero, then return optional outputs. per – 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 – Non-zero to suppress messages.

Outputs: (tck, {fp, ier, msg})

tck – (t,c,k) a tuple containing the vector of knots, the B-spline
coefficients, and the degree of the spline.

fp – The weighted sum of squared residuals of the spline approximation. ier – 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 – A message corresponding to the integer flag, ier.

Remarks:

See splev for evaluation of the spline and its derivatives.

Example:

x = linspace(0, 10, 10) y = sin(x) tck = splrep(x, y) x2 = linspace(0, 10, 200) y2 = splev(x2, tck) plot(x, y, ‘o’, x2, y2)

See also:

splprep, splev, sproot, spalde, splint - evaluation, roots, integral bisplrep, bisplev - bivariate splines UnivariateSpline, BivariateSpline - an alternative wrapping

of the FITPACK functions

Notes:

Based on algorithms described in:

Dierckx P.
[An algorithm for smoothing, differentiation and integ-] ration of experimental data using spline functions, J.Comp.Appl.Maths 1 (1975) 165-184.

Dierckx P.
[A fast algorithm for smoothing data on a rectangular] grid while using spline functions, SIAM J.Numer.Anal. 19 (1982) 1286-1304.

Dierckx P.
[An improved algorithm for curve fitting with spline] functions, report tw54, Dept. Computer Science,K.U. Leuven, 1981.

Dierckx P.
[Curve and surface fitting with splines, Monographs on] Numerical Analysis, Oxford University Press, 1993.

splprep(*x, w=None, u=None, ub=None, ue=None, k=3, task=0, s=None, t=None, full_output=0, nest=None, per=0, quiet=1*)

Find the B-spline representation of an N-dimensional curve.

Description:

Given a list of N rank-1 arrays, x, which represent a curve in N-dimensional space parametrized by u, find a smooth approximating spline curve g(u). Uses the FORTRAN routine parcur from FITPACK

Inputs:

x – A list of sample vector arrays representing the curve. u – An array of parameter values. If not given, these values are

calculated automatically as (M = len(x[0])): v[0] = 0 v[i] = v[i-1] + distance(x[i],x[i-1]) u[i] = v[i] / v[M-1]

ub, ue – The end-points of the parameters interval. Defaults to
u[0] and u[-1].

k – Degree of the spline. Cubic splines are recommended. Even values of
k should be avoided especially with a small s-value. 1 <= k <= 5.

task – 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.

If task=-1 find the weighted least square spline for a given set of
knots, t.

s – 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.

t – The knots needed for task=-1. full_output – If non-zero, then return optional outputs. nest – 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 – 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 – Non-zero to suppress messages.

Outputs: (tck, u, {fp, ier, msg})

tck – (t,c,k) a tuple containing the vector of knots, the B-spline
coefficients, and the degree of the spline.

u – An array of the values of the parameter.

fp – The weighted sum of squared residuals of the spline approximation. ier – 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 – A message corresponding to the integer flag, ier.

Remarks:

SEE splev for evaluation of the spline and its derivatives.

See also:
splrep, splev, sproot, spalde, splint - evaluation, roots, integral bisplrep, bisplev - bivariate splines UnivariateSpline, BivariateSpline - an alternative wrapping

of the FITPACK functions

Notes:

Dierckx P.
[Algorithms for smoothing data with periodic and] parametric splines, Computer Graphics and Image Processing 20 (1982) 171-184.

Dierckx P.
[Algorithms for smoothing data with periodic and param-] etric splines, report tw55, Dept. Computer Science, K.U.Leuven, 1981.

Dierckx P.
[Curve and surface fitting with splines, Monographs on] Numerical Analysis, Oxford University Press, 1993.

splev(*x, tck, der=0*)
Evaulate a B-spline and its derivatives.

Description:

Given the knots and coefficients of a B-spline representation, evaluate the value of the smoothing polynomial and it's derivatives. This is a wrapper around the FORTRAN routines splev and splder of FITPACK.

Inputs:

x (u) – a 1-D 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 – A sequence of length 3 returned by splrep or splprep containg the
knots, coefficients, and degree of the spline.

der – The order of derivative of the spline to compute (must be less than
or equal to k).

Outputs: (y,)

y – an array of values representing the spline function or curve.
If tck was returned from splrep, then this is a list of arrays representing the curve in N-dimensional space.

See also:

splprep, splrep, sproot, spalde, splint - evaluation, roots, integral bisplrep, bisplev - bivariate splines UnivariateSpline, BivariateSpline - an alternative wrapping

of the FITPACK functions

Notes:

de Boor C
[On calculating with b-splines, J. Approximation Theory] 6 (1972) 50-62.

Cox M.G.
[The numerical evaluation of b-splines, J. Inst. Maths] Applics 10 (1972) 134-149.

Dierckx P.
[Curve and surface fitting with splines, Monographs on] Numerical Analysis, Oxford University Press, 1993.

splint (*a, b, tck, full_output=0*)

Evaluate the definite integral of a B-spline.

Description:

Given the knots and coefficients of a B-spline, evaluate the definite integral of the smoothing polynomial between two given points.

Inputs:

a, b – The end-points of the integration interval. tck – A length 3 sequence describing the given spline (See splev). full_output – Non-zero to return optional output.

Outputs: (integral, {wrk})

integral – The resulting integral. wrk – An array containing the integrals of the normalized B-splines defined

on the set of knots.

See also:

splprep, splrep, sproot, spalde, splev - evaluation, roots, integral bisplrep, bisplev - bivariate splines UnivariateSpline, BivariateSpline - an alternative wrapping

of the FITPACK functions

Notes:

Gaffney P.W.

[The calculation of indefinite integrals of b-splines]

1. Inst. Maths Applics 17 (1976) 37-41.

Dierckx P.

[Curve and surface fitting with splines, Monographs on] Numerical Analysis, Oxford University Press, 1993.

sproot (*tck, mest=10*)

Find the roots of a cubic B-spline.

Description:

Given the knots (>=8) and coefficients of a cubic B-spline return the roots of the spline.

Inputs:

tck – A length 3 sequence describing the given spline (See splev).

The number of knots must be >= 8. The knots must be a montonically increasing sequence.

mest – An estimate of the number of zeros (Default is 10).

Outputs: (zeros,)

zeros – An array giving the roots of the spline.

See also:

splprep, splrep, splint, spalde, splev - evaluation, roots, integral bisplrep, bisplev - bivariate splines UnivariateSpline, BivariateSpline - an alternative wrapping

of the FITPACK functions

spalde (*x, tck*)

Evaluate all derivatives of a B-spline.

Description:

Given the knots and coefficients of a cubic B-spline compute all derivatives up to order k at a point (or set of points).

Inputs:

tck – A length 3 sequence describing the given spline (See splev). x – 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.

Outputs: (results,)

results – 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 - evaluation, roots, integral bisplrep, bisplev - bivariate splines UnivariateSpline, BivariateSpline - an alternative wrapping

of the FITPACK functions

Notes: Based on algorithms from:

de Boor C
[On calculating with b-splines, J. Approximation Theory] 6 (1972) 50-62.

Cox M.G.
[The numerical evaluation of b-splines, J. Inst. Maths] applics 10 (1972) 134-149.

Dierckx P.
[Curve and surface fitting with splines, Monographs on] Numerical Analysis, Oxford University Press, 1993.

bisplrep(*x, y, z, w=None, xb=None, xe=None, yb=None, ye=None, kx=3, ky=3, task=0, s=None, eps=9.9999999999999998e-17, tx=None, ty=None, full_output=0, nxest=None, nyest=None, quiet=1*)

Find a bivariate B-spline representation of a surface.

Description:

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.

Inputs:

x, y, z – Rank-1 arrays of data points. w – Rank-1 array of weights. By default w=ones(len(x)). xb, xe – End points of approximation interval in x. yb, ye – End points of approximation interval in y.

By default xb, xe, yb, ye = x.min(), x.max(), y.min(), y.max()

kx, ky – The degrees of the spline (1 <= kx, ky <= 5). Third order
(kx=ky=3) is recommended.

task – 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 – A non-negative smoothing factor. If weights correspond
to the inverse of the standard-deviation of the errors in z, then a good s-value should be found in the range (m-sqrt(2*m),m+sqrt(2*m)) where m=len(x)

eps – A threshold for determining the effective rank of an
over-determined linear system of equations (0 < eps < 1) — not likely to need changing.

tx, ty – Rank-1 arrays of the knots of the spline for task=-1 full_output – Non-zero to return optional outputs. nxest, nyest – Over-estimates of the total number of knots.

If None then nxest = max(kx+sqrt(m/2),2*kx+3),
nyest = max(ky+sqrt(m/2),2*ky+3)

quiet – Non-zero to suppress printing of messages.

Outputs: (tck, {fp, ier, msg})

tck – 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 – The weighted sum of squared residuals of the spline approximation. ier – 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 – A message corresponding to the integer flag, ier.

Remarks:

SEE bisplev to evaluate the value of the B-spline given its tck representation.

See also:
splprep, splrep, splint, sproot, splev - evaluation, roots, integral UnivariateSpline, BivariateSpline - an alternative wrapping

of the FITPACK functions

Notes: Based on algorithms from:

Dierckx P.
[An algorithm for surface fitting with spline functions] Ima J. Numer. Anal. 1 (1981) 267-283.

Dierckx P.
[An algorithm for surface fitting with spline functions] report tw50, Dept. Computer Science,K.U.Leuven, 1980.

Dierckx P.
[Curve and surface fitting with splines, Monographs on] Numerical Analysis, Oxford University Press, 1993.

bisplev(*x, y, tck, dx=0, dy=0*)
Evaluate a bivariate B-spline and its derivatives.

Description:

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.

Inputs:

x, y – Rank-1 arrays specifying the domain over which to evaluate the
spline or its derivative.

tck – 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 – The orders of the partial derivatives in x and y respectively.

Outputs: (vals,)

vals – The B-pline or its derivative evaluated over the set formed by
the cross-product of x and y.

Remarks:

SEE bisprep to generate the tck representation.

See also:

splprep, splrep, splint, sproot, splev - evaluation, roots, integral UnivariateSpline, BivariateSpline - an alternative wrapping

of the FITPACK functions

Notes: Based on algorithms from:

Dierckx P.
[An algorithm for surface fitting with spline functions] Ima J. Numer. Anal. 1 (1981) 267-283.

Dierckx P.
[An algorithm for surface fitting with spline functions] report tw50, Dept. Computer Science,K.U.Leuven, 1980.

Dierckx P.
[Curve and surface fitting with splines, Monographs on] Numerical Analysis, Oxford University Press, 1993.

3.5.4 2-D Splines

See Also:

scipy.ndimage.map_coordinates

BivariateSpline	Bivariate spline s(x,y) of degrees kx and ky on the rectangle [xb,xe] x [yb, ye] calculated from a given set of data points (x,y,z).
SmoothBivariateSpline(x, y, z, None, None[, ...])	Smooth bivariate spline approximation.
LSQBivariateSpline(x, y, z, tx, ty, None, None)	Weighted least-squares spline approximation.

class BivariateSpline()
Bivariate spline s(x,y) of degrees kx and ky on the rectangle [xb,xe] x [yb, ye] calculated from a given set of data points (x,y,z).

See also:

bisplrep, bisplev - an older wrapping of FITPACK UnivariateSpline - a similar class for univariate spline interpolation SmoothUnivariateSpline - to create a BivariateSpline through the

given points

LSQUnivariateSpline - to create a BivariateSpline using weighted
least-squares fitting

Methods

ev(xi, yi)	Evaluate spline at points (x[i], y[i]), i=0,...,len(x)-1
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].

ev(*xi, yi*)
Evaluate spline at points (x[i], y[i]), i=0,...,len(x)-1

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. 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.

get_residual()
Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

integral(*xa, xb, ya, yb*)
Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

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 SmoothBivariateSpline(*x, y, z, w=None, bbox=, [None, None, None, None], kx=3, ky=3, s=None, eps=None*)
Smooth bivariate spline approximation.

See also:

bisplrep, bisplev - an older wrapping of FITPACK UnivariateSpline - a similar class for univariate spline interpolation LSQUnivariateSpline - to create a BivariateSpline using weighted

least-squares fitting

Methods

ev(xi, yi)	Evaluate spline at points (x[i], y[i]), i=0,...,len(x)-1
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].

ev(*xi, yi*)
Evaluate spline at points (x[i], y[i]), i=0,...,len(x)-1

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. 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.

get_residual()
Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

integral(*xa, xb, ya, yb*)
Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

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 LSQBivariateSpline(*x, y, z, tx, ty, w=None, bbox=, [None, None, None, None], kx=3, ky=3, eps=None*)
Weighted least-squares spline approximation. See also:

bisplrep, bisplev - an older wrapping of FITPACK UnivariateSpline - a similar class for univariate spline interpolation SmoothUnivariateSpline - to create a BivariateSpline through the

given points

Methods

ev(xi, yi)	Evaluate spline at points (x[i], y[i]), i=0,...,len(x)-1
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].

ev(*xi, yi*)
Evaluate spline at points (x[i], y[i]), i=0,...,len(x)-1

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. 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.

get_residual()
Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

integral(*xa, xb, ya, yb*)
Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

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.

Low-level interface to FITPACK functions:

bisplrep(x, y, z[, w, xb, xe, yb, ye, kx, ...])	Find a bivariate B-spline representation of a surface.
bisplev(x, y, tck[, dx, dy])	Evaluate a bivariate B-spline and its derivatives.

bisplrep(*x, y, z, w=None, xb=None, xe=None, yb=None, ye=None, kx=3, ky=3, task=0, s=None, eps=9.9999999999999998e-17, tx=None, ty=None, full_output=0, nxest=None, nyest=None, quiet=1*)

Find a bivariate B-spline representation of a surface.

Description:

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.

Inputs:

x, y, z – Rank-1 arrays of data points. w – Rank-1 array of weights. By default w=ones(len(x)). xb, xe – End points of approximation interval in x. yb, ye – End points of approximation interval in y.

By default xb, xe, yb, ye = x.min(), x.max(), y.min(), y.max()

kx, ky – The degrees of the spline (1 <= kx, ky <= 5). Third order
(kx=ky=3) is recommended.

task – 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 – A non-negative smoothing factor. If weights correspond
to the inverse of the standard-deviation of the errors in z, then a good s-value should be found in the range (m-sqrt(2*m),m+sqrt(2*m)) where m=len(x)

eps – A threshold for determining the effective rank of an
over-determined linear system of equations (0 < eps < 1) — not likely to need changing.

tx, ty – Rank-1 arrays of the knots of the spline for task=-1 full_output – Non-zero to return optional outputs. nxest, nyest – Over-estimates of the total number of knots.

If None then nxest = max(kx+sqrt(m/2),2*kx+3),
nyest = max(ky+sqrt(m/2),2*ky+3)

quiet – Non-zero to suppress printing of messages.

Outputs: (tck, {fp, ier, msg})

tck – 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 – The weighted sum of squared residuals of the spline approximation. ier – 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 – A message corresponding to the integer flag, ier.

Remarks:

SEE bisplev to evaluate the value of the B-spline given its tck representation.

See also:

splprep, splrep, splint, sproot, splev - evaluation, roots, integral UnivariateSpline, BivariateSpline - an alternative wrapping

of the FITPACK functions

Notes: Based on algorithms from:

Dierckx P.
[An algorithm for surface fitting with spline functions] Ima J. Numer. Anal. 1 (1981) 267-283.

Dierckx P.
[An algorithm for surface fitting with spline functions] report tw50, Dept. Computer Science,K.U.Leuven, 1980.

Dierckx P.
[Curve and surface fitting with splines, Monographs on] Numerical Analysis, Oxford University Press, 1993.

bisplev(*x, y, tck, dx=0, dy=0*)

Evaluate a bivariate B-spline and its derivatives.

Description:

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.

Inputs:

x, y – Rank-1 arrays specifying the domain over which to evaluate the
spline or its derivative.

tck – 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 – The orders of the partial derivatives in x and y respectively.

Outputs: (vals,)

vals – The B-pline or its derivative evaluated over the set formed by
the cross-product of x and y.

Remarks:

SEE bisprep to generate the tck representation.

See also:

splprep, splrep, splint, sproot, splev - evaluation, roots, integral UnivariateSpline, BivariateSpline - an alternative wrapping

of the FITPACK functions

Notes: Based on algorithms from:

Dierckx P.
[An algorithm for surface fitting with spline functions] Ima J. Numer. Anal. 1 (1981) 267-283.

Dierckx P.
[An algorithm for surface fitting with spline functions] report tw50, Dept. Computer Science,K.U.Leuven, 1980.

Dierckx P.
[Curve and surface fitting with splines, Monographs on] Numerical Analysis, Oxford University Press, 1993.

3.5.5 Additional tools

lagrange(x, w)	Return the Lagrange interpolating polynomial of the data-points (x,w)
approximate_taylor_polynomial(f, x, degree, ...)	Estimate the Taylor polynomial of f at x by polynomial fitting

lagrange (*x, w*)
Return the Lagrange interpolating polynomial of the data-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.

approximate_taylor_polynomial (*f, x, degree, scale, order=None*)
Estimate the Taylor polynomial of f at x by polynomial fitting

A polynomial 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
[integer] 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
[integer or None] The order of the polynomial to be used in the fitting; f will be evaluated order+1 times. If None, use degree.

Returns
p : poly1d

the Taylor polynomial (translated to the origin, so that for example p(0)=f(x)).

Notes

The appropriate choice of “scale” is a tradeoff - too large and the function differs from its Taylor polynomial too much to get a good answer, too small and roundoff 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.

3.6 Input and output (scipy.io)

See Also:

numpy-reference.routines.io (in Numpy)

3.6.1 MATLAB® files

loadmat(file_name, **kwargs[, mdict, appendmat])	Load Matlab(tm) file
savemat(file_name, mdict[, appendmat, ...])	Save a dictionary of names and arrays into the MATLAB-style .mat file.

loadmat (*file_name, mdict=None, appendmat=True, **kwargs*)

Load Matlab(tm) file

Parameters

file_name : string

Name of the mat file (do not need .mat extension if appendmat==True) If name not a full path name, search for the file on the sys.path list and use the first one found (the current directory is searched first). Can also pass open file-like object

m_dict : dict, optional

dictionary in which to insert matfile variables

appendmat : {True, False} optional

True to append the .mat extension to the end of the given filename, if not already present

base_name : string, optional, unused

base name for unnamed variables. The code no longer uses this. We deprecate for this version of scipy, and will remove it in future versions

byte_order : {None, string}, optional

None by default, implying byte order guessed from mat file. Otherwise can be one of ('native', '=', 'little', '<', 'BIG', '>')

mat_dtype : {False, True} 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 : {False, True} optional

whether to squeeze unit matrix dimensions or not

chars_as_strings : {True, False} optional

whether to convert char arrays to string arrays

matlab_compatible : {False, True}

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 : {False, True} 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 behaviour of scipy version 0.6 (returning numpy object arrays). The preferred setting is True, because it allows easier round-trip load and save of matlab files. In a future version of scipy, we will change the default setting to True, and following versions may remove this flag entirely. For now, we set the default to False, for backwards compatibility, but issue a warning.

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.

savemat(*file_name, mdict, appendmat=True, format='5', long_field_names=False, do_compression=False, oned_as=None*)

Save a dictionary of names and arrays into the MATLAB-style .mat file.

This saves the arrayobjects in the given dictionary to a matlab style .mat file.

Parameters

file_name : {string, file-like object}

Name of the mat file (do not need .mat extension if appendmat==True) Can also pass open file-like object

m_dict : dict

dictionary from which to save matfile variables

appendmat : {True, False} optional

True to append the .mat extension to the end of the given filename, if not already present

format : {'5', '4'} string, optional

'5' for matlab 5 (up to matlab 7.2) '4' for matlab 4 mat files

long_field_names : boolean, optional, default=False

- False - 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 : {False, True} bool, optional

Whether to compress matrices on write. Default is False

oned_as : {'column', 'row'} string, optional

If 'column', write 1D numpy arrays as column vectors If 'row', write 1D numpy arrays as row vectors

3.6.2 Matrix Market files

mminfo(source)	Queries the contents of the Matrix Market file 'filename' to
mmread(source)	Reads the contents of a Matrix Market file 'filename' into a matrix.
mmwrite(target, a[, comment, field, precision])	Writes the sparse or dense matrix A to a Matrix Market formatted file.

mminfo(*source*)

Queries the contents of the Matrix Market file 'filename' to extract size and storage information.

Inputs:

source - Matrix Market filename (extension .mtx) or open file object

Outputs:

rows,cols - number of matrix rows and columns entries - number of non-zero entries of a sparse matrix

or rows*cols for a dense matrix

format - 'coordinate' | 'array' field - 'real' | 'complex' | 'pattern' | 'integer' symm - 'general' | 'symmetric' | 'skew-symmetric' | 'hermitian'

mmread(*source*)

Reads the contents of a Matrix Market file 'filename' into a matrix.

Inputs:

source - Matrix Market filename (extensions .mtx, .mtz.gz)
or open file object.

Outputs:

a - sparse or full matrix

mmwrite(*target, a, comment='', field=None, precision=None*)

Writes the sparse or dense matrix A to a Matrix Market formatted file.

Inputs:

target - Matrix Market filename (extension .mtx) or open file object a - sparse or full matrix comment - comments to be prepended to the Matrix Market file field - 'real' | 'complex' | 'pattern' | 'integer' precision - Number of digits to display for real or complex values.

3.6.3 Other

save_as_module([file_name, data])	Save the dictionary "data" into
npfile(*args, **kwds)	*npfile* is deprecated!

save_as_module(*file_name=None, data=None*)

Save the dictionary "data" into a module and shelf named save

npfile(**args, **kwds*)

npfile is deprecated!

You can achieve the same effect as using npfile using numpy.save and numpy.load.

You can use memory-mapped arrays and data-types to map out a file format for direct manipulation in NumPy.

Class for reading and writing numpy arrays to/from files

Inputs:

file_name – The complete path name to the file to open
or an open file-like object

permission – Open the file with given permissions: ('r', 'w', 'a')
for reading, writing, or appending. This is the same as the mode argument in the builtin open command.

format – The byte-ordering of the file:
(['native', 'n'], ['ieee-le', 'l'], ['ieee-be', 'B']) for native, little-endian, or big-endian respectively.

Attributes:
endian – default endian code for reading / writing order – default order for reading writing ('C' or 'F') file – file object containing read / written data

Methods:
seek, tell, close – as for file objects rewind – set read position to beginning of file read_raw – read string data from file (read method of file) write_raw – write string data to file (write method of file) read_array – read numpy array from binary file data write_array – write numpy array contents to binary file

Example use: >>> from StringIO import StringIO >>> import numpy as np >>> from scipy.io import npfile >>> arr = np.arange(10).reshape(5,2) >>> # Make file-like object (could also be file name) >>> my_file = StringIO() >>> npf = npfile(my_file) >>> npf.write_array(arr) >>> npf.rewind() >>> npf.read_array((5,2), arr.dtype) >>> npf.close() >>> # Or read write in Fortran order, Big endian >>> # and read back in C, system endian >>> my_file = StringIO() >>> npf = npfile(my_file, order='F', endian='>') >>> npf.write_array(arr) >>> npf.rewind() >>> npf.read_array((5,2), arr.dtype)

3.6.4 Wav sound files (`scipy.io.wavfile`)

read(file)	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

read (*file*)
Return the sample rate (in samples/sec) and data from a WAV file

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.

write (*filename, rate, data*)
Write a numpy array as a WAV file

filename – The name of the file to write (will be over-written) rate – The sample rate (in samples/sec). data – A 1-d or 2-d numpy array of integer data-type.

The bits-per-sample will be determined by the data-type To write multiple-channels, use a 2-d array of shape (Nsamples, Nchannels)

Writes a simple uncompressed WAV file.

3.6.5 Arff files (scipy.io.arff)

Module to read arff files (weka format).

arff is a simple file format which support numerical, string and data values. It supports sparse data too.

See http://weka.sourceforge.net/wekadoc/index.php/en:ARFF_(3.4.6) for more details about arff format and available datasets.

loadarff(filename)	Read an arff file.

loadarff (*filename*)

Read an arff file.

Parameters

filename : str

the name of the file

Returns

data : record array

the data of the arff file. Each record corresponds to one attribute.

meta : MetaData

this contains information about the arff file, like type and names of attributes, the relation (name of the dataset), etc...

Notes

This function should be able to read most arff files. Not implemented functionalities include:

- date type attributes
- string type attributes

It can read files with numeric and nominal attributes. It can read files with sparse data (? in the file).

3.6.6 Netcdf (scipy.io.netcdf)

netcdf_file(filename[, mode, mmap, version])	A netcdf_file object has two standard attributes: dimensions and variables.
netcdf_variable(data, typecode, shape, ...)	netcdf_variable objects are constructed by calling the method

class netcdf_file (*filename, mode='r', mmap=None, version=1*)

A netcdf_file object has two standard attributes: dimensions and variables. The values of both are dictionaries, mapping dimension names to their associated lengths and variable names to variables, respectively. Application programs should never modify these dictionaries.

All other attributes correspond to global attributes defined in the NetCDF file. Global file attributes are created by assigning to an attribute of the netcdf_file object.

Methods

close()
createDimension(name, length)
createVariable(name, type, dimensions)
flush()
sync()

close()

createDimension(*name, length*)

createVariable(*name, type, dimensions*)

flush()

sync()

class netcdf_variable(*data, typecode, shape, dimensions, attributes=None*)

`netcdf_variable` objects are constructed by calling the method `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 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.

Methods

assignValue(value)
getValue()
typecode()

assignValue(*value*)

getValue()

typecode()

3.7 Linear algebra (scipy.linalg)

3.7.1 Basics

inv(a[, overwrite_a])	Compute the inverse of a matrix.
solve(a, b[, sym_pos, lower, overwrite_a, ...])	Solve the equation a x = b for x
solve_banded(l, ab, b[, overwrite_ab, ...])	Solve the equation a x = b for x, assuming a is banded matrix.
solveh_banded(ab, b[, overwrite_ab, ...])	Solve equation a x = b.
det(a[, overwrite_a])	Compute the determinant of a matrix
norm(a[, ord])	Matrix or vector norm.
lstsq(a, b[, cond, overwrite_a, overwrite_b])	Compute least-squares solution to equation :m:‘a x = b‘
pinv(a[, cond, rcond])	Compute the (Moore-Penrose) pseudo-inverse of a matrix.
pinv2(a[, cond, rcond])	Compute the (Moore-Penrose) pseudo-inverse of a matrix.
kron(a, b)	Kronecker product of a and b.
hankel(c[, r])	Construct a Hankel matrix.
toeplitz(c[, r])	Construct a Toeplitz matrix.
tri(N[, M, k, dtype])	Construct (N, M) matrix filled with ones at and below the k-th diagonal.
tril(m[, k])	Construct a copy of a matrix with elements above the k-th diagonal zeroed.
triu(m[, k])	Construct a copy of a matrix with elements below the k-th diagonal zeroed.

inv (*a, overwrite_a=0*)

Compute the inverse of a matrix.

Parameters

a : array-like, shape (M, M)

Matrix to be inverted

Returns

ainv : array-like, shape (M, M)

Inverse of the matrix a

Raises LinAlgError if a is singular :

Examples

```
>>> a = array([[1., 2.], [3., 4.]])
>>> inv(a)
array([[-2. ,  1. ],
       [ 1.5, -0.5]])
>>> dot(a, inv(a))
array([[ 1.,  0.],
       [ 0.,  1.]])
```

solve (*a, b, sym_pos=0, lower=0, overwrite_a=0, overwrite_b=0, debug=0*)

Solve the equation a x = b for x

Parameters

a : array, shape (M, M)

b : array, shape (M,) or (M, N)

sym_pos : boolean

Assume a is symmetric and positive definite

lower : boolean

Use only data contained in the lower triangle of a, if sym_pos is true. Default is to use upper triangle.

overwrite_a : boolean

Allow overwriting data in a (may enhance performance)

overwrite_b : boolean

Allow overwriting data in b (may enhance performance)

Returns

x : array, shape (M,) or (M, N) depending on b

Solution to the system a x = b

Raises LinAlgError if a is singular :

solve_banded(*(l, u), ab, b, overwrite_ab=0, overwrite_b=0, debug=0*)

Solve the equation a x = b for x, assuming a is banded matrix.

The matrix a is stored in ab using the matrix diagonal orded form:

```
ab[u + i - j, j] == a[i,j]
```

Example of ab (shape of a is (6,6), u=1, l=2):

```
*    a01  a12  a23  a34  a45
a00  a11  a22  a33  a44  a55
a10  a21  a32  a43  a54   *
a20  a31  a42  a53   *    *
```

Parameters

(l, u) : (integer, integer)

Number of non-zero lower and upper diagonals

ab : array, shape (l+u+1, M)

Banded matrix

b : array, shape (M,) or (M, K)

Right-hand side

overwrite_ab : boolean

Discard data in ab (may enhance performance)

overwrite_b : boolean

Discard data in b (may enhance performance)

Returns

x : array, shape (M,) or (M, K)

The solution to the system a x = b

solveh_banded(*ab, b, overwrite_ab=0, overwrite_b=0, lower=0*)

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:
*   *   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

ab : array, shape (M, u + 1)

Banded matrix

b : array, shape (M,) or (M, K)

Right-hand side

overwrite_ab : boolean

Discard data in ab (may enhance performance)

overwrite_b : boolean

Discard data in b (may enhance performance)

lower : boolean

Is the matrix in the lower form. (Default is upper form)

Returns

c : array, shape (M, u+1)

Cholesky factorization of a, in the same banded format as ab

x : array, shape (M,) or (M, K)

The solution to the system a x = b

det(*a, overwrite_a=0*)

Compute the determinant of a matrix

Parameters

a : array, shape (M, M)

Returns

det : float or complex

Determinant of a

Notes

The determinant is computed via LU factorization, LAPACK routine z/dgetrf.

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

x : array_like, shape (M,) or (M, N)

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

n : 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:

ord	norm for matrices	norm for vectors
None	Frobenius norm	2-norm
'fro'	Frobenius norm	–
inf	max(sum(abs(x), axis=1))	max(abs(x))
-inf	min(sum(abs(x), axis=1))	min(abs(x))
0	–	sum(x != 0)
1	max(sum(abs(x), axis=0))	as below
-1	min(sum(abs(x), axis=0))	as below
2	2-norm (largest sing. value)	as below
-2	smallest singular value	as below
other	–	sum(abs(x)**ord)**(1./ord)

The Frobenius norm is given by [R4]:

$$||A||_F = [\sum_{i,j} abs(a_{i,j})^2]^{1/2}$$

References

[R4]

Examples

```
>>> from numpy import linalg as LA
>>> 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]])
```

```
>>> LA.norm(a)
7.745966692414834
>>> LA.norm(b)
7.745966692414834
>>> LA.norm(b, 'fro')
7.745966692414834
>>> LA.norm(a, np.inf)
4
>>> LA.norm(b, np.inf)
9
>>> LA.norm(a, -np.inf)
0
>>> LA.norm(b, -np.inf)
2

>>> LA.norm(a, 1)
20
>>> LA.norm(b, 1)
7
>>> LA.norm(a, -1)
-4.6566128774142013e-010
>>> LA.norm(b, -1)
6
>>> LA.norm(a, 2)
7.745966692414834
>>> LA.norm(b, 2)
7.3484692283495345

>>> LA.norm(a, -2)
nan
>>> LA.norm(b, -2)
1.8570331885190563e-016
>>> LA.norm(a, 3)
5.8480354764257312
>>> LA.norm(a, -3)
nan
```

lstsq(*a, b, cond=None, overwrite_a=0, overwrite_b=0*)

Compute least-squares solution to equation **:m:'a x = b'**

Compute a vector x such that the 2-norm **:m:'|b - a x|'** is minimised.

Parameters

a : array, shape (M, N)

b : array, shape (M,) or (M, K)

cond : float

Cutoff for 'small' singular values; used to determine effective rank of a. Singular values smaller than rcond*largest_singular_value are considered zero.

overwrite_a : boolean

Discard data in a (may enhance performance)

overwrite_b : boolean

Discard data in b (may enhance performance)

Returns

x : array, shape (N,) or (N, K) depending on shape of b

Least-squares solution

residues : array, shape () or (1,) or (K,)

Sums of residues, squared 2-norm for each column in **:m:'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 : integer

Effective rank of matrix a

s : array, shape (min(M,N),)

Singular values of a. The condition number of a is abs(s[0]/s[-1]).

Raises LinAlgError if computation does not converge :

pinv(*a, cond=None, rcond=None*)

Compute the (Moore-Penrose) pseudo-inverse of a matrix.

Calculate a generalized inverse of a matrix using a least-squares solver.

Parameters

a : array, shape (M, N)

Matrix to be pseudo-inverted

cond, rcond : float

Cutoff for 'small' singular values in the least-squares solver. Singular values smaller than rcond*largest_singular_value are considered zero.

Returns

B : array, shape (N, M)

Raises LinAlgError if computation does not converge :

Examples

```
>>> from numpy import *
>>> a = random.randn(9, 6)
>>> B = linalg.pinv(a)
>>> allclose(a, dot(a, dot(B, a)))
True
>>> allclose(B, dot(B, dot(a, B)))
True
```

pinv2(*a, cond=None, rcond=None*)

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 : array, shape (M, N)

Matrix to be pseudo-inverted

cond, rcond : float or None

Cutoff for 'small' singular values. Singular values smaller than rcond*largest_singular_value are considered zero.

If None or -1, suitable machine precision is used.

Returns

B : array, shape (N, M)

Raises LinAlgError if SVD computation does not converge :

Examples

```
>>> from numpy import *
>>> a = random.randn(9, 6)
>>> B = linalg.pinv2(a)
>>> allclose(a, dot(a, dot(B, a)))
True
>>> allclose(B, dot(B, dot(a, B)))
True
```

kron(*a, b*)

Kronecker product of a and b.

The result is the block matrix:

```
a[0,0]*b    a[0,1]*b  ... a[0,-1]*b
a[1,0]*b    a[1,1]*b  ... a[1,-1]*b
...
a[-1,0]*b   a[-1,1]*b ... a[-1,-1]*b
```

Parameters

a : array, shape (M, N)

b : array, shape (P, Q)

Returns

A : array, shape (M*P, N*Q)

Kronecker product of a and b

Examples

```
>>> from scipy import kron, array
>>> kron(array([[1,2],[3,4]]), array([[1,1,1]]))
array([[1, 1, 1, 2, 2, 2],
       [3, 3, 3, 4, 4, 4]])
```

hankel(*c, r=None*)

Construct a Hankel matrix.

The Hankel matrix has constant anti-diagonals, c as its first column, and r as its last row (if not given, r == 0 os assumed).

Parameters

c : array

First column of the matrix

r : array

Last row of the matrix. If None, r == 0 is assumed.

Returns

A : array, shape (len(c), len(r))

Constructed Hankel matrix. dtype is the same as (c[0] + r[0]).dtype

See Also:

toeplitz
Toeplitz matrix

Examples

```
>>> from scipy.linalg import hankel
>>> 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]])
```

toeplitz(*c, r=None*)

Construct a Toeplitz matrix.

The Toepliz matrix has constant diagonals, c as its first column, and r as its first row (if not given, r == c is assumed).

Parameters

c : array

First column of the matrix

r : array

First row of the matrix. If None, r == c is assumed.

Returns

A : array, shape (len(c), len(r))

Constructed Toeplitz matrix. dtype is the same as (c[0] + r[0]).dtype

See Also:

hankel
Hankel matrix

Examples

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

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 : integer

M : integer

Size of the matrix. If M is None, M == N is assumed.

k : integer

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

Data type of the matrix.

Returns

A : array, shape (N, M)

Examples

```
>>> from scipy.linalg import tri
>>> tri(3, 5, 2, dtype=int)
array([[1, 1, 1, 0, 0],
       [1, 1, 1, 1, 0],
       [1, 1, 1, 1, 1]])
>>> tri(3, 5, -1, dtype=int)
array([[0, 0, 0, 0, 0],
       [1, 0, 0, 0, 0],
       [1, 1, 0, 0, 0]])
```

tril(*m, k=0*)

Construct a copy of a matrix with elements above the k-th diagonal zeroed.

Parameters

m : array

Matrix whose elements to return

k : integer

Diagonal above which to zero elements. k == 0 is the main diagonal, k < 0 subdiagonal and k > 0 superdiagonal.

Returns

A : array, shape m.shape, dtype m.dtype

Examples

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

triu(*m, k=0*)

Construct a copy of a matrix with elements below the k-th diagonal zeroed.

Parameters

m : array

Matrix whose elements to return

k : integer

Diagonal below which to zero elements. k == 0 is the main diagonal, k < 0 subdiagonal and k > 0 superdiagonal.

Returns

A : array, shape m.shape, dtype m.dtype

Examples

```
>>> from scipy.linalg import tril
>>> 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]])
```

3.7.2 Eigenvalues and Decompositions

eig(a[, b, left, right, overwrite_a, ...])	Solve an ordinary or generalized eigenvalue problem of a square matrix.
eigvals(a[, b, overwrite_a])	Compute eigenvalues from an ordinary or generalized eigenvalue problem.
eigh(a[, b, lower, eigvals_only, ...])	Solve an ordinary or generalized eigenvalue problem for a complex
eigvalsh(a[, b, lower, overwrite_a, ...])	Solve an ordinary or generalized eigenvalue problem for a complex
eig_banded(a_band[, lower, eigvals_only, ...])	Solve real symmetric or complex hermetian band matrix eigenvalue problem.
eigvals_banded(a_band[, lower, ...])	Solve real symmetric or complex hermitian band matrix eigenvalue problem.
lu(a[, permute_l, overwrite_a])	Compute pivoted LU decompostion of a matrix.
lu_factor(a[, overwrite_a])	Compute pivoted LU decomposition of a matrix.
lu_solve(lu, b[, trans, overwrite_b])	Solve an equation system, a x = b, given the LU factorization of a
svd(a[, full_matrices, compute_uv, overwrite_a])	Singular Value Decomposition.
svdvals(a[, overwrite_a])	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])	Compute the Cholesky decomposition of a matrix.
cholesky_banded(ab[, overwrite_ab, lower])	Cholesky decompose a banded Hermitian positive-definite matrix
cho_factor(a[, lower, overwrite_a])	Compute the Cholesky decomposition of a matrix, to use in cho_solve
cho_solve(clow, b)	Solve a previously factored symmetric system of equations.
qr(a[, overwrite_a, lwork, econ, mode])	Compute QR decomposition of a matrix.
schur(a[, output, lwork, overwrite_a])	Compute Schur decomposition of a matrix.
rsf2csf(T, Z)	Convert real Schur form to complex Schur form.
hessenberg(a[, calc_q, overwrite_a])	Compute Hessenberg form of a matrix.

eig(*a, b=None, left=False, right=True, overwrite_a=False, overwrite_b=False*)

Solve an ordinary or generalized eigenvalue problem of a square matrix.

Find eigenvalues w and right or left eigenvectors of a general matrix:

```
a   vr[:,i] = w[i]        b   vr[:,i]
a.H vl[:,i] = w[i].conj() b.H vl[:,i]
```

where .H is the Hermitean conjugation.

Parameters

a : array, shape (M, M)

A complex or real matrix whose eigenvalues and eigenvectors will be computed.

b : array, shape (M, M)

Right-hand side matrix in a generalized eigenvalue problem. If omitted, identity matrix is assumed.

left : boolean

Whether to calculate and return left eigenvectors

right : boolean

Whether to calculate and return right eigenvectors

overwrite_a : boolean

Whether to overwrite data in a (may improve performance)

overwrite_b : boolean

Whether to overwrite data in b (may improve performance)

Returns

w : double or complex array, shape (M,)

The eigenvalues, each repeated according to its multiplicity.

(if left == True) :

vl : double or complex array, shape (M, M)

The normalized left eigenvector corresponding to the eigenvalue w[i] is the column v[:,i].

(if right == True) :

vr : double or complex array, shape (M, M)

The normalized right eigenvector corresponding to the eigenvalue w[i] is the column vr[:,i].

Raises LinAlgError if eigenvalue computation does not converge :

See Also:

eigh
eigenvalues and right eigenvectors for symmetric/Hermitian arrays

eigvals(*a, b=None, overwrite_a=0*)
Compute eigenvalues from an ordinary or generalized eigenvalue problem.

Find eigenvalues of a general matrix:

```
a   vr[:,i] = w[i]        b   vr[:,i]
```

Parameters

a : array, shape (M, M)

A complex or real matrix whose eigenvalues and eigenvectors will be computed.

b : array, shape (M, M)

Right-hand side matrix in a generalized eigenvalue problem. If omitted, identity matrix is assumed.

overwrite_a : boolean

Whether to overwrite data in a (may improve performance)

Returns

w : double or complex array, shape (M,)

The eigenvalues, each repeated according to its multiplicity, but not in any specific order.

Raises LinAlgError if eigenvalue computation does not converge :

See Also:

eigvalsh
eigenvalues of symmetric or Hemitiean arrays

eig
eigenvalues and right eigenvectors of general arrays

eigh
eigenvalues and eigenvectors of symmetric/Hermitean arrays.

eigh(*a, b=None, lower=True, eigvals_only=False, overwrite_a=False, overwrite_b=False, turbo=True, eigvals=None, type=1*)

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 v[:,i] = w[i] b v[:,i]
v[i,:].conj() a v[:,i] = w[i]
v[i,:].conj() b v[:,i] = 1
```

Parameters

a : array, shape (M, M)

A complex Hermitian or real symmetric matrix whose eigenvalues and eigenvectors will be computed.

b : array, shape (M, M)

A complex Hermitian or real symmetric definite positive matrix in. If omitted, identity matrix is assumed.

lower : boolean

Whether the pertinent array data is taken from the lower or upper triangle of a. (Default: lower)

eigvals_only : boolean

Whether to calculate only eigenvalues and no eigenvectors. (Default: both are calculated)

turbo : boolean

Use divide and conquer algorithm (faster but expensive in memory, only for generalized eigenvalue problem and if eigvals=None)

eigvals : tuple (lo, hi)

Indexes of the smallest and largest (in ascending order) eigenvalues and corresponding eigenvectors to be returned: 0 <= lo < hi <= M-1. If omitted, all eigenvalues and eigenvectors are returned.

type: integer :

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 : boolean

Whether to overwrite data in a (may improve performance)

overwrite_b : boolean

Whether to overwrite data in b (may improve performance)

Returns

w : real array, shape (N,)

The N (1<=N<=M) selected eigenvalues, in ascending order, each repeated according to its multiplicity.

(if eigvals_only == False) :

v : complex array, shape (M, N)

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:

eig
eigenvalues and right eigenvectors for non-symmetric arrays

eigvalsh(*a, b=None, lower=True, overwrite_a=False, overwrite_b=False, turbo=True, eigvals=None, type=1*)
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 : array, shape (M, M)

A complex Hermitian or real symmetric matrix whose eigenvalues and eigenvectors will be computed.

b : array, shape (M, M)

A complex Hermitian or real symmetric definite positive matrix in. If omitted, identity matrix is assumed.

lower : boolean

Whether the pertinent array data is taken from the lower or upper triangle of a. (Default: lower)

turbo : boolean

Use divide and conquer algorithm (faster but expensive in memory, only for generalized eigenvalue problem and if eigvals=None)

eigvals : tuple (lo, hi)

Indexes of the smallest and largest (in ascending order) eigenvalues and corresponding eigenvectors to be returned: 0 <= lo < hi <= M-1. If omitted, all eigenvalues and eigenvectors are returned.

type: integer :

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 : boolean

Whether to overwrite data in a (may improve performance)

overwrite_b : boolean

Whether to overwrite data in b (may improve performance)

Returns

w : real array, shape (N,)

The N (1<=N<=M) selected eigenvalues, in ascending order, each repeated according to its multiplicity.

Raises LinAlgError if eigenvalue computation does not converge, :

an error occurred, or b matrix is not definite positive. Note that :

if input matrices are not symmetric or hermitian, no error is reported :

but results will be wrong. :

See Also:

eigvals
eigenvalues of general arrays

eigh
eigenvalues and right eigenvectors for symmetric/Hermitian arrays

eig
eigenvalues and right eigenvectors for non-symmetric arrays

eig_banded(*a_band, lower=0, eigvals_only=0, overwrite_a_band=0, select='a', select_range=None, max_ev=0*)

Solve real symmetric or complex hermetian band matrix eigenvalue problem.

Find eigenvalues w and optionally right eigenvectors v of a:

```
a v[:,i] = w[i] v[:,i]
v.H v    = identity
```

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:
*   *   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 : array, shape (M, u+1)

Banded matrix whose eigenvalues to calculate

lower : boolean

Is the matrix in the lower form. (Default is upper form)

eigvals_only : boolean

Compute only the eigenvalues and no eigenvectors. (Default: calculate also eigenvectors)

overwrite_a_band: :

Discard data in a_band (may enhance performance)

select: {'a', 'v', 'i'} :

Which eigenvalues to calculate

select	calculated
'a'	All eigenvalues
'v'	Eigenvalues in the interval (min, max]
'i'	Eigenvalues with indices min <= i <= max

select_range : (min, max)

Range of selected eigenvalues

max_ev : integer

For select=='v', maximum number of eigenvalues expected. For other values of select, has no meaning.

In doubt, leave this parameter untouched.

Returns

w : array, shape (M,)

The eigenvalues, in ascending order, each repeated according to its multiplicity.

v : double or complex double array, shape (M, M)

The normalized eigenvector corresponding to the eigenvalue w[i] is the column v[:,i].

Raises LinAlgError if eigenvalue computation does not converge :

eigvals_banded(*a_band, lower=0, overwrite_a_band=0, select='a', select_range=None*)

Solve real symmetric or complex hermitian band matrix eigenvalue problem.

Find eigenvalues w of a:

```
a v[:,i] = w[i] v[:,i]
v.H v    = identity
```

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:
*   *   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 : array, shape (M, u+1)

Banded matrix whose eigenvalues to calculate

lower : boolean

Is the matrix in the lower form. (Default is upper form)

overwrite_a_band: :

Discard data in a_band (may enhance performance)

select: {'a', 'v', 'i'} :

Which eigenvalues to calculate

select	calculated
'a'	All eigenvalues
'v'	Eigenvalues in the interval (min, max]
'i'	Eigenvalues with indices min <= i <= max

select_range : (min, max)

Range of selected eigenvalues

Returns

w : array, shape (M,)

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

lu(*a, permute_l=0, overwrite_a=0*)
Compute pivoted LU decompostion 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 : array, shape (M, N)

Array to decompose

permute_l : boolean

Perform the multiplication P*L (Default: do not permute)

overwrite_a : boolean

Whether to overwrite data in a (may improve performance)

Returns

(If permute_l == False) :

p : array, shape (M, M)

Permutation matrix

l : array, shape (M, K)

Lower triangular or trapezoidal matrix with unit diagonal. K = min(M, N)

u : array, shape (K, N)

Upper triangular or trapezoidal matrix

(If permute_l == True) :

pl : array, shape (M, K)

Permuted L matrix. K = min(M, N)

u : array, shape (K, N)

Upper triangular or trapezoidal matrix

Notes

This is a LU factorization routine written for Scipy.

lu_factor (*a, overwrite_a=0*)

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 : array, shape (M, M)

Matrix to decompose

overwrite_a : boolean

Whether to overwrite data in A (may increase performance)

Returns

lu : array, shape (N, N)

Matrix containing U in its upper triangle, and L in its lower triangle. The unit diagonal elements of L are not stored.

piv : array, shape (N,)

Pivot indices representing the permutation matrix P: row i of matrix was interchanged with row piv[i].

See Also:

lu_solve

solve an equation system using the LU factorization of a matrix

Notes

This is a wrapper to the *GETRF routines from LAPACK.

lu_solve (*(lu, piv), b, trans=0, overwrite_b=0*)

Solve an equation system, a x = b, given the LU factorization of a

Parameters

(lu, piv) :

Factorization of the coefficient matrix a, as given by lu_factor

b : array

Right-hand side

trans : {0, 1, 2}

Type of system to solve:

trans	system
0	a x = b
1	a^T x = b
2	a^H x = b

Returns

x : array

Solution to the system

See Also:

lu_factor
LU factorize a matrix

svd(*a, full_matrices=1, compute_uv=1, overwrite_a=0*)
Singular Value Decomposition.

Factorizes the matrix a into two unitary matrices U and Vh and an 1d-array s of singular values (real, non-negative) such that a == U S Vh if S is an suitably shaped matrix of zeros whose main diagonal is s.

Parameters

a : array, shape (M, N)

Matrix to decompose

full_matrices : boolean

If true, U, Vh are shaped (M,M), (N,N) If false, the shapes are (M,K), (K,N) where K = min(M,N)

compute_uv : boolean

Whether to compute also U, Vh in addition to s (Default: true)

overwrite_a : boolean

Whether data in a is overwritten (may improve performance)

Returns

U: array, shape (M,M) or (M,K) depending on full_matrices :

s: array, shape (K,) :

The singular values, sorted so that s[i] >= s[i+1]. K = min(M, N)

Vh: array, 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
return singular values of a matrix

diagsvd
return the Sigma matrix, given the vector s

Examples

```
>>> from scipy import random, linalg, allclose, dot
>>> a = random.randn(9, 6) + 1j*random.randn(9, 6)
>>> U, s, Vh = linalg.svd(a)
>>> U.shape, Vh.shape, s.shape
((9, 9), (6, 6), (6,))
```

```
>>> U, s, Vh = linalg.svd(a, full_matrices=False)
>>> U.shape, Vh.shape, s.shape
((9, 6), (6, 6), (6,))
>>> S = linalg.diagsvd(s, 6, 6)
>>> allclose(a, dot(U, dot(S, Vh)))
True


>>> s2 = linalg.svd(a, compute_uv=False)
>>> allclose(s, s2)
True
```

svdvals(*a, overwrite_a=0*)

Compute singular values of a matrix.

Parameters

a : array, shape (M, N)

Matrix to decompose

overwrite_a : boolean

Whether data in a is overwritten (may improve performance)

Returns

s: array, shape (K,) :

The singular values, sorted so that s[i] >= s[i+1]. K = min(M, N)

Raises LinAlgError if SVD computation does not converge :

See Also:

svd

return the full singular value decomposition of a matrix

diagsvd

return the Sigma matrix, given the vector s

diagsvd(*s, M, N*)

Construct the sigma matrix in SVD from singular values and size M,N.

Parameters

s : array, shape (M,) or (N,)

Singular values

M : integer

N : integer

Size of the matrix whose singular values are s

Returns

S : array, shape (M, N)

The S-matrix in the singular value decomposition

orth(*A*)

Construct an orthonormal basis for the range of A using SVD

Parameters

A : array, shape (M, N)

Returns

Q : array, shape (M, K)

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

cholesky(*a, lower=0, overwrite_a=0*)

Compute the Cholesky decomposition of a matrix.

Returns the Cholesky decomposition, **:lm:'A = L L^*'** or **:lm:'A = U^* U'** of a Hermitian positive-definite matrix **:lm:'A'**.

Parameters

a : array, shape (M, M)

Matrix to be decomposed

lower : boolean

Whether to compute the upper or lower triangular Cholesky factorization (Default: upper-triangular)

overwrite_a : boolean

Whether to overwrite data in a (may improve performance)

Returns

B : array, shape (M, M)

Upper- or lower-triangular Cholesky factor of A

Raises LinAlgError if decomposition fails :

Examples

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

cholesky_banded(*ab, overwrite_ab=0, lower=0*)

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] (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:
*   *   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 : array, shape (M, u + 1)

Banded matrix

overwrite_ab : boolean

Discard data in ab (may enhance performance)

lower : boolean

Is the matrix in the lower form. (Default is upper form)

Returns

c : array, shape (M, u+1)

Cholesky factorization of a, in the same banded format as ab

cho_factor (*a, lower=0, overwrite_a=0*)

Compute the Cholesky decomposition of a matrix, to use in cho_solve

Returns a matrix containing the Cholesky decomposition, `A = L L*` or `A = U* U` of a Hermitian positive-definite matrix *a*. The return value can be directly used as the first parameter to cho_solve.

Warning: The returned matrix also contains random data in the entries not used by the Cholesky decomposition. If you need to zero these entries, use the function *cholesky* instead.

Parameters

a : array, shape (M, M)

Matrix to be decomposed

lower : boolean

Whether to compute the upper or lower triangular Cholesky factorization (Default: upper-triangular)

overwrite_a : boolean

Whether to overwrite data in a (may improve performance)

Returns

c : array, shape (M, M)

Matrix whose upper or lower triangle contains the Cholesky factor of *a*. Other parts of the matrix contain random data.

lower : boolean

Flag indicating whether the factor is in the lower or upper triangle

Raises

LinAlgError :

Raised if decomposition fails.

cho_solve (*clow, b*)
Solve a previously factored symmetric system of equations.

The equation system is

A x = b, A = U^H U = L L^H

and A is real symmetric or complex Hermitian.

Parameters
clow : tuple (c, lower)

Cholesky factor and a flag indicating whether it is lower triangular. The return value from cho_factor can be used.

b : array

Right-hand side of the equation system

First input is a tuple (LorU, lower) which is the output to cho_factor. :

Second input is the right-hand side. :

Returns
x : array

Solution to the equation system

qr (*a, overwrite_a=0, lwork=None, econ=None, mode='qr'*)
Compute QR decomposition of a matrix.

Calculate the decomposition **:lm:'A = Q R'** where Q is unitary/orthogonal and R upper triangular.

Parameters
a : array, shape (M, N)

Matrix to be decomposed

overwrite_a : boolean

Whether data in a is overwritten (may improve performance)

lwork : integer

Work array size, lwork >= a.shape[1]. If None or -1, an optimal size is computed.

econ : boolean

Whether to compute the economy-size QR decomposition, making shapes of Q and R (M, K) and (K, N) instead of (M,M) and (M,N). K=min(M,N). Default is False.

mode : {'qr', 'r'}

Determines what information is to be returned: either both Q and R or only R.

Returns
(if mode == 'qr') :

Q : double or complex array, shape (M, M) or (M, K) for econ==True

(for any mode) :

R : double or complex array, shape (M, N) or (K, N) for econ==True

Size K = min(M, N)

Raises LinAlgError if decomposition fails :

Notes

This is an interface to the LAPACK routines dgeqrf, zgeqrf, dorgqr, and zungqr.

Examples

```
>>> from scipy import random, linalg, dot
>>> a = random.randn(9, 6)
>>> q, r = linalg.qr(a)
>>> allclose(a, dot(q, r))
True
>>> q.shape, r.shape
((9, 9), (9, 6))


>>> r2 = linalg.qr(a, mode='r')
>>> allclose(r, r2)


>>> q3, r3 = linalg.qr(a, econ=True)
>>> q3.shape, r3.shape
((9, 6), (6, 6))
```

schur (*a, output='real', lwork=None, overwrite_a=0*)

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 : array, shape (M, M)

Matrix to decompose

output : {'real', 'complex'}

Construct the real or complex Schur decomposition (for real matrices).

lwork : integer

Work array size. If None or -1, it is automatically computed.

overwrite_a : boolean

Whether to overwrite data in a (may improve performance)

Returns

T : array, shape (M, M)

Schur form of A. It is real-valued for the real Schur decomposition.

Z : array, shape (M, M)

An unitary Schur transformation matrix for A. It is real-valued for the real Schur decomposition.

See Also:

rsf2csf

Convert real Schur form to complex Schur form

rsf2csf(*T, Z*)
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 : array, shape (M, M)

Real Schur form of the original matrix

Z : array, shape (M, M)

Schur transformation matrix

Returns
T : array, shape (M, M)

Complex Schur form of the original matrix

Z : array, shape (M, M)

Schur transformation matrix corresponding to the complex form

See Also:

schur
Schur decompose a matrix

hessenberg(*a, calc_q=0, overwrite_a=0*)
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 subdiagonal.

Parameters
a : array, shape (M,M)

Matrix to bring into Hessenberg form

calc_q : boolean

Whether to compute the transformation matrix

overwrite_a : boolean

Whether to ovewrite data in a (may improve performance)

Returns
H : array, shape (M,M)

Hessenberg form of A

(If calc_q == True) :

Q : array, shape (M,M)

Unitary/orthogonal similarity transformation matrix s.t. A = Q H Q^H

3.7.3 Matrix Functions

expm(A[, q])	Compute the matrix exponential using Pade approximation.
expm2(A)	Compute the matrix exponential using eigenvalue decomposition.
expm3(A[, q])	Compute the matrix exponential using Taylor series.
logm(A[, disp])	Compute matrix logarithm.
cosm(A)	Compute the matrix cosine.
sinm(A)	Compute the matrix sine.
tanm(A)	Compute the matrix tangent.
coshm(A)	Compute the hyperbolic matrix cosine.
sinhm(A)	Compute the hyperbolic matrix sine.
tanhm(A)	Compute the hyperbolic matrix tangent.
signm(a[, disp])	Matrix sign function.
sqrtm(A[, disp])	Matrix square root.
funm(A, func[, disp])	Evaluate a matrix function specified by a callable.

expm(*A, q=7*)

Compute the matrix exponential using Pade approximation.

Parameters

A : array, shape(M,M)

Matrix to be exponentiated

q : integer

Order of the Pade approximation

Returns

expA : array, shape(M,M)

Matrix exponential of A

expm2(*A*)

Compute the matrix exponential using eigenvalue decomposition.

Parameters

A : array, shape(M,M)

Matrix to be exponentiated

Returns

expA : array, shape(M,M)

Matrix exponential of A

expm3(*A, q=20*)

Compute the matrix exponential using Taylor series.

Parameters

A : array, shape(M,M)

Matrix to be exponentiated

q : integer

Order of the Taylor series

Returns

expA : array, shape(M,M)

Matrix exponential of A

logm(*A, disp=1*)
Compute matrix logarithm.

The matrix logarithm is the inverse of expm: expm(logm(A)) == A

Parameters
A : array, shape(M,M)

Matrix whose logarithm to evaluate

disp : boolean

Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)

Returns
logA : array, shape(M,M)

Matrix logarithm of A

(if disp == False) :

errest : float

1-norm of the estimated error, ||err||_1 / ||A||_1

cosm(*A*)
Compute the matrix cosine.

This routine uses expm to compute the matrix exponentials.

Parameters
A : array, shape(M,M)

Returns
cosA : array, shape(M,M)

Matrix cosine of A

sinm(*A*)
Compute the matrix sine.

This routine uses expm to compute the matrix exponentials.

Parameters
A : array, shape(M,M)

Returns
sinA : array, shape(M,M)

Matrix cosine of A

tanm(*A*)
Compute the matrix tangent.

This routine uses expm to compute the matrix exponentials.

Parameters
A : array, shape(M,M)

Returns
tanA : array, shape(M,M)

Matrix tangent of A

coshm(*A*)
Compute the hyperbolic matrix cosine.

This routine uses expm to compute the matrix exponentials.

Parameters
A : array, shape(M,M)

Returns
coshA : array, shape(M,M)

Hyperbolic matrix cosine of A

sinhm(*A*)
Compute the hyperbolic matrix sine.

This routine uses expm to compute the matrix exponentials.

Parameters
A : array, shape(M,M)

Returns
sinhA : array, shape(M,M)

Hyperbolic matrix sine of A

tanhm(*A*)
Compute the hyperbolic matrix tangent.

This routine uses expm to compute the matrix exponentials.

Parameters
A : array, shape(M,M)

Returns
tanhA : array, shape(M,M)

Hyperbolic matrix tangent of A

signm(*a, disp=1*)
Matrix sign function.

Extension of the scalar sign(x) to matrices.

Parameters
A : array, shape(M,M)

Matrix at which to evaluate the sign function

disp : boolean

Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)

Returns
sgnA : array, shape(M,M)

Value of the sign function at A

(if disp == False) :

errest : float

1-norm of the estimated error, ||err||_1 / ||A||_1

Examples

```
>>> 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])
```

sqrtm(*A, disp=1*)

Matrix square root.

Parameters

A : array, shape(M,M)

Matrix whose square root to evaluate

disp : boolean

Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)

Returns

sgnA : array, shape(M,M)

Value of the sign function at A

(if disp == False) :

errest : float

Frobenius norm of the estimated error, ||err||_F / ||A||_F

Notes

Uses algorithm by Nicholas J. Higham

funm(*A, func, disp=1*)

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 : array, shape(M,M)

Matrix at which to evaluate the function

func : callable

Callable object that evaluates a scalar function f. Must be vectorized (eg. using vectorize).

disp : boolean

Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)

Returns

fA : array, shape(M,M)

Value of the matrix function specified by func evaluated at A

(if disp == False) :

errest : float

1-norm of the estimated error, ||err||_1 / ||A||_1

3.7.4 Iterative linear systems solutions

These functions are deprecated - use scipy.sparse.linalg instead

cg(*args, **kwds)	scipy.linalg.cg is deprecated, use scipy.sparse.linalg.cg instead!
cgs(*args, **kwds)	scipy.linalg.cgs is deprecated, use scipy.sparse.linalg.cgs instead!
qmr(*args, **kwds)	scipy.linalg.qmr is deprecated, use scipy.sparse.linalg.qmr instead!
gmres(*args, **kwds)	scipy.linalg.gmres is deprecated, use scipy.sparse.linalg.gmres instead!
bicg(*args, **kwds)	scipy.linalg.bicg is deprecated, use scipy.sparse.linalg.bicg instead!
bicgstab(*args, **kwds)	scipy.linalg.bicgstab is deprecated, use scipy.sparse.linalg.bicgstab instead!

cg (**args, **kwds*)

scipy.linalg.cg is deprecated, use scipy.sparse.linalg.cg instead!

Use Conjugate Gradient iteration to solve A x = b

Parameters

A : {sparse matrix, dense matrix, LinearOperator}

The N-by-N matrix of the linear system.

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

cgs (**args, **kwds*)

scipy.linalg.cgs is deprecated, use scipy.sparse.linalg.cgs instead!

Use Conjugate Gradient Squared iteration to solve A x = b

Parameters

A : {sparse matrix, dense matrix, LinearOperator}

The N-by-N matrix of the linear system.

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

qmr (**args, **kwds*)

scipy.linalg.qmr is deprecated, use scipy.sparse.linalg.qmr instead!

Use Quasi-Minimal Residual iteration to solve A x = b

Parameters

A : {sparse matrix, dense matrix, LinearOperator}

The N-by-N matrix of the linear system.

b

[{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

gmres (**args, **kwds*)
scipy.linalg.gmres is deprecated, use scipy.sparse.linalg.gmres instead!

Use Generalized Minimal RESidual iteration to solve A x = b

Parameters
A : {sparse matrix, dense matrix, LinearOperator}

The N-by-N matrix of the linear system.

b
[{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

bicg (**args, **kwds*)
scipy.linalg.bicg is deprecated, use scipy.sparse.linalg.bicg instead!

Use BIConjugate Gradient iteration to solve A x = b

Parameters
A : {sparse matrix, dense matrix, LinearOperator}

The N-by-N matrix of the linear system.

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

bicgstab (**args, **kwds*)
scipy.linalg.bicgstab is deprecated, use scipy.sparse.linalg.bicgstab instead!

Use BIConjugate Gradient STABilized iteration to solve A x = b

Parameters
A : {sparse matrix, dense matrix, LinearOperator}

The N-by-N matrix of the linear system.

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

3.8 Maximum entropy models (scipy.maxentropy)

3.8.1 Routines for fitting maximum entropy models

Contains two classes for fitting maximum entropy models (also known as "exponential family" models) subject to linear constraints on the expectations of arbitrary feature statistics. One class, "model", is for small discrete sample spaces, using explicit summation. The other, "bigmodel", is for sample spaces that are either continuous (and perhaps high-dimensional) or discrete but too large to sum over, and uses importance sampling. conditional Monte Carlo methods.

The maximum entropy model has exponential form

$$p(\mathbf{x}) = \exp\left(\frac{\theta^{\mathsf{T}}\vec{f}(\mathbf{x})}{Z(\theta)}\right)$$

with a real parameter vector theta of the same length as the feature statistic f(x), For more background, see, for example, Cover and Thomas (1991), *Elements of Information Theory*.

See the file bergerexample.py for a walk-through of how to use these routines when the sample space is small enough to be enumerated.

See bergerexamplesimulated.py for a a similar walk-through using simulation.

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3.8.2 Models

class `model` (*f=None, samplespace=None*)

A maximum-entropy (exponential-form) model on a discrete sample space.

Methods

`beginlogging`(filename[, freq])	Enable logging params for each fn evaluation to files named 'filename.freq.pickle', 'filename.(2*freq).pickle', ...
`clearcache`()	Clears the interim results of computations depending on the
`crossentropy`(fx[, log_prior_x, base])	Returns the cross entropy H(q, p) of the empirical
`dual`([params, ignorepenalty, ignoretest])	Computes the Lagrangian dual L(theta) of the entropy of the
`endlogging`()	Stop logging param values whenever setparams() is called.
`entropydual`([params, ignorepenalty, ignoretest])	Computes the Lagrangian dual L(theta) of the entropy of the
`expectations`()	The vector E_p[f(X)] under the model p_params of the vector of
`fit`(K[, algorithm])	Fit the maxent model p whose feature expectations are given
`grad`([params, ignorepenalty])	Computes or estimates the gradient of the entropy dual.
`log`(params)	This method is called every iteration during the optimization process.
`lognormconst`()	Compute the log of the normalization constant (partition
`logparams`()	Saves the model parameters if logging has been
`logpmf`()	Returns an array indexed by integers representing the
`normconst`()	Returns the normalization constant, or partition function, for the current model.
`pmf`()	Returns an array indexed by integers representing the values of the probability mass function (pmf) at each point in the sample space under the current model (with the current parameter vector self.params).
`pmf_function`([f])	Returns the pmf p_theta(x) as a function taking values on the model's sample space.
`probdist`()	Returns an array indexed by integers representing the values of the probability mass function (pmf) at each point in the sample space under the current model (with the current parameter vector self.params).
`reset`([numfeatures])	Resets the parameters self.params to zero, clearing the cache variables dependent on them.
`setcallback`([callback, callback_dual, ...])	Sets callback functions to be called every iteration, every function evaluation, or every gradient evaluation.
`setfeaturesandsamplespace`(f, samplespace)	Creates a new matrix self.F of features f of all points in the
`setparams`(params)	Set the parameter vector to params, replacing the existing parameters.
`setsmooth`(sigma)	Speficies that the entropy dual and gradient should be computed with a quadratic penalty term on magnitude of the parameters.

model.beginlogging(filename[, freq])	Enable logging params for each fn evaluation to files named 'filename.freq.pickle', 'filename.(2*freq).pickle', ...
model.endlogging()	Stop logging param values whenever setparams() is called.
model.clearcache()	Clears the interim results of computations depending on the
model.crossentropy(fx[, log_prior_x, base])	Returns the cross entropy H(q, p) of the empirical
model.dual([params, ignorepenalty, ignoretest])	Computes the Lagrangian dual L(theta) of the entropy of the
model.fit(K[, algorithm])	Fit the maxent model p whose feature expectations are given
model.grad([params, ignorepenalty])	Computes or estimates the gradient of the entropy dual.
model.log(params)	This method is called every iteration during the optimization process.
model.logparams()	Saves the model parameters if logging has been
model.normconst()	Returns the normalization constant, or partition function, for the current model.
model.reset([numfeatures])	Resets the parameters self.params to zero, clearing the cache variables dependent on them.
model.setcallback([callback, callback_dual, ...])	Sets callback functions to be called every iteration, every function evaluation, or every gradient evaluation.
model.setparams(params)	Set the parameter vector to params, replacing the existing parameters.
model.setsmooth(sigma)	Speficies that the entropy dual and gradient should be computed with a quadratic penalty term on magnitude of the parameters.
model.expectations()	The vector E_p[f(X)] under the model p_params of the vector of
model.lognormconst()	Compute the log of the normalization constant (partition
model.logpmf()	Returns an array indexed by integers representing the
model.pmf_function([f])	Returns the pmf p_theta(x) as a function taking values on the model's sample space.
model.setfeaturesandsamplespace(f, samplespace)	Create a new matrix self.F of features f of all points in the

beginlogging (*filename, freq=10*)

Enable logging params for each fn evaluation to files named 'filename.freq.pickle', 'filename.(2*freq).pickle', ... each 'freq' iterations.

endlogging ()

Stop logging param values whenever setparams() is called.

clearcache ()

Clears the interim results of computations depending on the parameters and the sample.

crossentropy (*fx, log_prior_x=None, base=2.7182818284590451*)

Returns the cross entropy H(q, p) of the empirical distribution q of the data (with the given feature matrix fx) with respect to the model p. For discrete distributions this is defined as:

H(q, p) = - n^{-1} sum_{j=1}^n log p(x_j)

where x_j are the data elements assumed drawn from q whose features are given by the matrix fx = {f(x_j)}, j=1,...,n.

The 'base' argument specifies the base of the logarithm, which defaults to e.

For continuous distributions this makes no sense!

dual (*params=None, ignorepenalty=False, ignoretest=False*)

Computes the Lagrangian dual L(theta) of the entropy of the model, for the given vector theta=params. Minimizing this function (without constraints) should fit the maximum entropy model subject to the given constraints. These constraints are specified as the desired (target) values self.K for the expectations of the feature statistic.

This function is computed as:

L(theta) = log(Z) - theta^T . K

For 'bigmodel' objects, it estimates the entropy dual without actually computing p_theta. This is important if the sample space is continuous or innumerable in practice. We approximate the norm constant Z using importance sampling as in [Rosenfeld01whole]. This estimator is deterministic for any given sample. Note that the gradient of this estimator is equal to the importance sampling *ratio estimator* of the gradient of the entropy dual [see my thesis], justifying the use of this estimator in conjunction with grad() in optimization methods that use both the function and gradient. Note, however, that convergence guarantees break down for most optimization algorithms in the presence of stochastic error.

Note that, for 'bigmodel' objects, the dual estimate is deterministic for any given sample. It is given as:

L_est = log Z_est - sum_i{theta_i K_i}

where

Z_est = 1/m sum_{x in sample S_0} p_dot(x) / aux_dist(x),

and m = # observations in sample S_0, and K_i = the empirical expectation E_p_tilde f_i (X) = sum_x {p(x) f_i(x)}.

fit(*K, algorithm='CG'*)

Fit the maxent model p whose feature expectations are given by the vector K.

Model expectations are computed either exactly or using Monte Carlo simulation, depending on the 'func' and 'grad' parameters passed to this function.

For 'model' instances, expectations are computed exactly, by summing over the given sample space. If the sample space is continuous or too large to iterate over, use the 'bigmodel' class instead.

For 'bigmodel' instances, the model expectations are not computed exactly (by summing or integrating over a sample space) but approximately (by Monte Carlo simulation). Simulation is necessary when the sample space is too large to sum or integrate over in practice, like a continuous sample space in more than about 4 dimensions or a large discrete space like all possible sentences in a natural language.

Approximating the expectations by sampling requires an instrumental distribution that should be close to the model for fast convergence. The tails should be fatter than the model. This instrumental distribution is specified by calling setsampleFgen() with a user-supplied generator function that yields a matrix of features of a random sample and its log pdf values.

The algorithm can be 'CG', 'BFGS', 'LBFGSB', 'Powell', or 'Nelder-Mead'.

The CG (conjugate gradients) method is the default; it is quite fast and requires only linear space in the number of parameters, (not quadratic, like Newton-based methods).

The BFGS (Broyden-Fletcher-Goldfarb-Shanno) algorithm is a variable metric Newton method. It is perhaps faster than the CG method but requires O(N^2) instead of O(N) memory, so it is infeasible for more than about 10^3 parameters.

The Powell algorithm doesn't require gradients. For small models it is slow but robust. For big models (where func and grad are simulated) with large variance in the function estimates, this may be less robust than the gradient-based algorithms.

grad(*params=None, ignorepenalty=False*)

Computes or estimates the gradient of the entropy dual.

log(*params*)

This method is called every iteration during the optimization process. It calls the user-supplied callback function (if any), logs the evolution of the entropy dual and gradient norm, and checks whether the process appears to be diverging, which would indicate inconsistent constraints (or, for bigmodel instances, too large a variance in the estimates).

logparams()
Saves the model parameters if logging has been enabled and the # of iterations since the last save has reached self.paramslogfreq.

normconst()
Returns the normalization constant, or partition function, for the current model. Warning – this may be too large to represent; if so, this will result in numerical overflow. In this case use lognormconst() instead.

For 'bigmodel' instances, estimates the normalization term as Z = E_aux_dist [{exp (params.f(X))} / aux_dist(X)] using a sample from aux_dist.

reset(*numfeatures=None*)
Resets the parameters self.params to zero, clearing the cache variables dependent on them. Also resets the number of function and gradient evaluations to zero.

setcallback(*callback=None, callback_dual=None, callback_grad=None*)
Sets callback functions to be called every iteration, every function evaluation, or every gradient evaluation. All callback functions are passed one argument, the current model object.

Note that line search algorithms in e.g. CG make potentially several function and gradient evaluations per iteration, some of which we expect to be poor.

setparams(*params*)
Set the parameter vector to params, replacing the existing parameters. params must be a list or numpy array of the same length as the model's feature vector f.

setsmooth(*sigma*)
Speficies that the entropy dual and gradient should be computed with a quadratic penalty term on magnitude of the parameters. This 'smooths' the model to account for noise in the target expectation values or to improve robustness when using simulation to fit models and when the sampling distribution has high variance. The smoothing mechanism is described in Chen and Rosenfeld, 'A Gaussian prior for smoothing maximum entropy models' (1999).

The parameter 'sigma' will be squared and stored as self.sigma2.

expectations()
The vector E_p[f(X)] under the model p_params of the vector of feature functions f_i over the sample space.

lognormconst()
Compute the log of the normalization constant (partition function) Z=sum_{x in samplespace} p_0(x) exp(params . f(x)). The sample space must be discrete and finite.

logpmf()
Returns an array indexed by integers representing the logarithms of the probability mass function (pmf) at each point in the sample space under the current model (with the current parameter vector self.params).

pmf_function(*f=None*)
Returns the pmf p_theta(x) as a function taking values on the model's sample space. The returned pmf is defined as:

p_theta(x) = exp(theta.f(x) - log Z)

where theta is the current parameter vector self.params. The returned function p_theta also satisfies

all([p(x) for x in self.samplespace] == pmf()).

The feature statistic f should be a list of functions [f1(),...,fn(x)]. This must be passed unless the model already contains an equivalent attribute 'model.f'.

Requires that the sample space be discrete and finite, and stored as self.samplespace as a list or array.

setfeaturesandsamplespace(*f, samplespace*)

Creates a new matrix self.F of features f of all points in the sample space. f is a list of feature functions f_i mapping the sample space to real values. The parameter vector self.params is initialized to zero.

We also compute f(x) for each x in the sample space and store them as self.F. This uses lots of memory but is much faster.

This is only appropriate when the sample space is finite.

class bigmodel()

A maximum-entropy (exponential-form) model on a large sample space.

The model expectations are not computed exactly (by summing or integrating over a sample space) but approximately (by Monte Carlo estimation). Approximation is necessary when the sample space is too large to sum or integrate over in practice, like a continuous sample space in more than about 4 dimensions or a large discrete space like all possible sentences in a natural language.

Approximating the expectations by sampling requires an instrumental distribution that should be close to the model for fast convergence. The tails should be fatter than the model.

Methods

beginlogging(filename[, freq])	Enable logging params for each fn evaluation to files named 'filename.freq.pickle', 'filename.(2*freq).pickle', ...
clearcache()	Clears the interim results of computations depending on the
crossentropy(fx[, log_prior_x, base])	Returns the cross entropy H(q, p) of the empirical
dual([params, ignorepenalty, ignoretest])	Computes the Lagrangian dual L(theta) of the entropy of the
endlogging()	Stop logging param values whenever setparams() is called.
entropydual([params, ignorepenalty, ignoretest])	Computes the Lagrangian dual L(theta) of the entropy of the
estimate()	This function approximates both the feature expectation vector
expectations()	Estimates the feature expectations E_p[f(X)] under the current
fit(K[, algorithm])	Fit the maxent model p whose feature expectations are given
grad([params, ignorepenalty])	Computes or estimates the gradient of the entropy dual.
log(params)	This method is called every iteration during the optimization process.
lognormconst()	Estimate the normalization constant (partition function) using
logparams()	Saves the model parameters if logging has been
logpdf(fx[, log_prior_x])	Returns the log of the estimated density p(x) = p_theta(x) at the point x.
normconst()	Returns the normalization constant, or partition function, for the current model.
pdf(fx)	Returns the estimated density p_theta(x) at the point x with feature statistic fx = f(x).
pdf_function()	Returns the estimated density p_theta(x) as a function p(f) taking a vector f = f(x) of feature statistics at any point x.
resample()	(Re)samples the matrix F of sample features.
reset([numfeatures])	Resets the parameters self.params to zero, clearing the cache variables dependent on them.
setcallback([callback, callback_dual, ...])	Sets callback functions to be called every iteration, every function evaluation, or every gradient evaluation.
setparams(params)	Set the parameter vector to params, replacing the existing parameters.
setsampleFgen(sampler[, staticsample])	Initializes the Monte Carlo sampler to use the supplied
setsmooth(sigma)	Speficies that the entropy dual and gradient should be computed with a quadratic penalty term on magnitude of the parameters.
settestsamples(F_list, logprob_list[, ...])	Requests that the model be tested every 'testevery' iterations
stochapprox(K)	Tries to fit the model to the feature expectations K using
test()	Estimate the dual and gradient on the external samples, keeping track of the parameters that yield the minimum such dual.

bigmodel.estimate()	This function approximates both the feature expectation vector
bigmodel.logpdf(fx[, log_prior_x])	Returns the log of the estimated density p(x) = p_theta(x) at the point x.
bigmodel.pdf(fx)	Returns the estimated density p_theta(x) at the point x with feature statistic fx = f(x).
bigmodel.pdf_function()	Returns the estimated density p_theta(x) as a function p(f) taking a vector f = f(x) of feature statistics at any point x.
bigmodel.resample()	(Re)samples the matrix F of sample features.
bigmodel.setsampleFgen(sampler[, staticsample])	Initializes the Monte Carlo sampler to use the supplied
bigmodel.settestsamples(F_list, logprob_list)	Requests that the model be tested every 'testevery' iterations
bigmodel.stochapprox(K)	Tries to fit the model to the feature expectations K using
bigmodel.test()	Estimate the dual and gradient on the external samples, keeping track of the parameters that yield the minimum such dual.

estimate()

This function approximates both the feature expectation vector E_p f(X) and the log of the normalization term Z with importance sampling.

It also computes the sample variance of the component estimates of the feature expectations as: varE = var(E_1, ..., E_T) where T is self.matrixtrials and E_t is the estimate of E_p f(X) approximated using the 't'th auxiliary feature matrix.

It doesn't return anything, but stores the member variables logZapprox, mu and varE. (This is done because some optimization algorithms retrieve the dual fn and gradient fn in separate function calls, but we can compute them more efficiently together.)

It uses a supplied generator sampleFgen whose .next() method returns features of random observations s_j generated according to an auxiliary distribution aux_dist. It uses these either in a matrix (with multiple runs) or with a sequential procedure, with more updating overhead but potentially stopping earlier (needing fewer samples). In the matrix case, the features F={f_i(s_j)} and vector [log_aux_dist(s_j)] of log probabilities are generated by calling resample().

We use [Rosenfeld01Wholesentence]'s estimate of E_p[f_i] as:

{sum_j p(s_j)/aux_dist(s_j) f_i(s_j) }
/ {sum_j p(s_j) / aux_dist(s_j)}.

Note that this is consistent but biased.

This equals:

{sum_j p_dot(s_j)/aux_dist(s_j) f_i(s_j) }
/ {sum_j p_dot(s_j) / aux_dist(s_j)}

Compute the estimator E_p f_i(X) in log space as:
num_i / denom,

where

num_i = exp(logsumexp(theta.f(s_j) - log aux_dist(s_j)

- log f_i(s_j)))

and
denom = [n * Zapprox]

where Zapprox = exp(self.lognormconst()).

We can compute the denominator n*Zapprox directly as:

exp(logsumexp(log p_dot(s_j) - log aux_dist(s_j)))

= exp(logsumexp(theta.f(s_j) - log aux_dist(s_j)))

logpdf (*fx, log_prior_x=None*)

Returns the log of the estimated density p(x) = p_theta(x) at the point x. If log_prior_x is None, this is defined as:

log p(x) = theta.f(x) - log Z

where f(x) is given by the (m x 1) array fx.

If, instead, fx is a 2-d (m x n) array, this function interprets each of its rows j=0,...,n-1 as a feature vector f(x_j), and returns an array containing the log pdf value of each point x_j under the current model.

log Z is estimated using the sample provided with setsampleFgen().

The optional argument log_prior_x is the log of the prior density p_0 at the point x (or at each point x_j if fx is 2-dimensional). The log pdf of the model is then defined as

log p(x) = log p0(x) + theta.f(x) - log Z

and p then represents the model of minimum KL divergence D(p||p0) instead of maximum entropy.

pdf (*fx*)

Returns the estimated density p_theta(x) at the point x with feature statistic fx = f(x). This is defined as

p_theta(x) = exp(theta.f(x)) / Z(theta),

where Z is the estimated value self.normconst() of the partition function.

pdf_function ()

Returns the estimated density p_theta(x) as a function p(f) taking a vector f = f(x) of feature statistics at any point x. This is defined as:

p_theta(x) = exp(theta.f(x)) / Z

resample ()

(Re)samples the matrix F of sample features.

setsampleFgen (*sampler, staticsample=True*)

Initializes the Monte Carlo sampler to use the supplied generator of samples' features and log probabilities. This is an alternative to defining a sampler in terms of a (fixed size) feature matrix sampleF and accompanying vector samplelogprobs of log probabilities.

Calling sampler.next() should generate tuples (F, lp), where F is an (m x n) matrix of features of the n sample points x_1,...,x_n, and lp is an array of length n containing the (natural) log probability density (pdf or pmf) of each point under the auxiliary sampling distribution.

The output of sampler.next() can optionally be a 3-tuple (F, lp, sample) instead of a 2-tuple (F, lp). In this case the value 'sample' is then stored as a class variable self.sample. This is useful for inspecting the output and understanding the model characteristics.

If matrixtrials > 1 and staticsample = True, (which is useful for estimating variance between the different feature estimates), sampler.next() will be called once for each trial (0,...,matrixtrials) for each iteration. This allows using a set of feature matrices, each of which stays constant over all iterations.

We now insist that sampleFgen.next() return the entire sample feature matrix to be used each iteration to avoid overhead in extra function calls and memory copying (and extra code).

An alternative was to supply a list of samplers, sampler=[sampler0, sampler1, ..., sampler_{m-1}, samplerZ], one for each feature and one for estimating the normalization constant Z. But this code was unmaintained, and has now been removed (but it's in Ed's CVS repository :).

Example use: >>> import spmatrix >>> model = bigmodel() >>> def sampler(): ... n = 0 ... while True: ... f = spmatrix.ll_mat(1,3) ... f[0,0] = n+1; f[0,1] = n+1; f[0,2] = n+1 ... yield f, 1.0 ... n += 1 ... >>> model.setsampleFgen(sampler()) >>> type(model.sampleFgen) <type 'generator'> >>> [model.sampleF[0,i] for i in range(3)] [1.0, 1.0, 1.0]

We now set matrixtrials as a class property instead, rather than passing it as an argument to this function, where it can be written over (perhaps with the default function argument by accident) when we re-call this func (e.g. to change the matrix size.)

settestsamples(*F_list, logprob_list, testevery=1, priorlogprob_list=None*)

Requests that the model be tested every 'testevery' iterations during fitting using the provided list F_list of feature matrices, each representing a sample {x_j} from an auxiliary distribution q, together with the corresponding log probabiltiy mass or density values log {q(x_j)} in logprob_list. This is useful as an external check on the fitting process with sample path optimization, which could otherwise reflect the vagaries of the single sample being used for optimization, rather than the population as a whole.

If self.testevery > 1, only perform the test every self.testevery calls.

If priorlogprob_list is not None, it should be a list of arrays of log(p0(x_j)) values, j = 0,. ..., n - 1, specifying the prior distribution p0 for the sample points x_j for each of the test samples.

stochapprox(*K*)

Tries to fit the model to the feature expectations K using stochastic approximation, with the Robbins-Monro stochastic approximation algorithm: theta_{k+1} = theta_k + a_k g_k - a_k e_k where g_k is the gradient vector (= feature expectations E - K) evaluated at the point theta_k, a_k is the sequence a_k = a_0 / k, where a_0 is some step size parameter defined as self.a_0 in the model, and e_k is an unknown error term representing the uncertainty of the estimate of g_k. We assume e_k has nice enough properties for the algorithm to converge.

test()

Estimate the dual and gradient on the external samples, keeping track of the parameters that yield the minimum such dual. The vector of desired (target) feature expectations is stored as self.K.

class conditionalmodel(*F, counts, numcontexts*)

A conditional maximum-entropy (exponential-form) model p(x|w) on a discrete sample space. This is useful for classification problems: given the context w, what is the probability of each class x?

The form of such a model is

p(x | w) = exp(theta . f(w, x)) / Z(w; theta)

where Z(w; theta) is a normalization term equal to

Z(w; theta) = sum_x exp(theta . f(w, x)).

The sum is over all classes x in the set Y, which must be supplied to the constructor as the parameter 'samplespace'.

Such a model form arises from maximizing the entropy of a conditional model p(x | w) subject to the constraints:

K_i = E f_i(W, X)

where the expectation is with respect to the distribution

q(w) p(x | w)

where q(w) is the empirical probability mass function derived from observations of the context w in a training set. Normally the vector K = {K_i} of expectations is set equal to the expectation of f_i(w, x) with respect to the empirical distribution.

This method minimizes the Lagrangian dual L of the entropy, which is defined for conditional models as

L(theta) = sum_w q(w) log Z(w; theta)

- sum_{w,x} q(w,x) [theta . f(w,x)]

Note that both sums are only over the training set {w,x}, not the entire sample space, since q(w,x) = 0 for all w,x not in the training set.

The partial derivatives of L are:
dL / dtheta_i = K_i - E f_i(X, Y)

where the expectation is as defined above.

Methods

beginlogging(filename[, freq])	Enable logging params for each fn evaluation to files named 'filename.freq.pickle', 'filename.(2*freq).pickle', ...
clearcache()	Clears the interim results of computations depending on the
crossentropy(fx[, log_prior_x, base])	Returns the cross entropy H(q, p) of the empirical
dual([params, ignorepenalty])	The entropy dual function is defined for conditional models as
endlogging()	Stop logging param values whenever setparams() is called.
entropydual([params, ignorepenalty, ignoretest])	Computes the Lagrangian dual L(theta) of the entropy of the
expectations()	The vector of expectations of the features with respect to the
fit([algorithm])	Fits the conditional maximum entropy model subject to the
grad([params, ignorepenalty])	Computes or estimates the gradient of the entropy dual.
log(params)	This method is called every iteration during the optimization process.
lognormconst()	Compute the elementwise log of the normalization constant
logparams()	Saves the model parameters if logging has been
logpmf()	Returns a (sparse) row vector of logarithms of the conditional probability mass function (pmf) values p(x | c) for all pairs (c, x), where c are contexts and x are points in the sample space.
normconst()	Returns the normalization constant, or partition function, for the current model.
pmf()	Returns an array indexed by integers representing the values of the probability mass function (pmf) at each point in the sample space under the current model (with the current parameter vector self.params).
pmf_function([f])	Returns the pmf p_theta(x) as a function taking values on the model's sample space.
probdist()	Returns an array indexed by integers representing the values of the probability mass function (pmf) at each point in the sample space under the current model (with the current parameter vector self.params).
reset([numfeatures])	Resets the parameters self.params to zero, clearing the cache variables dependent on them.
setcallback([callback, callback_dual, ...])	Sets callback functions to be called every iteration, every function evaluation, or every gradient evaluation.
setfeaturesandsamplespace(f, samplespace)	Creates a new matrix self.F of features f of all points in the
setparams(params)	Set the parameter vector to params, replacing the existing parameters.
setsmooth(sigma)	Speficies that the entropy dual and gradient should be computed with a quadratic penalty term on magnitude of the parameters.

conditionalmodel.dual([params, ignorepenalty])	The entropy dual function is defined for conditional models as
conditionalmodel.expectations()	The vector of expectations of the features with respect to the
conditionalmodel.fit([algorithm])	Fits the conditional maximum entropy model subject to the
conditionalmodel.lognormconst()	Compute the elementwise log of the normalization constant
conditionalmodel.logpmf()	Returns a (sparse) row vector of logarithms of the conditional probability mass function (pmf) values p(x | c) for all pairs (c, x), where c are contexts and x are points in the sample space.

dual (*params=None, ignorepenalty=False*)

The entropy dual function is defined for conditional models as

L(theta) = sum_w q(w) log Z(w; theta)

- sum_{w,x} q(w,x) [theta . f(w,x)]

or equivalently as

L(theta) = sum_w q(w) log Z(w; theta) - (theta . k)

where K_i = sum_{w, x} q(w, x) f_i(w, x), and where q(w) is the empirical probability mass function derived from observations of the context w in a training set. Normally q(w, x) will be 1, unless the same class label is assigned to the same context more than once.

Note that both sums are only over the training set {w,x}, not the entire sample space, since q(w,x) = 0 for all w,x not in the training set.

The entropy dual function is proportional to the negative log likelihood.

Compare to the entropy dual of an unconditional model:

L(theta) = log(Z) - theta^T . K

expectations ()

The vector of expectations of the features with respect to the distribution p_tilde(w) p(x | w), where p_tilde(w) is the empirical probability mass function value stored as self.p_tilde_context[w].

fit (*algorithm='CG'*)

Fits the conditional maximum entropy model subject to the constraints

sum_{w, x} p_tilde(w) p(x | w) f_i(w, x) = k_i

for i=1,...,m, where k_i is the empirical expectation

k_i = sum_{w, x} p_tilde(w, x) f_i(w, x).

lognormconst ()

Compute the elementwise log of the normalization constant (partition function) Z(w)=sum_{y in Y(w)} exp(theta . f(w, y)). The sample space must be discrete and finite. This is a vector with one element for each context w.

logpmf ()

Returns a (sparse) row vector of logarithms of the conditional probability mass function (pmf) values p(x | c) for all pairs (c, x), where c are contexts and x are points in the sample space. The order of these is log p(x | c) = logpmf()[c * numsamplepoints + x].

3.8.3 Utilities

arrayexp(x)	Returns the elementwise antilog of the real array x.
arrayexpcomplex(x)	Returns the elementwise antilog of the vector x.
columnmeans(A)	This is a wrapper for general dense or sparse dot products.
columnvariances(A)	This is a wrapper for general dense or sparse dot products.
densefeaturematrix(f, sample)	Returns an (m x n) dense array of non-zero evaluations of the
densefeatures(f, x)	Returns a dense array of non-zero evaluations of the functions fi
dotprod(u, v)	This is a wrapper around general dense or sparse dot products.
flatten(a)	Flattens the sparse matrix or dense array/matrix 'a' into a
innerprod(A, v)	This is a wrapper around general dense or sparse dot products.
innerprodtranspose(A, v)	This is a wrapper around general dense or sparse dot products.
logsumexp(a)	Compute the log of the sum of exponentials log(e^{a_1}+...e^{a_n})
logsumexp_naive(values)	For testing logsumexp().
robustlog(x)	Returns log(x) if x > 0, the complex log cmath.log(x) if x < 0,
rowmeans(A)	This is a wrapper for general dense or sparse dot products.
sample_wr(population, k)	Chooses k random elements (with replacement) from a population.
sparsefeaturematrix(F, sample[, format])	Returns an (m x n) sparse matrix of non-zero evaluations of the scalar or vector functions f_1,...,f_m in the list f at the points x_1,...,x_n in the sequence 'sample'.
sparsefeatures(f, x[, format])	Returns an Mx1 sparse matrix of non-zero evaluations of the

arrayexp(*x*)

Returns the elementwise antilog of the real array x. We try to exponentiate with numpy.exp() and, if that fails, with python's math.exp(). numpy.exp() is about 10 times faster but throws an OverflowError exception for numerical underflow (e.g. exp(-800), whereas python's math.exp() just returns zero, which is much more helpful.

arrayexpcomplex(*x*)

Returns the elementwise antilog of the vector x. We try to exponentiate with numpy.exp() and, if that fails, with python's math.exp(). numpy.exp() is about 10 times faster but throws an OverflowError exception for numerical underflow (e.g. exp(-800), whereas python's math.exp() just returns zero, which is much more helpful.

columnmeans(*A*)

This is a wrapper for general dense or sparse dot products. It is only necessary as a common interface for supporting ndarray, scipy spmatrix, and PySparse arrays.

Returns a dense (1 x n) vector with the column averages of A, which can be an (m x n) sparse or dense matrix.

```
>>> a = numpy.array([[1,2],[3,4]],'d')
>>> columnmeans(a)
array([ 2.,  3.])
```

columnvariances(*A*)

This is a wrapper for general dense or sparse dot products. It is not necessary except as a common interface for supporting ndarray, scipy spmatrix, and PySparse arrays.

Returns a dense (1 x n) vector with unbiased estimators for the column variances for each column of the (m x n) sparse or dense matrix A. (The normalization is by (m - 1).)

```
>>> a = numpy.array([[1,2], [3,4]], 'd')
>>> columnvariances(a)
array([ 2.,  2.])
```

densefeaturematrix (*f, sample*)
Returns an (m x n) dense array of non-zero evaluations of the scalar functions fi in the list f at the points x_1,...,x_n in the list sample.

densefeatures (*f, x*)
Returns a dense array of non-zero evaluations of the functions fi in the list f at the point x.

dotprod (*u, v*)
This is a wrapper around general dense or sparse dot products. It is not necessary except as a common interface for supporting ndarray, scipy spmatrix, and PySparse arrays.

Returns the dot product of the (1 x m) sparse array u with the (m x 1) (dense) numpy array v.

flatten (*a*)
Flattens the sparse matrix or dense array/matrix 'a' into a 1-dimensional array

innerprod (*A, v*)
This is a wrapper around general dense or sparse dot products. It is not necessary except as a common interface for supporting ndarray, scipy spmatrix, and PySparse arrays.

Returns the inner product of the (m x n) dense or sparse matrix A with the n-element dense array v. This is a wrapper for A.dot(v) for dense arrays and spmatrix objects, and for A.matvec(v, result) for PySparse matrices.

innerprodtranspose (*A, v*)
This is a wrapper around general dense or sparse dot products. It is not necessary except as a common interface for supporting ndarray, scipy spmatrix, and PySparse arrays.

Computes A^T V, where A is a dense or sparse matrix and V is a numpy array. If A is sparse, V must be a rank-1 array, not a matrix. This function is efficient for large matrices A. This is a wrapper for u.T.dot(v) for dense arrays and spmatrix objects, and for u.matvec_transp(v, result) for pysparse matrices.

logsumexp (*a*)
Compute the log of the sum of exponentials log(e^{a_1}+...e^{a_n}) of the components of the array a, avoiding numerical overflow.

logsumexp_naive (*values*)
For testing logsumexp(). Subject to numerical overflow for large values (e.g. 720).

robustlog (*x*)
Returns log(x) if x > 0, the complex log cmath.log(x) if x < 0, or float('-inf') if x == 0.

rowmeans (*A*)
This is a wrapper for general dense or sparse dot products. It is only necessary as a common interface for supporting ndarray, scipy spmatrix, and PySparse arrays.

Returns a dense (m x 1) vector representing the mean of the rows of A, which be an (m x n) sparse or dense matrix.

```
>>> a = numpy.array([[1,2],[3,4]], float)
>>> rowmeans(a)
array([ 1.5,  3.5])
```

sample_wr (*population, k*)
Chooses k random elements (with replacement) from a population. (From the Python Cookbook).

sparsefeaturematrix (*f, sample, format='csc_matrix'*)
Returns an (m x n) sparse matrix of non-zero evaluations of the scalar or vector functions f_1,...,f_m in the list f at the points x_1,...,x_n in the sequence 'sample'.

If format='ll_mat', the PySparse module (or a symlink to it) must be available in the Python site-packages/ directory. A trimmed-down version, patched for NumPy compatibility, is available in the SciPy sandbox/pysparse directory.

sparsefeatures (*f, x, format='csc_matrix'*)
Returns an Mx1 sparse matrix of non-zero evaluations of the scalar functions f_1,...,f_m in the list f at the point x.

If format='ll_mat', the PySparse module (or a symlink to it) must be available in the Python site-packages/ directory. A trimmed-down version, patched for NumPy compatibility, is available in the SciPy sandbox/pysparse directory.

3.9 Miscellaneous routines (scipy.misc)

Warning: This documentation is work-in-progress and unorganized.

Various utilities that don't have another home.

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

```
>>> 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.whos(d)
Name            Shape            Bytes            Type
===========================================================
y               3                24               float64
x               2                16               float64
Upper bound on total bytes  =       40
```

source (*object, output=<open file '<stdout>', mode 'w' at 0x2aaaaaac9198>*)
Print or write to a file the source code for a Numpy object.

The source code is only returned for objects written in Python. Many functions and classes are defined in C and will therefore not return useful information.

Parameters

object : numpy object

Input object. This can be any object (function, class, module, ...).

output : file object, optional

If *output* not supplied then source code is printed to screen (sys.stdout). File object must be created with either write 'w' or append 'a' modes.

See Also:

`lookfor`, `info`

Examples

```
>>> np.source(np.interp)
In file: /usr/lib/python2.6/dist-packages/numpy/lib/function_base.py
def interp(x, xp, fp, left=None, right=None):
    """.... (full docstring printed)"""
    if isinstance(x, (float, int, number)):
        return compiled_interp([x], xp, fp, left, right).item()
    else:
        return compiled_interp(x, xp, fp, left, right)
```

The source code is only returned for objects written in Python.

```
>>> np.source(np.array)
Not available for this object.
```

info(*object=None, maxwidth=76, output=<open file '<stdout>', mode 'w' at 0x2aaaaaac9198>, 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. ***
```

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

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.

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, the pal keyword, and the mode keyword.

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

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.

if the

The numpy array must be either 2 dimensional or 3 dimensional.

imsave(*name, arr*)
Save an array to an image file.

imread(*name, flatten=0*)
Read an image file from a filename.

Optional arguments:

•flatten (0): if true, the image is flattened by calling convert('F') on

the resulting image object. This flattens the color layers into a single grayscale layer.

imrotate(*arr, angle, interp='bilinear'*)
Rotate an image counter-clockwise by angle degrees.

Interpolation methods can be:
'nearest' : for nearest neighbor 'bilinear' : for bilinear 'cubic' or 'bicubic' : for bicubic

imresize(*arr, size*)
Resize an image.

If size is an integer it is a percentage of current size. If size is a float it is a fraction of current size. If size is a tuple it is the size of the output image.

imshow(*arr*)
Simple showing of an image through an external viewer.

imfilter(*arr, ftype*)
Simple filtering of an image.

type can be:
'blur', 'contour', 'detail', 'edge_enhance', 'edge_enhance_more', 'emboss', 'find_edges', 'smooth', 'smooth_more', 'sharpen'

factorial(*n, exact=0*)
n! = special.gamma(n+1)

If exact==0, then floating point precision is used, otherwise exact long integer is computed.

Notes:

- Array argument accepted only for exact=0 case.
- If n<0, the return value is 0.

factorial2(*n, exact=False*)
Double factorial.

This is the factorial with every second value is skipped, i.e., `7!!  = 7 * 5 * 3 * 1`. It can be approximated numerically as:

```
n!! = special.gamma(n/2+1)*2**((m+1)/2)/sqrt(pi)  n odd
    = 2**(n/2) * (n/2)!                           n even
```

Parameters
n : int, 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*.

References

[R39]

factorialk (*n, k, exact=1*)
n(!!...!) = multifactorial of order k k times

comb (*N, k, exact=0*)
Combinations of N things taken k at a time.

If exact==0, then floating point precision is used, otherwise exact long integer is computed.

Notes:

- Array arguments accepted only for exact=0 case.
- If k > N, N < 0, or k < 0, then a 0 is returned.

central_diff_weights (*Np, ndiv=1*)
Return weights for an Np-point central derivative of order ndiv assuming equally-spaced function points.

If weights are in the vector w, then derivative is w[0] * f(x-ho*dx) + ... + w[-1] * f(x+h0*dx)

Can be inaccurate for large number of points.

derivative (*func, x0, dx=1.0, n=1, args=(), order=3*)
Given a function, use a central difference formula with spacing dx to compute the nth derivative at x0.

order is the number of points to use and must be odd.

Warning: Decreasing the step size too small can result in round-off error.

pade (*an, m*)
Given Taylor series coefficients in an, return a Pade approximation to the function as the ratio of two polynomials p / q where the order of q is m.

3.10 Multi-dimensional image processing (scipy.ndimage)

Functions for multi-dimensional image processing.

3.10.1 Filters `scipy.ndimage.filters`

convolve(input, weights[, output, mode, ...])	Multi-dimensional convolution.
convolve1d(input, weights[, axis, output, ...])	Calculate a one-dimensional convolution along the given axis.
correlate(input, weights[, output, mode, ...])	Multi-dimensional correlation.
correlate1d(input, weights[, axis, output, ...])	Calculate a one-dimensional correlation along the given axis.
gaussian_filter(input, sigma[, order, ...])	Multi-dimensional Gaussian filter.
gaussian_filter1d(input, sigma[, axis, ...])	One-dimensional Gaussian filter.
gaussian_gradient_magnitude(input, sigma[, ...])	Calculate a multidimensional gradient magnitude using gaussian derivatives.
gaussian_laplace(input, sigma[, output, ...])	Calculate a multidimensional laplace filter using gaussian second derivatives.
generic_filter(input, function[, size, ...])	Calculates a multi-dimensional filter using the given function.
generic_filter1d(input, function, filter_size)	Calculate a one-dimensional filter along the given axis.
generic_gradient_magnitude(input, derivative)	Calculate a gradient magnitude using the provided function for the gradient.
generic_laplace(input, derivative2[, ...])	Calculate a multidimensional laplace filter using the provided second derivative function.
laplace(input[, output, mode, cval])	Calculate a multidimensional laplace filter using an estimation for the second derivative based on differences.
maximum_filter(input[, size, footprint, ...])	Calculates a multi-dimensional maximum filter.
maximum_filter1d(input, size[, axis, ...])	Calculate a one-dimensional maximum filter along the given axis.
median_filter(input[, size, footprint, ...])	Calculates a multi-dimensional median filter.
minimum_filter(input[, size, footprint, ...])	Calculates a multi-dimensional minimum filter.
minimum_filter1d(input, size[, axis, ...])	Calculate a one-dimensional minimum filter along the given axis.
percentile_filter(input, percentile[, size, ...])	Calculates a multi-dimensional percentile filter.
prewitt(input[, axis, output, mode, cval])	Calculate a Prewitt filter.
rank_filter(input, rank[, size, footprint, ...])	Calculates a multi-dimensional rank filter.
sobel(input[, axis, output, mode, cval])	Calculate a Sobel filter.
uniform_filter(input[, size, output, mode, ...])	Multi-dimensional uniform filter.
uniform_filter1d(input, size[, axis, ...])	Calculate a one-dimensional uniform filter along the given axis.

convolve(*input, weights, output=None, mode='reflect', cval=0.0, origin=0*)

Multi-dimensional convolution.

The array is convolved 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

See Also:

correlate
Correlate an image with a kernel.

convolve1d(*input, weights, axis=-1, output=None, mode='reflect', cval=0.0, origin=0*)
Calculate a one-dimensional convolution along the given axis.

The lines of the array along the given axis are convolved with the given weights.

Parameters

input : array-like

input array to filter

weights : ndarray

one-dimensional sequence of numbers

axis : integer, optional

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 :

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

See Also:

convolve
Convolve an image with a kernel.

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 : integer, optional

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 :

gaussian_filter(*input, sigma, order=0, output=None, mode='reflect', cval=0.0*)
Multi-dimensional 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

Notes

The multi-dimensional 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.

gaussian_filter1d(*input, sigma, axis=-1, order=0, output=None, mode='reflect', cval=0.0*)
One-dimensional Gaussian filter.

Parameters
input : array-like

input array to filter

sigma : scalar

standard deviation for Gaussian kernel

axis : integer, optional

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

gaussian_gradient_magnitude(*input, sigma, output=None, mode='reflect', cval=0.0*)

Calculate a 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

gaussian_laplace(*input, sigma, output=None, mode='reflect', cval=0.0*)

Calculate a 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

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 :

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

generic_filter1d(*input, function, filter_size, axis=-1, output=None, mode='reflect', cval=0.0, origin=0, extra_arguments=(), extra_keywords=None*)

Calculate a one-dimensional filter along the given axis.

generic_filter1d iterates over the lines of the array, calling the given function at each line. The arguments of the line are the input line, and the output line. The input and output lines are 1D double arrays. The input line is extended appropriately according to the filter size and origin. The output line must be modified in-place with the result.

Parameters

input : array-like

input array to filter

function : callable

function to apply along given axis

filter_size : scalar

length of the filter

axis : integer, optional

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 :

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

generic_gradient_magnitude(*input, derivative, output=None, mode='reflect', cval=0.0, extra_arguments=(), extra_keywords=None*)

Calculate a gradient magnitude using the provided function for the gradient.

Parameters

input : array-like

input array to filter

derivative : callable

Callable with the following signature::

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

generic_laplace(*input, derivative2, output=None, mode='reflect', cval=0.0, extra_arguments=(), extra_keywords=None*)

Calculate a multidimensional laplace filter using the provided second derivative function.

Parameters

input : array-like

input array to filter

derivative2 : callable

Callable with the following signature::

derivative2(input, axis, output, mode, cval,
*extra_arguments, **extra_keywords)

See `extra_arguments`, `extra_keywords` below

output : array, 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

laplace(*input, output=None, mode='reflect', cval=0.0*)

Calculate a multidimensional laplace filter using an estimation for the second derivative based on differences.

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

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 :

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 1D maximum

axis : integer, optional

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 :

median_filter(*input, size=None, footprint=None, output=None, mode='reflect', cval=0.0, origin=0*)
Calculates a multi-dimensional 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

minimum_filter(*input, size=None, footprint=None, output=None, mode='reflect', cval=0.0, origin=0*)
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 :

minimum_filter1d(*input, size, axis=-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 : integer, optional

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 :

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 :

prewitt(*input, axis=-1, output=None, mode='reflect', cval=0.0*)
Calculate a Prewitt filter.

Parameters

input : array-like

input array to filter

axis : integer, optional

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

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 : integer

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 :

sobel(*input, axis=-1, output=None, mode='reflect', cval=0.0*)

Calculate a Sobel filter.

Parameters

input : array-like

input array to filter

axis : integer, optional

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

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

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 :

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.

uniform_filter1d(*input, size, axis=-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 : integer

length of uniform filter

axis : integer, optional

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 :

3.10.2 Fourier filters `scipy.ndimage.fourier`

`fourier_ellipsoid`(input, size[, n, axis, output])	Multi-dimensional ellipsoid fourier filter.
`fourier_gaussian`(input, sigma[, n, axis, output])	Multi-dimensional Gaussian fourier filter.
`fourier_shift`(input, shift[, n, axis, output])	Multi-dimensional fourier shift filter.
`fourier_uniform`(input, size[, n, axis, output])	Multi-dimensional Uniform fourier filter.

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. If the parameter n is negative, then the input is assumed to be the result of a complex fft. If n is larger or equal to zero, the input is assumed to be the result of a real fft, and n gives the length of the of the array before transformation along the the real transform direction. The axis of the real transform is given by the axis parameter. This function is implemented for arrays of rank 1, 2, or 3.

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. If the parameter n is negative, then the input is assumed to be the result of a complex fft. If n is larger or equal to zero, the input is assumed to be the result of a real fft, and n gives the length of the of the array before transformation along the the real transform direction. The axis of the real transform is given by the axis parameter.

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 If the parameter n is negative, then the input is assumed to be the result of a complex fft. If n is larger or equal to zero, the input is assumed to be the result of a real fft, and n gives the length of the of the array before transformation along the the real transform direction. The axis of the real transform is given by the axis parameter.

fourier_uniform(*input, size, n=-1, axis=-1, output=None*)
Multi-dimensional Uniform fourier filter.

The array is multiplied with the fourier transform of a box of given sizes. If the parameter n is negative, then the input is assumed to be the result of a complex fft. If n is larger or equal to zero, the input is assumed to be the result of a real fft, and n gives the length of the of the array before transformation along the the real transform direction. The axis of the real transform is given by the axis parameter.

3.10.3 Interpolation `scipy.ndimage.interpolation`

affine_transform(input, matrix[, offset, ...])	Apply an affine transformation.
geometric_transform(input, mapping[, ...])	Apply an arbritrary 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_type, output, ...])	Shift an array.
spline_filter(input[, order, output, ...])	Multi-dimensional spline filter.
spline_filter1d(input[, order, axis, ...])	Calculates a one-dimensional spline filter along the given axis.
zoom(input, zoom[, output_type, output, ...])	Zoom an array.

affine_transform(*input, matrix, offset=0.0, output_shape=None, output_type=None, output=None, order=3, mode='constant', cval=0.0, prefilter=True*)
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. The output shape can optionally be given. If not given it is equal to the input shape. The parameter prefilter determines if the input is pre-filtered before interpolation, if False it is assumed that the input is already filtered.

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.

geometric_transform(*input, mapping, output_shape=None, output_type=None, output=None, order=3, mode='constant', cval=0.0, prefilter=True, extra_arguments=(), extra_keywords={}*)

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.

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. Points outside the boundaries of the input are filled according to the given mode ('constant', 'nearest', 'reflect' or 'wrap'). The output shape can optionally be given. If not given, it is equal to the input shape. The parameter prefilter determines if the input is pre-filtered before interpolation (necessary for spline interpolation of order > 1). If False it is assumed that the input is already filtered. The extra_arguments and extra_keywords arguments can be used to provide extra arguments and keywords that are passed to the mapping function at each call.

map_coordinates(*input, coordinates, output_type=None, output=None, order=3, mode='constant', cval=0.0, prefilter=True*)

Map the input array to new coordinates by interpolation.

The array of coordinates is used to find, for each point in the output, the corresponding coordinates in the input. The value of the input at those coordinates is determined by spline interpolation of the requested order.

The shape of the output is derived from that of the coordinate array by dropping the first axis. The values of the array along the first axis are the coordinates in the input array at which the output value is found.

Parameters

input : ndarray

The input array

coordinates : array_like

The coordinates at which *input* is evaluated.

output_type : deprecated

Use *output* instead.

output : dtype, optional

If the output has to have a certain type, specify the dtype. The default behavior is for the output to have the same type as *input*.

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.

Returns

return_value : 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

```
>>> import scipy.ndimage
>>> a = np.arange(12.).reshape((4,3))
>>> print a
array([[  0.,   1.,   2.],
       [  3.,   4.,   5.],
       [  6.,   7.,   8.],
       [  9.,  10.,  11.]])
>>> sp.ndimage.map_coordinates(a, [[0.5, 2], [0.5, 1]], order=1)
[ 2.  7.]
```

Above, the interpolated value of a[0.5, 0.5] gives output[0], while a[2, 1] is output[1].

```
>>> inds = np.array([[0.5, 2], [0.5, 4]])
>>> sp.ndimage.map_coordinates(a, inds, order=1, cval=-33.3)
array([  2. , -33.3])
>>> sp.ndimage.map_coordinates(a, inds, order=1, mode='nearest')
array([ 2.,  8.])
>>> sp.ndimage.map_coordinates(a, inds, order=1, cval=0, output=bool)
array([ True, False], dtype=bool
```

rotate(*input, angle, axes=(1, 0), reshape=True, output_type=None, output=None, order=3, mode='constant', cval=0.0, prefilter=True*)

Rotate an array.

The array is rotated in the plane defined by the two axes given by the axes parameter using spline interpolation of the requested order. The angle is given in degrees. Points outside the boundaries of the input are filled according to the given mode. If reshape is true, the output shape is adapted so that the input array is contained completely in the output. The parameter prefilter determines if the input is pre- filtered before interpolation, if False it is assumed that the input is already filtered.

shift(*input, shift, output_type=None, 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. The parameter prefilter determines if the input is pre-filtered before interpolation, if False it is assumed that the input is already filtered.

spline_filter(*input, order=3, output=<type 'numpy.float64'>, output_type=None*)

Multi-dimensional spline filter.

Note: 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.

spline_filter1d(*input, order=3, axis=-1, output=<type 'numpy.float64'>, output_type=None*)

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.

zoom(*input, zoom, output_type=None, 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. Points outside the boundaries of the input are filled according to the given mode. The parameter prefilter determines if the input is pre- filtered before interpolation, if False it is assumed that the input is already filtered.

3.10.4 Measurements `scipy.ndimage.measurements`

center_of_mass(input[, labels, index])	Calculate the center of mass of of the array.
extrema(input[, labels, index])	Calculate the minimum, the maximum and their positions of the values of the array.
find_objects(input[, max_label])	Find objects in a labeled array.
histogram(input, min, max, bins[, labels, index])	Calculate a histogram of of the array.
label(input[, structure, output])	Label features in an array.
maximum(input[, labels, index])	Return the maximum input value.
maximum_position(input[, labels, index])	Find the position of the maximum of the values of the array.
mean(input[, labels, index])	Calculate the mean of the values of the array.
minimum(input[, labels, index])	Calculate the minimum of the values of the array.
minimum_position(input[, labels, index])	Find the position of the minimum of the values of the array.
standard_deviation(input[, labels, index])	Calculate the standard deviation of the values of the array.
sum(input[, labels, index])	Calculate the sum of the values of the array.
variance(input[, labels, index])	Calculate the variance of the values of the array.
watershed_ift(input, markers[, structure, ...])	Apply watershed from markers using a iterative forest transform algorithm.

center_of_mass(*input, labels=None, index=None*)
Calculate the center of mass of of the array.

The index parameter is a single label number or a sequence of label numbers of the objects to be measured. If index is None, all values are used where labels is larger than zero.

extrema(*input, labels=None, index=None*)

Calculate the minimum, the maximum and their positions of the
values of the array.

The index parameter is a single label number or a sequence of label numbers of the objects to be measured. If index is None, all values are used where labels is larger than zero.

find_objects(*input, max_label=0*)
Find objects in a labeled array.

The input must be an array with labeled objects. A list of slices into the array is returned that contain the objects. The list represents a sequence of the numbered objects. If a number is missing, None is returned instead of a slice. If max_label > 0, it gives the largest object number that is searched for, otherwise all are returned.

histogram(*input, min, max, bins, labels=None, index=None*)
Calculate a histogram of of the array.

The histogram is defined by its minimum and maximum value and the number of bins.

The index parameter is a single label number or a sequence of label numbers of the objects to be measured. If index is None, all values are used where labels is larger than zero.

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 2D *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

Returns

labeled_array : array_like

An array-like object where each unique feature has a unique value

num_features : int

If 'output' is None or a data type, this function returns a tuple, :

('labeled_array', 'num_features'). :

If 'output' is an array, 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:

```
>>> a = 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]])
>>> labeled_array, num_features = label(a)
```

Each of the 4 features are labeled with a different integer:

```
>>> print num_features
4
>>> print labeled_array
array([[0, 0, 1, 1, 0, 0],
       [0, 0, 0, 1, 0, 0],
       [2, 2, 0, 0, 3, 0],
       [0, 0, 0, 4, 0, 0]])
```

Generate a structuring element that will consider features connected even if they touch diagonally:

```
>>> s = generate_binary_structure(2,2)
```

or,

```
>>> s = [[1,1,1],
         [1,1,1],
         [1,1,1]]
```

Label the image using the new structuring element:

```
>>> 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):

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

maximum(*input, labels=None, index=None*)
Return the maximum input value.

The index parameter is a single label number or a sequence of label numbers of the objects to be measured. If index is None, all values are used where labels is larger than zero.

maximum_position(*input, labels=None, index=None*)
Find the position of the maximum of the values of the array.

The index parameter is a single label number or a sequence of label numbers of the objects to be measured. If index is None, all values are used where labels is larger than zero.

mean(*input, labels=None, index=None*)
Calculate the mean of the values of the array.

The index parameter is a single label number or a sequence of label numbers of the objects to be measured. If index is None, all values are used where labels is larger than zero.

minimum(*input, labels=None, index=None*)
Calculate the minimum of the values of the array.

The index parameter is a single label number or a sequence of label numbers of the objects to be measured. If index is None, all values are used where labels is larger than zero.

minimum_position(*input, labels=None, index=None*)
Find the position of the minimum of the values of the array.

The index parameter is a single label number or a sequence of label numbers of the objects to be measured. If index is None, all values are used where labels is larger than zero.

standard_deviation(*input, labels=None, index=None*)
Calculate the standard deviation of the values of the array.

The index parameter is a single label number or a sequence of label numbers of the objects to be measured. If index is None, all values are used where labels is larger than zero.

sum(*input, labels=None, index=None*)
Calculate the sum of the values of the array.

Parameters

labels
[array of integers, same shape as input] Assign labels to the values of the array.

index
[scalar or array] A single label number or a sequence of label numbers of the objects to be measured. If index is None, all values are used where 'labels' is larger than zero.

Examples

```
>>> input =  [0,1,2,3]
>>> labels = [1,1,2,2]
>>> sum(input, labels, index=[1,2])
[1.0, 5.0]
```

variance(*input, labels=None, index=None*)
Calculate the variance of the values of the array.

The index parameter is a single label number or a sequence of label numbers of the objects to be measured. If index is None, all values are used where labels is larger than zero.

watershed_ift(*input, markers, structure=None, output=None*)
Apply watershed from markers using a iterative forest transform algorithm.

Negative markers are considered background markers which are processed after the other markers. A structuring element defining the connectivity of the object can be provided. If none is provided an element is generated iwth a squared connecitiviy equal to one. An output array can optionally be provided.

3.10.5 Morphology scipy.ndimage.morphology

binary_closing(input[, structure, ...])	Multi-dimensional binary closing with the given structure.
binary_dilation(input[, structure, ...])	Multi-dimensional binary dilation with the given structure.
binary_erosion(input[, structure, ...])	Multi-dimensional binary erosion with the given structure.
binary_fill_holes(input[, structure, ...])	Fill the holes in binary objects.
binary_hit_or_miss(input[, structure1, ...])	Multi-dimensional binary hit-or-miss transform.
binary_opening(input[, structure, ...])	Multi-dimensional binary opening with the given structure.
binary_propagation(input[, structure, mask, ...])	Multi-dimensional binary propagation with the given structure.
black_tophat(input[, size, footprint, ...])	Multi-dimensional black tophat filter.
distance_transform_bf(input[, metric, ...])	Distance transform function by a brute force algorithm.
distance_transform_cdt(input[, metric, ...])	Distance transform for chamfer type of transforms.
distance_transform_edt(input[, sampling, ...])	Exact euclidean distance transform.
generate_binary_structure(rank, connectivity)	Generate a binary structure for binary morphological operations.
grey_closing(input[, size, footprint, ...])	Multi-dimensional grey valued closing.
grey_dilation(input[, size, footprint, ...])	Calculate a grey values dilation.
grey_erosion(input[, size, footprint, ...])	Calculate a grey values erosion.
grey_opening(input[, size, footprint, ...])	Multi-dimensional grey valued opening.
iterate_structure(structure, iterations[, ...])	Iterate a structure by dilating it with itself.
morphological_gradient(input[, size, ...])	Multi-dimensional morphological gradient.
morphological_laplace(input[, size, ...])	Multi-dimensional morphological laplace.
white_tophat(input[, size, footprint, ...])	Multi-dimensional white tophat filter.

binary_closing(*input, structure=None, iterations=1, output=None, origin=0*)
Multi-dimensional binary closing with the given structure.

An output array can optionally be provided. The origin parameter controls the placement of the filter. If no structuring element is provided an element is generated with a squared connectivity equal to one. The iterations parameter gives the number of times the dilations and then the erosions are done.

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 structure.

An output array can optionally be provided. The origin parameter controls the placement of the filter. If no structuring element is provided an element is generated with a squared connectivity equal to one. The dilation operation is repeated iterations times. If iterations is less than 1, the dilation is repeated until the result does not change anymore. If a mask is given, only those elements with a true value at the corresponding mask element are modified at each iteration.

binary_erosion(*input, structure=None, iterations=1, mask=None, output=None, border_value=0, origin=0, brute_force=False*)
Multi-dimensional binary erosion with the given structure.

An output array can optionally be provided. The origin parameter controls the placement of the filter. If no structuring element is provided an element is generated with a squared connectivity equal to one. The border_value parameter gives the value of the array outside the border. The erosion operation is repeated iterations times. If iterations is less than 1, the erosion is repeated until the result does not change anymore. If a mask is given, only those elements with a true value at the corresponding mask element are modified at each iteration.

binary_fill_holes(*input, structure=None, output=None, origin=0*)
Fill the holes in binary objects.

An output array can optionally be provided. The origin parameter controls the placement of the filter. If no structuring element is provided an element is generated with a squared connectivity equal to one.

binary_hit_or_miss(*input, structure1=None, structure2=None, output=None, origin1=0, origin2=None*)
Multi-dimensional binary hit-or-miss transform.

An output array can optionally be provided. The origin parameters controls the placement of the structuring elements. If the first structuring element is not given one is generated with a squared connectivity equal to one. If the second structuring element is not provided, it set equal to the inverse of the first structuring element. If the origin for the second structure is equal to None it is set equal to the origin of the first.

binary_opening(*input, structure=None, iterations=1, output=None, origin=0*)
Multi-dimensional binary opening with the given structure.

An output array can optionally be provided. The origin parameter controls the placement of the filter. If no structuring element is provided an element is generated with a squared connectivity equal to one. The iterations parameter gives the number of times the erosions and then the dilations are done.

binary_propagation(*input, structure=None, mask=None, output=None, border_value=0, origin=0*)
Multi-dimensional binary propagation with the given structure.

An output array can optionally be provided. The origin parameter controls the placement of the filter. If no structuring element is provided an element is generated with a squared connectivity equal to one. If a mask is given, only those elements with a true value at the corresponding mask element are.

This function is functionally equivalent to calling binary_dilation with the number of iterations less then one: iterative dilation until the result does not change anymore.

black_tophat(*input, size=None, footprint=None, structure=None, output=None, mode='reflect', cval=0.0, origin=0*)
Multi-dimensional black tophat filter.

Either a size or a footprint, or the structure must be provided. An output array can optionally be provided. The origin parameter controls the placement of the filter. The mode parameter determines how the array borders are handled, where cval is the value when mode is equal to 'constant'.

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). Three types of distance metric are supported: 'euclidean', 'taxicab' and '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.

This function employs a slow brute force algorithm, see also the function distance_transform_cdt for more efficient taxicab and chessboard algorithms.

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).

distance_transform_cdt(*input, metric='chessboard', return_distances=True, return_indices=False, distances=None, indices=None*)
Distance transform for chamfer type of transforms.

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 rank of the array. These choices correspond to the common interpretations of the taxicab and the chessboard distance metrics in two dimensions.

In addition to the distance transform, the feature transform can be calculated. In this case the index of the closest background element is returned along the first axis of the result.

The return_distances, and return_indices flags can be used to indicate if the distance transform, the feature transform, or both must be returned.

The distances and indices arguments can be used to give optional output arrays that must be of the correct size and type (both int32).

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.

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).

generate_binary_structure(*rank, connectivity*)

Generate a binary structure for binary morphological operations.

The inputs are the rank of the array to which the structure will be applied and the square of the connectivity of the structure.

grey_closing(*input, size=None, footprint=None, structure=None, output=None, mode='reflect', cval=0.0, origin=0*)

Multi-dimensional grey valued closing.

Either a size or a footprint, or the structure must be provided. An output array can optionally be provided. The origin parameter controls the placement of the filter. The mode parameter determines how the array borders are handled, where cval is the value when mode is equal to 'constant'.

grey_dilation(*input, size=None, footprint=None, structure=None, output=None, mode='reflect', cval=0.0, origin=0*)

Calculate a grey values dilation.

Either a size or a footprint, or the structure must be provided. An output array can optionally be provided. The origin parameter controls the placement of the filter. The mode parameter determines how the array borders are handled, where cval is the value when mode is equal to 'constant'.

grey_erosion(*input, size=None, footprint=None, structure=None, output=None, mode='reflect', cval=0.0, origin=0*)

Calculate a grey values erosion.

Either a size or a footprint, or the structure must be provided. An output array can optionally be provided. The origin parameter controls the placement of the filter. The mode parameter determines how the array borders are handled, where cval is the value when mode is equal to 'constant'.

grey_opening(*input, size=None, footprint=None, structure=None, output=None, mode='reflect', cval=0.0, origin=0*)

Multi-dimensional grey valued opening.

Either a size or a footprint, or the structure must be provided. An output array can optionally be provided. The origin parameter controls the placement of the filter. The mode parameter determines how the array borders are handled, where cval is the value when mode is equal to 'constant'.

iterate_structure(*structure, iterations, origin=None*)
Iterate a structure by dilating it with itself.

If origin is None, only the iterated structure is returned. If not, a tuple of the iterated structure and the modified origin is returned.

morphological_gradient(*input, size=None, footprint=None, structure=None, output=None, mode='reflect', cval=0.0, origin=0*)
Multi-dimensional morphological gradient.

Either a size or a footprint, or the structure must be provided. An output array can optionally be provided. The origin parameter controls the placement of the filter. The mode parameter determines how the array borders are handled, where cval is the value when mode is equal to 'constant'.

morphological_laplace(*input, size=None, footprint=None, structure=None, output=None, mode='reflect', cval=0.0, origin=0*)
Multi-dimensional morphological laplace.

Either a size or a footprint, or the structure must be provided. An output array can optionally be provided. The origin parameter controls the placement of the filter. The mode parameter determines how the array borders are handled, where cval is the value when mode is equal to 'constant'.

white_tophat(*input, size=None, footprint=None, structure=None, output=None, mode='reflect', cval=0.0, origin=0*)
Multi-dimensional white tophat filter.

Either a size or a footprint, or the structure must be provided. An output array can optionally be provided. The origin parameter controls the placement of the filter. The mode parameter determines how the array borders are handled, where cval is the value when mode is equal to 'constant'.

3.11 Orthogonal distance regression (scipy.odr)

Orthogonal Distance Regression

3.11.1 Introduction

Why Orthogonal Distance Regression (ODR)? Sometimes one has measurement errors in the explanatory variable, not just the response variable. Ordinary Least Squares (OLS) fitting procedures treat the data for explanatory variables as fixed. Furthermore, OLS procedures require that the response variable be an explicit function of the explanatory variables; sometimes making the equation explicit is unwieldy and introduces errors. ODR can handle both of these cases with ease and can even reduce to the OLS case if necessary.

ODRPACK is a FORTRAN-77 library for performing ODR with possibly non-linear fitting functions. It uses a modified trust-region Levenberg-Marquardt-type algorithm to estimate the function parameters. The fitting functions are provided by Python functions operating on NumPy arrays. The required derivatives may be provided by Python functions as well or may be numerically estimated. ODRPACK can do explicit or implicit ODR fits or can do OLS. Input and output variables may be multi-dimensional. Weights can be provided to account for different variances of the observations (even covariances between dimensions of the variables).

odr provides two interfaces: a single function and a set of high-level classes that wrap that function. Please refer to their docstrings for more information. While the docstring of the function, odr, does not have a full explanation of its arguments, the classes do, and the arguments with the same name usually have the same requirements. Furthermore, it is highly suggested that one at least skim the ODRPACK User's Guide. Know Thy Algorithm.

3.11.2 Use

See the docstrings of odr.odrpack and the functions and classes for usage instructions. The ODRPACK User's Guide is also quite helpful. It can be found on one of the ODRPACK's original author's website:

http://www.boulder.nist.gov/mcsd/Staff/JRogers/odrpack.html

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class `Data` (*x, y=None, we=None, wd=None, fix=None, meta={}*)

The Data class stores the data to fit.

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 structures of wd and we are described below. meta is an freeform dictionary for application-specific use.

we weights the effect a deviation in the response variable has on the fit. wd 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.

we – 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 – 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 – fix 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 – optional, freeform dictionary for metadata

Methods

set_meta(**kwds)	Update the metadata dictionary with the keywords and data provided

set_meta (***kwds*)
Update the metadata dictionary with the keywords and data provided by keywords.

class 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.

The initialization method stores these into members of the same name.

fcn – fit function: fcn(beta, x) –> y

fjacb – Jacobian of fcn wrt the fit parameters beta:
fjacb(beta, x) –> @f_i(x,B)/@B_j

fjacd – Jacobian of fcn wrt the (possibly multidimensional) input variable:
fjacd(beta, x) –> @f_i(x,B)/@x_j

extra_args – if specified, extra_args should be a tuple of extra
arguments to pass to fcn, fjacb, and fjacd. Each will be called like the following: apply(fcn, (beta, x) + extra_args)

estimate – provide estimates of the fit parameters from the data:
estimate(data) –> estbeta

implicit – boolean variable which, if TRUE, specifies that the model
is implicit; i.e fcn(beta, x) ~= 0 and there is no y data to fit against.

meta – an optional, freeform dictionary of metadata for the model

Note that the fcn, fjacb, and fjacd operate on NumPy arrays and return a NumPy array. estimate takes an instance of the Data class.

Here are the rules for the shapes of the argument and return arrays:

x – if the input data is single-dimensional, then x is rank-1
array; i.e. x = array([1, 2, 3, ...]); x.shape = (n,) If the input data is multi-dimensional, then x is a rank-2 array; i.e. x = array([[1, 2, ...], [2, 4, ...]]); x.shape = (m, n) In all cases, it has the same shape as the input data array passed to odr(). m is the dimensionality of the input data, n is the number of observations.

y – if the response variable is single-dimensional, then y is a rank-1
array; i.e. y = array([2, 4, ...]); y.shape = (n,) If the response variable is multi-dimensional, then y is a rank-2 array; i.e. y = array([[2, 4, ...], [3, 6, ...]]); y.shape = (q, n) where q is the dimensionality of the response variable.

beta – rank-1 array of length p where p is the number of parameters;
i.e. beta = array([B_1, B_2, ..., B_p])

fjacb – if the response variable is multi-dimensional, then the return
array's shape is (q, p, n) such that fjacb(x,beta)[l,k,i] = @f_l(X,B)/@B_k evaluated at the i'th data point. If q == 1, then the return array is only rank-2 and with shape (p, n).

fjacd – as with fjacb, only the return array's shape is (q, m, n) such that
fjacd(x,beta)[l,j,i] = @f_l(X,B)/@X_j at the i'th data point. If q == 1, then the return array's shape is (m, n). If m == 1, the shape is (q, n). If m == q == 1, the shape is (n,).

Methods

set_meta(**kwds)	Update the metadata dictionary with the keywords and data provided

set_meta(***kwds*)
Update the metadata dictionary with the keywords and data provided here.

class ODR(*data, model, beta0=None, delta0=None, ifixb=None, ifixx=None, job=None, iprint=None, errfile=None, rptfile=None, ndigit=None, taufac=None, sstol=None, partol=None, maxit=None, stpb=None, stpd=None, sclb=None, scld=None, work=None, iwork=None*)
The ODR class gathers all information and coordinates the running of the main fitting routine.

Members of instances of the ODR class have the same names as the arguments to the initialization routine.

Parameters
Required: :

data – instance of the Data class

model – instance of the Model class

beta0 – a rank-1 sequence of initial parameter values. Optional if
model provides an "estimate" function to estimate these values.

Optional:

delta0 – 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 – 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 – 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 – 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 – 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 – string with the filename to print ODRPACK errors to. *Do Not Open

This File Yourself!*

rptfile – string with the filename to print ODRPACK summaries to. *Do Not

Open This File Yourself!*

ndigit – integer specifying the number of reliable digits in the computation

of the function.

taufac – 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 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 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 – 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 – sequence (len(stpb) == len(beta0)) of relative step sizes to compute
finite difference derivatives wrt the parameters.

stpd – 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 – 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 (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 – array to hold the double-valued working data for ODRPACK. When

restarting, takes the value of self.output.work .

iwork – array to hold the integer-valued working data for ODRPACK. When

restarting, takes the value of self.output.iwork .

Other Members (not supplied as initialization arguments):

output – an instance if the Output class containing all of the returned
data from an invocation of ODR.run() or ODR.restart()

Methods

restart([iter])	Restarts the run with iter more iterations.
run()	Run the fitting routine with all of the information given.
set_iprint([init, so_init, iter, so_iter, ...])	Set the iprint parameter for the printing of computation reports.
set_job([fit_type, deriv, var_calc, ...])	Sets the "job" parameter is a hopefully comprehensible way.

restart (*iter=None*)
Restarts the run with iter more iterations.

Parameters
iter : int, optional

ODRPACK's default for the number of new iterations is 10.

Returns
output : Output instance

This object is also assigned to the attribute .output .

run ()
Run the fitting routine with all of the information given.

Returns
output : Output instance

This object is also assigned to the attribute .output .

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.

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.

Parameter	Value	Meaning
fit_type	0	explicit ODR
	1	implicit ODR
	2	ordinary least-squares
deriv	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	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	initial input variable offsets set to 0
	1	initial offsets provided by user in variable "work"
restart	0	fit is not a restart
	1	fit is a restart

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.

class `Output`(*output*)

The Output class stores the output of an ODR run.

Takes one argument for initialization: the return value from the function odr().

Attributes

Methods

`pprint`()	Pretty-print important results.

pprint()

Pretty-print important results.

exception `odr_error`

exception `odr_stop`

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, stpd=None, sclb=None, scld=None, work=None, iwork=None, full_output=0*)

3.12 Optimization and root finding (scipy.optimize)

3.12.1 Optimization

General-purpose

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, ...])	Minimize a function using the Newton-CG method.
leastsq(func, x0[, args, Dfun, full_output, ...])	Minimize the sum of squares of a set of equations.

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

Minimize a function using the downhill simplex algorithm.

Parameters

func : callable func(x,*args)

The objective function to be minimized.

x0 : ndarray

Initial guess.

args : tuple

Extra arguments passed to func, i.e. `f(x,*args)`.

callback : callable

Called after each iteration, as callback(xk), where xk is the current parameter vector.

Returns

xopt : ndarray

Parameter that minimizes function.

fopt : float

Value of function at minimum: `fopt = func(xopt)`.

iter : int

Number of iterations performed.

funcalls : int

Number of function calls made.

warnflag : int

1 : Maximum number of function evaluations made. 2 : Maximum number of iterations reached.

allvecs : list

Solution at each iteration.

Notes

Uses a Nelder-Mead simplex algorithm to find the minimum of a function of one or more variables.

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.

Parameters

func : callable f(x,*args)

Objective function to be minimized.

x0 : ndarray

Initial guess.

args : tuple

Eextra arguments passed to func.

callback : callable

An optional user-supplied function, called after each iteration. Called as `callback(xk)`, where `xk` is the current parameter vector.

direc : ndarray

Initial direction set.

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.

Notes

Uses a modification of Powell's method to find the minimum of a function of N variables.

fmin_cg (*f, x0, fprime=None, args=(), gtol=1.0000000000000001e-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.

x0 : ndarray

Initial guess.

fprime : callable f'(x,*args)

Function which computes the gradient of f.

args : tuple

Extra arguments passed to f and fprime.

gtol : float

Stop when norm of gradient is less than gtol.

norm : float

Order of vector norm to use. -Inf is min, Inf is max.

epsilon : float or ndarray

If fprime is approximated, use this value for the step size (can be scalar or vector).

callback : callable

An optional user-supplied function, called after each iteration. Called as callback(xk), where xk is the current parameter vector.

Returns

xopt : ndarray

Parameters which minimize f, i.e. f(xopt) == fopt.

fopt : float

Minimum value found, f(xopt).

func_calls : int

The number of function_calls made.

grad_calls : int

The number of gradient calls made.

warnflag : int

1 : Maximum number of iterations exceeded. 2 : Gradient and/or function calls not changing.

allvecs : ndarray

If retall is True (see other parameters below), then this vector containing the result at each iteration is returned.

Notes

Optimize the function, f, whose gradient is given by fprime using the nonlinear conjugate gradient algorithm of Polak and Ribiere. See Wright & Nocedal, 'Numerical Optimization', 1999, pg. 120-122.

fmin_bfgs (*f, x0, fprime=None, args=(), gtol=1.0000000000000001e-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)

Gradient of f.

args : tuple

Extra arguments passed to f and fprime.

gtol : float

Gradient norm must be less than gtol before succesful termination.

norm : float

Order of norm (Inf is max, -Inf is min)

epsilon : int or ndarray

If fprime is approximated, use this value for the step size.

callback : callable

An optional user-supplied function to call after each iteration. Called as callback(xk), where xk is the current parameter vector.

Returns

xopt : ndarray

Parameters which minimize f, i.e. f(xopt) == fopt.

fopt : float

Minimum value.

gopt : ndarray

Value of gradient at minimum, f'(xopt), which should be near 0.

Bopt : ndarray

Value of 1/f''(xopt), i.e. the inverse hessian matrix.

func_calls : int

Number of function_calls made.

grad_calls : int

Number of gradient calls made.

warnflag : integer

1 : Maximum number of iterations exceeded. 2 : Gradient and/or function calls not changing.

allvecs : list

Results at each iteration. Only returned if retall is True.

Notes

Optimize the function, f, whose gradient is given by fprime using the quasi-Newton method of Broyden, Fletcher, Goldfarb, and Shanno (BFGS) See Wright, and Nocedal 'Numerical Optimization', 1999, pg. 198.

fmin_ncg (*f, x0, fprime, fhess_p=None, fhess=None, args=(), avextol=1.0000000000000001e-05, epsilon=1.4901161193847656e-08, maxiter=None, full_output=0, disp=1, retall=0, callback=None*)

Minimize 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)

Function which computes the Hessian of f times an arbitrary vector, p.

fhess : callable fhess(x,*args)

Function to compute the Hessian matrix of f.

args : tuple

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

If fhess is approximated, use this value for the step size.

callback : callable

An optional user-supplied function which is called after each iteration. Called as callback(xk), where xk is the current parameter vector.

Returns

xopt : ndarray

Parameters which minimizer f, i.e. `f(xopt) == fopt`.

fopt : float

Value of the function at xopt, i.e. `fopt = f(xopt)`.

fcalls : int

Number of function calls made.

gcalls : int

Number of gradient calls made.

hcalls : int

Number of hessian calls made.

warnflag : int

Warnings generated by the algorithm. 1 : Maximum number of iterations exceeded.

allvecs : list

The result at each iteration, if retall is True (see below).

Notes

Only one of *fhess_p* or *fhess* need to be given. If *fhess* is provided, then *fhess_p* will be ignored. If neither *fhess* nor *fhess_p* is provided, then the hessian product will be approximated using finite differences on *fprime*. *fhess_p* must compute the hessian times an arbitrary vector. If it is not given, finite-differences on *fprime* are used to compute it. See Wright & Nocedal, 'Numerical Optimization', 1999, pg. 140.

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=0.0, factor=100, diag=None, warning=True*)

Minimize the sum of squares of a set of equations.

```
x = arg min(sum(func(y)**2,axis=0))
         y
```

Parameters

func : callable

should take at least one (possibly length N vector) argument and returns M floating point numbers.

x0 : ndarray

The starting estimate for the minimization.

args : tuple

Any extra arguments to func are placed in this tuple.

Dfun : callable

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

non-zero to return all optional outputs.

col_deriv : bool

non-zero to specify that the Jacobian function computes derivatives down the columns (faster, because there is no transpose operation).

ftol : float

Relative error desired in the sum of squares.

xtol : float

Relative error desired in the approximate solution.

gtol : float

Orthogonality desired between the function vector and the columns of the Jacobian.

maxfev : int

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.

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.

factor : float

A parameter determining the initial step bound (`factor * || diag * x||`). Should be in interval `(0.1, 100)`.

diag : sequence

N positive entries that serve as a scale factors for the variables.

warning : bool

Whether to print a warning message when the call is unsuccessful. Deprecated, use the warnings module instead.

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 standard deviation to get the covariance of the parameter estimates – see curve_fit.

infodict : dict

a dictionary of optional outputs with the keys:

```
- '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 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 elements 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.

Constrained (multivariate)

fmin_l_bfgs_b(func, x0[, fprime, args, ...])	Minimize a function func using the L-BFGS-B algorithm.
fmin_tnc(func, x0[, fprime, args, ...])	Minimize a function with variables subject to bounds, using gradient information.
fmin_cobyla(func, x0, cons[, args, ...])	Minimize a function using the Constrained Optimization BY Linear
fmin_slsqp(func, x0[, eqcons, f_eqcons, ...])	Minimize a function using Sequential Least SQuares Programming
nnls(A, b)	Solve argmin_x || Ax - b ||_2 for x>=0.

fmin_l_bfgs_b(*func, x0, fprime=None, args=(), approx_grad=0, bounds=None, m=10, factr=10000000.0, pgtol=1.0000000000000001e-05, epsilon=1e-08, iprint=-1, maxfun=15000*)

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)] 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
[tuple] Arguments to pass to *func* and *fprime*.

approx_grad
[bool] Whether to approximate the gradient numerically (in which case *func* returns only the function value).

bounds
[list] `(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.

m
[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} <= 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] 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] Step size used when *approx_grad* is True, for numerically calculating the gradient

iprint
[int] Controls the frequency of output. `iprint < 0` means no output.

maxfun
[int] Maximum number of function evaluations.

Returns

x : ndarray

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, 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.

Notes

License of L-BFGS-B (Fortran code):

The version included here (in fortran code) is 2.1 (released in 1997). 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.

References

- R. H. Byrd, P. Lu and J. Nocedal. A Limited Memory Algorithm for Bound Constrained Optimization, (1995), SIAM Journal on Scientific and Statistical Computing , 16, 5, pp. 1190-1208.
- C. Zhu, R. H. Byrd and J. Nocedal. L-BFGS-B: Algorithm 778: L-BFGS-B, FORTRAN routines for large scale bound constrained optimization (1997), ACM Transactions on Mathematical Software, Vol 23, Num. 4, pp. 550 - 560.

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*)

Minimize a function with variables subject to bounds, using gradient information.

Parameters

func : callable func(x, *args)

Function to minimize. Should return f and g, where f is the value of the function and g its gradient (a list of floats). If the function returns None, the minimization is aborted.

x0 : list of floats

Initial estimate of minimum.

fprime : callable fprime(x, *args)

Gradient of func. If None, then func must return the function value and the gradient (f,g = func(x, *args)).

args : tuple

Arguments to pass to function.

approx_grad : bool

If true, approximate the gradient numerically.

bounds : list

(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.

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] fo the others. Defaults to None

offset : float

Value to substract from each variable. If None, the offsets are (up+low)/2 for interval bounded variables and x for the others.

messages : :

Bit mask used to select messages display during minimization values defined in the MSGS dict. Defaults to MGS_ALL.

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.

maxfun : int

Maximum number of function evaluation. if None, maxfun 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.

fmin : float

Minimum function value estimate. Defaults to 0.

ftol : float

Precision goal for the value of f in the stoping 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.

pgtol : float

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

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.

Returns

x : list of floats

The solution.

nfeval : int

The number of function evaluations.

rc : :

Return code as defined in the RCSTRINGS dict.

fmin_cobyla (*func, x0, cons, args=(), consargs=None, rhobeg=1.0, rhoend=0.0001, iprint=1, maxfun=1000*)

Minimize a function using the Constrained Optimization BY Linear Approximation (COBYLA) method.

Parameters

func : callable f(x, *args)

Function to minimize.

x0 : ndarray

Initial guess.

cons : sequence

Constraint functions; must all be `>=0` (a single function if only 1 constraint).

args : tuple

Extra arguments to pass to function.

consargs : tuple

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 : :

Reasonable initial changes to the variables.

rhoend : :

Final accuracy in the optimization (not precisely guaranteed).

iprint : {0, 1, 2, 3}

Controls the frequency of output; 0 implies no output.

maxfun : int

Maximum number of function evaluations.

Returns

x : ndarray

The argument that minimises *f*.

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=9.9999999999999995e-07, iprint=1, full_output=0, epsilon=1.4901161193847656e-08*)

Minimize a function using Sequential Least SQuares Programming

Python interface function for the SLSQP Optimization subroutine originally implemented by Dieter Kraft.

Parameters

func : callable f(x,*args)

Objective function.

x0 : ndarray of float

Initial guess for the independent variable(s).

eqcons : list

A list of functions of length n such that eqcons[j](x0,*args) == 0.0 in a successfully optimized problem.

f_eqcons : callable f(x,*args)

Returns an array in which each element must equal 0.0 in a successfully optimized problem. If f_eqcons is specified, eqcons is ignored.

ieqcons : list

A list of functions of length n such that ieqcons[j](x0,*args) >= 0.0 in a successfully optimized problem.

f_ieqcons : callable f(x0,*args)

Returns an array 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

A list of tuples specifying the lower and upper bound for each independent variable [(xl0, xu0),(xl1, xu1),...]

fprime : callable *f(x,*args)*

A function that evaluates the partial derivatives of func.

fprime_eqcons : callable *f(x,*args)*

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)*

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

Additional arguments passed to func and fprime.

iter : int

The maximum number of iterations.

acc : float

Requested accuracy.

iprint : int

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

full_output : bool

If False, return only the minimizer of func (default). Otherwise, output final objective function and summary information.

epsilon : float

The step size for finite-difference derivative estimates.

Returns

x : 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.

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*.

nnls(*A*, *b*)

Solve `argmin_x || Ax - b ||_2` for `x>=0`.

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

This is a wrapper for `NNLS.F`.

Global

`anneal`(func, x0[, args, schedule, ...])	Minimize a function using simulated annealing.
`brute`(func, ranges[, args, Ns, full_output, ...])	Minimize a function over a given range by brute force.

anneal(*func, x0, args=(), schedule='fast', full_output=0, T0=None, Tf=9.9999999999999998e-13, maxeval=None, maxaccept=None, maxiter=400, boltzmann=1.0, learn_rate=0.5, feps=9.9999999999999995e-07, quench=1.0, m=1.0, n=1.0, lower=-100, upper=100, dwell=50*)

Minimize a function using simulated annealing.

Schedule is a schedule class implementing the annealing schedule. Available ones are 'fast', 'cauchy', 'boltzmann'

Parameters

func : callable f(x, *args)

Function to be optimized.

x0 : ndarray

Initial guess.

args : tuple

Extra parameters to *func*.

schedule : base_schedule

Annealing schedule to use (a class).

full_output : bool

Whether to return optional outputs.

T0 : float

Initial Temperature (estimated as 1.2 times the largest cost-function deviation over random points in the range).

Tf : float

Final goal temperature.

maxeval : int

Maximum function evaluations.

maxaccept : int

Maximum changes to accept.

maxiter : int

Maximum cooling iterations.

learn_rate : float

Scale constant for adjusting guesses.

boltzmann : float

Boltzmann constant in acceptance test (increase for less stringent test at each temperature).

feps : float

Stopping relative error tolerance for the function value in last four coolings.

quench, m, n : float

Parameters to alter fast_sa schedule.

lower, upper : float or ndarray

Lower and upper bounds on *x*.

dwell : int

The number of times to search the space at each temperature.

brute (*func, ranges, args=(), Ns=20, full_output=0, finish=<function fmin at 0x149ee578>*)

Minimize a function over a given range by brute force.

Parameters

func : callable `f(x,*args)`

Objective function to be minimized.

ranges : tuple

Each element is a tuple of parameters or a slice object to be handed to `numpy.mgrid`.

args : tuple

Extra arguments passed to function.

Ns : int

Default number of samples, if those are not provided.

full_output : bool

If True, return the evaluation grid.

Returns

x0 : ndarray

Value of arguments to *func*, giving minimum over the grid.

fval : int

Function value at minimum.

grid : tuple

Representation of the evaluation grid. It has the same length as x0.

Jout : ndarray

Function values over grid: `Jout = func(*grid)`.

Notes

Find the minimum of a function evaluated on a grid given by the tuple ranges.

Scalar function minimizers

`fminbound`(func, x1, x2[, args, xtol, ...])	Bounded minimization for scalar functions.
`golden`(func[, args, brack, tol, full_output])	Given a function of one-variable and a possible bracketing interval, return the minimum of the function isolated to a fractional precision of tol.
`bracket`(func[, xa, xb, args, grow_limit, ...])	Given a function and distinct initial points, search in the downhill direction (as defined by the initital points) and return new points xa, xb, xc that bracket the minimum of the function f(xa) > f(xb) < f(xc).
`brent`(func[, args, brack, tol, full_output, ...])	Given a function of one-variable and a possible bracketing interval, return the minimum of the function isolated to a fractional precision of tol.

fminbound (*func, x1, x2, args=(), xtol=1.0000000000000001e-05, maxfun=500, full_output=0, disp=1*)

Bounded minimization for scalar functions.

Parameters

func : callable f(x,*args)

Objective function to be minimized (must accept and return scalars).

x1, x2 : float or array scalar

The optimization bounds.

args : tuple

Extra arguments passed to function.

xtol : float

The convergence tolerance.

maxfun : int

Maximum number of function evaluations allowed.

full_output : bool

If True, return optional outputs.

disp : int

If non-zero, print messages.
0 : no message printing. 1 : non-convergence notification messages only. 2 : print a message on convergence too. 3 : print iteration results.

Returns

xopt : ndarray

Parameters (over given interval) which minimize the objective function.

fval : number

The function value at the minimum point.

ierr : int

An error flag (0 if converged, 1 if maximum number of function calls reached).

numfunc : int

The number of function calls made.

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).

golden (*func, args=(), brack=None, tol=1.4901161193847656e-08, full_output=0*)

Given a function of one-variable and a possible bracketing interval, return the minimum of the function isolated to a fractional precision of tol.

Parameters

func : callable func(x,*args)

Objective function to minimize.

args : tuple

Additional arguments (if present), passed to func.

brack : tuple

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

x tolerance stop criterion

full_output : bool

If True, return optional outputs.

Notes

Uses analog of bisection method to decrease the bracketed interval.

bracket (*func, xa=0.0, xb=1.0, args=(), grow_limit=110.0, maxiter=1000*)

Given a function and distinct initial points, search in the downhill direction (as defined by the initital points) and return new points xa, xb, xc that bracket the minimum of the function f(xa) > f(xb) < f(xc). It doesn't always mean that obtained solution will satisfy xa<=x<=xb

Parameters

func : callable f(x,*args)

Objective function to minimize.

xa, xb : float

Bracketing interval.

args : tuple

Additional arguments (if present), passed to *func*.

grow_limit : float

Maximum grow limit.

maxiter : int

Maximum number of iterations to perform.

Returns

xa, xb, xc : float

Bracket.

fa, fb, fc : float

Objective function values in bracket.

funcalls : int

Number of function evaluations made.

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 :

Additional arguments (if present).

brack : tuple

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.

full_output : bool

If True, return all output args (xmin, fval, iter, funcalls).

Returns

xmin : ndarray

Optimum point.

fval : float

Optimum value.

iter : int

Number of iterations.

funcalls : int

Number of objective function evaluations made.

Notes

Uses inverse parabolic interpolation when possible to speed up convergence of golden section method.

3.12.2 Fitting

curve_fit(f, xdata, ydata, **kw[, p0, sigma])	Use non-linear least squares to fit a function, f, to data.

curve_fit (*f, xdata, ydata, p0=None, sigma=None, **kw*)

Use non-linear least squares to fit a function, f, to data.

Assumes `ydata = f(xdata, *params) + eps`

Parameters

f : callable

The model function, f(x, ...). It must take the independent variable as the first argument and the parameters to fit as separate remaining arguments.

xdata : An N-length sequence or an (k,N)-shaped array

for functions with k predictors. The independent variable where the data is measured.

ydata : N-length sequence

The dependent data — nominally f(xdata, ...)

p0 : None, scalar, or M-length sequence

Initial guess for the parameters. If None, then the initial values will all be 1 (if the number of parameters for the function can be determined using introspection, otherwise a ValueError is raised).

sigma : None or N-length sequence

If not None, it represents the standard-deviation of ydata. This vector, if given, will be used as weights in the least-squares problem.

Returns

popt : array

Optimal values for the parameters so that the sum of the squared error of `f(xdata, *popt) - ydata` is minimized

pcov : 2d array

The estimated covariance of popt. The diagonals provide the variance of the parameter estimate.

Notes

The algorithm uses the Levenburg-Marquardt algorithm: scipy.optimize.leastsq. Additional keyword arguments are passed directly to that algorithm.

Examples

```
>>> import numpy as np
>>> from scipy.optimize import curve_fit
>>> def func(x, a, b, c):
...     return a*np.exp(-b*x) + c
```

```
>>> x = np.linspace(0,4,50)
>>> y = func(x, 2.5, 1.3, 0.5)
>>> yn = y + 0.2*np.random.normal(size=len(x))

>>> popt, pcov = curve_fit(func, x, yn)
```

3.12.3 Root finding

fsolve(func, x0[, args, fprime, ...])	Find the roots of a function.

fsolve (*func, x0, args=(), fprime=None, full_output=0, col_deriv=0, xtol=1.49012e-08, maxfev=0, band=None, epsfcn=0.0, factor=100, diag=None, warning=True*)

Find the roots of a function.

Return the roots of the (non-linear) equations defined by `func(x) = 0` given a starting estimate.

Parameters

func : callable f(x, *args)

A function that takes at least one (possibly vector) argument.

x0 : ndarray

The starting estimate for the roots of `func(x) = 0`.

args : tuple

Any extra arguments to *func*.

fprime : callable(x)

A function to compute the Jacobian of *func* with derivatives across the rows. By default, the Jacobian will be estimated.

full_output : bool

If True, return optional outputs.

col_deriv : bool

Specify whether the Jacobian function computes derivatives down the columns (faster, because there is no transpose operation).

warning : bool

Whether to print a warning message when the call is unsuccessful. This option is deprecated, use the warnings module instead.

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 same
           matrix
    * '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.

Notes

`fsolve` is a wrapper around MINPACK's hybrd and hybrj algorithms.

Scalar function solvers

`brentq`(f, a, b[, args, xtol, rtol, maxiter, ...])	Find a root of a function in given interval.
`brenth`(f, a, b[, args, xtol, rtol, maxiter, ...])	Find root of f in [a,b].
`ridder`(f, a, b[, args, xtol, rtol, maxiter, ...])	Find a root of a function in an interval.
`bisect`(f, a, b[, args, xtol, rtol, maxiter, ...])	Find root of f in [a,b].
`newton`(func, x0[, fprime, args, tol, maxiter])	Find a zero using the Newton-Raphson or secant method.

brentq(*f, a, b, args=(), xtol=9.9999999999999998e-13, 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-Deker-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.

maxiter : number, optional

if convergence is not achieved in maxiter iterations, and error is raised. Must be >= 0.

args : tuple, optional

containing extra arguments for the function *f*. *f* is called by `apply(f, (x)+args)`.

full_output : bool, optional

If *full_output* is False, the root is returned. If *full_output* is True, the return value is `(x, r)`, where *x* is the root, and *r* is a RootResults object.

disp : {True, 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
fmin, *fmin_powell*, *fmin_cg*, *fmin_bfgs*, *fmin_ncg*

nonlinear
leastsq

constrained
fmin_l_bfgs_b, *fmin_tnc*, *fmin_cobyla*

global
anneal, *brute*

local
fminbound, *brent*, *golden*, *bracket*

n-dimensional
fsolve

one-dimensional
brentq, *brenth*, *ridder*, `bisect`, *newton*

scalar
fixed_point

Notes

f must be continuous. f(a) and f(b) must have opposite signs.

brenth(*f, a, b, args=(), xtol=9.9999999999999998e-13, rtol=4.4408920985006262e-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) can not 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 >= 0. The routine modifies this to take into account the relative precision of doubles.

maxiter : number, optional

if convergence is not achieved in maxiter iterations, and error is raised. Must be >= 0.

args : tuple, optional

containing extra arguments for the function *f*. *f* is called by `apply(f, (x)+args)`.

full_output : bool, optional

If *full_output* is False, the root is returned. If *full_output* is True, the return value is `(x, r)`, where *x* is the root, and *r* is a RootResults object.

disp : {True, 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.

ridder(*f, a, b, args=(), xtol=9.9999999999999998e-13, 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 >= 0. The routine modifies this to take into account the relative precision of doubles.

maxiter : number, optional

if convergence is not achieved in maxiter iterations, and error is raised. Must be >= 0.

args : tuple, optional

containing extra arguments for the function *f*. *f* is called by `apply(f, (x)+args)`.

full_output : bool, optional

If *full_output* is False, the root is returned. If *full_output* is True, the return value is `(x, r)`, where *x* is the root, and *r* is a RootResults object.

disp : {True, 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:

`brentq`, `brenth`, `bisect`, `newton`

`fixed_point`
scalar fixed-point finder

Notes

Uses [Ridders1979] method to find a zero of the function *f* between the arguments *a* and *b*. Ridders' method is faster than bisection, but not generally as fast as the Brent rountines. [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]

bisect(*f, a, b, args=(), xtol=9.9999999999999998e-13, rtol=4.4408920985006262e-16, maxiter=100, full_output=False, disp=True*)

Find root of f in [a,b].

Basic bisection routine to find a zero of the function f between the arguments a and b. f(a) and f(b) can not have the same signs. Slow but sure.

Parameters

f : function

Python function returning a number. f must be continuous, and f(a) and f(b) must have opposite signs.

a : 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.

maxiter : number, optional

if convergence is not achieved in maxiter iterations, and error is raised. Must be >= 0.

args : tuple, optional

containing extra arguments for the function *f*. *f* is called by `apply(f, (x)+args)`.

full_output : bool, optional

If *full_output* is False, the root is returned. If *full_output* is True, the return value is `(x, r)`, where *x* is the root, and *r* is a RootResults object.

disp : {True, 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:

fixed_point

scalar fixed-point finder fsolve – n-dimensional root-finding

newton (*func, x0, fprime=None, args=(), tol=1.48e-08, maxiter=50*)
Find a zero using the Newton-Raphson or secant method.

Find a zero of the function *func* given a nearby starting point *x0*. The Newton-Rapheson method is used if the derivative *fprime* of *func* is provided, otherwise the secant method is used.

Parameters

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 *args* parameter.

x0 : float

An initial estimate of the zero that should be somewhere near the actual zero.

fprime : {None, function}, optional

The derivative of the function when available and convenient. If it is None, then the secant method is used. The default is None.

args : tuple, optional

Extra arguments to be used in the function call.

tol : float, optional

The allowable error of the zero value.

maxiter : int, optional

Maximum number of iterations.

Returns

zero : float

Estimated location where function is zero.

See Also:

brentq, brenth, ridder, bisect, fsolve

Notes

The convergence rate of the Newton-Rapheson method is quadratic while that of the secant method is somewhat less. This means that if the function is well behaved the actual error in the estimated zero is approximatly the square of the requested tolerance up to roundoff error. However, the stopping criterion used here is the step size and there is no quarantee that a zero has been found. Consequently the result should be verified. Safer algorithms are brentq, brenth, 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 dimemsional problems when such an interval has been found.

Fixed point finding:

fixed_point(func, x0[, args, xtol, maxiter])	Find the point where func(x) == x

fixed_point (*func, x0, args=(), xtol=1e-08, maxiter=500*)
Find the point where func(x) == x

Given a function of one or more variables and a starting point, find a fixed-point of the function: i.e. where func(x)=x.

Uses Steffensen's Method using Aitken's Del^2 convergence acceleration. See Burden, Faires, "Numerical Analysis", 5th edition, pg. 80

General-purpose nonlinear (multidimensional)

broyden1(F, xin[, iter, alpha, verbose])	Broyden's first method.
broyden2(F, xin[, iter, alpha, verbose])	Broyden's second method.
broyden3(F, xin[, iter, alpha, verbose])	Broyden's second method.
broyden_generalized(F, xin[, iter, alpha, ...])	Generalized Broyden's method.
anderson(F, xin[, iter, alpha, M, w0, verbose])	Extended Anderson method.
anderson2(F, xin[, iter, alpha, M, w0, verbose])	Anderson method.

broyden1 (*F, xin, iter=10, alpha=0.10000000000000001, verbose=False*)
Broyden's first method.

Updates Jacobian and computes inv(J) by a matrix inversion at every iteration. It's very slow.

The best norm |F(x)|=0.005 achieved in ~45 iterations.

broyden2 (*F, xin, iter=10, alpha=0.40000000000000002, verbose=False*)
Broyden's second method.

Updates inverse Jacobian by an optimal formula. There is NxN matrix multiplication in every iteration.

The best norm |F(x)|=0.003 achieved in ~20 iterations.

Recommended.

broyden3 (*F, xin, iter=10, alpha=0.40000000000000002, verbose=False*)
Broyden's second method.

Updates inverse Jacobian by an optimal formula. The NxN matrix multiplication is avoided.

The best norm |F(x)|=0.003 achieved in ~20 iterations.

Recommended.

broyden_generalized (*F, xin, iter=10, alpha=0.10000000000000001, M=5, verbose=False*)
Generalized Broyden's method.

Computes an approximation to the inverse Jacobian from the last M interations. Avoids NxN matrix multiplication, it only has MxM matrix multiplication and inversion.

M=0 .... linear mixing M=1 .... Anderson mixing with 2 iterations M=2 .... Anderson mixing with 3 iterations etc. optimal is M=5

anderson (*F, xin, iter=10, alpha=0.10000000000000001, M=5, w0=0.01, verbose=False*)
Extended Anderson method.

Computes an approximation to the inverse Jacobian from the last M interations. Avoids NxN matrix multiplication, it only has MxM matrix multiplication and inversion.

M=0 .... linear mixing M=1 .... Anderson mixing with 2 iterations M=2 .... Anderson mixing with 3 iterations etc. optimal is M=5

anderson2 (*F, xin, iter=10, alpha=0.10000000000000001, M=5, w0=0.01, verbose=False*)
Anderson method.

M=0 .... linear mixing M=1 .... Anderson mixing with 2 iterations M=2 .... Anderson mixing with 3 iterations etc. optimal is M=5

3.12.4 Utility Functions

line_search(f, myfprime, xk, pk, gfk, ...[, ...])	Find alpha that satisfies strong Wolfe conditions.
check_grad(func, grad, x0, *args)	

line_search (*f, myfprime, xk, pk, gfk, old_fval, old_old_fval, args=(), c1=0.0001, c2=0.90000000000000002, 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 (can be None).

xk : ndarray

Starting point.

pk : ndarray

Search direction.

gfk : ndarray

Gradient value for x=xk (xk being the current parameter estimate).

args : tuple

Additional arguments passed to objective function.

c1 : float

Parameter for Armijo condition rule.

c2 : float

Parameter for curvature condition rule.

Returns

alpha0 : float

Alpha for which `x_new = x0 + alpha * pk`.

fc : int

Number of function evaluations made.

gc : int

Number of gradient evaluations made.

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 [...].

check_grad (*func, grad, x0, *args*)

3.13 Signal processing (scipy.signal)

3.13.1 Convolution

convolve(in1, in2[, mode, old_behavior])	Convolve two N-dimensional arrays.
correlate(in1, in2[, mode, old_behavior])	Cross-correlate two N-dimensional arrays.
fftconvolve(in1, in2[, mode])	Convolve two N-dimensional arrays using FFT. See convolve.
convolve2d(in1, in2[, mode, boundary, ...])	Convolve two 2-dimensional arrays.
correlate2d(in1, in2[, mode, boundary, ...])	Cross-correlate two 2-dimensional arrays.
sepfir2d	sepfir2d(input, hrow, hcol) -> output

convolve(*in1, in2, mode='full', old_behavior=True*)

Convolve two N-dimensional arrays.

Convolve in1 and in2 with output size determined by mode.

Returns

out: array :

an N-dimensional array containing a subset of the discrete linear cross-correlation of in1 with in2.

correlate(*in1, in2, mode='full', old_behavior=True*)

Cross-correlate two N-dimensional arrays.

Cross-correlate in1 and in2 with the output size determined by the mode argument.

Returns

out: array :

an N-dimensional array containing a subset of the discrete linear cross-correlation of in1 with in2.

fftconvolve(*in1, in2, mode='full'*)

Convolve two N-dimensional arrays using FFT. See convolve.

convolve2d(*in1, in2, mode='full', boundary='fill', fillvalue=0, old_behavior=True*)

Convolve two 2-dimensional arrays.

Description:

Convolve in1 and in2 with output size determined by mode and boundary conditions determined by boundary and fillvalue.

Inputs:

in1 – a 2-dimensional array. in2 – a 2-dimensional array. mode – a flag indicating the size of the output

'valid' (0): The output consists only of those elements that
do not rely on the zero-padding.

'same' (1): The output is the same size as the input centered
with respect to the 'full' output.

'full' (2): The output is the full discrete linear convolution
of the inputs. (*Default*)

boundary – a flag indicating how to handle boundaries
'fill' : pad input arrays with fillvalue. (*Default*) 'wrap' : circular boundary conditions. 'symm' : symmetrical boundary conditions.

fillvalue – value to fill pad input arrays with (*Default* = 0)

Outputs: (out,)

out – a 2-dimensional array containing a subset of the discrete linear
convolution of in1 with in2.

correlate2d(*in1, in2, mode='full', boundary='fill', fillvalue=0, old_behavior=True*)
Cross-correlate two 2-dimensional arrays.

Description:

Cross correlate in1 and in2 with output size determined by mode and boundary conditions determined by boundary and fillvalue.

Inputs:

in1 – a 2-dimensional array. in2 – a 2-dimensional array. mode – a flag indicating the size of the output

'valid' (0): The output consists only of those elements that
do not rely on the zero-padding.

'same' (1): The output is the same size as the input centered
with respect to the 'full' output.

'full' (2): The output is the full discrete linear convolution
of the inputs. (*Default*)

boundary – a flag indicating how to handle boundaries
'fill' : pad input arrays with fillvalue. (*Default*) 'wrap' : circular boundary conditions. 'symm' : symmetrical boundary conditions.

fillvalue – value to fill pad input arrays with (*Default* = 0)

Outputs: (out,)

out – a 2-dimensional array containing a subset of the discrete linear
cross-correlation of in1 with in2.

sepfir2d()
sepfir2d(input, hrow, hcol) -> output

Description:

Convolve the rank-2 input array with the separable filter defined by the rank-1 arrays hrow, and hcol. Mirror symmetric boundary conditions are assumed. This function can be used to find an image given its B-spline representation.

3.13.2 B-splines

bspline(x, n)	bspline(x,n): B-spline basis function of order n.
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	cspline2d(input {, lambda, precision}) -> ck
qspline2d	qspline2d(input {, lambda, precision}) -> qk
spline_filter(Iin[, lmbda])	Smoothing spline (cubic) filtering of a rank-2 array.

bspline(*x, n*)
bspline(x,n): B-spline basis function of order n. uses numpy.piecewise and automatic function-generator.

gauss_spline(*x, n*)
Gaussian approximation to B-spline basis function of order n.

cspline1d(*signal, lamb=0.0*)
Compute cubic spline coefficients for rank-1 array.

Description:

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 .

Inputs:

signal – a rank-1 array representing samples of a signal. lamb – smoothing coefficient (default = 0.0)

Output:

c – cubic spline coefficients.

qspline1d(*signal, lamb=0.0*)
Compute quadratic spline coefficients for rank-1 array.

Description:

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 .

Inputs:

signal – a rank-1 array representing samples of a signal. lamb – smoothing coefficient (must be zero for now.)

Output:

c – cubic spline coefficients.

cspline2d()
cspline2d(input {, lambda, precision}) -> ck

Description:

Return the third-order B-spline coefficients over a regularly spacedi 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.

qspline2d()
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.

spline_filter(*Iin, lmbda=5.0*)
Smoothing spline (cubic) filtering of a rank-2 array.

Filter an input data set, Iin, using a (cubic) smoothing spline of fall-off lmbda.

3.13.3 Filtering

order_filter(a, domain, rank)	Perform an order filter on an N-dimensional array.
medfilt(volume[, kernel_size])	Perform a median filter on an N-dimensional array.
medfilt2d(input[, kernel_size])	Median filter two 2-dimensional arrays.
wiener(im[, mysize, noise])	Perform a Wiener filter on an N-dimensional array.
symiirorder1	symiirorder1(input, c0, z1 {, precision}) -> output
symiirorder2	symiirorder2(input, r, omega {, precision}) -> output
lfilter(b, a, x[, axis, zi])	Filter data along one-dimension with an IIR or FIR filter.
lfiltic(b, a, y[, x])	Construct initial conditions for lfilter
deconvolve(signal, divisor)	Deconvolves divisor out of signal.
hilbert(x[, N, axis])	Compute the analytic signal.
get_window(window, Nx[, fftbins])	Return a window of length Nx and type window.
detrend(data[, axis, type, bp])	Remove linear trend along axis from data.
resample(x, num[, t, axis, window])	Resample to num samples using Fourier method along the given axis.

order_filter(*a, domain, rank*)

Perform an order filter on an N-dimensional array.

Description:

Perform an order filter on the array in. The domain argument acts as a mask centered over each pixel. The non-zero elements of domain are used to select elements surrounding each input pixel which are placed in a list. The list is sorted, and the output for that pixel is the element corresponding to rank in the sorted list.

Inputs:

in – an N-dimensional input array. domain – a mask array with the same number of dimensions as in. Each

dimension should have an odd number of elements.

rank – an non-negative integer which selects the element from the
sorted list (0 corresponds to the largest element, 1 is the next largest element, etc.)

Output: (out,)

out – the results of the order filter in an array with the same
shape as in.

medfilt(*volume, kernel_size=None*)

Perform a median filter on an N-dimensional array.

Description:

Apply a median filter to the input array using a local window-size given by kernel_size.

Inputs:

in – An N-dimensional input array. kernel_size – 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.

Outputs: (out,)

out – An array the same size as input containing the median filtered
result.

medfilt2d(*input, kernel_size=3*)
Median filter two 2-dimensional arrays.

Description:

Apply a median filter to the input array using a local window-size given by kernel_size (must be odd).

Inputs:

in – An 2 dimensional input array. kernel_size – A scalar or an length-2 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.

Outputs: (out,)

out – An array the same size as input containing the median filtered
result.

wiener(*im, mysize=None, noise=None*)
Perform a Wiener filter on an N-dimensional array.

Description:

Apply a Wiener filter to the N-dimensional array in.

Inputs:

in – an N-dimensional array. kernel_size – A scalar or an N-length list giving the size of the

Wiener 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.

noise – The noise-power to use. If None, then noise is estimated as
the average of the local variance of the input.

Outputs: (out,)

out – Wiener filtered result with the same shape as in.

symiirorder1()
symiirorder1(input, c0, z1 {, precision}) -> output

Description:

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.

$$H(z) = \frac{c0}{(1-z1/z)\,(1 - z1\,z)}$$

The resulting signal will have mirror symmetric boundary conditions as well.

Inputs:

input – the input signal. c0, z1 – parameters in the transfer function. precision – specifies the precision for calculating initial conditions

of the recursive filter based on mirror-symmetric input.

Output:

output – filtered signal.

symiirorder2()

symiirorder2(input, r, omega {, precision}) -> output

Description:

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:

cs^2

H(z) = ——————————————————
(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

Inputs:

input – the input signal. r, omega – parameters in the transfer function. precision – specifies the precision for calculating initial conditions

of the recursive filter based on mirror-symmetric input.

Output:

output – filtered 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

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* = -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(len(a),len(b))-1. If zi=None or is not given then initial rest is assumed. SEE signal.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]*y[n] = b[0]*x[n] + b[1]*x[n-1] + ... + b[nb]*x[n-nb]
                      - a[1]*y[n-1] - ... - a[na]*y[n-na]
```

using the following difference equations:

```
y[m] = b[0]*x[m] + z[0,m-1]
z[0,m] = b[1]*x[m] + z[1,m-1] - a[1]*y[m]
...
z[n-3,m] = b[n-2]*x[m] + z[n-2,m-1] - a[n-2]*y[m]
z[n-2,m] = b[n-1]*x[m] - a[n-1]*y[m]
```

where m is the output sample number and n=max(len(a),len(b)) is the model order.

The rational transfer function describing this filter in the z-transform domain is:

```
                     -1               -nb
         b[0] + b[1]z  + ... + b[nb] z
Y(z) = ---------------------------------- X(z)
                     -1               -na
         a[0] + a[1]z  + ... + a[na] z
```

lfiltic(*b, a, y, x=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 inital conditions on the state vector zi which is used by lfilter to generate the output given the input.

If M=len(b)-1 and N=len(a)-1. Then, the initial conditions are given in the vectors x and y as:

```
x = {x[-1],x[-2],...,x[-M]}
y = {y[-1],y[-2],...,y[-N]}
```

If x is not given, its inital conditions are assumed zero. If either vector is too short, then zeros are added to achieve the proper length.

The output vector zi contains:

```
zi = {z_0[-1], z_1[-1], ..., z_K-1[-1]}  where K=max(M,N).
```

deconvolve(*signal, divisor*)
Deconvolves divisor out of signal.

hilbert(*x, N=None, axis=-1*)
Compute the analytic signal.

The transformation is done along the last axis by default.

Parameters

x : array-like

Signal data

N : int, optional

Number of Fourier components. Default: `x.shape[axis]`

axis : int, optional

Returns

xa : ndarray

Analytic signal of *x*, of each 1d array along axis

Notes

The analytic signal *x_a(t)* of *x(t)* is:

```
x_a = F^{-1}(F(x) 2U) = x + i y
```

where `F` is the Fourier transform, `U` the unit step function, and `y` the Hilbert transform of `x`. [1]

changes in scipy 0.8.0: new axis argument, new default axis=-1

References

[R5]

get_window(*window, Nx, fftbins=1*)

Return a window of length Nx and type window.

If fftbins is 1, create a "periodic" window ready to use with ifftshift and be multiplied by the result of an fft (SEE ALSO fftfreq).

Window types: boxcar, triang, blackman, hamming, hanning, bartlett,
parzen, bohman, blackmanharris, nuttall, barthann, kaiser (needs beta), gaussian (needs std), general_gaussian (needs power, width), slepian (needs width)

If the window requires no parameters, then it can be a string. If the window requires parameters, the window argument should 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.

detrend(*data, axis=-1, type='linear', bp=0*)

Remove linear trend along axis from data.

If type is 'constant' then remove mean only.

If bp is given, then it is a sequence of points at which to
break a piecewise-linear fit to the data.

resample(*x, num, t=None, axis=0, window=None*)

Resample to num samples using Fourier method along the given axis.

The resampled signal starts at the same value of x but is sampled with a spacing of len(x) / num * (spacing of x). Because a Fourier method is used, the signal is assumed periodic.

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).

If window is a string then use the named window. If window is a float, then it represents a value of beta for a kaiser window. If window is a tuple, then the first component is a string representing the window, and the next arguments are parameters for that window.

Possible windows are:

'flattop' – 'flat', 'flt' 'boxcar' – 'ones', 'box' 'triang' – 'traing', 'tri' 'parzen' – 'parz', 'par' 'bohman' – 'bman', 'bmn' 'blackmanharris' – 'blackharr', 'bkh' 'nuttall', – 'nutl', 'nut' 'barthann' – 'brthan', 'bth' 'blackman' – 'black', 'blk' 'hamming' – 'hamm', 'ham' 'bartlett' – 'bart', 'brt' 'hanning' – 'hann', 'han' ('kaiser', beta) – 'ksr' ('gaussian', std) – 'gauss', 'gss' ('general gauss', power, width) – 'general', 'ggs' ('slepian', width) – 'slep', 'optimal', 'dss'

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.

3.13.4 Filter design

remez(numtaps, bands, desired[, weight, Hz, ...])	Calculate the minimax optimal filter using Remez exchange algorithm.
firwin(N, cutoff[, width, window])	FIR Filter Design using windowed ideal filter method.
iirdesign(wp, ws, gpass, gstop[, analog, ...])	Complete IIR digital and analog filter design.
iirfilter(N, Wn[, rp, rs, btype, analog, ...])	IIR digital and analog filter design given order and critical points.
freqs(b, a[, worN, plot])	Compute frequency response of analog filter.
freqz(b[, a, worN, whole, plot])	Compute frequency response of a digital filter.
unique_roots(p[, tol, rtype])	Determine the unique roots and their multiplicities in two lists
residue(b, a[, tol, rtype])	Compute partial-fraction expansion of b(s) / a(s).
residuez(b, a[, tol, rtype])	Compute partial-fraction expansion of b(z) / a(z).
invres(r, p, k[, tol, rtype])	Compute b(s) and a(s) from partial fraction expansion: r,p,k

remez (*numtaps, bands, desired, weight=None, Hz=1, type='bandpass', maxiter=25, grid_density=16*)

Calculate the minimax optimal filter using Remez exchange algorithm.

Description:

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 bands using the remez exchange algorithm.

Inputs:

numtaps – The desired number of taps in the filter. bands – A montonic sequence containing the band edges. All elements

must be non-negative and less than 1/2 the sampling frequency as given by Hz.

desired – A sequency half the size of bands containing the desired gain
in each of the specified bands

weight – A relative weighting to give to each band region. type — The type of filter:

'bandpass' : flat response in bands. 'differentiator' : frequency proportional response in bands.

Outputs: (out,)

out – A rank-1 array containing the coefficients of the optimal (in a minimax sense) filter.

firwin (*N, cutoff, width=None, window='hamming'*)

FIR Filter Design using windowed ideal filter method.

Parameters

N – order of filter (number of taps) :

cutoff – cutoff frequency of filter (normalized so that 1 corresponds to :

Nyquist or pi radians / sample)

width – if width is not None, then assume it is the approximate width of :

the transition region (normalized so that 1 corresonds to pi) for use in kaiser FIR filter design.

window – desired window to use. See get_window for a list :

of windows and required parameters.

Returns

h – coefficients of length N fir filter. :

iirdesign (*wp, ws, gpass, gstop, analog=0, 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') or pole-zero ('zpk') form.

Parameters

wp, ws – Passband and stopband edge frequencies, normalized from 0 :

to 1 (1 corresponds to pi radians / 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]

gpass – The maximum loss in the passband (dB). :

gstop – The minimum attenuation in the stopband (dB). :

analog – Non-zero to design an analog filter (in this case wp and :

ws are in radians / second).

ftype – The type of iir filter to design: :

elliptic : 'ellip' Butterworth : 'butter', Chebyshev I : 'cheby1', Chebyshev II: 'cheby2', Bessel : 'bessel'

output – Type of output: numerator/denominator ('ba') or pole-zero ('zpk') :

Returns

b,a – Numerator and denominator of the iir filter. :

z,p,k – Zeros, poles, and gain of the iir filter.

iirfilter (*N, Wn, rp=None, rs=None, btype='band', analog=0, ftype='butter', output='ba'*)

IIR digital and analog filter design given order and critical points.

Design an Nth order lowpass digital or analog filter and return the filter coefficients in (B,A) (numerator, denominator) or (Z,P,K) form.

Parameters

N – the order of the filter. :

Wn – a scalar or length-2 sequence giving the critical frequencies. :

rp, rs – For chebyshev and elliptic filters provides the maximum ripple :

in the passband and the minimum attenuation in the stop band.

btype – the type of filter (lowpass, highpass, bandpass, or bandstop). :

analog – non-zero to return an analog filter, otherwise :

a digital filter is returned.

ftype – the type of IIR filter (Butterworth, Cauer (Elliptic), :

Bessel, Chebyshev1, Chebyshev2)

output – 'ba' for (b,a) output, 'zpk' for (z,p,k) output. :

SEE ALSO butterord, cheb1ord, cheb2ord, ellipord :

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.

b[0]*(jw)**(nb-1) + b[1]*(jw)**(nb-2) + ... + b[nb-1]

H(w) = ——————————————————————————

a[0]*(jw)**(na-1) + a[1]*(jw)**(na-2) + ... + a[na-1]

Parameters

b : ndarray

numerator of a linear filter

a : ndarray

numerator 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, the compute at that many frequencies. Otherwise, compute the response at frequencies given in worN.

Returns

w : ndarray

The frequencies at which h was computed.

h : ndarray

The frequency response.

freqz (*b, a=1, worN=None, whole=0, plot=None*)

Compute frequency response of a digital filter.

Given the numerator (b) and denominator (a) of a digital filter compute its frequency response.

jw -jw -jmw

jw B(e) b[0] + b[1]e + ... + b[m]e

H(e) = —- = ————————————————

jw -jw -jnw

A(e) a[0] + a[2]e + ... + a[n]e

Parameters

b : ndarray

numerator of a linear filter

a : ndarray

numerator of a linear filter

worN : {None, int}, optional

If None, then compute at 512 frequencies around the unit circle. If a single integer, the compute at that many frequencies. Otherwise, compute the response at frequencies given in worN

whole : {0,1}, optional

Normally, frequencies are computed from 0 to pi (upper-half of unit-circle. If whole is non-zero compute frequencies from 0 to 2*pi.

Returns

w : ndarray

The frequencies at which h was computed.

h : ndarray

The frequency response.

unique_roots(*p, tol=0.001, rtype='min'*)

Determine the unique roots and their multiplicities in two lists

Inputs:

p – The list of roots tol — The tolerance for two roots to be considered equal. rtype — How to determine the returned root from the close

ones: 'max': pick the maximum

'min': pick the minimum 'avg': average roots

Outputs: (pout, mult)

pout – The list of sorted roots mult – The multiplicity of each root

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)

b(s) b[0] s**(M-1) + b[1] s**(M-2) + ... + b[M-1]

H(s) = —— = ————————————————————-

a(s) a[0] s**(N-1) + a[1] s**(N-2) + ... + a[N-1]

r[0] r[1] r[-1]

= ——— + ——— + ... + ——— + k(s)
(s-p[0]) (s-p[1]) (s-p[-1])

If there are any repeated roots (closer than tol), then the partial fraction expansion has terms like

r[i] r[i+1] r[i+n-1]

——— + ——— + ... + ——— (s-p[i]) (s-p[i])**2 (s-p[i])**n

Returns

r : ndarray

Residues

p : ndarray

Poles

k : ndarray

Coefficients of the direct polynomial term.

See Also:

invres, poly, polyval, unique_roots

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)

b(z) b[0] + b[1] z**(-1) + ... + b[M-1] z**(-M+1)

H(z) = ——— = ——————————————————————-

a(z) a[0] + a[1] z**(-1) + ... + a[N-1] z**(-N+1)

r[0] r[-1]

= ————— + ... + ————————- + k[0] + k[1]z(-1) ...**
(1-p[0]z**(-1)) (1-p[-1]z**(-1))

If there are any repeated roots (closer than tol), then the partial fraction expansion has terms like

r[i] r[i+1] r[i+n-1]

————— + ————————— + ... + ————————— (1-p[i]z**(-1)) (1-p[i]z**(-1))**2 (1-p[i]z**(-1))**n

See also: invresz, poly, polyval, unique_roots

invres (*r, p, k, tol=0.001, rtype='avg'*)

Compute b(s) and a(s) from partial fraction expansion: r,p,k

If M = len(b) and N = len(a)

b(s) b[0] x**(M-1) + b[1] x**(M-2) + ... + b[M-1]

H(s) = ——— = ————————————————————-

a(s) a[0] x**(N-1) + a[1] x**(N-2) + ... + a[N-1]

r[0] r[1] r[-1]

= ——— + ——— + ... + ——— + k(s)
(s-p[0]) (s-p[1]) (s-p[-1])

If there are any repeated roots (closer than tol), then the partial fraction expansion has terms like

r[i] r[i+1] r[i+n-1]

——— + ——— + ... + ——— (s-p[i]) (s-p[i])**2 (s-p[i])**n

See Also:

`residue`, `poly`, `polyval`, `unique_roots`

3.13.5 Matlab-style IIR filter design

`butter`(N, Wn[, btype, analog, output])	Butterworth digital and analog filter design.
`buttord`(wp, ws, gpass, gstop[, analog])	Butterworth filter order selection.
`cheby1`(N, rp, Wn[, btype, analog, output])	Chebyshev type I digital and analog filter design.
`cheb1ord`(wp, ws, gpass, gstop[, analog])	Chebyshev type I filter order selection.
`cheby2`(N, rs, Wn[, btype, analog, output])	Chebyshev type I digital and analog filter design.
`cheb2ord`(wp, ws, gpass, gstop[, analog])	Chebyshev type II filter order selection.
`ellip`(N, rp, rs, Wn[, btype, analog, output])	Elliptic (Cauer) digital and analog filter design.
`ellipord`(wp, ws, gpass, gstop[, analog])	Elliptic (Cauer) filter order selection.
`bessel`(N, Wn[, btype, analog, output])	Bessel digital and analog filter design.

butter(*N, Wn, btype='low', analog=0, output='ba'*)
Butterworth digital and analog filter design.

Description:

Design an Nth order lowpass digital or analog Butterworth filter and return the filter coefficients in (B,A) or (Z,P,K) form.

See also buttord.

buttord(*wp, ws, gpass, gstop, analog=0*)
Butterworth filter order selection.

Return the order of the lowest order digital 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 – Passband and stopband edge frequencies, normalized from 0 :

to 1 (1 corresponds to pi radians / 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]

gpass – The maximum loss in the passband (dB). :

gstop – The minimum attenuation in the stopband (dB). :

analog – Non-zero to design an analog filter (in this case wp and :

ws are in radians / second).

Returns

ord – The lowest order for a Butterworth filter which meets specs. :

Wn – The Butterworth natural frequency (i.e. the "3dB frequency"). :

Should be used with scipy.signal.butter to give filter results.

cheby1 (*N, rp, Wn, btype='low', analog=0, output='ba'*)

Chebyshev type I digital and analog filter design.

Description:

Design an Nth order lowpass digital or analog Chebyshev type I filter and return the filter coefficients in (B,A) or (Z,P,K) form.

See also cheb1ord.

cheb1ord (*wp, ws, gpass, gstop, analog=0*)

Chebyshev type I filter order selection.

Return the order of the lowest order digital 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 – Passband and stopband edge frequencies, normalized from 0 :

to 1 (1 corresponds to pi radians / 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]

gpass – The maximum loss in the passband (dB). :

gstop – The minimum attenuation in the stopband (dB). :

analog – Non-zero to design an analog filter (in this case wp and :

ws are in radians / second).

Returns

ord – The lowest order for a Chebyshev type I filter that meets specs. :

Wn – The Chebyshev natural frequency (the "3dB frequency") for :

use with scipy.signal.cheby1 to give filter results.

cheby2 (*N, rs, Wn, btype='low', analog=0, output='ba'*)

Chebyshev type I digital and analog filter design.

Description:

Design an Nth order lowpass digital or analog Chebyshev type I filter and return the filter coefficients in (B,A) or (Z,P,K) form.

See also cheb2ord.

cheb2ord (*wp, ws, gpass, gstop, analog=0*)

Chebyshev type II filter order selection.

Description:

Return the order of the lowest order digital 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 – Passband and stopband edge frequencies, normalized from 0 :

to 1 (1 corresponds to pi radians / 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]

gpass – The maximum loss in the passband (dB). :

gstop – The minimum attenuation in the stopband (dB). :

analog – Non-zero to design an analog filter (in this case wp and :

ws are in radians / second).

Returns

ord – The lowest order for a Chebyshev type II filter that meets specs. :

Wn – The Chebyshev natural frequency for :

use with scipy.signal.cheby2 to give the filter.

ellip (*N, rp, rs, Wn, btype='low', analog=0, output='ba'*)
Elliptic (Cauer) digital and analog filter design.

Description:

Design an Nth order lowpass digital or analog elliptic filter and return the filter coefficients in (B,A) or (Z,P,K) form.

See also ellipord.

ellipord (*wp, ws, gpass, gstop, analog=0*)
Elliptic (Cauer) filter order selection.

Return the order of the lowest order digital elliptic filter that loses no more than gpass dB in the passband and has at least gstop dB attenuation in the stopband.

Parameters

wp, ws – Passband and stopband edge frequencies, normalized from 0 :

to 1 (1 corresponds to pi radians / 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]

gpass – The maximum loss in the passband (dB). :

gstop – The minimum attenuation in the stopband (dB). :

analog – Non-zero to design an analog filter (in this case wp and :

ws are in radians / second).

Returns

ord – The lowest order for an Elliptic (Cauer) filter that meets specs. :

Wn – The natural frequency for use with scipy.signal.ellip :

to give the filter.

bessel (*N, Wn, btype='low', analog=0, output='ba'*)
Bessel digital and analog filter design.

Description:

Design an Nth order lowpass digital or analog Bessel filter and return the filter coefficients in (B,A) or (Z,P,K) form.

3.13.6 Linear Systems

lti(*args, **kwords)	Linear Time Invariant class which simplifies representation.
lsim(system, U, T[, X0, interp])	Simulate output of a continuous-time linear system.
impulse(system[, X0, T, N])	Impulse response of continuous-time system.
step(system[, X0, T, N])	Step response of continuous-time system.

class lti (**args, **kwords*)

Linear Time Invariant class which simplifies representation.

Methods

impulse([X0, T, N])
output(U, T[, X0])
step([X0, T, N])

impulse (*X0=None, T=None, N=None*)

output (*U, T, X0=None*)

step (*X0=None, T=None, N=None*)

lsim (*system, U, T, X0=None, interp=1*)

Simulate output of a continuous-time linear system.

Inputs:

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 – 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 – the time steps at which the input is defined and at which
the output is desired.

X0 – (optional, default=0) the initial conditions on the state vector. interp – linear (1) or zero-order hold (0) interpolation

Outputs: (T, yout, xout)

T – the time values for the output. yout – the response of the system. xout – the time-evolution of the state-vector.

impulse (*system, X0=None, T=None, N=None*)

Impulse response of continuous-time system.

Inputs:

system – an instance of the LTI class or a tuple with 2, 3, or 4
elements representing (num, den), (zero, pole, gain), or (A, B, C, D) representation of the system.

X0 – (optional, default = 0) inital state-vector. T – (optional) time points (autocomputed if not given). N – (optional) number of time points to autocompute (100 if not given).

Ouptuts: (T, yout)

T – output time points, yout – impulse response of system (except possible singularities at 0).

step (*system, X0=None, T=None, N=None*)
Step response of continuous-time system.

Inputs:

system – an instance of the LTI class or a tuple with 2, 3, or 4
elements representing (num, den), (zero, pole, gain), or (A, B, C, D) representation of the system.

X0 – (optional, default = 0) inital state-vector. T – (optional) time points (autocomputed if not given). N – (optional) number of time points to autocompute (100 if not given).

Ouptuts: (T, yout)

T – output time points, yout – step response of system.

3.13.7 LTI Reresentations

tf2zpk(b, a)	Return zero, pole, gain (z,p,k) representation from a numerator, denominator representation of a linear filter.
zpk2tf(z, p, k)	Return polynomial transfer function representation from zeros
tf2ss(num, den)	Transfer function to state-space representation.
ss2tf(A, B, C, D[, input])	State-space to transfer function.
zpk2ss(z, p, k)	Zero-pole-gain representation to state-space representation
ss2zpk(A, B, C, D[, input])	State-space representation to zero-pole-gain representation.

tf2zpk (*b, a*)
Return zero, pole, gain (z,p,k) representation from a numerator, denominator representation of a linear filter.

Parameters
b : ndarray

numerator polynomial.

a : ndarray

numerator and denominator polynomials.

Returns
z : ndarray

zeros of the transfer function.

p : ndarray

poles of the transfer function.

k : float

system gain.

If some values of b are too close to 0, they are removed. In that case, a :

BadCoefficients warning is emitted. :

zpk2tf (*z, p, k*)
Return polynomial transfer function representation from zeros and poles

Parameters

z : ndarray

zeros of the transfer function.

p : ndarray

poles of the transfer function.

k : float

system gain.

Returns

b : ndarray

numerator polynomial.

a : ndarray

numerator and denominator polynomials.

tf2ss (*num, den*)

Transfer function to state-space representation.

Inputs:

num, den – sequences representing the numerator and denominator polynomials.

Outputs:

A, B, C, D – state space representation of the system.

ss2tf (*A, B, C, D, input=0*)

State-space to transfer function.

Inputs:

A, B, C, D – state-space representation of linear system. input – For multiple-input systems, the input to use.

Outputs:

num, den – Numerator and denominator polynomials (as sequences)
respectively.

zpk2ss (*z, p, k*)

Zero-pole-gain representation to state-space representation

Inputs:

z, p, k – zeros, poles (sequences), and gain of system

Outputs:

A, B, C, D – state-space matrices.

ss2zpk (*A, B, C, D, input=0*)

State-space representation to zero-pole-gain representation.

Inputs:

A, B, C, D – state-space matrices. input – for multiple-input systems, the input to use.

Outputs:

z, p, k – zeros and poles in sequences and gain constant.

3.13.8 Waveforms

sawtooth(t[, width])	Returns a periodic sawtooth waveform with period 2*pi
square(t[, duty])	Returns a periodic square-wave waveform with period 2*pi
gausspulse(t[, fc, bw, bwr, tpr, retquad, ...])	Return a gaussian modulated sinusoid: exp(-a t^2) exp(1j*2*pi*fc)
chirp(t[, f0, t1, f1, method, phi, qshape])	Frequency-swept cosine generator.

sawtooth(*t, width=1*)

Returns a periodic sawtooth waveform with period 2*pi which rises from -1 to 1 on the interval 0 to width*2*pi and drops from 1 to -1 on the interval width*2*pi to 2*pi width must be in the interval [0,1]

square(*t, duty=0.5*)

Returns a periodic square-wave waveform with period 2*pi which is +1 from 0 to 2*pi*duty and -1 from 2*pi*duty to 2*pi duty must be in the interval [0,1]

gausspulse(*t, fc=1000, bw=0.5, bwr=-6, tpr=-60, retquad=0, retenv=0*)

Return a gaussian modulated sinusoid: exp(-a t^2) exp(1j*2*pi*fc)

If retquad is non-zero, then return the real and imaginary parts
(inphase and quadrature)

If retenv is non-zero, then return the envelope (unmodulated signal). Otherwise, return the real part of the modulated sinusoid.

Inputs:

t – Input array. fc – Center frequency (Hz). bw – Fractional bandwidth in frequency domain of pulse (Hz). bwr – Reference level at which fractional bandwidth is calculated (dB). tpr – If t is 'cutoff', then the function returns the cutoff time for when the

pulse amplitude falls below tpr (in dB).

retquad – Return the quadrature (imaginary) as well as the real part of the signal retenv – Return the envelope of th signal.

chirp(*t, f0=0, t1=1, f1=100, method='linear', phi=0, qshape=None*)

Frequency-swept cosine generator.

Parameters

t : ndarray

Times at which to evaluate the waveform.

f0 : float or ndarray, optional

Frequency (in Hz) of the waveform at time 0. If *f0* is an ndarray, it specifies the frequency change as a polynomial in *t* (see Notes below).

t1 : float, optional

Time at which *f1* is specified.

f1 : float, optional

Frequency (in Hz) of the waveform at time *t1*.

method : {'linear', 'quadratic', 'logarithmic'}, optional

Kind of frequency sweep.

phi : float

Phase offset, in degrees.

qshape : {'convex', 'concave'}

If method is 'quadratic', *qshape* specifies its shape.

Notes

If *f0* is an array, it forms the coefficients of a polynomial in *t* (see *numpy.polval*). The polynomial determines the waveform frequency change in time. In this case, the values of *f1*, *t1*, *method*, and *qshape* are ignored.

3.13.9 Window functions

boxcar(M[, sym])	The M-point boxcar window.
triang(M[, sym])	The M-point triangular window.
parzen(M[, sym])	The M-point Parzen window.
bohman(M[, sym])	The M-point Bohman window.
blackman(M[, sym])	The M-point Blackman window.
blackmanharris(M[, sym])	The M-point minimum 4-term Blackman-Harris window.
nuttall(M[, sym])	A minimum 4-term Blackman-Harris window according to Nuttall.
flattop(M[, sym])	The M-point Flat top window.
bartlett(M[, sym])	The M-point Bartlett window.
hann(M[, sym])	The M-point Hanning window.
barthann(M[, sym])	Return the M-point modified Bartlett-Hann window.
hamming(M[, sym])	The M-point Hamming window.
kaiser(M, beta[, sym])	Return a Kaiser window of length M with shape parameter beta.
gaussian(M, std[, sym])	Return a Gaussian window of length M with standard-deviation std.
general_gaussian(M, p, sig[, sym])	Return a window with a generalized Gaussian shape.
slepian(M, width[, sym])	Return the M-point slepian window.

boxcar(*M, sym=1*)
The M-point boxcar window.

triang(*M, sym=1*)
The M-point triangular window.

parzen(*M, sym=1*)
The M-point Parzen window.

bohman(*M, sym=1*)
The M-point Bohman window.

blackman(*M, sym=1*)
The M-point Blackman window.

blackmanharris(*M, sym=1*)
The M-point minimum 4-term Blackman-Harris window.

nuttall(*M, sym=1*)
A minimum 4-term Blackman-Harris window according to Nuttall.

flattop(*M, sym=1*)
The M-point Flat top window.

bartlett(*M, sym=1*)
The M-point Bartlett window.

hann(*M, sym=1*)
The M-point Hanning window.

barthann(*M, sym=1*)
Return the M-point modified Bartlett-Hann window.

hamming(*M, sym=1*)
The M-point Hamming window.

kaiser(*M, beta, sym=1*)
Return a Kaiser window of length M with shape parameter beta.

gaussian(*M, std, sym=1*)
Return a Gaussian window of length M with standard-deviation std.

general_gaussian(*M, p, sig, sym=1*)
Return a window with a generalized Gaussian shape.

exp(-0.5*(x/sig)**(2*p))

half power point is at (2*log(2)))**(1/(2*p))*sig

slepian(*M, width, sym=1*)
Return the M-point slepian window.

3.13.10 Wavelets

daub(p)	The coefficients for the FIR low-pass filter producing Daubechies wavelets.
qmf(hk)	Return high-pass qmf filter from low-pass
cascade(hk[, J])	(x,phi,psi) at dyadic points K/2**J from filter coefficients.

daub(*p*)
The coefficients for the FIR low-pass filter producing Daubechies wavelets.

p>=1 gives the order of the zero at f=1/2. There are 2p filter coefficients.

qmf(*hk*)
Return high-pass qmf filter from low-pass

cascade(*hk, J=7*)
(x,phi,psi) at dyadic points K/2**J from filter coefficients.

Inputs:
hk – coefficients of low-pass filter J – values will be computed at grid points $K/2^J$

Outputs:

x – the dyadic points $K/2^J$ for $K=0...N*(2^J)-1$
where len(hk)=len(gk)=N+1

phi – the scaling function phi(x) at x
$phi(x) = sum_{k=0}^{N} h_k phi(2x-k)$

psi – the wavelet function psi(x) at x

$psi(x) = sum_{k=0}^N g_k phi(2x-k)$

Only returned if gk is not None

Algorithm:

Uses the vector cascade algorithm described by Strang and Nguyen in “Wavelets and Filter Banks”

Builds a dictionary of values and slices for quick reuse. Then inserts vectors into final vector at then end

3.14 Sparse matrices (scipy.sparse)

3.14.1 Sparse Matrices

Scipy 2D sparse matrix module.

Original code by Travis Oliphant. Modified and extended by Ed Schofield, Robert Cimrman, and Nathan Bell.

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 lil_matrix (recommended) or dok_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.

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.

3.14.2 Example 1

Construct a 1000x1000 lil_matrix and add some values to it:

```
>>> from scipy import sparse, linsolve
>>> from numpy import linalg
>>> from numpy.random import rand
>>> A = sparse.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:

```
>>> A = A.tocsr()
>>> b = rand(1000)
>>> x = linsolve.spsolve(A, b)
```

Convert it to a dense matrix and solve, and check that the result is the same:

```
>>> x_ = linalg.solve(A.todense(), b)
```

Now we can compute norm of the error with:

```
>>> err = linalg.norm(x-x_)
>>> err < 1e-10
True
```

It should be small :)

3.14.3 Example 2

Construct a matrix in COO format:

```
>>> 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.

```
>>> 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.

3.14.4 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).

3.14.5 Sparse matrix classes

csc_matrix(arg1[, shape, dtype, copy, dims, ...])	Compressed Sparse Column matrix
csr_matrix(arg1[, shape, dtype, copy, dims, ...])	Compressed Sparse Row matrix
bsr_matrix(arg1[, shape, dtype, copy, blocksize])	Block Sparse Row matrix
lil_matrix(arg1[, shape, dtype, copy])	Row-based linked list sparse matrix
dok_matrix(arg1[, shape, dtype, copy])	Dictionary Of Keys based sparse matrix.
coo_matrix(arg1[, shape, dtype, copy, dims])	A sparse matrix in COOrdinate format.
dia_matrix(arg1[, shape, dtype, copy])	Sparse matrix with DIAgonal storage

class csc_matrix(*arg1, shape=None, dtype=None, copy=False, dims=None, nzmax=None*)

Compressed Sparse Column matrix

This can be instantiated in several ways:

csc_matrix(D)

with a dense matrix or rank-2 ndarray D

csc_matrix(S)
with another sparse matrix S (equivalent to S.tocsc())

csc_matrix((M, N), [dtype])
to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype='d'.

csc_matrix((data, ij), [shape=(M, N)])
where `data` and `ij` satisfy the relationship `a[ij[0, k], ij[1, k]] = data[k]`

csc_matrix((data, indices, indptr), [shape=(M, N)])
is the standard CSC representation where the row indices for column i are stored in `indices[indptr[i]:indices[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

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

```
>>> from scipy.sparse import *
>>> from scipy import *
>>> csc_matrix( (3,4), dtype=int8 ).todense()
matrix([[0, 0, 0, 0],
        [0, 0, 0, 0],
        [0, 0, 0, 0]], dtype=int8)


>>> row = array([0,2,2,0,1,2])
>>> col = array([0,0,1,2,2,2])
>>> data = array([1,2,3,4,5,6])
>>> csc_matrix( (data,(row,col)), shape=(3,3) ).todense()
matrix([[1, 0, 4],
        [0, 0, 5],
        [2, 3, 6]])


>>> indptr = array([0,2,3,6])
>>> indices = array([0,2,2,0,1,2])
>>> data = array([1,2,3,4,5,6])
>>> csc_matrix( (data,indices,indptr), shape=(3,3) ).todense()
matrix([[1, 0, 4],
        [0, 0, 5],
        [2, 3, 6]])
```

Methods

asformat(format)	Return this matrix in a given sparse format
asfptype()	Upcast matrix to a floating point format (if necessary)
astype(t)	
check_format([full_check])	check whether the matrix format is valid
conj()	
conjugate()	
copy()	
diagonal()	Returns the main diagonal of the matrix
dot(*args, **kwds)	*dot* is deprecated!
eliminate_zeros()	Remove zero entries from the matrix
ensure_sorted_indices([inplace])	Return a copy of this matrix where the column indices are sorted
getH()	
get_shape()	
getcol(j)	Returns a copy of column j of the matrix, as an (m x 1) sparse
getdata(*args, **kwds)	*getdata* is deprecated!
getformat()	
getmaxprint()	
getnnz()	
getrow(i)	Returns a copy of row i of the matrix, as a (1 x n) sparse
listprint(*args, **kwds)	*listprint* is deprecated!
matmat(*args, **kwds)	*matmat* is deprecated!
matvec(*args, **kwds)	*matvec* is deprecated!
mean([axis])	Average the matrix over the given axis.
multiply(other)	Point-wise multiplication by another matrix
nonzero()	nonzero indices
prune()	Remove empty space after all non-zero elements.
reshape(shape)	
rmatvec(*args, **kwds)	*rmatvec* is deprecated!
rowcol(*args, **kwds)	*rowcol* is deprecated!
save(file_name[, format])	
set_shape(shape)	
setdiag(values[, k])	Fills the diagonal elements {a_ii} with the values from the given sequence.
sort_indices()	Sort the indices of this matrix *in place*
sorted_indices()	Return a copy of this matrix with sorted indices
sum([axis])	Sum the matrix over the given axis.
sum_duplicates()	Eliminate duplicate matrix entries by adding them together
toarray()	
tobsr([blocksize])	
tocoo([copy])	Return a COOrdinate representation of this matrix
tocsc([copy])	
tocsr()	
todense()	
todia()	
todok()	
tolil()	
transpose([copy])	

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

asfptype()
Upcast matrix to a floating point format (if necessary)

astype(*t*)

check_format(*full_check=True*)
check whether the matrix format is valid

Parameters
- full_check : {bool}

- True - rigorous check, O(N) operations : default
- False - basic check, O(1) operations

conj()

conjugate()

copy()

diagonal()
Returns the main diagonal of the matrix

dot(**args, **kwds*)
dot is deprecated!

eliminate_zeros()
Remove zero entries from the matrix

The is an *in place* operation

ensure_sorted_indices(*inplace=False*)
Return a copy of this matrix where the column indices are sorted

getH()

get_shape()

getcol(*j*)
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

getdata(**args, **kwds*)
getdata is deprecated!

getformat()

getmaxprint()

getnnz()

getrow(*i*)
Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

listprint(**args, **kwds*)
listprint is deprecated!

Provides a way to print over a single index.

matmat(**args, **kwds*)
matmat is deprecated!

matvec(**args, **kwds*)
matvec is deprecated!

mean(*axis=None*)
Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning a scalar.

multiply(*other*)
Point-wise multiplication by another matrix

nonzero()
nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

prune()
Remove empty space after all non-zero elements.

reshape(*shape*)

rmatvec(**args, **kwds*)
rmatvec is deprecated!

Multiplies the vector 'other' by the sparse matrix, returning a
dense vector as a result.

If 'conjugate' is True:

- returns A.transpose().conj() * other

Otherwise:

- returns A.transpose() * other.

rowcol(**args, **kwds*)
rowcol is deprecated!

save(*file_name, format='%d %d %fn'*)

set_shape(*shape*)

setdiag(*values, k=0*)
Fills the diagonal elements {a_ii} with the values from the given sequence. If k != 0, fills the off-diagonal elements {a_{i,i+k}} instead.

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.

sort_indices()
Sort the indices of this matrix *in place*

sorted_indices()
Return a copy of this matrix with sorted indices

sum(*axis=None*)
Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

sum_duplicates()
Eliminate duplicate matrix entries by adding them together

The is an *in place* operation

toarray()

tobsr(*blocksize=None*)

tocoo(*copy=True*)
Return a COOrdinate representation of this matrix

When copy=False the index and data arrays are not copied.

tocsc(*copy=False*)

tocsr()

todense()

todia()

todok()

tolil()

transpose(*copy=False*)

class csr_matrix(*arg1, shape=None, dtype=None, copy=False, dims=None, nzmax=None*)
Compressed Sparse Row matrix

This can be instantiated in several ways:

csr_matrix(D)
with a dense matrix or rank-2 ndarray D

csr_matrix(S)
with another sparse matrix S (equivalent to S.tocsr())

csr_matrix((M, N), [dtype])
to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype='d'.

csr_matrix((data, ij), [shape=(M, N)])
where `data` and `ij` satisfy the relationship `a[ij[0, k], ij[1, 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]:indices[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

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

```
>>> from scipy.sparse import *
>>> from scipy import *
>>> csr_matrix( (3,4), dtype=int8 ).todense()
matrix([[0, 0, 0, 0],
        [0, 0, 0, 0],
        [0, 0, 0, 0]], dtype=int8)


>>> row = array([0,0,1,2,2,2])
>>> col = array([0,2,2,0,1,2])
>>> data = array([1,2,3,4,5,6])
>>> csr_matrix( (data,(row,col)), shape=(3,3) ).todense()
matrix([[1, 0, 2],
        [0, 0, 3],
        [4, 5, 6]])


>>> indptr = array([0,2,3,6])
>>> indices = array([0,2,2,0,1,2])
>>> data = array([1,2,3,4,5,6])
>>> csr_matrix( (data,indices,indptr), shape=(3,3) ).todense()
matrix([[1, 0, 2],
        [0, 0, 3],
        [4, 5, 6]])
```

Methods

asformat(format)	Return this matrix in a given sparse format
asfptype()	Upcast matrix to a floating point format (if necessary)
astype(t)	
check_format([full_check])	check whether the matrix format is valid
conj()	
conjugate()	
copy()	
diagonal()	Returns the main diagonal of the matrix
dot(*args, **kwds)	*dot* is deprecated!
eliminate_zeros()	Remove zero entries from the matrix
ensure_sorted_indices([inplace])	Return a copy of this matrix where the column indices are sorted
getH()	
get_shape()	
getcol(j)	Returns a copy of column j of the matrix, as an (m x 1) sparse
getdata(*args, **kwds)	*getdata* is deprecated!
getformat()	
getmaxprint()	
getnnz()	
getrow(i)	Returns a copy of row i of the matrix, as a (1 x n) sparse
listprint(*args, **kwds)	*listprint* is deprecated!
matmat(*args, **kwds)	*matmat* is deprecated!
matvec(*args, **kwds)	*matvec* is deprecated!
mean([axis])	Average the matrix over the given axis.
multiply(other)	Point-wise multiplication by another matrix
nonzero()	nonzero indices
prune()	Remove empty space after all non-zero elements.
reshape(shape)	
rmatvec(*args, **kwds)	*rmatvec* is deprecated!
rowcol(*args, **kwds)	*rowcol* is deprecated!
save(file_name[, format])	
set_shape(shape)	
setdiag(values[, k])	Fills the diagonal elements {a_ii} with the values from the given sequence.
sort_indices()	Sort the indices of this matrix *in place*
sorted_indices()	Return a copy of this matrix with sorted indices
sum([axis])	Sum the matrix over the given axis.
sum_duplicates()	Eliminate duplicate matrix entries by adding them together
toarray()	
tobsr([blocksize, copy])	
tocoo([copy])	Return a COOrdinate representation of this matrix
tocsc()	
tocsr([copy])	
todense()	
todia()	
todok()	
tolil()	
transpose([copy])	

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

asfptype()
Upcast matrix to a floating point format (if necessary)

astype(*t*)

check_format(*full_check=True*)
check whether the matrix format is valid

Parameters
- full_check : {bool}

- True - rigorous check, O(N) operations : default
- False - basic check, O(1) operations

conj()

conjugate()

copy()

diagonal()
Returns the main diagonal of the matrix

dot(**args, **kwds*)
dot is deprecated!

eliminate_zeros()
Remove zero entries from the matrix

The is an *in place* operation

ensure_sorted_indices(*inplace=False*)
Return a copy of this matrix where the column indices are sorted

getH()

get_shape()

getcol(*j*)
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

getdata(**args, **kwds*)
getdata is deprecated!

getformat()

getmaxprint()

getnnz()

getrow(*i*)
Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

listprint(**args, **kwds*)
listprint is deprecated!

Provides a way to print over a single index.

matmat(**args, **kwds*)
matmat is deprecated!

matvec(**args, **kwds*)
matvec is deprecated!

mean(*axis=None*)
Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning a scalar.

multiply(*other*)
Point-wise multiplication by another matrix

nonzero()
nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

prune()
Remove empty space after all non-zero elements.

reshape(*shape*)

rmatvec(**args, **kwds*)
rmatvec is deprecated!

Multiplies the vector 'other' by the sparse matrix, returning a
dense vector as a result.

If 'conjugate' is True:

- returns A.transpose().conj() * other

Otherwise:

- returns A.transpose() * other.

rowcol(**args, **kwds*)
rowcol is deprecated!

save(*file_name, format='%d %d %fn'*)

set_shape(*shape*)

setdiag(*values, k=0*)
Fills the diagonal elements {a_ii} with the values from the given sequence. If k != 0, fills the off-diagonal elements {a_{i,i+k}} instead.

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.

sort_indices()
Sort the indices of this matrix *in place*

sorted_indices()
Return a copy of this matrix with sorted indices

sum(*axis=None*)
Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

sum_duplicates()
Eliminate duplicate matrix entries by adding them together

The is an *in place* operation

toarray()

tobsr(*blocksize=None, copy=True*)

tocoo(*copy=True*)
Return a COOrdinate representation of this matrix

When copy=False the index and data arrays are not copied.

tocsc()

tocsr(*copy=False*)

todense()

todia()

todok()

tolil()

transpose(*copy=False*)

class bsr_matrix(*arg1, shape=None, dtype=None, copy=False, blocksize=None*)
Block Sparse Row matrix

This can be instantiated in several ways:

bsr_matrix(D, [blocksize=(R,C)])
with a dense matrix or rank-2 ndarray D

bsr_matrix(S, [blocksize=(R,C)])
with another sparse matrix S (equivalent to S.tobsr())

bsr_matrix((M, N), [blocksize=(R,C), dtype])
to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype='d'.

bsr_matrix((data, ij), [blocksize=(R,C), shape=(M, N)])
where `data` and `ij` satisfy `a[ij[0, k], ij[1, k]] = data[k]`

bsr_matrix((data, indices, indptr), [shape=(M, N)])
is the standard BSR representation where the block column indices for row i are stored in `indices[indptr[i]:indices[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

Summary

- 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

```
>>> from scipy.sparse import *
>>> from scipy import *
>>> bsr_matrix( (3,4), dtype=int8 ).todense()
matrix([[0, 0, 0, 0],
        [0, 0, 0, 0],
        [0, 0, 0, 0]], dtype=int8)


>>> row  = array([0,0,1,2,2,2])
>>> col  = array([0,2,2,0,1,2])
>>> data = array([1,2,3,4,5,6])
>>> bsr_matrix( (data,(row,col)), shape=(3,3) ).todense()
matrix([[1, 0, 2],
        [0, 0, 3],
        [4, 5, 6]])


>>> indptr  = array([0,2,3,6])
>>> indices = array([0,2,2,0,1,2])
>>> data    = array([1,2,3,4,5,6]).repeat(4).reshape(6,2,2)
>>> bsr_matrix( (data,indices,indptr), shape=(6,6) ).todense()
matrix([[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]])
```

Methods

asformat(format)	Return this matrix in a given sparse format
asfptype()	Upcast matrix to a floating point format (if necessary)
astype(t)	
check_format([full_check])	check whether the matrix format is valid
conj()	
conjugate()	
copy()	
diagonal()	Returns the main diagonal of the matrix
dot(*args, **kwds)	*dot* is deprecated!
eliminate_zeros()	
ensure_sorted_indices([inplace])	Return a copy of this matrix where the column indices are sorted
getH()	
get_shape()	
getcol(j)	Returns a copy of column j of the matrix, as an (m x 1) sparse
getdata(ind)	
getformat()	
getmaxprint()	
getnnz()	
getrow(i)	Returns a copy of row i of the matrix, as a (1 x n) sparse
listprint(*args, **kwds)	*listprint* is deprecated!
matmat(other)	
matvec(other)	
mean([axis])	Average the matrix over the given axis.
multiply(other)	Point-wise multiplication by another matrix
nonzero()	nonzero indices
prune()	Remove empty space after all non-zero elements.
reshape(shape)	
rmatvec(*args, **kwds)	*rmatvec* is deprecated!
rowcol(*args, **kwds)	*rowcol* is deprecated!
save(file_name[, format])	
set_shape(shape)	
setdiag(values[, k])	Fills the diagonal elements {a_ii} with the values from the given sequence.
sort_indices()	Sort the indices of this matrix *in place*
sorted_indices()	Return a copy of this matrix with sorted indices
sum([axis])	Sum the matrix over the given axis.
sum_duplicates()	
toarray()	
tobsr([blocksize, copy])	
tocoo([copy])	Convert this matrix to COOrdinate format.
tocsc()	
tocsr()	
todense()	
todia()	
todok()	
tolil()	
transpose()	

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

asfptype()
Upcast matrix to a floating point format (if necessary)

astype(*t*)

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

conj()

conjugate()

copy()

diagonal()
Returns the main diagonal of the matrix

dot(**args, **kwds*)
dot is deprecated!

eliminate_zeros()

ensure_sorted_indices(*inplace=False*)
Return a copy of this matrix where the column indices are sorted

getH()

get_shape()

getcol(*j*)
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

getdata(*ind*)

getformat()

getmaxprint()

getnnz()

getrow(*i*)
Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

listprint(**args, **kwds*)
listprint is deprecated!

Provides a way to print over a single index.

matmat(*other*)

matvec(*other*)

mean(*axis=None*)
Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning a scalar.

multiply(*other*)
Point-wise multiplication by another matrix

nonzero()
nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

prune()
Remove empty space after all non-zero elements.

reshape(*shape*)

rmatvec(**args, **kwds*)
rmatvec is deprecated!

Multiplies the vector 'other' by the sparse matrix, returning a
dense vector as a result.

If 'conjugate' is True:

- returns A.transpose().conj() * other

Otherwise:

- returns A.transpose() * other.

rowcol(**args, **kwds*)
rowcol is deprecated!

save(*file_name, format='%d %d %fn'*)

set_shape(*shape*)

setdiag(*values, k=0*)
Fills the diagonal elements {a_ii} with the values from the given sequence. If k != 0, fills the off-diagonal elements {a_{i,i+k}} instead.

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.

sort_indices()
Sort the indices of this matrix *in place*

sorted_indices()
Return a copy of this matrix with sorted indices

sum(*axis=None*)
Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

sum_duplicates()

toarray()

tobsr(*blocksize=None, copy=False*)

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.

tocsc()

tocsr()

todense()

todia()

todok()

tolil()

transpose()

class lil_matrix(*arg1, shape=None, dtype=None, copy=False*)
Row-based linked list sparse matrix

This is an efficient structure for constructing sparse matrices incrementally.

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.tocsc())

lil_matrix((M, N), [dtype])
to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype='d'.

Notes

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`.

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(*args, **kwds)	*dot* is deprecated!
getH()	
get_shape()	
getcol(j)	Returns a copy of column j of the matrix, as an (m x 1) sparse
getdata(*args, **kwds)	*getdata* is deprecated!
getformat()	
getmaxprint()	

Continued on next page

Table 3.5 – continued from previous page

getnnz()	
getrow(i)	Returns a copy of the ‘i’th row.
getrowview(i)	Returns a view of the ‘i’th row (without copying).
listprint(*args, **kwds)	*listprint* is deprecated!
matmat(*args, **kwds)	*matmat* is deprecated!
matvec(*args, **kwds)	*matvec* is deprecated!
mean([axis])	Average the matrix over the given axis.
multiply(other)	Point-wise multiplication by another matrix
nonzero()	nonzero indices
reshape(shape)	
rmatvec(*args, **kwds)	*rmatvec* is deprecated!
rowcol(*args, **kwds)	*rowcol* is deprecated!
save(file_name[, format])	
set_shape(shape)	
setdiag(values[, k])	Fills the diagonal elements {a_ii} with the values from the given sequence.
sum([axis])	Sum the matrix over the given axis.
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()	
todia()	
todok()	
tolil([copy])	
transpose()	

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

asfptype()

Upcast matrix to a floating point format (if necessary)

astype(*t*)

conj()

conjugate()

copy()

diagonal()
Returns the main diagonal of the matrix

dot(**args, **kwds*)
dot is deprecated!

getH()

get_shape()

getcol(*j*)
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

getdata(**args, **kwds*)
getdata is deprecated!

getformat()

getmaxprint()

getnnz()

getrow(*i*)
Returns a copy of the 'i'th row.

getrowview(*i*)
Returns a view of the 'i'th row (without copying).

listprint(**args, **kwds*)
listprint is deprecated!

Provides a way to print over a single index.

matmat(**args, **kwds*)
matmat is deprecated!

matvec(**args, **kwds*)
matvec is deprecated!

mean(*axis=None*)
Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning a scalar.

multiply(*other*)
Point-wise multiplication by another matrix

nonzero()
nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

reshape(*shape*)

rmatvec(**args, **kwds*)
rmatvec is deprecated!

Multiplies the vector 'other' by the sparse matrix, returning a
dense vector as a result.

If 'conjugate' is True:

- returns A.transpose().conj() * other

Otherwise:

- returns A.transpose() * other.

rowcol(**args, **kwds*)
rowcol is deprecated!

save(*file_name, format='%d %d %fn'*)

set_shape(*shape*)

setdiag(*values, k=0*)
Fills the diagonal elements {a_ii} with the values from the given sequence. If k != 0, fills the off-diagonal elements {a_{i,i+k}} instead.

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.

sum(*axis=None*)
Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

toarray()

tobsr(*blocksize=None*)

tocoo()

tocsc()
Return Compressed Sparse Column format arrays for this matrix.

tocsr()
Return Compressed Sparse Row format arrays for this matrix.

todense()

todia()

todok()

tolil(*copy=False*)

transpose()

class 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 instatiated 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

Allows for efficient O(1) access of individual elements. Duplicates are not allowed. Can be efficiently converted to a coo_matrix once constructed.

Examples

```
>>> from scipy.sparse import *
>>> from scipy import *
>>> S = dok_matrix((5,5), dtype=float32)
>>> for i in range(5):
>>>     for j in range(5):
>>>         S[i,j] = i+j # Update element
```

Methods

asformat(format)	Return this matrix in a given sparse format
asfptype()	Upcast matrix to a floating point format (if necessary)
astype(t)	
clear	D.clear() -> None. Remove all items from D.
conj()	
conjtransp()	Return the conjugate transpose
conjugate()	
copy()	
diagonal()	Returns the main diagonal of the matrix
dot(*args, **kwds)	*dot* is deprecated!
fromkeys	
get(key[, default])	This overrides the dict.get method, providing type checking
getH()	
get_shape()	
getcol(j)	Returns a copy of column j of the matrix, as an (m x 1) sparse
getdata(*args, **kwds)	*getdata* is deprecated!
getformat()	
getmaxprint()	
getnnz()	
getrow(i)	Returns a copy of row i of the matrix, as a (1 x n) sparse
has_key	D.has_key(k) -> True if D has a key k, else False
items	D.items() -> list of D's (key, value) pairs, as 2-tuples
iteritems	D.iteritems() -> an iterator over the (key, value) items of D

Continued on next page

Table 3.6 – continued from previous page

iterkeys	D.iterkeys() -> an iterator over the keys of D
itervalues	D.itervalues() -> an iterator over the values of D
keys	D.keys() -> list of D's keys
listprint(*args, **kwds)	*listprint* is deprecated!
matmat(*args, **kwds)	*matmat* is deprecated!
matvec(*args, **kwds)	*matvec* is deprecated!
mean([axis])	Average the matrix over the given axis.
multiply(other)	Point-wise multiplication by another matrix
nonzero()	nonzero indices
pop	D.pop(k[,d]) -> v, remove specified key and return the corresponding value
popitem	D.popitem() -> (k, v), remove and return some (key, value) pair as a
reshape(shape)	
resize(shape)	Resize the matrix to dimensions given by 'shape', removing any
rmatvec(*args, **kwds)	*rmatvec* is deprecated!
rowcol(*args, **kwds)	*rowcol* is deprecated!
save(file_name[, format])	
set_shape(shape)	
setdefault	D.setdefault(k[,d]) -> D.get(k,d), also set D[k]=d if k not in D
setdiag(values[, k])	Fills the diagonal elements {a_ii} with the values from the given sequence.
split(cols_or_rows[, columns])	
sum([axis])	Sum the matrix over the given axis.
take(cols_or_rows[, columns])	
toarray()	
tobsr([blocksize])	
tocoo()	Return a copy of this matrix in COOrdinate format
tocsc()	Return a copy of this matrix in Compressed Sparse Column format
tocsr()	Return a copy of this matrix in Compressed Sparse Row format
todense()	
todia()	
todok([copy])	
tolil()	
transpose()	Return the transpose
update	D.update(E, **F) -> None. Update D from E and F: for k in E: D[k] = E[k]
values	D.values() -> list of D's values

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

asfptype()

Upcast matrix to a floating point format (if necessary)

astype(*t*)

clear()
D.clear() -> None. Remove all items from D.

conj()

conjtransp()
Return the conjugate transpose

conjugate()

copy()

diagonal()
Returns the main diagonal of the matrix

dot(**args, **kwds*)
dot is deprecated!

get(*key, default=0.0*)
This overrides the dict.get method, providing type checking but otherwise equivalent functionality.

getH()

get_shape()

getcol(*j*)
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

getdata(**args, **kwds*)
getdata is deprecated!

getformat()

getmaxprint()

getnnz()

getrow(*i*)
Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

has_key()
D.has_key(k) -> True if D has a key k, else False

items()
D.items() -> list of D's (key, value) pairs, as 2-tuples

iteritems()
D.iteritems() -> an iterator over the (key, value) items of D

iterkeys()
D.iterkeys() -> an iterator over the keys of D

itervalues()
D.itervalues() -> an iterator over the values of D

keys()
D.keys() -> list of D's keys

listprint(**args, **kwds*)
listprint is deprecated!

Provides a way to print over a single index.

matmat(**args, **kwds*)
matmat is deprecated!

matvec(**args, **kwds*)
matvec is deprecated!

mean(*axis=None*)
Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning a scalar.

multiply(*other*)
Point-wise multiplication by another matrix

nonzero()
nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

pop()
D.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

popitem()
D.popitem() -> (k, v), remove and return some (key, value) pair as a 2-tuple; but raise KeyError if D is empty

reshape(*shape*)

resize(*shape*)
Resize the matrix to dimensions given by 'shape', removing any non-zero elements that lie outside.

rmatvec(**args, **kwds*)
rmatvec is deprecated!

Multiplies the vector 'other' by the sparse matrix, returning a
dense vector as a result.

If 'conjugate' is True:

- returns A.transpose().conj() * other

Otherwise:

- returns A.transpose() * other.

rowcol(**args, **kwds*)
rowcol is deprecated!

save(*file_name, format='%d %d %fn'*)

set_shape(*shape*)

setdefault()
D.setdefault(k[,d]) -> D.get(k,d), also set D[k]=d if k not in D

setdiag(*values, k=0*)
Fills the diagonal elements {a_ii} with the values from the given sequence. If k != 0, fills the off-diagonal elements {a_{i,i+k}} instead.

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.

split(*cols_or_rows, columns=1*)

sum(*axis=None*)
Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

take(*cols_or_rows, columns=1*)

toarray()

tobsr(*blocksize=None*)

tocoo()
Return a copy of this matrix in COOrdinate format

tocsc()
Return a copy of this matrix in Compressed Sparse Column format

tocsr()
Return a copy of this matrix in Compressed Sparse Row format

todense()

todia()

todok(*copy=False*)

tolil()

transpose()
Return the transpose

update()
D.update(E, **F) -> None. Update D from E and F: for k in E: D[k] = E[k] (if E has keys else: for (k, v) in E: D[k] = v) then: for k in F: D[k] = F[k]

values()
D.values() -> list of D's values

class coo_matrix(*arg1, shape=None, dtype=None, copy=False, dims=None*)
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, ij), [shape=(M, N)])

The arguments 'data' and 'ij' represent three arrays:

1. data[:] the entries of the matrix, in any order
2. ij[0][:] the row indices of the matrix entries
3. ij[1][:] the column indices of the matrix entries

Where `A[ij[0][k], ij[1][k] = data[k]`. When shape is not specified, it is inferred from the index arrays

Notes

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

```
>>> from scipy.sparse import *
>>> from scipy import *
>>> coo_matrix( (3,4), dtype=int8 ).todense()
```

```
matrix([[0, 0, 0, 0],
        [0, 0, 0, 0],
        [0, 0, 0, 0]], dtype=int8)


>>> row  = array([0,3,1,0])
>>> col  = array([0,3,1,2])
>>> data = array([4,5,7,9])
>>> coo_matrix( (data,(row,col)), shape=(4,4) ).todense()
matrix([[4, 0, 9, 0],
        [0, 7, 0, 0],
        [0, 0, 0, 0],
        [0, 0, 0, 5]])


>>> # example with duplicates
>>> 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])
>>> coo_matrix( (data,(row,col)), shape=(4,4)).todense()
matrix([[3, 0, 1, 0],
        [0, 2, 0, 0],
        [0, 0, 0, 0],
        [0, 0, 0, 1]])
```

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(*args, **kwds)	*dot* is deprecated!
getH()	
get_shape()	
getcol(j)	Returns a copy of column j of the matrix, as an (m x 1) sparse
getdata(*args, **kwds)	*getdata* is deprecated!
getformat()	
getmaxprint()	
getnnz()	
getrow(i)	Returns a copy of row i of the matrix, as a (1 x n) sparse
listprint(*args, **kwds)	*listprint* is deprecated!
matmat(*args, **kwds)	*matmat* is deprecated!
matvec(*args, **kwds)	*matvec* is deprecated!
mean([axis])	Average the matrix over the given axis.
multiply(other)	Point-wise multiplication by another matrix
nonzero()	nonzero indices
reshape(shape)	
rmatvec(*args, **kwds)	*rmatvec* is deprecated!
rowcol(*args, **kwds)	*rowcol* is deprecated!
save(file_name[, format])	
set_shape(shape)	
setdiag(values[, k])	Fills the diagonal elements {a_ii} with the values from the given sequence.

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Table 3.7 – continued from previous page

sum([axis])	Sum the matrix over the given axis.
toarray()	
tobsr([blocksize])	
tocoo([copy])	
tocsc()	Return a copy of this matrix in Compressed Sparse Column format
tocsr()	Return a copy of this matrix in Compressed Sparse Row format
todense()	
todia()	
todok()	
tolil()	
transpose([copy])	

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

asfptype()
Upcast matrix to a floating point format (if necessary)

astype(*t*)

conj()

conjugate()

copy()

diagonal()
Returns the main diagonal of the matrix

dot(**args, **kwds*)
dot is deprecated!

getH()

get_shape()

getcol(*j*)
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

getdata(**args, **kwds*)
getdata is deprecated!

getformat()

getmaxprint()

getnnz()

getrow(*i*)
Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

listprint(**args, **kwds*)
listprint is deprecated!

Provides a way to print over a single index.

matmat(**args, **kwds*)
matmat is deprecated!

matvec(**args, **kwds*)
matvec is deprecated!

mean(*axis=None*)
Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning a scalar.

multiply(*other*)
Point-wise multiplication by another matrix

nonzero()
nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

reshape(*shape*)

rmatvec(**args, **kwds*)
rmatvec is deprecated!

Multiplies the vector 'other' by the sparse matrix, returning a
dense vector as a result.

If 'conjugate' is True:

- returns A.transpose().conj() * other

Otherwise:

- returns A.transpose() * other.

rowcol(**args, **kwds*)
rowcol is deprecated!

save(*file_name, format='%d %d %fn'*)

set_shape(*shape*)

setdiag(*values, k=0*)
Fills the diagonal elements {a_ii} with the values from the given sequence. If k != 0, fills the off-diagonal elements {a_{i,i+k}} instead.

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.

sum(*axis=None*)
Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

toarray()

tobsr(*blocksize=None*)

tocoo(*copy=False*)

tocsc()
Return a copy of this matrix in Compressed Sparse Column format

Duplicate entries will be summed together.

tocsr()
Return a copy of this matrix in Compressed Sparse Row format

Duplicate entries will be summed together.

todense()

todia()

todok()

tolil()

transpose(*copy=False*)

class **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)

Examples

```
>>> from scipy.sparse import *
>>> from scipy import *
>>> dia_matrix( (3,4), dtype=int8).todense()
matrix([[0, 0, 0, 0],
        [0, 0, 0, 0],
        [0, 0, 0, 0]], dtype=int8)


>>> data = array([[1,2,3,4]]).repeat(3,axis=0)
>>> offsets = array([0,-1,2])
>>> dia_matrix( (data,offsets), shape=(4,4)).todense()
matrix([[1, 0, 3, 0],
        [1, 2, 0, 4],
        [0, 2, 3, 0],
        [0, 0, 3, 4]])
```

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(*args, **kwds)	*dot* is deprecated!
getH()	
get_shape()	
getcol(j)	Returns a copy of column j of the matrix, as an (m x 1) sparse
getdata(*args, **kwds)	*getdata* is deprecated!
getformat()	
getmaxprint()	
getnnz()	number of nonzero values
getrow(i)	Returns a copy of row i of the matrix, as a (1 x n) sparse
listprint(*args, **kwds)	*listprint* is deprecated!
matmat(*args, **kwds)	*matmat* is deprecated!
matvec(*args, **kwds)	*matvec* is deprecated!
mean([axis])	Average the matrix over the given axis.
multiply(other)	Point-wise multiplication by another matrix
nonzero()	nonzero indices
reshape(shape)	
rmatvec(*args, **kwds)	*rmatvec* is deprecated!
rowcol(*args, **kwds)	*rowcol* is deprecated!
save(file_name[, format])	
set_shape(shape)	
setdiag(values[, k])	Fills the diagonal elements {a_ii} with the values from the given sequence.
sum([axis])	Sum the matrix over the given axis.
toarray()	
tobsr([blocksize])	
tocoo()	
tocsc()	
tocsr()	

Continued on next page

Table 3.8 – continued from previous page

todense()
todia([copy])
todok()
tolil()
transpose()

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

asfptype()
Upcast matrix to a floating point format (if necessary)

astype(*t*)

conj()

conjugate()

copy()

diagonal()
Returns the main diagonal of the matrix

dot(**args, **kwds*)
dot is deprecated!

getH()

get_shape()

getcol(*j*)
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

getdata(**args, **kwds*)
getdata is deprecated!

getformat()

getmaxprint()

getnnz()
number of nonzero values

explicit zero values are included in this number

getrow(*i*)
Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

listprint(**args, **kwds*)
listprint is deprecated!

Provides a way to print over a single index.

matmat(**args, **kwds*)
matmat is deprecated!

matvec(**args, **kwds*)
matvec is deprecated!

mean(*axis=None*)
Average the matrix over the given axis. If the axis is None, average over both rows and columns, returning a scalar.

multiply(*other*)
Point-wise multiplication by another matrix

nonzero()
nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

reshape(*shape*)

rmatvec(**args, **kwds*)
rmatvec is deprecated!

Multiplies the vector 'other' by the sparse matrix, returning a
dense vector as a result.

If 'conjugate' is True:

- returns A.transpose().conj() * other

Otherwise:

- returns A.transpose() * other.

rowcol(**args, **kwds*)
rowcol is deprecated!

save(*file_name, format='%d %d %fn'*)

set_shape(*shape*)

setdiag(*values, k=0*)
Fills the diagonal elements {a_ii} with the values from the given sequence. If k != 0, fills the off-diagonal elements {a_{i,i+k}} instead.

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.

sum(*axis=None*)
Sum the matrix over the given axis. If the axis is None, sum over both rows and columns, returning a scalar.

toarray()

tobsr(*blocksize=None*)

tocoo()

tocsc()

tocsr()

todense()

todia(*copy=False*)

todok()

tolil()

transpose()

3.14.6 Functions

Building sparse matrices:

eye(m, n[, k, dtype, format])	eye(m, n) returns a sparse (m x n) matrix where the k-th diagonal
identity(n[, dtype, format])	Identity matrix in sparse format
kron(A, B[, format])	kronecker product of sparse matrices A and B
kronsum(A, B[, format])	kronecker sum of sparse matrices A and B
lil_eye(r[, k, dtype])	Generate a lil_matrix of dimensions (r,c) with the k-th diagonal set to 1.
lil_diags(diags, offsets, m[, dtype])	Generate a lil_matrix with the given diagonals.
spdiags(data, diags, m, n[, format])	Return a sparse matrix from diagonals.
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)

eye(*m, n, k=0, dtype='d', format=None*)
eye(m, n) returns a sparse (m x n) matrix where the k-th diagonal is all ones and everything else is zeros.

identity(*n, dtype='d', format=None*)
Identity matrix in sparse format

Returns an identity matrix with shape (n,n) using a given sparse format and dtype.

Parameters

n : integer

Shape of the identity matrix.

dtype : :

Data type of the matrix

format : string

Sparse format of the result, e.g. format="csr", etc.

Examples

```
>>> identity(3).todense()
matrix([[ 1.,  0.,  0.],
        [ 0.,  1.,  0.],
        [ 0.,  0.,  1.]])
>>> identity(3, dtype='int8', format='dia')
<3x3 sparse matrix of type '<type 'numpy.int8'>'
        with 3 stored elements (1 diagonals) in DIAgonal format>
```

kron(*A, B, format=None*)

kronecker product of sparse matrices A and B

Parameters

A : sparse or dense matrix

first matrix of the product

B : sparse or dense matrix

second matrix of the product

format : string

format of the result (e.g. "csr")

Returns

kronecker product in a sparse matrix format :

Examples

```
>>> A = csr_matrix(array([[0,2],[5,0]]))
>>> B = csr_matrix(array([[1,2],[3,4]]))
>>> kron(A,B).todense()
matrix([[ 0,  0,  2,  4],
        [ 0,  0,  6,  8],
        [ 5, 10,  0,  0],
        [15, 20,  0,  0]])


>>> kron(A,[[1,2],[3,4]]).todense()
matrix([[ 0,  0,  2,  4],
        [ 0,  0,  6,  8],
        [ 5, 10,  0,  0],
        [15, 20,  0,  0]])
```

kronsum(*A, B, format=None*)

kronecker sum of sparse matrices A and B

Kronecker sum of two sparse matrices is a sum of two Kronecker products kron(I_n,A) + kron(B,I_m) where A has shape (m,m) and B has shape (n,n) and I_m and I_n are identity matrices of shape (m,m) and (n,n) respectively.

Parameters

A :

square matrix

B :

square matrix

format : string

format of the result (e.g. "csr")

Returns

kronecker sum in a sparse matrix format :

lil_eye (*(r, c), k=0, dtype='d'*)

Generate a lil_matrix of dimensions (r,c) with the k-th diagonal set to 1.

Parameters

r,c : int

row and column-dimensions of the output.

k : int

- diagonal offset. In the output matrix,
- out[m,m+k] == 1 for all m.

dtype : dtype

data-type of the output array.

lil_diags (*diags, offsets, (m, n), dtype='d'*)

Generate a lil_matrix with the given diagonals.

Parameters

diags : list of list of values e.g. [[1,2,3],[4,5]]

values to be placed on each indicated diagonal.

offsets : list of ints

diagonal offsets. This indicates the diagonal on which the given values should be placed.

(r,c) : tuple of ints

row and column dimensions of the output.

dtype : dtype

output data-type.

Examples

```
>>> lil_diags([[1,2,3],[4,5],[6]],[0,1,2],(3,3)).todense()
matrix([[ 1.,  4.,  6.],
        [ 0.,  2.,  5.],
        [ 0.,  0.,  3.]])
```

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 : format of the result (e.g. "csr")

By default (format=None) an appropriate sparse matrix format is returned. This choice is subject to change.

See Also:

dia_matrix
the sparse DIAgonal format.

Examples

```
>>> data = array([[1,2,3,4],[1,2,3,4],[1,2,3,4]])
>>> diags = array([0,-1,2])
>>> spdiags(data, diags, 4, 4).todense()
matrix([[1, 0, 3, 0],
        [1, 2, 0, 4],
        [0, 2, 3, 0],
        [0, 0, 3, 4]])
```

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 trianglar 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

```
>>> 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.todense()
matrix([[1, 2, 0, 0, 3],
        [4, 5, 0, 6, 7],
        [0, 0, 8, 9, 0]])
>>> tril(A).todense()
matrix([[1, 0, 0, 0, 0],
        [4, 5, 0, 0, 0],
        [0, 0, 8, 0, 0]])
>>> tril(A).nnz
4
>>> tril(A, k=1).todense()
matrix([[1, 2, 0, 0, 0],
        [4, 5, 0, 0, 0],
        [0, 0, 8, 9, 0]])
>>> tril(A, k=-1).todense()
matrix([[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>
```

triu(*A, k=0, format=None*)

Return the upper triangular portion of a matrix in sparse format

Returns the elements on or above the k-th diagonal of the matrix A.

- k = 0 corresponds to the main diagonal
- k > 0 is above the main diagonal
- k < 0 is below the main diagonal

Parameters

A : dense or sparse matrix

Matrix whose upper trianglar 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.todense()
matrix([[1, 2, 0, 0, 3],
        [4, 5, 0, 6, 7],
        [0, 0, 8, 9, 0]])
>>> triu(A).todense()
matrix([[1, 2, 0, 0, 3],
        [0, 5, 0, 6, 7],
        [0, 0, 8, 9, 0]])
>>> triu(A).nnz
8
>>> triu(A, k=1).todense()
matrix([[0, 2, 0, 0, 3],
        [0, 0, 0, 6, 7],
        [0, 0, 0, 9, 0]])
>>> triu(A, k=-1).todense()
matrix([[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>
```

bmat(*blocks, format=None, dtype=None*)

Build a sparse matrix from sparse sub-blocks

Parameters

blocks :

grid of sparse matrices with compatible shapes an entry of None implies an all-zero matrix

format : sparse format of the result (e.g. "csr")

by default an appropriate sparse matrix format is returned. This choice is subject to change.

Examples

```
>>> 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]] ).todense()
matrix([[1, 2, 5],
```

```
        [3, 4, 6],
        [0, 0, 7]])

>>> bmat( [[A,None],[None,C]] ).todense()
matrix([[1, 2, 0],
        [3, 4, 0],
        [0, 0, 7]])
```

hstack(*blocks, format=None, dtype=None*)

Stack sparse matrices horizontally (column wise)

Parameters

blocks :

sequence of sparse matrices with compatible shapes

format : string

sparse format of the result (e.g. "csr") by default an appropriate sparse matrix format is returned. This choice is subject to change.

See Also:

vstack

stack sparse matrices vertically (row wise)

Examples

```
>>> from scipy.sparse import coo_matrix, vstack
>>> A = coo_matrix([[1,2],[3,4]])
>>> B = coo_matrix([[5],[6]])
>>> hstack( [A,B] ).todense()
matrix([[1, 2, 5],
        [3, 4, 6]])
```

vstack(*blocks, format=None, dtype=None*)

Stack sparse matrices vertically (row wise)

Parameters

blocks :

sequence of sparse matrices with compatible shapes

format : string

sparse format of the result (e.g. "csr") by default an appropriate sparse matrix format is returned. This choice is subject to change.

See Also:

hstack

stack sparse matrices horizontally (column wise)

Examples

```
>>> from scipy.sparse import coo_matrix, vstack
>>> A = coo_matrix([[1,2],[3,4]])
>>> B = coo_matrix([[5,6]])
>>> vstack( [A,B] ).todense()
```

```
    matrix([[1, 2],
            [3, 4],
            [5, 6]])
```

Identifying sparse matrices:

issparse(x)
isspmatrix(x)
isspmatrix_csc(x)
isspmatrix_csr(x)
isspmatrix_bsr(x)
isspmatrix_lil(x)
isspmatrix_dok(x)
isspmatrix_coo(x)
isspmatrix_dia(x)

issparse(*x*)

isspmatrix(*x*)

isspmatrix_csc(*x*)

isspmatrix_csr(*x*)

isspmatrix_bsr(*x*)

isspmatrix_lil(*x*)

isspmatrix_dok(*x*)

isspmatrix_coo(*x*)

isspmatrix_dia(*x*)

3.14.7 Exceptions

exception SparseEfficiencyWarning

exception SparseWarning

3.15 Sparse linear algebra (scipy.sparse.linalg)

Warning: This documentation is work-in-progress and unorganized.

3.15.1 Sparse Linear Algebra

The submodules of sparse.linalg:

1. eigen: sparse eigenvalue problem solvers
2. isolve: iterative methods for solving linear systems
3. dsolve: direct factorization methods for solving linear systems

3.15.2 Examples

class `LinearOperator`(*shape, matvec, rmatvec=None, matmat=None, dtype=None*)

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.

Parameters

shape : tuple

Matrix dimensions (M,N)

matvec : callable f(v)

Returns returns A * v.

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.

Examples

```
>>> from scipy.sparse.linalg import LinearOperator
>>> from scipy import *
>>> def mv(v):
...     return array([ 2*v[0], 3*v[1]])
...
>>> A = LinearOperator( (2,2), matvec=mv )
>>> A
<2x2 LinearOperator with unspecified dtype>
>>> A.matvec( ones(2) )
array([ 2.,  3.])
>>> A * ones(2)
array([ 2.,  3.])
```

Methods

`matmat`(X)	Matrix-matrix multiplication
`matvec`(x)	Matrix-vector multiplication

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 to ensure that y has the correct type.

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 rank-1 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 to ensure that y has the correct shape and type.

Tester
alias of `NoseTester`

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 additonal information.

Examples

```
>>> from scipy import matrix
>>> M = matrix( [[1,2,3],[4,5,6]], dtype='int32' )
>>> aslinearoperator( M )
<2x3 LinearOperator with dtype=int32>
```

bicg(*A, b, x0=None, tol=1.0000000000000001e-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 N-by-N matrix of the linear system.

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

bicgstab(*A, b, x0=None, tol=1.0000000000000001e-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 N-by-N matrix of the linear system.

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

cg(*A, b, x0=None, tol=1.0000000000000001e-05, maxiter=None, xtype=None, M=None, callback=None*)
Use Conjugate Gradient iteration to solve A x = b

Parameters

A : {sparse matrix, dense matrix, LinearOperator}

The N-by-N matrix of the linear system.

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

cgs(*A, b, x0=None, tol=1.0000000000000001e-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 N-by-N matrix of the linear system.

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

eigen(*A, k=6, M=None, sigma=None, which='LM', v0=None, ncv=None, maxiter=None, tol=0, return_eigenvectors=True*)
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].

Parameters

A : matrix, array, or object with matvec(x) method

An N x N matrix, array, or an object with matvec(x) method to perform the matrix vector product A * x. The sparse matrix formats in scipy.sparse are appropriate for A.

k : integer

The number of eigenvalues and eigenvectors desired

Returns

w : array

Array of k eigenvalues

v : array

An array of k eigenvectors The v[i] is the eigenvector corresponding to the eigenvector w[i]

See Also:

eigen_symmetric
eigenvalues and eigenvectors for symmetric matrix A

eigen_symmetric(*A, k=6, M=None, sigma=None, which='LM', v0=None, ncv=None, maxiter=None, tol=0, return_eigenvectors=True*)

Find k eigenvalues and eigenvectors of the real symmetric square matrix A.

Solves A * x[i] = w[i] * x[i], the standard eigenvalue problem for w[i] eigenvalues with corresponding eigenvectors x[i].

Parameters

A : matrix or array with real entries or object with matvec(x) method

An N x N real symmetric matrix or array or an object with matvec(x) method to perform the matrix vector product A * x. The sparse matrix formats in scipy.sparse are appropriate for A.

k : integer

The number of eigenvalues and eigenvectors desired

Returns

w : array

Array of k eigenvalues

v : array

An array of k eigenvectors The v[i] is the eigenvector corresponding to the eigenvector w[i]

See Also:

eigen
eigenvalues and eigenvectors for a general (nonsymmetric) matrix A

factorized(*A*)

Return a fuction for solving a sparse linear system, with A pre-factorized.

Example:

solve = factorized(A) # Makes LU decomposition. x1 = solve(rhs1) # Uses the LU factors. x2 = solve(rhs2) # Uses again the LU factors.

gmres(*A, b, x0=None, tol=1.0000000000000001e-05, restrt=20, 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 N-by-N matrix of the linear system.

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

See Also:

LinearOperator

lgmres(*A, b, x0=None, tol=1.0000000000000001e-05, maxiter=1000, M=None, callback=None, inner_m=30, outer_k=3, outer_v=None, store_outer_Av=True*)
Solve a matrix equation using the LGMRES algorithm.

The LGMRES algorithm [BJM] [BPh] 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 N-by-N matrix of the linear system.

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

x0 : {array, matrix}

Starting guess for the solution.

tol : 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.

Returns

x : array or 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

Notes

The LGMRES algorithm [BJM] [BPh] 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

[BJM], [BPh]

lobpcg(*A, X, B=None, M=None, Y=None, tol=None, maxiter=20, largest=True, verbosityLevel=0, retLambdaHistory=False, retResidualNormsHistory=False*)
Solve symmetric partial eigenproblems with optional preconditioning

This function implements the Locally Optimal Block Preconditioned Conjugate Gradient Method (LOBPCG).

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).

Returns
w : array

Array of k eigenvalues

v : array

An array of k eigenvectors. V has the same shape as X.

Notes

If both retLambdaHistory and retResidualNormsHistory are True, the return tuple has the following format (lambda, V, lambda history, residual norms history)

minres(*A, b, x0=None, shift=0.0, tol=1.0000000000000001e-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 the 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 N-by-N matrix of the linear system.

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

Notes

THIS FUNCTION IS EXPERIMENTAL AND SUBJECT TO CHANGE!

References

Solution of sparse indefinite systems of linear equations,
C. C. Paige and M. A. Saunders (1975), SIAM J. Numer. Anal. 12(4), pp. 617-629. 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/

qmr(*A, b, x0=None, tol=1.0000000000000001e-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 N-by-N matrix of the linear system.

b : {array, matrix}

Right hand side of the linear system. Has shape (N,) or (N,1).

See Also:

LinearOperator

splu(*A, permc_spec=2, diag_pivot_thresh=1.0, drop_tol=0.0, relax=1, panel_size=10*)
A linear solver, for a sparse, square matrix A, using LU decomposition where L is a lower triangular matrix and U is an upper triagular matrix.

Returns a factored_lu object. (scipy.sparse.linalg.dsolve._superlu.SciPyLUType)

See scipy.sparse.linalg.dsolve._superlu.dgstrf for more info.

spsolve(*A, b, permc_spec=2*)
Solve the sparse linear system Ax=b

test
Run tests for module using nose.

Parameters
label : {'fast', 'full', '', attribute identifier}, optional

Identifies the tests to run. This can be a string to pass to the nosetests executable with the '-A' option, or one of several special values. Special values are:

'fast' - the default - which corresponds to the `nosetests -A`
option of 'not slow'.

'full' - fast (as above) and slow tests as in the
'no -A' option to nosetests - this is the same as ''.

None or '' - run all tests. attribute_identifier - string passed directly to nosetests as '-A'.

verbose : int, optional

Verbosity value for test outputs, in the range 1-10. Default is 1.

extra_argv : list, optional

List with any extra arguments to pass to nosetests.

doctests : bool, optional

If True, run doctests in module. Default is False.

coverage : bool, optional

If True, report coverage of NumPy code. Default is False. (This requires the ‘coverage module:

<http://nedbatchelder.com/code/modules/coverage.html>‘_).

Returns

result : object

Returns the result of running the tests as a `nose.result.TextTestResult` object.

Notes

Each NumPy module exposes `test` in its namespace to run all tests for it. For example, to run all tests for numpy.lib:

```
>>> np.lib.test()
```

Examples

```
>>> result = np.lib.test()
Running unit tests for numpy.lib
...
Ran 976 tests in 3.933s

OK

>>> result.errors
[]
>>> result.knownfail
[]
```

use_solver(***kwargs*)

Valid keyword arguments with defaults (other ignored):

useUmfpack = True assumeSortedIndices = False

The default sparse solver is umfpack when available. This can be changed by passing useUmfpack = False, which then causes the always present SuperLU based solver to be used.

Umfpack requires a CSR/CSC matrix to have sorted column/row indices. If sure that the matrix fulfills this, pass assumeSortedIndices=True to gain some speed.

3.16 Spatial algorithms and data structures (`scipy.spatial`)

Warning: This documentation is work-in-progress and unorganized.

3.16.1 Distance computations (`scipy.spatial.distance`)

Function Reference

Distance matrix computation from a collection of raw observation vectors stored in a rectangular array.

Function	*Description*
pdist	pairwise distances between observation vectors.
cdist	distances between between two collections of observation vectors.
squareform	converts a square distance matrix to a condensed one and vice versa.

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.

Function	*Description*
is_valid_dm	checks for a valid distance matrix.
is_valid_y	checks for a valid condensed distance matrix.
num_obs_dm	# of observations in a distance matrix.
num_obs_y	# of observations in a condensed distance matrix.

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.

Function	*Description*
braycurtis	the Bray-Curtis distance.
canberra	the Canberra distance.
chebyshev	the Chebyshev distance.
cityblock	the Manhattan distance.
correlation	the Correlation distance.
cosine	the Cosine distance.
dice	the Dice dissimilarity (boolean).
euclidean	the Euclidean distance.
hamming	the Hamming distance (boolean).
jaccard	the Jaccard distance (boolean).
kulsinski	the Kulsinski distance (boolean).
mahalanobis	the Mahalanobis distance.
matching	the matching dissimilarity (boolean).
minkowski	the Minkowski distance.
rogerstanimoto	the Rogers-Tanimoto dissimilarity (boolean).
russellrao	the Russell-Rao dissimilarity (boolean).
seuclidean	the normalized Euclidean distance.
sokalmichener	the Sokal-Michener dissimilarity (boolean).
sokalsneath	the Sokal-Sneath dissimilarity (boolean).
sqeuclidean	the squared Euclidean distance.
yule	the Yule dissimilarity (boolean).

References

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`braycurtis` (*u, v*)

Computes the Bray-Curtis distance between two n-vectors `u` and `v`, which is defined as

$$\sum |u_i - v_i| / \sum |u_i + v_i|.$$

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The Bray-Curtis distance between vectors `u` and `v`.

canberra(*u, v*)
Computes the Canberra distance between two n-vectors u and v, which is defined as

$$\frac{\sum_i |u_i - v_i|}{\sum_i |u_i| + |v_i|}.$$

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The Canberra distance between vectors `u` and `v`.

cdist(*XA, XB, metric='euclidean', p=2, V=None, VI=None, w=None*)
Computes distance between each pair of observation vectors in the Cartesian product of two collections of vectors. `XA` is a m_A by n array while `XB` is a m_B by n array. A m_A by m_B array is returned. An exception is thrown if `XA` and `XB` do not have the same number of columns.

A rectangular distance matrix `Y` is returned. For each i and j, the metric `dist(u=XA[i], v=XB[j])` is computed and stored in the ij th entry.

The following are common calling conventions:

1. `Y = 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 = cdist(XA, XB, 'minkowski', p)`

   Computes the distances using the Minkowski distance $||u - v||_p$ (p-norm) where $p \geq 1$.

3. `Y = cdist(XA, XB, 'cityblock')`

   Computes the city block or Manhattan distance between the points.

4. `Y = 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 = cdist(XA, XB, 'sqeuclidean')`

   Computes the squared Euclidean distance $||u-v||_2^2$ between the vectors.

6. `Y = cdist(XA, XB, 'cosine')`

   Computes the cosine distance between vectors u and v,

$$\frac{1 - uv^T}{|u|_2|v|_2}$$

   where $|*|_2$ is the 2-norm of its argument *.

7. `Y = cdist(XA, XB, 'correlation')`

   Computes the correlation distance between vectors u and v. This is

$$\frac{1 - (u - n|u|_1)(v - n|v|_1)^T}{|(u - n|u|_1)|_2|(v - n|v|_1)|^T}$$

   where $|*|_1$ is the Manhattan (or 1-norm) of its argument, and n is the common dimensionality of the vectors.

8. `Y = 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 = 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 = 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

$$d(u, v) = \max_i |u_i - v_i|.$$

1. `Y = cdist(XA, XB, 'canberra')`

   Computes the Canberra distance between the points. The Canberra distance between two points `u` and `v` is

$$d(u, v) = \sum_u \frac{|u_i - v_i|}{(|u_i| + |v_i|)}$$

1. `Y = cdist(XA, XB, 'braycurtis')`

   Computes the Bray-Curtis distance between the points. The Bray-Curtis distance between two points `u` and `v` is

$$d(u, v) = \frac{\sum_i (u_i - v_i)}{\sum_i (u_i + v_i)}$$

1. `Y = cdist(XA, XB, '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.

1.`Y = cdist(XA, XB, 'yule')`

Computes the Yule distance between the boolean vectors. (see yule function documentation)

1.`Y = cdist(XA, XB, 'matching')`

Computes the matching distance between the boolean vectors. (see matching function documentation)

1.`Y = cdist(XA, XB, 'dice')`

Computes the Dice distance between the boolean vectors. (see dice function documentation)

1.`Y = cdist(XA, XB, 'kulsinski')`

Computes the Kulsinski distance between the boolean vectors. (see kulsinski function documentation)

1.`Y = cdist(XA, XB, 'rogerstanimoto')`

Computes the Rogers-Tanimoto distance between the boolean vectors. (see rogerstanimoto function documentation)

1.`Y = cdist(XA, XB, 'russellrao')`

Computes the Russell-Rao distance between the boolean vectors. (see russellrao function documentation)

1.`Y = cdist(XA, XB, 'sokalmichener')`

Computes the Sokal-Michener distance between the boolean vectors. (see sokalmichener function documentation)

1.`Y = cdist(XA, XB, 'sokalsneath')`

Computes the Sokal-Sneath distance between the vectors. (see sokalsneath function documentation)

1.`Y = cdist(XA, XB, 'wminkowski')`

Computes the weighted Minkowski distance between the vectors. (see sokalsneath function documentation)

1.`Y = 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:

```
dm = cdist(XA, XB, (lambda u, v: np.sqrt(((u-v)*(u-v).T).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.

XB
[ndarray] An m_B by n array of m_B original observations in an n-dimensional space.

metric
[string or function] 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', 'wminkowski', 'yule'.

w
[ndarray] The weight vector (for weighted Minkowski).

p
[double] The p-norm to apply (for Minkowski, weighted and unweighted)

V
[ndarray] The variance vector (for standardized Euclidean).

VI
[ndarray] The inverse of the covariance matrix (for Mahalanobis).

Returns

Y
[ndarray] A m_A by m_B distance matrix.

chebyshev(*u, v*)
Computes the Chebyshev distance between two n-vectors u and v, which is defined as

$$\max_i |u_i - v_i|.$$

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The Chebyshev distance between vectors u and v.

cityblock(*u, v*)
Computes the Manhattan distance between two n-vectors u and v, which is defined as

$$\sum_i (u_i - v_i).$$

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The City Block distance between vectors u and v.

correlation(*u, v*)
Computes the correlation distance between two n-vectors u and v, which is defined as

$$\frac{1 - (u - \bar{u})(v - \bar{v})^T}{||(u - \bar{u})||_2 ||(v - \bar{v})||_2^T}$$

where $\bar{u}$ is the mean of a vectors elements and n is the common dimensionality of u and v.

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The correlation distance between vectors u and v.

cosine(*u, v*)
Computes the Cosine distance between two n-vectors u and v, which is defined as

$$\frac{1 - uv^T}{||u||_2 ||v||_2}.$$

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The Cosine distance between vectors u and v.

dice(*u, v*)
Computes the Dice dissimilarity between two boolean n-vectors u and v, which is

$$\frac{c_{TF} + c_{FT}}{2c_{TT} + c_{FT} + c_{TF}}$$

where c_{ij} is the number of occurrences of $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$.

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The Dice dissimilarity between vectors u and v.

euclidean(*u, v*)
Computes the Euclidean distance between two n-vectors u and v, which is defined as

$$||u - v||_2$$

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The Euclidean distance between vectors u and v.

hamming(*u, v*)
Computes the Hamming distance between two n-vectors u and v, which 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 $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$.

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The Hamming distance between vectors `u` and `v`.

is_valid_dm(*D, tol=0.0, throw=False, name='D', warning=False*)
Returns True if the variable D passed 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
[double] The distance matrix should be symmetric. tol is the maximum difference between the :math:‘ij‘th entry and the :math:‘ji‘th entry for the distance metric to be considered symmetric.

throw
[bool] An exception is thrown if the distance matrix passed is not valid.

name
[string] the name of the variable to checked. This is useful ifa throw is set to `True` so the offending variable can be identified in the exception message when an exception is thrown.

warning
[boolx] Instead of throwing an exception, a warning message is raised.

Returns
Returns `True` if the variable `D` passed is a valid distance matrix. 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(*y, warning=False, throw=False, name=None*)
Returns `True` if the variable `y` passed 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] 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.

throws
[throw] Throws an exception if the variable passed is not a valid condensed distance matrix.

name
[bool] Used when referencing the offending variable in the warning or exception message.

jaccard(*u, v*)
Computes the Jaccard-Needham dissimilarity between two boolean n-vectors u and v, which is

$$racc_{TF} + c_{FT}c_{TT} + c_{FT} + c_{TF}$$

where c_{ij} is the number of occurrences of $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$.

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The Jaccard distance between vectors `u` and `v`.

kulsinski(*u, v*)
Computes the Kulsinski dissimilarity between two boolean n-vectors u and v, which is defined as

$$racc_{TF} + c_{FT} - c_{TT} + nc_{FT} + c_{TF} + n$$

where c_{ij} is the number of occurrences of $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$.

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The Kulsinski distance between vectors `u` and `v`.

mahalanobis(*u, v, VI*)
Computes the Mahalanobis distance between two n-vectors `u` and `v`, which is defiend as

$$(u - v)V^{-1}(u - v)^T$$

where `VI` is the inverse covariance matrix V^{-1}.

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The Mahalanobis distance between vectors `u` and `v`.

matching(*u, v*)
Computes the Matching dissimilarity between two boolean n-vectors u and v, which is defined as

$$\frac{c_{TF} + c_{FT}}{n}$$

where c_{ij} is the number of occurrences of $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$.

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The Matching dissimilarity between vectors `u` and `v`.

minkowski(*u, v, p*)
Computes the Minkowski distance between two vectors `u` and `v`, defined as

$$||u - v||_p = (\sum |u_i - v_i|^p)^{1/p}.$$

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

p
[ndarray] The norm of the difference $||u - v||_p$.

Returns

d
[double] The Minkowski distance between vectors `u` and `v`.

num_obs_dm(*d*)
Returns the number of original observations that correspond to a square, redudant distance matrix `D`.

Parameters

d
[ndarray] The target distance matrix.

Returns
The number of observations in the redundant distance matrix.

num_obs_y(*Y*)

Returns the number of original observations that correspond to a condensed distance matrix `Y`.

Parameters

Y

[ndarray] The number of original observations in the condensed observation `Y`.

Returns

n

[int] The number of observations in the condensed distance matrix passed.

pdist(*X, metric='euclidean', p=2, V=None, VI=None*)

Computes the pairwise distances between m original observations in n-dimensional space. 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 the :math:‘ij‘th entry.

See `squareform` for information on how to calculate the index of this entry or to convert the condensed distance matrix to a redundant square matrix.

The following are common calling conventions.

1. `Y = 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

   $$\sqrt{\sum (u_i - v_i)^2 / V[x_i]}.$$

   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 = pdist(X, 'sqeuclidean')`

   Computes the squared Euclidean distance $||u-v||_2^2$ between the vectors.

6. `Y = pdist(X, 'cosine')`

   Computes the cosine distance between vectors u and v,

   $$\frac{1 - uv^T}{|u|_2 |v|_2}$$

   where |*|_2 is the 2 norm of its argument *.

7. `Y = pdist(X, 'correlation')`

Computes the correlation distance between vectors u and v. This is

$$\frac{1 - (u - \bar{u})(v - \bar{v})^T}{|(u - \bar{u})||(v - \bar{v})|^T}$$

where $\bar{v}$ is the mean of the elements of vector v.

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

$$d(u, v) = \max_i |u_i - v_i|.$$

1. `Y = pdist(X, 'canberra')`

   Computes the Canberra distance between the points. The Canberra distance between two points `u` and `v` is

$$d(u, v) = \sum_u \frac{|u_i - v_i|}{(|u_i| + |v_i|)}$$

1. `Y = pdist(X, 'braycurtis')`

   Computes the Bray-Curtis distance between the points. The Bray-Curtis distance between two points `u` and `v` is

$$d(u, v) = \frac{\sum_i u_i - v_i}{\sum_i u_i + v_i}$$

1. `Y = 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.

1. `Y = pdist(X, 'yule')`

   Computes the Yule distance between each pair of boolean vectors. (see yule function documentation)

1. `Y = pdist(X, 'matching')`

   Computes the matching distance between each pair of boolean vectors. (see matching function documentation)

1.`Y = pdist(X, 'dice')`

Computes the Dice distance between each pair of boolean vectors. (see dice function documentation)

1.`Y = pdist(X, 'kulsinski')`

Computes the Kulsinski distance between each pair of boolean vectors. (see kulsinski function documentation)

1.`Y = pdist(X, 'rogerstanimoto')`

Computes the Rogers-Tanimoto distance between each pair of boolean vectors. (see rogerstanimoto function documentation)

1.`Y = pdist(X, 'russellrao')`

Computes the Russell-Rao distance between each pair of boolean vectors. (see russellrao function documentation)

1.`Y = pdist(X, 'sokalmichener')`

Computes the Sokal-Michener distance between each pair of boolean vectors. (see sokalmichener function documentation)

1.`Y = pdist(X, 'sokalsneath')`

Computes the Sokal-Sneath distance between each pair of boolean vectors. (see sokalsneath function documentation)

1.`Y = pdist(X, 'wminkowski')`

Computes the weighted Minkowski distance between each pair of vectors. (see wminkowski function documentation)

1.`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:

```
dm = pdist(X, (lambda u, v: np.sqrt(((u-v)*(u-v).T).sum())))
```

Note that you should avoid passing a reference to one of the distance functions defined in this library. For example,:

```
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.:

```
dm = pdist(X, 'sokalsneath')
```

Parameters

X
[ndarray] An m by n array of m original observations in an n-dimensional space.

metric
[string or function] 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] The weight vector (for weighted Minkowski).

p
[double] The p-norm to apply (for Minkowski, weighted and unweighted)

V
[ndarray] The variance vector (for standardized Euclidean).

VI
[ndarray] The inverse of the covariance matrix (for Mahalanobis).

Returns

Y
[ndarray] A condensed distance matrix.

Seealso

squareform
[converts between condensed distance matrices and] square distance matrices.

rogerstanimoto(*u, v*)
Computes the Rogers-Tanimoto dissimilarity between two boolean n-vectors u and v, which is defined as

$$\frac{R}{c_{TT} + c_{FF} + R}$$

where c_{ij} is the number of occurrences of $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$ and $R = 2(c_{TF} + c_{FT})$.

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The Rogers-Tanimoto dissimilarity between vectors u and v.

russellrao(*u, v*)
Computes the Russell-Rao dissimilarity between two boolean n-vectors u and v, which is defined as

$$\frac{n - c_{TT}}{n}$$

where c_{ij} is the number of occurrences of $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$.

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The Russell-Rao dissimilarity between vectors u and v.

seuclidean(*u, v, V*)
Returns the standardized Euclidean distance between two n-vectors u and v. V is an m-dimensional vector of component variances. It is usually computed among a larger collection vectors.

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The standardized Euclidean distance between vectors u and v.

sokalmichener(*u, v*)
Computes the Sokal-Michener dissimilarity between two boolean vectors u and v, which is defined as

$$\frac{2R}{S + 2R}$$

where c_{ij} is the number of occurrences of $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$, $R = 2 * (c_{TF} + c_{FT})$ and $S = c_{FF} + c_{TT}$.

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The Sokal-Michener dissimilarity between vectors u and v.

sokalsneath(*u, v*)

Computes the Sokal-Sneath dissimilarity between two boolean vectors u and v,

$$\frac{2R}{c_{TT} + 2R}$$

where c_{ij} is the number of occurrences of $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$ and $R = 2(c_{TF} + c_{FT})$.

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The Sokal-Sneath dissimilarity between vectors u and v.

sqeuclidean(*u, v*)

Computes the squared Euclidean distance between two n-vectors u and v, which is defined as

$$||u - v||_2^2.$$

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The squared Euclidean distance between vectors u and v.

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.

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.

force
[string] 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] 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.

wminkowski (*u, v, p, w*)
Computes the weighted Minkowski distance between two vectors `u` and `v`, defined as

$$\left(\sum (w_i|u_i - v_i|^p)\right)^{1/p}.$$

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

p
[ndarray] The norm of the difference $||u - v||_p$.

w
[ndarray] The weight vector.

Returns

d
[double] The Minkowski distance between vectors `u` and `v`.

yule (*u, v*)
Computes the Yule dissimilarity between two boolean n-vectors u and v, which is defined as

$$\frac{R}{c_{TT} + c_{FF} + \frac{R}{2}}$$

where c_{ij} is the number of occurrences of $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$ and $R = 2.0 * (c_{TF} + c_{FT})$.

Parameters

u
[ndarray] An n-dimensional vector.

v
[ndarray] An n-dimensional vector.

Returns

d
[double] The Yule dissimilarity between vectors `u` and `v`.

3.16.2 Spatial data structures and algorithms

Nearest-neighbor queries:

KDTree – class for efficient nearest-neighbor queries distance – module containing many different distance measures

class 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.

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.
innernode	
leafnode	
node	
query(x[, k, eps, p, distance_upper_bound])	query the kd-tree for nearest neighbors
query_ball_point(x, r[, p, eps])	Find all points within r of x
query_ball_tree(other, r[, p, eps])	Find all pairs of points whose distance is at most r
query_pairs(r[, p, eps])	Find all pairs of points whose distance is at most r
sparse_distance_matrix(other, max_distance)	Compute a sparse distance matrix

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

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

Which Minkowski p-norm to use

Returns

result : integer or one-dimensional array of integers

The number of pairs. Note that this is internally stored in a numpy int, and so may overflow if very large (two billion).

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 : integer

The number of nearest neighbors to return.

eps : nonnegative float

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

Which Minkowski p-norm to use. 1 is the sum-of-absolute-values "Manhattan" distance 2 is the usual Euclidean distance infinity is the maximum-coordinate-difference distance

distance_upper_bound : nonnegative float

Return only neighbors within this distance. This is used to prune tree searches, so if you are doing a series of nearest-neighbor queries, it may help to supply the distance to the nearest neighbor of the most recent point.

Returns

d : 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 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 : array of integers

The locations of the neighbors in self.data. i is the same shape as d.

Examples

```
>>> from scipy.spatial import KDTree
>>> x, y = np.mgrid[0:5, 2:8]
>>> tree = KDTree(zip(x.ravel(), y.ravel()))
>>> tree.data
array([[0, 2],
       [0, 3],
       [0, 4],
       [0, 5],
       [0, 6],
       [0, 7],
       [1, 2],
       [1, 3],
       [1, 4],
       [1, 5],
       [1, 6],
       [1, 7],
       [2, 2],
       [2, 3],
```

```
            [2, 4],
            [2, 5],
            [2, 6],
            [2, 7],
            [3, 2],
            [3, 3],
            [3, 4],
            [3, 5],
            [3, 6],
            [3, 7],
            [4, 2],
            [4, 3],
            [4, 4],
            [4, 5],
            [4, 6],
            [4, 7]])
>>> pts = np.array([[0, 0], [2.1, 2.9]])
>>> tree.query(pts)
(array([ 2.        ,  0.14142136]), array([ 0, 13]))
```

query_ball_point(*x, r, p=2.0, eps=0*)

Find all points within r of 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 1<=p<=infinity

Which Minkowski p-norm to use

eps : nonnegative float

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.

Note: 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. :

query_ball_tree(*other, r, p=2.0, eps=0*)

Find all pairs of points whose distance is at most r

Parameters

other : KDTree

The tree containing points to search against

r : positive float

The maximum distance

p : float 1<=p<=infinity

Which Minkowski norm to use

eps : nonnegative float

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 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.

query_pairs(*r, p=2.0, eps=0*)

Find all pairs of points whose distance is at most r

Parameters

r : positive float

The maximum distance

p : float 1<=p<=infinity

Which Minkowski norm to use

eps : nonnegative float

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 : set

set of pairs (i,j), i<j, for which the corresponing positions are close.

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 max_distance.

Parameters

other : KDTree

max_distance : positive float

Returns

result : dok_matrix

Sparse matrix representing the results in "dictionary of keys" format.

class Rectangle(*maxes, mins*)

Hyperrectangle class.

Represents a Cartesian product of intervals.

Methods

max_distance_point(x[, p])	Compute the maximum distance between x and a point in the hyperrectangle.
max_distance_rectangle(other[, p])	Compute the maximum distance between points in the two hyperrectangles.
min_distance_point(x[, p])	Compute the minimum distance between x and a point in the hyperrectangle.
min_distance_rectangle(other[, p])	Compute the minimum distance between points in the two hyperrectangles.
split(d, split)	Produce two hyperrectangles by splitting along axis d.
volume()	Total volume.

max_distance_point (*x, p=2.0*)
Compute the maximum distance between x and a point in the hyperrectangle.

max_distance_rectangle (*other, p=2.0*)
Compute the maximum distance between points in the two hyperrectangles.

min_distance_point (*x, p=2.0*)
Compute the minimum distance between x and a point in the hyperrectangle.

min_distance_rectangle (*other, p=2.0*)
Compute the minimum distance between points in the two hyperrectangles.

split (*d, split*)
Produce two hyperrectangles by splitting along axis d.

In general, if you need to compute maximum and minimum distances to the children, it can be done more efficiently by updating the maximum and minimum distances to the parent.

volume ()
Total volume.

class 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.

Methods

query	query the kd-tree for nearest neighbors

query ()
query the kd-tree for nearest neighbors

distance_matrix(*x, y, p=2, threshold=1000000*)
Compute the distance matrix.

Computes the matrix of all pairwise distances.

Parameters
x : array-like, m by k

y : array-like, n by k

p : float 1<=p<=infinity

Which Minkowski p-norm to use.

threshold : positive integer

If m*n*k>threshold use a python loop instead of creating a very large temporary.

Returns
result : array-like, m by n

heappop()
Pop the smallest item off the heap, maintaining the heap invariant.

heappush()
Push item onto heap, maintaining the heap invariant.

minkowski_distance(*x, y, p=2*)
Compute the L**p distance between x and y

minkowski_distance_p(*x, y, p=2*)
Compute the pth power of the L**p distance between x and y

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.

3.17 Special functions (scipy.special)

Nearly all of the functions below are universal functions and follow broadcasting and automatic array-looping rules. Exceptions are noted.

3.17.1 Error handling

Errors are handled by returning nans, or other appropriate values. Some of the special function routines will print an error message when an error occurs. By default this printing is disabled. To enable such messages use errprint(1) To disable such messages use errprint(0).

Example:

```
>>> print scipy.special.bdtr(-1,10,0.3)
>>> scipy.special.errprint(1)
>>> print scipy.special.bdtr(-1,10,0.3)
```

errprint	errprint({flag}) sets the error printing flag for special functions
errstate(**kwargs)	Context manager for floating-point error handling.

errprint()
errprint({flag}) sets the error printing flag for special functions (from the cephesmodule). The output is the previous state. With errprint(0) no error messages are shown; the default is errprint(1). If no argument is given the current state of the flag is returned and no change occurs.

class errstate(***kwargs*)
Context manager for floating-point error handling.

Using an instance of *errstate* as a context manager allows statements in that context to execute with a known error handling behavior. Upon entering the context the error handling is set with *seterr* and *seterrcall*, and upon exiting it is reset to what it was before.

Parameters
kwargs : {divide, over, under, invalid}

Keyword arguments. The valid keywords are the possible floating-point exceptions. Each keyword should have a string value that defines the treatment for the particular error. Possible values are {'ignore', 'warn', 'raise', 'call', 'print', 'log'}.

See Also:

`seterr`, `geterr`, `seterrcall`, `geterrcall`

Notes

The `with` statement was introduced in Python 2.5, and can only be used there by importing it: `from __future__ import with_statement`. In earlier Python versions the `with` statement is not available.

For complete documentation of the types of floating-point exceptions and treatment options, see *seterr*.

Examples

```
>>> from __future__ import with_statement  # use 'with' in Python 2.5
>>> olderr = np.seterr(all='ignore')  # Set error handling to known state.


>>> np.arange(3) / 0.
array([ NaN,  Inf,  Inf])
>>> with np.errstate(divide='warn'):
...     np.arange(3) / 0.
...
__main__:2: RuntimeWarning: divide by zero encountered in divide
array([ NaN,  Inf,  Inf])


>>> np.sqrt(-1)
nan
>>> with np.errstate(invalid='raise'):
...     np.sqrt(-1)
...
Traceback (most recent call last):
  File "<stdin>", line 2, in <module>
FloatingPointError: invalid value encountered in sqrt
```

Outside the context the error handling behavior has not changed:

```
>>> np.geterr()
{'over': 'ignore', 'divide': 'ignore', 'invalid': 'ignore',
'under': 'ignore'}
```

3.17.2 Available functions

Airy functions

airy(out1, out2, out3)	(Ai,Aip,Bi,Bip)=airy(z) calculates the Airy functions and their derivatives
airye(out1, out2, out3)	(Aie,Aipe,Bie,Bipe)=airye(z) calculates the exponentially scaled Airy functions and
ai_zeros(nt)	Compute the zeros of Airy Functions Ai(x) and Ai'(x), a and a'
bi_zeros(nt)	Compute the zeros of Airy Functions Bi(x) and Bi'(x), b and b'

airy
(Ai,Aip,Bi,Bip)=airy(z) calculates the Airy functions and their derivatives evaluated at real or complex number z. The Airy functions Ai and Bi are two independent solutions of y''(x)=xy. Aip and Bip are the first derivatives evaluated at x of Ai and Bi respectively.

airye
(Aie,Aipe,Bie,Bipe)=airye(z) calculates the exponentially scaled Airy functions and their derivatives evaluated at real or complex number z. airye(z)[0:1] = airy(z)[0:1] * exp(2.0/3.0*z*sqrt(z)) airye(z)[2:3] = airy(z)[2:3] * exp(-abs((2.0/3.0*z*sqrt(z)).real))

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).

Outputs:

a[l-1] – the lth zero of Ai(x) ap[l-1] – the lth zero of Ai'(x) ai[l-1] – Ai(ap[l-1]) aip[l-1] – Ai'(a[l-1])

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).

Outputs:

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])

Elliptic Functions and Integrals

ellipj(x1, out1, out2, out3)	(sn,cn,dn,ph)=ellipj(u,m) calculates the Jacobian elliptic functions of
ellipk()	y=ellipk(m) returns the complete integral of the first kind:
ellipkinc(x1)	y=ellipkinc(phi,m) returns the incomplete elliptic integral of the first
ellipe()	y=ellipe(m) returns the complete integral of the second kind:
ellipeinc(x1)	y=ellipeinc(phi,m) returns the incomplete elliptic integral of the

ellipj
(sn,cn,dn,ph)=ellipj(u,m) calculates the Jacobian elliptic functions of parameter m between 0 and 1, and real u. The returned functions are often written sn(u|m), cn(u|m), and dn(u|m). The value of ph is such that if u = ellik(ph,m), then sn(u|m) = sin(ph) and cn(u|m) = cos(ph).

ellipk
y=ellipk(m) returns the complete integral of the first kind: integral(1/sqrt(1-m*sin(t)**2),t=0..pi/2)

ellipkinc
y=ellipkinc(phi,m) returns the incomplete elliptic integral of the first kind: integral(1/sqrt(1-m*sin(t)**2),t=0..phi)

ellipe
y=ellipe(m) returns the complete integral of the second kind: integral(sqrt(1-m*sin(t)**2),t=0..pi/2)

ellipeinc
y=ellipeinc(phi,m) returns the incomplete elliptic integral of the second kind: integral(sqrt(1-m*sin(t)**2),t=0..phi)

Bessel Functions

jn(x1)	y=jv(v,z) returns the Bessel function of real order v at complex z.
jv(x1)	y=jv(v,z) returns the Bessel function of real order v at complex z.
jve(x1)	y=jve(v,z) returns the exponentially scaled Bessel function of real order
yn(x1)	y=yn(n,x) returns the Bessel function of the second kind of integer
yv(x1)	y=yv(v,z) returns the Bessel function of the second kind of real
yve(x1)	y=yve(v,z) returns the exponentially scaled Bessel function of the second
kn(x1)	y=kn(n,x) returns the modified Bessel function of the second kind (sometimes called the third kind) for
kv(x1)	y=kv(v,z) returns the modified Bessel function of the second kind (sometimes called the third kind) for
kve(x1)	y=kve(v,z) returns the exponentially scaled, modified Bessel function
iv(x1)	y=iv(v,z) returns the modified Bessel function of real order v of
ive(x1)	y=ive(v,z) returns the exponentially scaled modified Bessel function of
hankel1(x1)	y=hankel1(v,z) returns the Hankel function of the first kind for real order v and complex argument z.
hankel1e(x1)	y=hankel1e(v,z) returns the exponentially scaled Hankel function of the first
hankel2(x1)	y=hankel2(v,z) returns the Hankel function of the second kind for real order v and complex argument z.
hankel2e(x1)	y=hankel2e(v,z) returns the exponentially scaled Hankel function of the second

jn
y=jv(v,z) returns the Bessel function of real order v at complex z.

jv
y=jv(v,z) returns the Bessel function of real order v at complex z.

jve
y=jve(v,z) returns the exponentially scaled Bessel function of real order v at complex z: jve(v,z) = jv(v,z) * exp(-abs(z.imag))

yn
y=yn(n,x) returns the Bessel function of the second kind of integer order n at x.

yv
y=yv(v,z) returns the Bessel function of the second kind of real order v at complex z.

yve
y=yve(v,z) returns the exponentially scaled Bessel function of the second kind of real order v at complex z: yve(v,z) = yv(v,z) * exp(-abs(z.imag))

kn
y=kn(n,x) returns the modified Bessel function of the second kind (sometimes called the third kind) for integer order n at x.

kv
y=kv(v,z) returns the modified Bessel function of the second kind (sometimes called the third kind) for real order v at complex z.

kve
y=kve(v,z) 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) * exp(z)

iv
y=iv(v,z) returns the modified Bessel function of real order v of z. If z is of real type and negative, v must be integer valued.

ive
y=ive(v,z) returns the exponentially scaled modified Bessel function of real order v and complex z: ive(v,z) = iv(v,z) * exp(-abs(z.real))

hankel1
y=hankel1(v,z) returns the Hankel function of the first kind for real order v and complex argument z.

hankel1e
y=hankel1e(v,z) returns the exponentially scaled Hankel function of the first kind for real order v and complex argument z: hankel1e(v,z) = hankel1(v,z) * exp(-1j * z)

hankel2
y=hankel2(v,z) returns the Hankel function of the second kind for real order v and complex argument z.

hankel2e
y=hankel2e(v,z) returns the exponentially scaled Hankel function of the second kind for real order v and complex argument z: hankel1e(v,z) = hankel1(v,z) * exp(1j * z)

The following is not an universal function:

lmbda(v, x)	Compute sequence of lambda functions with arbitrary order v and their derivatives.

lmbda (*v, x*)
Compute sequence of lambda functions with arbitrary order v and their derivatives. Lv0(x)..Lv(x) are computed with v0=v-int(v).

Zeros of Bessel Functions

These are not universal functions:

jnjnp_zeros(nt)	Compute nt (<=1200) zeros of the bessel functions Jn and Jn'
jnyn_zeros(n, nt)	Compute nt zeros of the Bessel functions Jn(x), Jn'(x), Yn(x), and
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])	Returns nt (complex or real) zeros of Y0(z), z0, and the value
y1_zeros(nt[, complex])	Returns nt (complex or real) zeros of Y1(z), z1, and the value
y1p_zeros(nt[, complex])	Returns nt (complex or real) zeros of Y1'(z), z1', and the value

jnjnp_zeros (*nt*)
Compute nt (<=1200) zeros of the bessel functions Jn and Jn' and arange them in order of their magnitudes.

Outputs (all are arrays of length nt):

zo[l-1] – Value of the lth zero of of Jn(x) and Jn'(x) n[l-1] – Order of the Jn(x) or Jn'(x) associated with lth zero m[l-1] – Serial number of the zeros of Jn(x) or Jn'(x) associated

with lth zero.

t[l-1] – 0 if lth zero in zo is zero of Jn(x), 1 if it is a zero
of Jn'(x)

See jn_zeros, jnp_zeros to get separated arrays of zeros.

jnyn_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.

y1p_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

j0()	y=j0(x) returns the Bessel function of order 0 at x.
j1()	y=j1(x) returns the Bessel function of order 1 at x.
y0()	y=y0(x) returns the Bessel function of the second kind of order 0 at x.
y1()	y=y1(x) returns the Bessel function of the second kind of order 1 at x.
i0()	y=i0(x) returns the modified Bessel function of order 0 at x.
i0e()	y=i0e(x) returns the exponentially scaled modified Bessel function
i1()	y=i1(x) returns the modified Bessel function of order 1 at x.
i1e()	y=i1e(x) returns the exponentially scaled modified Bessel function
k0()	y=k0(x) returns the modified Bessel function of the second kind (sometimes called the third kind) of
k0e()	y=k0e(x) returns the exponentially scaled modified Bessel function
k1()	y=i1(x) returns the modified Bessel function of the second kind (sometimes called the third kind) of
k1e()	y=k1e(x) returns the exponentially scaled modified Bessel function

j0
y=j0(x) returns the Bessel function of order 0 at x.

j1
y=j1(x) returns the Bessel function of order 1 at x.

y0
y=y0(x) returns the Bessel function of the second kind of order 0 at x.

y1
y=y1(x) returns the Bessel function of the second kind of order 1 at x.

i0
y=i0(x) returns the modified Bessel function of order 0 at x.

i0e
y=i0e(x) returns the exponentially scaled modified Bessel function of order 0 at x. i0e(x) = exp(-|x|) * i0(x).

i1
y=i1(x) returns the modified Bessel function of order 1 at x.

i1e
y=i1e(x) returns the exponentially scaled modified Bessel function of order 0 at x. i1e(x) = exp(-|x|) * i1(x).

k0
y=k0(x) returns the modified Bessel function of the second kind (sometimes called the third kind) of order 0 at x.

k0e
y=k0e(x) returns the exponentially scaled modified Bessel function of the second kind (sometimes called the third kind) of order 0 at x. k0e(x) = exp(x) * k0(x).

k1
y=i1(x) returns the modified Bessel function of the second kind (sometimes called the third kind) of order 1 at x.

k1e
y=k1e(x) returns the exponentially scaled modified Bessel function of the second kind (sometimes called the third kind) of order 1 at x. k1e(x) = exp(x) * k1(x)

Integrals of Bessel Functions

itj0y0(out1)	(ij0,iy0)=itj0y0(x) returns simple integrals from 0 to x of the zeroth order
it2j0y0(out1)	(ij0,iy0)=it2j0y0(x) returns the integrals int((1-j0(t))/t,t=0..x) and
iti0k0(out1)	(ii0,ik0)=iti0k0(x) returns simple integrals from 0 to x of the zeroth order
it2i0k0(out1)	(ii0,ik0)=it2i0k0(x) returns the integrals int((i0(t)-1)/t,t=0..x) and
besselpoly(x1, x2)	y=besselpoly(a,lam,nu) returns the value of the integral:

itj0y0
(ij0,iy0)=itj0y0(x) returns simple integrals from 0 to x of the zeroth order bessel functions j0 and y0.

it2j0y0
(ij0,iy0)=it2j0y0(x) returns the integrals int((1-j0(t))/t,t=0..x) and int(y0(t)/t,t=x..infinitity).

iti0k0
(ii0,ik0)=iti0k0(x) returns simple integrals from 0 to x of the zeroth order modified bessel functions i0 and k0.

it2i0k0
(ii0,ik0)=it2i0k0(x) returns the integrals int((i0(t)-1)/t,t=0..x) and int(k0(t)/t,t=x..infinitity).

besselpoly
y=besselpoly(a,lam,nu) returns the value of the integral: integral(x**lam * jv(nu,2*a*x),x=0..1).

Derivatives of Bessel Functions

jvp(v, z[, n])	Return the nth derivative of Jv(z) with respect to z.
yvp(v, z[, n])	Return the nth derivative of Yv(z) with respect to z.
kvp(v, z[, n])	Return the nth derivative of Kv(z) with respect to z.
ivp(v, z[, n])	Return the nth derivative of Iv(z) with respect to z.
h1vp(v, z[, n])	Return the nth derivative of H1v(z) with respect to z.
h2vp(v, z[, n])	Return the nth derivative of H2v(z) with respect to z.

jvp(*v, z, n=1*)
Return the nth derivative of Jv(z) with respect to z.

yvp(*v, z, n=1*)
Return the nth derivative of Yv(z) with respect to z.

kvp(*v, z, n=1*)
Return the nth derivative of Kv(z) with respect to z.

ivp(*v, z, n=1*)
Return the nth derivative of Iv(z) with respect to z.

h1vp (*v, z, n=1*)
Return the nth derivative of H1v(z) with respect to z.

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
sph_yn(n, z)	Compute the spherical Bessel function yn(z) and its derivative for
sph_jnyn(n, z)	Compute the spherical Bessel functions, jn(z) and yn(z) and their
sph_in(n, z)	Compute the spherical Bessel function in(z) and its derivative for
sph_kn(n, z)	Compute the spherical Bessel function kn(z) and its derivative for
sph_inkn(n, z)	Compute the spherical Bessel functions, in(z) and kn(z) and their

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_jnyn (*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.

Ricatti-Bessel Functions

These are not universal functions:

riccati_jn(n, x)	Compute the Ricatti-Bessel function of the first kind and its
riccati_yn(n, x)	Compute the Ricatti-Bessel function of the second kind and its

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.

Struve Functions

struve(x1)	y=struve(v,x) returns the Struve function Hv(x) of order v at x, x
modstruve(x1)	y=modstruve(v,x) returns the modified Struve function Lv(x) of order
itstruve0()	y=itstruve0(x) returns the integral of the Struve function of order 0
it2struve0()	y=it2struve0(x) returns the integral of the Struve function of order 0
itmodstruve0()	y=itmodstruve0(x) returns the integral of the modified Struve function

struve
y=struve(v,x) returns the Struve function Hv(x) of order v at x, x must be positive unless v is an integer.

modstruve
y=modstruve(v,x) returns the modified Struve function Lv(x) of order v at x, x must be positive unless v is an integer and it is recommended that |v|<=20.

itstruve0
y=itstruve0(x) returns the integral of the Struve function of order 0 from 0 to x: integral(H0(t), t=0..x).

it2struve0
y=it2struve0(x) returns the integral of the Struve function of order 0 divided by t from x to infinity: integral(H0(t)/t, t=x..inf).

itmodstruve0
y=itmodstruve0(x) returns the integral of the modified Struve function of order 0 from 0 to x: integral(L0(t), t=0..x).

Raw Statistical Functions

See Also:

scipy.stats: Friendly versions of these functions.

bdtr(x1, x2)	y=bdtr(k,n,p) returns the sum of the terms 0 through k of the
bdtrc(x1, x2)	y=bdtrc(k,n,p) returns the sum of the terms k+1 through n of the
bdtri(x1, x2)	p=bdtri(k,n,y) finds the probability p such that the sum of the
btdtr(x1, x2)	y=btdtr(a,b,x) returns the area from zero to x under the beta
btdtri(x1, x2)	x=btdtri(a,b,p) returns the pth quantile of the beta distribution. It is
fdtr(x1, x2)	y=fdtr(dfn,dfd,x) returns the area from zero to x under the F density
fdtrc(x1, x2)	y=fdtrc(dfn,dfd,x) returns the complemented F distribution function.
fdtri(x1, x2)	x=fdtri(dfn,dfd,p) finds the F density argument x such that
gdtr(x1, x2)	y=gdtr(a,b,x) returns the integral from zero to x of the gamma
gdtrc(x1, x2)	y=gdtrc(a,b,x) returns the integral from x to infinity of the gamma
gdtria(x1, x2)	
gdtrib(x1, x2)	
gdtrix(x1, x2)	
nbdtr(x1, x2)	y=nbdtr(k,n,p) returns the sum of the terms 0 through k of the
nbdtrc(x1, x2)	y=nbdtrc(k,n,p) returns the sum of the terms k+1 to infinity of the
nbdtri(x1, x2)	p=nbdtri(k,n,y) finds the argument p such that nbdtr(k,n,p)=y.
pdtr(x1)	y=pdtr(k,m) returns the sum of the first k terms of the Poisson
pdtrc(x1)	y=pdtrc(k,m) returns the sum of the terms from k+1 to infinity of the
pdtri(x1)	m=pdtri(k,y) returns the Poisson variable m such that the sum
stdtr(x1)	p=stdtr(df,t) returns the integral from minus infinity to t of the Student t
stdtridf(x1)	t=stdtridf(p,t) returns the argument df such that stdtr(df,t) is equal to p.
stdtrit(x1)	t=stdtrit(df,p) returns the argument t such that stdtr(df,t) is equal to p.
chdtr(x1)	p=chdtr(v,x) Returns the area under the left hand tail (from 0 to x) of the Chi
chdtrc(x1)	p=chdtrc(v,x) returns the area under the right hand tail (from x to
chdtri(x1)	x=chdtri(v,p) returns the argument x such that chdtrc(v,x) is equal
ndtr()	y=ndtr(x) returns the area under the standard Gaussian probability
ndtri()	x=ndtri(y) returns the argument x for which the area udnder the
smirnov(x1)	y=smirnov(n,e) returns the exact Kolmogorov-Smirnov complementary
smirnovi(x1)	e=smirnovi(n,y) returns e such that smirnov(n,e) = y.
kolmogorov()	p=kolmogorov(y) returns the complementary cumulative distribution
kolmogi()	y=kolmogi(p) returns y such that kolmogorov(y) = p
tklmbda(x1)	

bdtr

y=bdtr(k,n,p) returns the sum of the terms 0 through k of the Binomial probability density: sum(nCj p**j (1-p)**(n-j),j=0..k)

bdtrc
y=bdtrc(k,n,p) returns the sum of the terms k+1 through n of the Binomial probability density: sum(nCj p**j (1-p)**(n-j), j=k+1..n)

bdtri
p=bdtri(k,n,y) finds the probability p such that the sum of the terms 0 through k of the Binomial probability density is equal to the given cumulative probability y.

btdtr
y=btdtr(a,b,x) returns the area from zero to x under the beta density function: gamma(a+b)/(gamma(a)*gamma(b)))*integral(t**(a-1) (1-t)**(b-1), t=0..x). SEE ALSO betainc

btdtri
x=btdtri(a,b,p) returns the pth quantile of the beta distribution. It is effectively the inverse of btdtr returning the value of x for which btdtr(a,b,x) = p. SEE ALSO betaincinv

fdtr
y=fdtr(dfn,dfd,x) 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.

fdtrc
y=fdtrc(dfn,dfd,x) returns the complemented F distribution function.

fdtri
x=fdtri(dfn,dfd,p) finds the F density argument x such that fdtr(dfn,dfd,x)=p.

gdtr
y=gdtr(a,b,x) returns the integral from zero to x of the gamma probability density function: a**b / gamma(b) * integral(t**(b-1) exp(-at),t=0..x). The arguments a and b are used differently here than in other definitions.

gdtrc
y=gdtrc(a,b,x) returns the integral from x to infinity of the gamma probability density function. SEE gdtr, gdtri

gdtria

gdtrib

gdtrix

nbdtr
y=nbdtr(k,n,p) returns the sum of the terms 0 through k of the negative binomial distribution: sum((n+j-1)Cj p**n (1-p)**j,j=0..k). In a sequence of Bernoulli trials this is the probability that k or fewer failures precede the nth success.

nbdtrc
y=nbdtrc(k,n,p) returns the sum of the terms k+1 to infinity of the negative binomial distribution.

nbdtri
p=nbdtri(k,n,y) finds the argument p such that nbdtr(k,n,p)=y.

pdtr
y=pdtr(k,m) returns the sum of the first k terms of the Poisson distribution: sum(exp(-m) * m**j / j!, j=0..k) = gammaincc(k+1, m). Arguments must both be positive and k an integer.

pdtrc
y=pdtrc(k,m) returns the sum of the terms from k+1 to infinity of the Poisson distribution: sum(exp(-m) * m**j / j!, j=k+1..inf) = gammainc(k+1, m). Arguments must both be positive and k an integer.

pdtri
m=pdtri(k,y) 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.

stdtr
p=stdtr(df,t) returns the integral from minus infinity to t of the Student t distribution with df > 0 degrees of freedom: gamma((df+1)/2)/(sqrt(df*pi)*gamma(df/2)) * integral((1+x**2/df)**(-df/2-1/2), x=-inf..t)

stdtridf
t=stdtridf(p,t) returns the argument df such that stdtr(df,t) is equal to p.

stdtrit
t=stdtrit(df,p) returns the argument t such that stdtr(df,t) is equal to p.

chdtr
p=chdtr(v,x) Returns the area under the left hand tail (from 0 to x) of the Chi square probability density function with v degrees of freedom: 1/(2**(v/2) * gamma(v/2)) * integral(t**(v/2-1) * exp(-t/2), t=0..x)

chdtrc
p=chdtrc(v,x) returns the area under the right hand tail (from x to infinity) of the Chi square probability density function with v degrees of freedom: 1/(2**(v/2) * gamma(v/2)) * integral(t**(v/2-1) * exp(-t/2), t=x..inf)

chdtri
x=chdtri(v,p) returns the argument x such that chdtrc(v,x) is equal to p.

ndtr
y=ndtr(x) returns the area under the standard Gaussian probability density function, integrated from minus infinity to x: 1/sqrt(2*pi) * integral(exp(-t**2 / 2),t=-inf..x)

ndtri
x=ndtri(y) returns the argument x for which the area udnder the Gaussian probability density function (integrated from minus infinity to x) is equal to y.

smirnov
y=smirnov(n,e) 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.

smirnovi
e=smirnovi(n,y) returns e such that smirnov(n,e) = y.

kolmogorov
p=kolmogorov(y) 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.

kolmogi
y=kolmogi(p) returns y such that kolmogorov(y) = p

tklmbda

Gamma and Related Functions

gamma()	y=gamma(z) returns the gamma function of the argument. The gamma
gammaln()	y=gammaln(z) returns the base e logarithm of the absolute value of the
gammainc(x1)	y=gammainc(a,x) returns the incomplete gamma integral defined as
gammaincinv(x1)	gammaincinv(a, y) returns x such that gammainc(a, x) = y.
gammaincc(x1)	y=gammaincc(a,x) returns the complemented incomplete gamma integral
gammainccinv(x1)	x=gammainccinv(a,y) returns x such that gammaincc(a,x) = y.
beta(x1)	y=beta(a,b) returns gamma(a) * gamma(b) / gamma(a+b)
betaln(x1)	y=betaln(a,b) returns the natural logarithm of the absolute value of
betainc(x1, x2)	y=betainc(a,b,x) returns the incomplete beta integral of the
betaincinv(x1, x2)	x=betaincinv(a,b,y) returns x such that betainc(a,b,x) = y.
psi()	y=psi(z) is the derivative of the logarithm of the gamma function
rgamma()	y=rgamma(z) returns one divided by the gamma function of x.
polygamma(n, x)	Polygamma function which is the nth derivative of the digamma (psi)
multigammaln(a, d)	returns the log of multivariate gamma, also sometimes called the

gamma
y=gamma(z) returns the gamma function of the argument. The gamma function is often referred to as the generalized factorial since z*gamma(z) = gamma(z+1) and gamma(n+1) = n! for natural number n.

gammaln
y=gammaln(z) returns the base e logarithm of the absolute value of the gamma function of z: ln(|**gamma(z)**|)

gammainc
y=gammainc(a,x) returns the incomplete gamma integral defined as 1 / gamma(a) * integral(exp(-t) * t**(a-1), t=0..x). Both arguments must be positive.

gammaincinv
gammaincinv(a, y) returns x such that gammainc(a, x) = y.

gammaincc
y=gammaincc(a,x) returns the complemented incomplete gamma integral defined as 1 / gamma(a) * integral(exp(-t) * t**(a-1), t=x..inf) = 1 - gammainc(a,x). Both arguments must be positive.

gammainccinv
x=gammainccinv(a,y) returns x such that gammaincc(a,x) = y.

beta
y=beta(a,b) returns gamma(a) * gamma(b) / gamma(a+b)

betaln
y=betaln(a,b) returns the natural logarithm of the absolute value of beta: ln(|**beta(x)**|).

betainc
y=betainc(a,b,x) returns the incomplete beta integral of the arguments, evaluated from zero to x:

gamma(a+b) / (gamma(a)*gamma(b)) * integral(t**(a-1) (1-t)**(b-1), t=0..x).

betaincinv
x=betaincinv(a,b,y) returns x such that betainc(a,b,x) = y.

psi
y=psi(z) is the derivative of the logarithm of the gamma function evaluated at z (also called the digamma function).

rgamma
y=rgamma(z) returns one divided by the gamma function of x.

polygamma (*n, x*)
Polygamma function which is the nth derivative of the digamma (psi) function.

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

Reference:

R. J. Muirhead, Aspects of multivariate statistical theory (Wiley Series in probability and mathematical statistics).

Error Function and Fresnel Integrals

erf()	y=erf(z) returns the error function of complex argument defined as
erfc()	y=erfc(x) returns 1 - erf(x).
erfinv(y)	
erfcinv(y)	
erf_zeros(nt)	Compute nt complex zeros of the error function erf(z).
fresnel(out1)	(ssa,cca)=fresnel(z) returns the fresnel sin and cos integrals: integral(sin(pi/2
fresnel_zeros(nt)	Compute nt complex zeros of the sine and cosine fresnel integrals
modfresnelp(out1)	(fp,kp)=modfresnelp(x) returns the modified fresnel integrals F_+(x) and K_+(x)
modfresnelm(out1)	(fm,km)=modfresnelp(x) returns the modified fresnel integrals F_-(x) amd K_-(x)

erf
y=erf(z) returns the error function of complex argument defined as as 2/sqrt(pi)*integral(exp(-t**2),t=0..z)

erfc
y=erfc(x) returns 1 - erf(x).

erfinv(*y*)

erfcinv(*y*)

erf_zeros(*nt*)
Compute nt complex zeros of the error function erf(z).

fresnel
(ssa,cca)=fresnel(z) returns the fresnel sin and cos integrals: integral(sin(pi/2 * t**2),t=0..z) and integral(cos(pi/2 * t**2),t=0..z) for real or complex z.

fresnel_zeros(*nt*)
Compute nt complex zeros of the sine and cosine fresnel integrals S(z) and C(z).

modfresnelp
(fp,kp)=modfresnelp(x) returns the modified fresnel integrals F_+(x) and K_+(x) as fp=integral(exp(1j*t*t),t=x..inf) and kp=1/sqrt(pi)*exp(-1j*(x*x+pi/4))*fp

modfresnelm
(fm,km)=modfresnelp(x) returns the modified fresnel integrals F_-(x) amd K_-(x) as fp=integral(exp(-1j*t*t),t=x..inf) and kp=1/sqrt(pi)*exp(1j*(x*x+pi/4))*fp

These are not universal functions:

fresnelc_zeros(nt)	Compute nt complex zeros of the cosine fresnel integral C(z).
fresnels_zeros(nt)	Compute nt complex zeros of the sine fresnel integral S(z).

fresnelc_zeros (*nt*)
Compute nt complex zeros of the cosine fresnel integral C(z).

fresnels_zeros (*nt*)
Compute nt complex zeros of the sine fresnel integral S(z).

Legendre Functions

lpmv(x1, x2)	y=lpmv(m,v,x) returns the associated legendre function of integer order
sph_harm	Compute spherical harmonics.

lpmv
y=lpmv(m,v,x) returns the associated legendre function of integer order m and nonnegative degree v: |x|<=1.

sph_harm
Compute spherical harmonics.

This is a ufunc and may take scalar or array arguments like any other ufunc. The inputs will be broadcasted against each other.

Parameters

- *m* : int |m| <= n The order of the harmonic.
- *n* : int >= 0 The degree of the harmonic.
- *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*.

These are not universal functions:

lpn(n, z)	Compute sequence of Legendre functions of the first kind (polynomials),
lqn(n, z)	Compute sequence of Legendre functions of the second kind,
lpmn(m, n, z)	Associated Legendre functions of the first kind, Pmn(z) and its
lqmn(m, n, z)	Associated Legendre functions of the second kind, Qmn(z) and its

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.

lqn (*n, z*)
Compute sequence of Legendre functions of the second kind, Qn(z) and derivatives for all degrees from 0 to n (inclusive).

lpmn (*m, n, z*)
Associated Legendre functions of the first kind, Pmn(z) and its derivative, Pmn'(z) of order m and degree n. 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.

z can be complex.

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.

Orthogonal polynomials

The following functions evaluate values of orthogonal polynomials:

eval_legendre	Evaluate Legendre polynomial at a point.
eval_chebyt	Evaluate Chebyshev T polynomial at a point.
eval_chebyu	Evaluate Chebyshev U polynomial at a point.
eval_chebyc	Evaluate Chebyshev C polynomial at a point.
eval_chebys	Evaluate Chebyshev S polynomial at a point.
eval_jacobi	Evaluate Jacobi polynomial at a point.
eval_laguerre	Evaluate Laguerre polynomial at a point.
eval_genlaguerre	Evaluate generalized Laguerre polynomial at a point.
eval_hermite	Evaluate Hermite polynomial at a point.
eval_hermitenorm	Evaluate normalized Hermite polynomial at a point.
eval_gegenbauer	Evaluate Gegenbauer polynomial at a point.
eval_sh_legendre	Evaluate shifted Legendre polynomial at a point.
eval_sh_chebyt	Evaluate shifted Chebyshev T polynomial at a point.
eval_sh_chebyu	Evaluate shifted Chebyshev U polynomial at a point.
eval_sh_jacobi	Evaluate shifted Jacobi polynomial at a point.

eval_legendre()
Evaluate Legendre polynomial at a point.

eval_chebyt()
Evaluate Chebyshev T polynomial at a point.

This routine is numerically stable for *x* in `[-1, 1]` at least up to order `10000`.

eval_chebyu()
Evaluate Chebyshev U polynomial at a point.

eval_chebyc()
Evaluate Chebyshev C polynomial at a point.

eval_chebys()
Evaluate Chebyshev S polynomial at a point.

eval_jacobi()
Evaluate Jacobi polynomial at a point.

eval_laguerre()
Evaluate Laguerre polynomial at a point.

eval_genlaguerre()
Evaluate generalized Laguerre polynomial at a point.

eval_hermite()
Evaluate Hermite polynomial at a point.

eval_hermitenorm()
Evaluate normalized Hermite polynomial at a point.

eval_gegenbauer()
Evaluate Gegenbauer polynomial at a point.

eval_sh_legendre()
Evaluate shifted Legendre polynomial at a point.

eval_sh_chebyt()
Evaluate shifted Chebyshev T polynomial at a point.

eval_sh_chebyu()
Evaluate shifted Chebyshev U polynomial at a point.

eval_sh_jacobi()
Evaluate shifted Jacobi polynomial at a point.

The functions below, in turn, return *orthopoly1d* objects, which functions similarly as *numpy.poly1d*. The *orthopoly1d* class also has an attribute `weights` which returns the roots, weights, and total weights for the appropriate form of Gaussian quadrature. These are returned in an `n x 3` array with roots in the first column, weights in the second column, and total weights in the final column.

legendre(n[, monic])	Returns the nth order Legendre polynomial, P_n(x), orthogonal over
chebyt(n[, monic])	Return nth order Chebyshev polynomial of first kind, Tn(x). Orthogonal
chebyu(n[, monic])	Return nth order Chebyshev polynomial of second kind, Un(x). Orthogonal
chebyc(n[, monic])	Return nth order Chebyshev polynomial of first kind, Cn(x). Orthogonal
chebys(n[, monic])	Return nth order Chebyshev polynomial of second kind, Sn(x). Orthogonal
jacobi(n, alpha, beta[, monic])	Returns the nth order Jacobi polynomial, P^(alpha,beta)_n(x)
laguerre(n[, monic])	Return the nth order Laguerre polynoimal, L_n(x), orthogonal over
genlaguerre(n, alpha[, monic])	Returns the nth order generalized (associated) Laguerre polynomial,
hermite(n[, monic])	Return the nth order Hermite polynomial, H_n(x), orthogonal over
hermitenorm(n[, monic])	Return the nth order normalized Hermite polynomial, He_n(x), orthogonal
gegenbauer(n, alpha[, monic])	Return the nth order Gegenbauer (ultraspherical) polynomial,
sh_legendre(n[, monic])	Returns the nth order shifted Legendre polynomial, P^*_n(x), orthogonal
sh_chebyt(n[, monic])	Return nth order shifted Chebyshev polynomial of first kind, Tn(x).
sh_chebyu(n[, monic])	Return nth order shifted Chebyshev polynomial of second kind, Un(x).
sh_jacobi(n, p, q[, monic])	Returns the nth order Jacobi polynomial, G_n(p,q,x)

legendre(*n, monic=0*)
Returns the nth order Legendre polynomial, P_n(x), orthogonal over [-1,1] with weight function 1.

chebyt(*n, monic=0*)
Return nth order Chebyshev polynomial of first kind, Tn(x). Orthogonal over [-1,1] with weight function (1-x**2)**(-1/2).

chebyu(*n, monic=0*)
Return nth order Chebyshev polynomial of second kind, Un(x). Orthogonal over [-1,1] with weight function (1-x**2)**(1/2).

chebyc(*n, monic=0*)
Return nth order Chebyshev polynomial of first kind, Cn(x). Orthogonal over [-2,2] with weight function (1-(x/2)**2)**(-1/2).

chebys(*n, monic=0*)
Return nth order Chebyshev polynomial of second kind, Sn(x). Orthogonal over [-2,2] with weight function (1-(x/)**2)**(1/2).

jacobi (*n, alpha, beta, monic=0*)
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.

laguerre (*n, monic=0*)
Return the nth order Laguerre polynoimal, L_n(x), orthogonal over [0,inf) with weighting function exp(-x)

genlaguerre (*n, alpha, monic=0*)
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

hermite (*n, monic=0*)
Return the nth order Hermite polynomial, H_n(x), orthogonal over (-inf,inf) with weighting function exp(-x**2)

hermitenorm (*n, monic=0*)
Return the nth order normalized Hermite polynomial, He_n(x), orthogonal over (-inf,inf) with weighting function exp(-(x/2)**2)

gegenbauer (*n, alpha, monic=0*)
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

sh_legendre (*n, monic=0*)
Returns the nth order shifted Legendre polynomial, P^*_n(x), orthogonal over [0,1] with weighting function 1.

sh_chebyt (*n, monic=0*)
Return nth order shifted Chebyshev polynomial of first kind, Tn(x). Orthogonal over [0,1] with weight function (x-x**2)**(-1/2).

sh_chebyu (*n, monic=0*)
Return nth order shifted Chebyshev polynomial of second kind, Un(x). Orthogonal over [0,1] with weight function (x-x**2)**(1/2).

sh_jacobi (*n, p, q, monic=0*)
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: Large-order polynomials obtained from these functions are numerically unstable. `orthopoly1d` objects are converted to `poly1d`, when doing arithmetic. `numpy.poly1d` works in power basis and cannot represent high-order polynomials accurately, which can cause significant inaccuracy.

Hypergeometric Functions

`hyp2f1`(x1, x2, x3)	y=hyp2f1(a,b,c,z) returns the gauss hypergeometric function
`hyp1f1`(x1, x2)	y=hyp1f1(a,b,x) returns the confluent hypergeometeric function
`hyperu`(x1, x2)	y=hyperu(a,b,x) returns the confluent hypergeometric function of the
`hyp0f1`(v, z)	Confluent hypergeometric limit function 0F1.
`hyp2f0`(x1, x2, x3, out1)	(y,err)=hyp2f0(a,b,x,type) returns (y,err) with the hypergeometric function 2F0 in y and an error estimate in err. The input type determines a convergence factor and
`hyp1f2`(x1, x2, x3, out1)	(y,err)=hyp1f2(a,b,c,x) returns (y,err) with the hypergeometric function 1F2 in y and an error estimate in err.
`hyp3f0`(x1, x2, x3, out1)	(y,err)=hyp3f0(a,b,c,x) returns (y,err) with the hypergeometric function 3F0 in y and an error estimate in err.

hyp2f1
y=hyp2f1(a,b,c,z) returns the gauss hypergeometric function (2F1(a,b;c;z)).

hyp1f1
y=hyp1f1(a,b,x) returns the confluent hypergeometeric function (1F1(a,b;x)) evaluated at the values a, b, and x.

hyperu
y=hyperu(a,b,x) returns the confluent hypergeometric function of the second kind U(a,b,x).

hyp0f1(*v, z*)
Confluent hypergeometric limit function 0F1. Limit as q->infinity of 1F1(q;a;z/q)

hyp2f0
(y,err)=hyp2f0(a,b,x,type) returns (y,err) with the hypergeometric function 2F0 in y and an error estimate in err. The input type determines a convergence factor and can be either 1 or 2.

hyp1f2
(y,err)=hyp1f2(a,b,c,x) returns (y,err) with the hypergeometric function 1F2 in y and an error estimate in err.

hyp3f0
(y,err)=hyp3f0(a,b,c,x) returns (y,err) with the hypergeometric function 3F0 in y and an error estimate in err.

Parabolic Cylinder Functions

pbdv(x1, out1)	(d,dp)=pbdv(v,x) returns (d,dp) with the parabolic cylinder function Dv(x) in
pbvv(x1, out1)	(v,vp)=pbvv(v,x) returns (v,vp) with the parabolic cylinder function Vv(x) in
pbwa(x1, out1)	(w,wp)=pbwa(a,x) returns (w,wp) with the parabolic cylinder function W(a,x) in

pbdv
(d,dp)=pbdv(v,x) returns (d,dp) with the parabolic cylinder function Dv(x) in d and the derivative, Dv'(x) in dp.

pbvv
(v,vp)=pbvv(v,x) returns (v,vp) with the parabolic cylinder function Vv(x) in v and the derivative, Vv'(x) in vp.

pbwa
(w,wp)=pbwa(a,x) returns (w,wp) with the parabolic cylinder function W(a,x) in w and the derivative, W'(a,x) in wp. May not be accurate for large (>5) arguments in a and/or x.

These are not universal functions:

pbdv_seq(v, x)	Compute sequence of parabolic cylinder functions Dv(x) and
pbvv_seq(v, x)	Compute sequence of parabolic cylinder functions Dv(x) and
pbdn_seq(n, z)	Compute sequence of parabolic cylinder functions Dn(z) and

pbdv_seq(*v, x*)
Compute sequence of parabolic cylinder functions Dv(x) and their derivatives for Dv0(x)..Dv(x) with v0=v-int(v).

pbvv_seq(*v, x*)
Compute sequence of parabolic cylinder functions Dv(x) and their derivatives for Dv0(x)..Dv(x) with v0=v-int(v).

pbdn_seq(*n, z*)
Compute sequence of parabolic cylinder functions Dn(z) and their derivatives for D0(z)..Dn(z).

Mathieu and Related Functions

mathieu_a(x1)	lmbda=mathieu_a(m,q) returns the characteristic value for the even solution,
mathieu_b(x1)	lmbda=mathieu_b(m,q) returns the characteristic value for the odd solution,

mathieu_a
lmbda=mathieu_a(m,q) returns the characteristic value for the even solution, ce_m(z,q), of Mathieu's equation

mathieu_b
lmbda=mathieu_b(m,q) 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
mathieu_odd_coef(m, q)	Compute expansion coefficients for even mathieu functions and

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(x1, x2, out1)	(y,yp)=mathieu_cem(m,q,x) returns the even Mathieu function, ce_m(x,q),
mathieu_sem(x1, x2, out1)	(y,yp)=mathieu_sem(m,q,x) returns the odd Mathieu function, se_m(x,q),
mathieu_modcem1(x1, x2, out1)	(y,yp)=mathieu_modcem1(m,q,x) evaluates the even modified Matheiu function
mathieu_modcem2(x1, x2, out1)	(y,yp)=mathieu_modcem2(m,q,x) evaluates the even modified Matheiu function
mathieu_modsem1(x1, x2, out1)	(y,yp)=mathieu_modsem1(m,q,x) evaluates the odd modified Matheiu function
mathieu_modsem2(x1, x2, out1)	(y,yp)=mathieu_modsem2(m,q,x) evaluates the odd modified Matheiu function

mathieu_cem
(y,yp)=mathieu_cem(m,q,x) 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)

mathieu_sem
(y,yp)=mathieu_sem(m,q,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).

mathieu_modcem1
(y,yp)=mathieu_modcem1(m,q,x) evaluates the even modified Matheiu function of the first kind, Mc1m(x,q), and its derivative at x for order m and parameter q.

mathieu_modcem2
(y,yp)=mathieu_modcem2(m,q,x) evaluates the even modified Matheiu function of the second kind, Mc2m(x,q), and its derivative at x (given in degrees) for order m and parameter q.

mathieu_modsem1
(y,yp)=mathieu_modsem1(m,q,x) evaluates the odd modified Matheiu function of the first kind, Ms1m(x,q), and its derivative at x (given in degrees) for order m and parameter q.

mathieu_modsem2
(y,yp)=mathieu_modsem2(m,q,x) evaluates the odd modified Matheiu function of the second kind, Ms2m(x,q), and its derivative at x (given in degrees) for order m and parameter q.

Spheroidal Wave Functions

pro_ang1(x1, x2, x3, out1)	(s,sp)=pro_ang1(m,n,c,x) computes the prolate sheroidal angular function
pro_rad1(x1, x2, x3, out1)	(s,sp)=pro_rad1(m,n,c,x) computes the prolate sheroidal radial function
pro_rad2(x1, x2, x3, out1)	(s,sp)=pro_rad2(m,n,c,x) computes the prolate sheroidal radial function
obl_ang1(x1, x2, x3, out1)	(s,sp)=obl_ang1(m,n,c,x) computes the oblate sheroidal angular function
obl_rad1(x1, x2, x3, out1)	(s,sp)=obl_rad1(m,n,c,x) computes the oblate sheroidal radial function
obl_rad2(x1, x2, x3, out1)	(s,sp)=obl_rad2(m,n,c,x) computes the oblate sheroidal radial function
pro_cv(x1, x2)	cv=pro_cv(m,n,c) computes the characteristic value of prolate spheroidal
obl_cv(x1, x2)	cv=obl_cv(m,n,c) computes the characteristic value of oblate spheroidal
pro_cv_seq(m, n, c)	Compute a sequence of characteristic values for the prolate
obl_cv_seq(m, n, c)	Compute a sequence of characteristic values for the oblate

pro_ang1
(s,sp)=pro_ang1(m,n,c,x) computes the prolate sheroidal angular function of the first kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0.

pro_rad1
(s,sp)=pro_rad1(m,n,c,x) computes the prolate sheroidal radial function of the first kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0.

pro_rad2
(s,sp)=pro_rad2(m,n,c,x) computes the prolate sheroidal radial function of the second kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0.

obl_ang1
(s,sp)=obl_ang1(m,n,c,x) computes the oblate sheroidal angular function of the first kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0.

obl_rad1
(s,sp)=obl_rad1(m,n,c,x) computes the oblate sheroidal radial function of the first kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0.

obl_rad2
(s,sp)=obl_rad2(m,n,c,x) computes the oblate sheroidal radial function of the second kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0.

pro_cv
cv=pro_cv(m,n,c) computes the characteristic value of prolate spheroidal wave functions of order m,n (n>=m) and spheroidal parameter c.

obl_cv
cv=obl_cv(m,n,c) computes the characteristic value of oblate spheroidal wave functions of order m,n (n>=m) and spheroidal parameter c.

pro_cv_seq(*m, n, c*)
Compute a sequence of characteristic values for the prolate spheroidal wave functions for mode m and n'=m..n and spheroidal parameter c.

obl_cv_seq(*m, n, c*)
Compute 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:

pro_ang1_cv(x1, x2, x3, x4, out1)	(s,sp)=pro_ang1_cv(m,n,c,cv,x) computes the prolate sheroidal angular function
pro_rad1_cv(x1, x2, x3, x4, out1)	(s,sp)=pro_rad1_cv(m,n,c,cv,x) computes the prolate sheroidal radial function
pro_rad2_cv(x1, x2, x3, x4, out1)	(s,sp)=pro_rad2_cv(m,n,c,cv,x) computes the prolate sheroidal radial function
obl_ang1_cv(x1, x2, x3, x4, out1)	(s,sp)=obl_ang1_cv(m,n,c,cv,x) computes the oblate sheroidal angular function
obl_rad1_cv(x1, x2, x3, x4, out1)	(s,sp)=obl_rad1_cv(m,n,c,cv,x) computes the oblate sheroidal radial function
obl_rad2_cv(x1, x2, x3, x4, out1)	(s,sp)=obl_rad2_cv(m,n,c,cv,x) computes the oblate sheroidal radial function

pro_ang1_cv

(s,sp)=pro_ang1_cv(m,n,c,cv,x) computes the prolate sheroidal angular function of the first kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0. Requires pre-computed characteristic value.

pro_rad1_cv

(s,sp)=pro_rad1_cv(m,n,c,cv,x) computes the prolate sheroidal radial function of the first kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0. Requires pre-computed characteristic value.

pro_rad2_cv

(s,sp)=pro_rad2_cv(m,n,c,cv,x) computes the prolate sheroidal radial function of the second kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0. Requires pre-computed characteristic value.

obl_ang1_cv

(s,sp)=obl_ang1_cv(m,n,c,cv,x) computes the oblate sheroidal angular function of the first kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0. Requires pre-computed characteristic value.

obl_rad1_cv

(s,sp)=obl_rad1_cv(m,n,c,cv,x) computes the oblate sheroidal radial function of the first kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0. Requires pre-computed characteristic value.

obl_rad2_cv

(s,sp)=obl_rad2_cv(m,n,c,cv,x) computes the oblate sheroidal radial function of the second kind and its derivative (with respect to x) for mode paramters m>=0 and n>=m, spheroidal parameter c and |x|<1.0. Requires pre-computed characteristic value.

Kelvin Functions

kelvin(out1, out2, out3)	(Be, Ke, Bep, Kep)=kelvin(x) returns the tuple (Be, Ke, Bep, Kep) which containes
kelvin_zeros(nt)	Compute nt zeros of all the kelvin functions returned in a length 8 tuple of arrays of length nt.
ber()	y=ber(x) returns the Kelvin function ber x
bei()	y=bei(x) returns the Kelvin function bei x
berp()	y=berp(x) returns the derivative of the Kelvin function ber x
beip()	y=beip(x) returns the derivative of the Kelvin function bei x
ker()	y=ker(x) returns the Kelvin function ker x
kei()	y=kei(x) returns the Kelvin function ker x
kerp()	y=kerp(x) returns the derivative of the Kelvin function ker x
keip()	y=keip(x) returns the derivative of the Kelvin function kei x

kelvin
(Be, Ke, Bep, Kep)=kelvin(x) returns the tuple (Be, Ke, Bep, Kep) which containes 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.

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')

ber
y=ber(x) returns the Kelvin function ber x

bei
y=bei(x) returns the Kelvin function bei x

berp
y=berp(x) returns the derivative of the Kelvin function ber x

beip
y=beip(x) returns the derivative of the Kelvin function bei x

ker
y=ker(x) returns the Kelvin function ker x

kei
y=kei(x) returns the Kelvin function ker x

kerp
y=kerp(x) returns the derivative of the Kelvin function ker x

keip
y=keip(x) returns the derivative of the Kelvin function kei x

These are not universal functions:

ber_zeros(nt)	Compute nt zeros of the kelvin function ber x
bei_zeros(nt)	Compute nt zeros of the kelvin function bei x
berp_zeros(nt)	Compute nt zeros of the kelvin function ber' x
beip_zeros(nt)	Compute nt zeros of the kelvin function bei' x
ker_zeros(nt)	Compute nt zeros of the kelvin function ker x
kei_zeros(nt)	Compute nt zeros of the kelvin function kei x
kerp_zeros(nt)	Compute nt zeros of the kelvin function ker' x
keip_zeros(nt)	Compute nt zeros of the kelvin function kei' x

ber_zeros(*nt*)
Compute nt zeros of the kelvin function ber x

bei_zeros(*nt*)
Compute nt zeros of the kelvin function bei x

berp_zeros(*nt*)
Compute nt zeros of the kelvin function ber' x

beip_zeros(*nt*)
Compute nt zeros of the kelvin function bei' x

ker_zeros(*nt*)
Compute nt zeros of the kelvin function ker x

kei_zeros(*nt*)
Compute nt zeros of the kelvin function kei x

kerp_zeros(*nt*)
Compute nt zeros of the kelvin function ker' x

keip_zeros(*nt*)
Compute nt zeros of the kelvin function kei' x

Other Special Functions

expn(x1)	y=expn(n,x) returns the exponential integral for integer n and
exp1()	y=exp1(z) returns the exponential integral (n=1) of complex argument
expi()	y=expi(x) returns an exponential integral of argument x defined as
wofz()	y=wofz(z) returns the value of the fadeeva function for complex argument
dawsn()	y=dawsn(x) returns dawson's integral: exp(-x**2) *
shichi(out1)	(shi,chi)=shichi(x) returns the hyperbolic sine and cosine integrals:
sici(out1)	(si,ci)=sici(x) returns in si the integral of the sinc function from 0 to x:
spence()	y=spence(x) returns the dilogarithm integral: -integral(log t /
lambertw(z[, k, tol])	Lambert W function.
zeta(x1)	y=zeta(x,q) returns the Riemann zeta function of two arguments:
zetac()	y=zetac(x) returns 1.0 - the Riemann zeta function: sum(k**(-x), k=2..inf)

expn
y=expn(n,x) returns the exponential integral for integer n and non-negative x and n: integral(exp(-x*t) / t**n, t=1..inf).

exp1
y=exp1(z) returns the exponential integral (n=1) of complex argument z: integral(exp(-z*t)/t,t=1..inf).

expi
y=expi(x) returns an exponential integral of argument x defined as integral(exp(t)/t,t=-inf..x). See expn for a different exponential integral.

wofz
y=wofz(z) returns the value of the fadeeva function for complex argument z: exp(-z**2)*erfc(-i*z)

dawsn
y=dawsn(x) returns dawson's integral: exp(-x**2) * integral(exp(t**2),t=0..x).

shichi
(shi,chi)=shichi(x) returns the hyperbolic sine and cosine integrals: integral(sinh(t)/t,t=0..x) and eul + ln x + integral((cosh(t)-1)/t,t=0..x) where eul is Euler's Constant.

sici
(si,ci)=sici(x) returns in si the integral of the sinc function from 0 to x: integral(sin(t)/t,t=0..x). It returns in ci the cosine integral: eul + ln x + integral((cos(t) - 1)/t,t=0..x).

spence
y=spence(x) returns the dilogarithm integral: -integral(log t / (t-1),t=1..x)

lambertw(*z, k=0, tol=1e-8*)
Lambert W function.

The Lambert W function *W(z)* is defined as the inverse function of $w \exp(w)$. In other words, the value of $W(z)$ is such that $z = W(z) \exp(W(z))$ 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 $w \exp(w)$. Here, the branches are indexed by the integer *k*.

Parameters

z : array_like

Input argument

k : integer, optional

Branch index

tol : float

Evaluation tolerance

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* . 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 Corless et al, "On the Lambert W function", Adv. Comp. Math. 5 (1996) 329-359, available online here: http://www.apmaths.uwo.ca/~djeffrey/Offprints/W-adv-cm.pdf

TODO: use a series expansion when extremely close to the branch point at *-1/e* and make sure that the proper branch is chosen there

Examples

The Lambert W function is the inverse of *w exp(w)*:

```
>>> from scipy.special import lambertw
>>> w = lambertw(1)
>>> w
```

0.56714329040978387299996866221035555 >>> w*exp(w) 1.0

Any branch gives a valid inverse:

```
>>> w = lambertw(1, k=3)
>>> w
```

(-2.8535817554090378072068187234910812 + 17.113535539412145912607826671159289j) >>> w*exp(w) (1.0 + 3.5075477124212226194278700785075126e-36j)

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^{z^{ldots}}}*:

```
>>> def tower(z, n):
```

... if n == 0: ... return z ... return z ** tower(z, n-1) ... >>> tower(0.5, 100) 0.641185744504986 >>> -lambertw(-log(0.5))/log(0.5) 0.64118574450498598448620048211482366656282095719 11

Properties

The Lambert W function grows roughly like the natural logarithm for large arguments:

```
>>> lambertw(1000)
```

5.2496028524016 >>> log(1000) 6.90775527898214 >>> lambertw(10**100) 224.843106445119 >>> log(10**100) 230.258509299405

The principal branch of the Lambert W function has a rational Taylor series expansion around *z = 0*:

```
>>> nprint(taylor(lambertw, 0, 6), 10)
```

[0.0, 1.0, -1.0, 1.5, -2.666666667, 5.208333333, -10.8]

Some special values and limits are:

```
>>> lambertw(0)
```

0.0 >>> lambertw(1) 0.567143290409784 >>> lambertw(e) 1.0 >>> lambertw(inf) +inf >>> lambertw(0, k=-1) -inf >>> lambertw(0, k=3) -inf >>> lambertw(inf, k=3) (+inf + 18.8495559215388j)

The *k = 0* and *k = -1* branches join at *z = -1/e* where *W(z) = -1* for both branches. Since *-1/e* can only be represented approximately with mpmath numbers, evaluating the Lambert W function at this point only gives *-1* approximately:

```
>>> lambertw(-1/e, 0)
```

-0.99999999999837133022867 >>> lambertw(-1/e, -1) -1.00000000000016286697718

If *-1/e* happens to round in the negative direction, there might be a small imaginary part:

```
>>> lambertw(-1/e)
```

(-1.0 + 8.22007971511612e-9j)

zeta

y=zeta(x,q) returns the Riemann zeta function of two arguments: sum((k+q)**(-x),k=0..inf)

zetac
y=zetac(x) returns 1.0 - the Riemann zeta function: sum(k**(-x), k=2..inf)

Convenience Functions

cbrt()	y=cbrt(x) returns the real cube root of x.
exp10()	y=exp10(x) returns 10 raised to the x power.
exp2()	y=exp2(x) returns 2 raised to the x power.
radian(x1, x2)	y=radian(d,m,s) returns the angle given in (d)egrees, (m)inutes, and
cosdg()	y=cosdg(x) calculates the cosine of the angle x given in degrees.
sindg()	y=sindg(x) calculates the sine of the angle x given in degrees.
tandg()	y=tandg(x) calculates the tangent of the angle x given in degrees.
cotdg()	y=cotdg(x) calculates the cotangent of the angle x given in degrees.
log1p()	y=log1p(x) calculates log(1+x) for use when x is near zero.
expm1()	y=expm1(x) calculates exp(x) - 1 for use when x is near zero.
cosm1()	y=calculates cos(x) - 1 for use when x is near zero.
round()	y=Returns the nearest integer to x as a double precision

cbrt
y=cbrt(x) returns the real cube root of x.

exp10
y=exp10(x) returns 10 raised to the x power.

exp2
y=exp2(x) returns 2 raised to the x power.

radian
y=radian(d,m,s) returns the angle given in (d)egrees, (m)inutes, and (s)econds in radians.

cosdg
y=cosdg(x) calculates the cosine of the angle x given in degrees.

sindg
y=sindg(x) calculates the sine of the angle x given in degrees.

tandg
y=tandg(x) calculates the tangent of the angle x given in degrees.

cotdg
y=cotdg(x) calculates the cotangent of the angle x given in degrees.

log1p
y=log1p(x) calculates log(1+x) for use when x is near zero.

expm1
y=expm1(x) calculates exp(x) - 1 for use when x is near zero.

cosm1
y=calculates cos(x) - 1 for use when x is near zero.

round
y=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.

3.18 Statistical functions (scipy.stats)

This module contains a large number of probability distributions as well as a growing library of statistical functions.

Each included continuous distribution is an instance of the class rv_continous:

rv_continuous([momtype, a, b, xa, xb, xtol, ...])	A Generic continuous random variable.
rv_continuous.pdf(x, *args, **kwds)	Probability density function at x of the given RV.
rv_continuous.cdf(x, *args, **kwds)	Cumulative distribution function at x of the given RV.
rv_continuous.sf(x, *args, **kwds)	Survival function (1-cdf) at x of the given RV.
rv_continuous.ppf(q, *args, **kwds)	Percent point function (inverse of cdf) at q of the given RV.
rv_continuous.isf(q, *args, **kwds)	Inverse survival function at q of the given RV.
rv_continuous.stats(*args, **kwds)	Some statistics of the given RV

class rv_continuous (*momtype=1, a=None, b=None, xa=-10.0, xb=10.0, xtol=1e-14, badvalue=None, name=None, longname=None, shapes=None, extradoc=None*)

A Generic continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = generic.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = generic(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = generic.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-generic.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = generic.rvs(<shape(s)>,size=100)
```

Methods

generic.rvs(<shape(s)>,loc=0,scale=1,size=1)	•random variates
generic.pdf(x,<shape(s)>,loc=0,scale=1)	•probability density function
generic.cdf(x,<shape(s)>,loc=0,scale=1)	•cumulative density function
generic.sf(x,<shape(s)>,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
generic.ppf(q,<shape(s)>,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
generic.isf(q,<shape(s)>,loc=0,scale=1)	•inverse survival function (inverse of sf)
generic.stats(<shape(s)>,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
generic.entropy(<shape(s)>,loc=0,scale=1)	•(differential) entropy of the RV.
generic.fit(data,<shape(s)>,loc=0,scale=1)	•Parameter estimates for generic data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = generic(<shape(s)>,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

pdf (*x, *args, **kwds*)

Probability density function at x of the given RV.

Parameters

x : array-like

quantiles

arg1, arg2, arg3,... : array-like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

Returns

pdf : array-like

Probability density function evaluated at x

cdf (*x, *args, **kwds*)

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

cdf : array-like

Cumulative distribution function evaluated at x

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

ppf(*q, *args, **kwds*)
Percent point function (inverse of cdf) at q of the given RV.

Parameters

q : array-like

lower tail probability

arg1, arg2, arg3,... : array-like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

Returns

x : array-like

quantile corresponding to the lower tail probability q.

isf(*q, *args, **kwds*)
Inverse survival function at q of the given RV.

Parameters

q : array-like

upper tail probability

arg1, arg2, arg3,... : array-like

The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

Returns

x : array-like

quantile corresponding to the upper tail probability q.

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

scale parameter (default=1)

moments : string, optional

composed of letters ['mvsk'] defining which moments to compute: 'm' = mean, 'v' = variance, 's' = (Fisher's) skew, 'k' = (Fisher's) kurtosis. (default='mv')

Returns

stats : sequence

of requested moments.

Each discrete distribution is an instance of the class rv_discrete:

rv_discrete([a, b, name, badvalue, ...])	A Generic discrete random variable.
rv_discrete.pmf(k, *args, **kwds)	Probability mass function at k of the given RV.
rv_discrete.cdf(k, *args, **kwds)	Cumulative distribution function at k of the given RV
rv_discrete.sf(k, *args, **kwds)	Survival function (1-cdf) at k of the given RV
rv_discrete.ppf(q, *args, **kwds)	Percent point function (inverse of cdf) at q of the given RV
rv_discrete.isf(q, *args, **kwds)	Inverse survival function (1-sf) at q of the given RV
rv_discrete.stats(*args, **kwds)	Some statistics of the given discrete RV

class rv_discrete(*a=0, b=inf, name=None, badvalue=None, moment_tol=1e-08, values=None, inc=1, longname=None, shapes=None, extradoc=None*)

A Generic discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = generic.numargs
>>> [ <shape(s)> ] = ['Replace with resonable value',]*numargs
```

Display frozen pmf:

```
>>> rv = generic(<shape(s)>)
>>> x = np.arange(0,np.min(rv.dist.b,3)+1)
>>> h = plt.plot(x,rv.pmf(x))
```

Check accuracy of cdf and ppf:

```
>>> prb = generic.cdf(x,<shape(s)>)
>>> h = plt.semilogy(np.abs(x-generic.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation:

```
>>> R = generic.rvs(<shape(s)>,size=100)
```

Custom made discrete distribution:

```
>>> vals = [arange(7),(0.1,0.2,0.3,0.1,0.1,0.1,0.1)]
>>> custm = rv_discrete(name='custm',values=vals)
>>> h = plt.plot(vals[0],custm.pmf(vals[0]))
```

Methods

generic.rvs(<shape(s)>,loc=0,size=1)	•random variates
generic.pmf(x,<shape(s)>,loc=0)	•probability mass function
generic.cdf(x,<shape(s)>,loc=0)	•cumulative density function
generic.sf(x,<shape(s)>,loc=0)	•survival function (1-cdf — sometimes more accurate)
generic.ppf(q,<shape(s)>,loc=0)	•percent point function (inverse of cdf — percentiles)
generic.isf(q,<shape(s)>,loc=0)	•inverse survival function (inverse of sf)
generic.stats(<shape(s)>,loc=0,moments='mv')	•mean('m',axis=0), variance('v'), skew('s'), and/or kurtosis('k')
generic.entropy(<shape(s)>,loc=0)	•entropy of the RV
Alternatively, the object may be called (as a function) to fix the shape and location parameters returning a "frozen" discrete RV object: myrv = generic(<shape(s)>,loc=0)	•frozen RV object with the same methods but holding the given shape and location fixed.
You can construct an aribtrary discrete rv where P{X=xk} = pk by passing to the rv_discrete initialization method (through the values= keyword) a tuple of sequences (xk,pk) which describes only those values of X (xk) that occur with nonzero probability (pk).	

pmf(*k, *args, **kwds*)

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

cdf(*k, *args, **kwds*)

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

cdf : array-like

Cumulative distribution function evaluated at k

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

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.

isf(*q, *args, **kwds*)

Inverse survival function (1-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 : array-like

quantile corresponding to the upper tail probability, q.

stats(**args, **kwds*)

Some statistics of the given discrete 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)

moments : string, optional

composed of letters ['mvsk'] defining which moments to compute: 'm' = mean, 'v' = variance, 's' = (Fisher's) skew, 'k' = (Fisher's) kurtosis. (default='mv')

Returns

stats : sequence

of requested moments.

3.18.1 Continuous distributions

norm	A	normal	continuous	random	variable.
alpha	A	alpha	continuous	random	variable.
anglit	A	anglit	continuous	random	variable.
arcsine	A	arcsine	continuous	random	variable.
beta	A	beta	continuous	random	variable.
betaprime	A	betaprime	continuous	random	variable.
bradford	A	Bradford	continuous	random	variable.
burr	Burr	continuous	random	variable.	
fisk	A	funk	continuous	random	variable.

Continued on next page

Table 3.10 – continued from previous page

cauchy	Cauchy continuous random variable.
chi	A chi continuous random variable.
chi2	A chi-squared continuous random variable.
cosine	A cosine continuous random variable.
dgamma	A double gamma continuous random variable.
dweibull	A double Weibull continuous random variable.
erlang	An Erlang continuous random variable.
expon	An exponential continuous random variable.
exponweib	An exponentiated Weibull continuous random variable.
exponpow	An exponential power continuous random variable.
fatiguelife	A fatigue-life (Birnbaum-Sanders) continuous random variable.
foldcauchy	A folded Cauchy continuous random variable.
f	An F continuous random variable.
foldnorm	A folded normal continuous random variable.
fretchet_r	
fretcher_l	
genlogistic	A generalized logistic continuous random variable.
genpareto	A generalized Pareto continuous random variable.
genexpon	A generalized exponential continuous random variable.
genextreme	A generalized extreme value continuous random variable.
gausshyper	A Gauss hypergeometric continuous random variable.
gamma	A gamma continuous random variable.
gengamma	A generalized gamma continuous random variable.
genhalflogistic	A generalized half-logistic continuous random variable.
gompertz	A Gompertz (truncated Gumbel) distribution continuous random variable.
gumbel_r	A (right-skewed) Gumbel continuous random variable.
gumbel_l	A left-skewed Gumbel continuous random variable.
halfcauchy	A Half-Cauchy continuous random variable.
halflogistic	A half-logistic continuous random variable.
halfnorm	A half-normal continuous random variable.
hypsecant	A hyperbolic secant continuous random variable.
invgamma	An inverted gamma continuous random variable.
invnorm	An inverse normal continuous random variable.
invweibull	An inverted Weibull continuous random variable.
johnsonsb	A Johnson SB continuous random variable.
johnsonsu	A Johnson SU continuous random variable.
laplace	A Laplace continuous random variable.
logistic	A logistic continuous random variable.
loggamma	A log gamma continuous random variable.
loglaplace	A log-Laplace continuous random variable.
lognorm	A lognormal continuous random variable.
gilbrat	A Gilbrat continuous random variable.
lomax	A Lomax (Pareto of the second kind) continuous random variable.
maxwell	A Maxwell continuous random variable.
mielke	A Mielke's Beta-Kappa continuous random variable.
nakagami	A Nakagami continuous random variable.
ncx2	A non-central chi-squared continuous random variable.
ncf	A non-central F distribution continuous random variable.
t	Student's T continuous random variable.
nct	A Noncentral T continuous random variable.
pareto	A Pareto continuous random variable.
powerlaw	A power-function continuous random variable.

Continued on next page

Table 3.10 – continued from previous page

powerlognorm	A power log-normal continuous random variable.
powernorm	A power normal continuous random variable.
rdist	An R-distributed continuous random variable.
reciprocal	A reciprocal continuous random variable.
rayleigh	A Rayleigh continuous random variable.
rice	A Rice continuous random variable.
recipinvgauss	A reciprocal inverse Gaussian continuous random variable.
semicircular	A semicircular continuous random variable.
triang	A Triangular continuous random variable.
truncexpon	A truncated exponential continuous random variable.
truncnorm	A truncated normal continuous random variable.
tukeylambda	A Tukey-Lambda continuous random variable.
uniform	A uniform continuous random variable.
von_mises	
wald	A Wald continuous random variable.
weibull_min	A Weibull minimum continuous random variable.
weibull_max	A Weibull maximum continuous random variable.
wrapcauchy	A wrapped Cauchy continuous random variable.
ksone	Kolmogorov-Smirnov A one-sided test statistic. continuous random variable.
kstwobign	Kolmogorov-Smirnov two-sided (for large N) continuous random variable.

norm

A normal continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = norm.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = norm(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = norm.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-norm.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = norm.rvs(size=100)
```

Normal distribution

The location (loc) keyword specifies the mean. The scale (scale) keyword specifies the standard deviation.

normal.pdf(x) = exp(-x**2/2)/sqrt(2*pi)

Methods

norm.rvs(loc=0,scale=1,size=1)	•random variates
norm.pdf(x,loc=0,scale=1)	•probability density function
norm.cdf(x,loc=0,scale=1)	•cumulative density function
norm.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
norm.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
norm.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
norm.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
norm.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
norm.fit(data,loc=0,scale=1)	•Parameter estimates for norm data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = norm(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

alpha

A alpha continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

a : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = alpha.numargs
>>> [ a ] = [0.9,]*numargs
>>> rv = alpha(a)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = alpha.cdf(x,a)
>>> h=plt.semilogy(np.abs(x-alpha.ppf(prb,a))+1e-20)
```

Random number generation

```
>>> R = alpha.rvs(a,size=100)
```

Alpha distribution

alpha.pdf(x,a) = 1/(x**2*Phi(a)*sqrt(2*pi)) * exp(-1/2 * (a-1/x)**2) where Phi(alpha) is the normal CDF, x > 0, and a > 0.

Methods

alpha.rvs(a,loc=0,scale=1,size=1)	•random variates
alpha.pdf(x,a,loc=0,scale=1)	•probability density function
alpha.cdf(x,a,loc=0,scale=1)	•cumulative density function
alpha.sf(x,a,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
alpha.ppf(q,a,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
alpha.isf(q,a,loc=0,scale=1)	•inverse survival function (inverse of sf)
alpha.stats(a,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
alpha.entropy(a,loc=0,scale=1)	•(differential) entropy of the RV.
alpha.fit(data,a,loc=0,scale=1)	•Parameter estimates for alpha data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = alpha(a,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

anglit

A anglit continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = anglit.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = anglit(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = anglit.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-anglit.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = anglit.rvs(size=100)
```

Anglit distribution

anglit.pdf(x) = sin(2*x+pi/2) = cos(2*x) for -pi/4 <= x <= pi/4

Methods

anglit.rvs(loc=0,scale=1,size=1)	•random variates
anglit.pdf(x,loc=0,scale=1)	•probability density function
anglit.cdf(x,loc=0,scale=1)	•cumulative density function
anglit.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
anglit.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
anglit.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
anglit.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
anglit.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
anglit.fit(data,loc=0,scale=1)	•Parameter estimates for anglit data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = anglit(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`arcsine`

A arcsine continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = arcsine.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = arcsine(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = arcsine.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-arcsine.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = arcsine.rvs(size=100)
```

Arcsine distribution

arcsine.pdf(x) = 1/(pi*sqrt(x*(1-x))) for 0 < x < 1.

Methods

arcsine.rvs(loc=0,scale=1,size=1)	•random variates
arcsine.pdf(x,loc=0,scale=1)	•probability density function
arcsine.cdf(x,loc=0,scale=1)	•cumulative density function
arcsine.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
arcsine.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
arcsine.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
arcsine.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
arcsine.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
arcsine.fit(data,loc=0,scale=1)	•Parameter estimates for arcsine data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = arcsine(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

beta

A beta continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

a,b : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = beta.numargs
>>> [ a,b ] = [0.9,]*numargs
>>> rv = beta(a,b)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = beta.cdf(x,a,b)
>>> h=plt.semilogy(np.abs(x-beta.ppf(prb,a,b))+1e-20)
```

Random number generation

```
>>> R = beta.rvs(a,b,size=100)
```

Beta distribution

beta.pdf(x, a, b) = gamma(a+b)/(gamma(a)*gamma(b)) * x**(a-1) * (1-x)**(b-1) for 0 < x < 1, a, b > 0.

Methods

beta.rvs(a,b,loc=0,scale=1,size=1)	•random variates
beta.pdf(x,a,b,loc=0,scale=1)	•probability density function
beta.cdf(x,a,b,loc=0,scale=1)	•cumulative density function
beta.sf(x,a,b,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
beta.ppf(q,a,b,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
beta.isf(q,a,b,loc=0,scale=1)	•inverse survival function (inverse of sf)
beta.stats(a,b,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
beta.entropy(a,b,loc=0,scale=1)	•(differential) entropy of the RV.
beta.fit(data,a,b,loc=0,scale=1)	•Parameter estimates for beta data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = beta(a,b,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`betaprime`

A betaprime continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

a,b : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = betaprime.numargs
>>> [ a,b ] = [0.9,]*numargs
>>> rv = betaprime(a,b)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = betaprime.cdf(x,a,b)
>>> h=plt.semilogy(np.abs(x-betaprime.ppf(prb,a,b))+1e-20)
```

Random number generation

```
>>> R = betaprime.rvs(a,b,size=100)
```

Beta prime distribution

betaprime.pdf(x, a, b) = gamma(a+b)/(gamma(a)*gamma(b))

- x**(a-1) * (1-x)**(-a-b)

for x > 0, a, b > 0.

Methods

betaprime.rvs(a,b,loc=0,scale=1,size=1)	•random variates
betaprime.pdf(x,a,b,loc=0,scale=1)	•probability density function
betaprime.cdf(x,a,b,loc=0,scale=1)	•cumulative density function
betaprime.sf(x,a,b,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
betaprime.ppf(q,a,b,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
betaprime.isf(q,a,b,loc=0,scale=1)	•inverse survival function (inverse of sf)
betaprime.stats(a,b,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
betaprime.entropy(a,b,loc=0,scale=1)	•(differential) entropy of the RV.
betaprime.fit(data,a,b,loc=0,scale=1)	•Parameter estimates for betaprime data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = betaprime(a,b,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

bradford

A Bradford continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = bradford.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = bradford(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = bradford.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-bradford.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = bradford.rvs(c,size=100)
```

Bradford distribution

bradford.pdf(x,c) = c/(k*(1+c*x)) for 0 < x < 1, c > 0 and k = log(1+c).

Methods

bradford.rvs(c,loc=0,scale=1,size=1)	•random variates
bradford.pdf(x,c,loc=0,scale=1)	•probability density function
bradford.cdf(x,c,loc=0,scale=1)	•cumulative density function
bradford.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
bradford.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
bradford.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
bradford.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
bradford.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
bradford.fit(data,c,loc=0,scale=1)	•Parameter estimates for bradford data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = bradford(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

burr

Burr continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c,d : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = burr.numargs
>>> [ c,d ] = [0.9,]*numargs
>>> rv = burr(c,d)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = burr.cdf(x,c,d)
>>> h=plt.semilogy(np.abs(x-burr.ppf(prb,c,d))+1e-20)
```

Random number generation

```
>>> R = burr.rvs(c,d,size=100)
```

Burr distribution

burr.pdf(x,c,d) = c*d * x**(-c-1) * (1+x**(-c))**(-d-1) for x > 0.

Methods

burr.rvs(c,d,loc=0,scale=1,size=1)	•random variates
burr.pdf(x,c,d,loc=0,scale=1)	•probability density function
burr.cdf(x,c,d,loc=0,scale=1)	•cumulative density function
burr.sf(x,c,d,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
burr.ppf(q,c,d,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
burr.isf(q,c,d,loc=0,scale=1)	•inverse survival function (inverse of sf)
burr.stats(c,d,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
burr.entropy(c,d,loc=0,scale=1)	•(differential) entropy of the RV.
burr.fit(data,c,d,loc=0,scale=1)	•Parameter estimates for burr data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = burr(c,d,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

fisk

A funk continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = fink.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = fink(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = fink.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-fink.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = fink.rvs(c,size=100)
```

Fink distribution.

Burr distribution with d=1.

Methods

fink.rvs(c,loc=0,scale=1,size=1)	•random variates
fink.pdf(x,c,loc=0,scale=1)	•probability density function
fink.cdf(x,c,loc=0,scale=1)	•cumulative density function
fink.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
fink.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
fink.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
fink.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
fink.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
fink.fit(data,c,loc=0,scale=1)	•Parameter estimates for fink data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = fink(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

cauchy

Cauchy continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = cauchy.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = cauchy(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = cauchy.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-cauchy.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = cauchy.rvs(size=100)
```

Cauchy distribution

cauchy.pdf(x) = 1/(pi*(1+x**2))

This is the t distribution with one degree of freedom.

Methods

cauchy.rvs(loc=0,scale=1,size=1)	•random variates
cauchy.pdf(x,loc=0,scale=1)	•probability density function
cauchy.cdf(x,loc=0,scale=1)	•cumulative density function
cauchy.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
cauchy.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
cauchy.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
cauchy.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
cauchy.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
cauchy.fit(data,loc=0,scale=1)	•Parameter estimates for cauchy data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = cauchy(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

chi

A chi continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

df : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = chi.numargs
>>> [ df ] = [0.9,]*numargs
>>> rv = chi(df)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = chi.cdf(x,df)
>>> h=plt.semilogy(np.abs(x-chi.ppf(prb,df))+1e-20)
```

Random number generation

```
>>> R = chi.rvs(df,size=100)
```

Chi distribution

chi.pdf(x,df) = x**(df-1)*exp(-x**2/2)/(2**(df/2-1)*gamma(df/2)) for x > 0.

Methods

chi.rvs(df,loc=0,scale=1,size=1)	•random variates
chi.pdf(x,df,loc=0,scale=1)	•probability density function
chi.cdf(x,df,loc=0,scale=1)	•cumulative density function
chi.sf(x,df,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
chi.ppf(q,df,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
chi.isf(q,df,loc=0,scale=1)	•inverse survival function (inverse of sf)
chi.stats(df,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
chi.entropy(df,loc=0,scale=1)	•(differential) entropy of the RV.
chi.fit(data,df,loc=0,scale=1)	•Parameter estimates for chi data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = chi(df,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

chi2

A chi-squared continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

df : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = chi2.numargs
>>> [ df ] = [0.9,]*numargs
>>> rv = chi2(df)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = chi2.cdf(x,df)
>>> h=plt.semilogy(np.abs(x-chi2.ppf(prb,df))+1e-20)
```

Random number generation

```
>>> R = chi2.rvs(df,size=100)
```

Chi-squared distribution

chi2.pdf(x,df) = 1/(2*gamma(df/2)) * (x/2)**(df/2-1) * exp(-x/2)

Methods

chi2.rvs(df,loc=0,scale=1,size=1)	•random variates
chi2.pdf(x,df,loc=0,scale=1)	•probability density function
chi2.cdf(x,df,loc=0,scale=1)	•cumulative density function
chi2.sf(x,df,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
chi2.ppf(q,df,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
chi2.isf(q,df,loc=0,scale=1)	•inverse survival function (inverse of sf)
chi2.stats(df,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
chi2.entropy(df,loc=0,scale=1)	•(differential) entropy of the RV.
chi2.fit(data,df,loc=0,scale=1)	•Parameter estimates for chi2 data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = chi2(df,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

cosine

A cosine continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = cosine.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = cosine(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = cosine.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-cosine.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = cosine.rvs(size=100)
```

Cosine distribution (approximation to the normal)

cosine.pdf(x) = 1/(2*pi) * (1+cos(x)) for -pi <= x <= pi.

Methods

cosine.rvs(loc=0,scale=1,size=1)	•random variates
cosine.pdf(x,loc=0,scale=1)	•probability density function
cosine.cdf(x,loc=0,scale=1)	•cumulative density function
cosine.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
cosine.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
cosine.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
cosine.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
cosine.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
cosine.fit(data,loc=0,scale=1)	•Parameter estimates for cosine data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = cosine(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

dgamma

A double gamma continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

a : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = dgamma.numargs
>>> [ a ] = [0.9,]*numargs
>>> rv = dgamma(a)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = dgamma.cdf(x,a)
>>> h=plt.semilogy(np.abs(x-dgamma.ppf(prb,a))+1e-20)
```

Random number generation

```
>>> R = dgamma.rvs(a,size=100)
```

Double gamma distribution

dgamma.pdf(x,a) = 1/(2*gamma(a))*abs(x)**(a-1)*exp(-abs(x)) for a > 0.

Methods

dgamma.rvs(a,loc=0,scale=1,size=1)	•random variates
dgamma.pdf(x,a,loc=0,scale=1)	•probability density function
dgamma.cdf(x,a,loc=0,scale=1)	•cumulative density function
dgamma.sf(x,a,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
dgamma.ppf(q,a,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
dgamma.isf(q,a,loc=0,scale=1)	•inverse survival function (inverse of sf)
dgamma.stats(a,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
dgamma.entropy(a,loc=0,scale=1)	•(differential) entropy of the RV.
dgamma.fit(data,a,loc=0,scale=1)	•Parameter estimates for dgamma data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = dgamma(a,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

dweibull

A double Weibull continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = dweibull.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = dweibull(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = dweibull.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-dweibull.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = dweibull.rvs(c,size=100)
```

Double Weibull distribution

dweibull.pdf(x,c) = c/2*abs(x)**(c-1)*exp(-abs(x)**c)

Methods

dweibull.rvs(c,loc=0,scale=1,size=1)	•random variates
dweibull.pdf(x,c,loc=0,scale=1)	•probability density function
dweibull.cdf(x,c,loc=0,scale=1)	•cumulative density function
dweibull.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
dweibull.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
dweibull.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
dweibull.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
dweibull.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
dweibull.fit(data,c,loc=0,scale=1)	•Parameter estimates for dweibull data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = dweibull(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

erlang

An Erlang continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

n : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = erlang.numargs
>>> [ n ] = [0.9,]*numargs
>>> rv = erlang(n)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = erlang.cdf(x,n)
>>> h=plt.semilogy(np.abs(x-erlang.ppf(prb,n))+1e-20)
```

Random number generation

```
>>> R = erlang.rvs(n,size=100)
```

Erlang distribution (Gamma with integer shape parameter)

Methods

erlang.rvs(n,loc=0,scale=1,size=1)	•random variates
erlang.pdf(x,n,loc=0,scale=1)	•probability density function
erlang.cdf(x,n,loc=0,scale=1)	•cumulative density function
erlang.sf(x,n,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
erlang.ppf(q,n,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
erlang.isf(q,n,loc=0,scale=1)	•inverse survival function (inverse of sf)
erlang.stats(n,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
erlang.entropy(n,loc=0,scale=1)	•(differential) entropy of the RV.
erlang.fit(data,n,loc=0,scale=1)	•Parameter estimates for erlang data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = erlang(n,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

expon

An exponential continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = expon.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = expon(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = expon.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-expon.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = expon.rvs(size=100)
```

Exponential distribution

expon.pdf(x) = exp(-x) for x >= 0.

scale = 1.0 / lambda

Methods

expon.rvs(loc=0,scale=1,size=1)	•random variates
expon.pdf(x,loc=0,scale=1)	•probability density function
expon.cdf(x,loc=0,scale=1)	•cumulative density function
expon.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
expon.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
expon.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
expon.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
expon.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
expon.fit(data,loc=0,scale=1)	•Parameter estimates for expon data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = expon(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

exponweib

An exponentiated Weibull continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

a,c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = exponweib.numargs
>>> [ a,c ] = [0.9,]*numargs
>>> rv = exponweib(a,c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = exponweib.cdf(x,a,c)
>>> h=plt.semilogy(np.abs(x-exponweib.ppf(prb,a,c))+1e-20)
```

Random number generation

```
>>> R = exponweib.rvs(a,c,size=100)
```

Exponentiated Weibull distribution

exponweib.pdf(x,a,c) = a*c*(1-exp(-x**c))**(a-1)*exp(-x**c)*x**(c-1) for x > 0, a, c > 0.

Methods

exponweib.rvs(a,c,loc=0,scale=1,size=1)	•random variates
exponweib.pdf(x,a,c,loc=0,scale=1)	•probability density function
exponweib.cdf(x,a,c,loc=0,scale=1)	•cumulative density function
exponweib.sf(x,a,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
exponweib.ppf(q,a,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
exponweib.isf(q,a,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
exponweib.stats(a,c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
exponweib.entropy(a,c,loc=0,scale=1)	•(differential) entropy of the RV.
exponweib.fit(data,a,c,loc=0,scale=1)	•Parameter estimates for exponweib data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = exponweib(a,c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

exponpow

An exponential power continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

b : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = exponpow.numargs
>>> [ b ] = [0.9,]*numargs
>>> rv = exponpow(b)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = exponpow.cdf(x,b)
>>> h=plt.semilogy(np.abs(x-exponpow.ppf(prb,b))+1e-20)
```

Random number generation

```
>>> R = exponpow.rvs(b,size=100)
```

Exponential Power distribution

exponpow.pdf(x,b) = b*x**(b-1) * exp(1+x**b - exp(x**b)) for x >= 0, b > 0.

Methods

exponpow.rvs(b,loc=0,scale=1,size=1)	•random variates
exponpow.pdf(x,b,loc=0,scale=1)	•probability density function
exponpow.cdf(x,b,loc=0,scale=1)	•cumulative density function
exponpow.sf(x,b,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
exponpow.ppf(q,b,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
exponpow.isf(q,b,loc=0,scale=1)	•inverse survival function (inverse of sf)
exponpow.stats(b,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
exponpow.entropy(b,loc=0,scale=1)	•(differential) entropy of the RV.
exponpow.fit(data,b,loc=0,scale=1)	•Parameter estimates for exponpow data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = exponpow(b,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

fatiguelife

A fatigue-life (Birnbaum-Sanders) continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = fatiguelife.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = fatiguelife(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = fatiguelife.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-fatiguelife.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = fatiguelife.rvs(c,size=100)
```

Fatigue-life (Birnbaum-Sanders) distribution

fatiguelife.pdf(x,c) = (x+1)/(2*c*sqrt(2*pi*x**3)) * exp(-(x-1)**2/(2*x*c**2)) for x > 0.

Methods

fatiguelife.rvs(c,loc=0,scale=1,size=1)	•random variates
fatiguelife.pdf(x,c,loc=0,scale=1)	•probability density function
fatiguelife.cdf(x,c,loc=0,scale=1)	•cumulative density function
fatiguelife.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
fatiguelife.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
fatiguelife.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
fatiguelife.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
fatiguelife.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
fatiguelife.fit(data,c,loc=0,scale=1)	•Parameter estimates for fatiguelife data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = fatiguelife(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`foldcauchy`

A folded Cauchy continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = foldcauchy.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = foldcauchy(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = foldcauchy.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-foldcauchy.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = foldcauchy.rvs(c,size=100)
```

A folded Cauchy distributions

foldcauchy.pdf(x,c) = 1/(pi*(1+(x-c)**2)) + 1/(pi*(1+(x+c)**2)) for x >= 0.

Methods

foldcauchy.rvs(c,loc=0,scale=1,size=1)	•random variates
foldcauchy.pdf(x,c,loc=0,scale=1)	•probability density function
foldcauchy.cdf(x,c,loc=0,scale=1)	•cumulative density function
foldcauchy.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
foldcauchy.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
foldcauchy.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
foldcauchy.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
foldcauchy.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
foldcauchy.fit(data,c,loc=0,scale=1)	•Parameter estimates for foldcauchy data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = foldcauchy(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

f

An F continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

dfn,dfd : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = f.numargs
>>> [ dfn,dfd ] = [0.9,]*numargs
>>> rv = f(dfn,dfd)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = f.cdf(x,dfn,dfd)
>>> h=plt.semilogy(np.abs(x-f.ppf(prb,dfn,dfd))+1e-20)
```

Random number generation

```
>>> R = f.rvs(dfn,dfd,size=100)
```

F distribution

$$\mathbf{F.pdf(x,df1,df2)} = \frac{\mathrm{df2}^{(\mathrm{df2}/2)} * \mathrm{df1}^{(\mathrm{df1}/2)} * x^{(\mathrm{df1}/2-1)}}{(\mathrm{df2}+\mathrm{df1}*x)^{((\mathrm{df1}+\mathrm{df2})/2)} * B(\mathrm{df1}/2, \mathrm{df2}/2)}$$

for $x > 0$.

Methods

f.rvs(dfn,dfd,loc=0,scale=1,size=1)	•random variates
f.pdf(x,dfn,dfd,loc=0,scale=1)	•probability density function
f.cdf(x,dfn,dfd,loc=0,scale=1)	•cumulative density function
f.sf(x,dfn,dfd,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
f.ppf(q,dfn,dfd,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
f.isf(q,dfn,dfd,loc=0,scale=1)	•inverse survival function (inverse of sf)
f.stats(dfn,dfd,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
f.entropy(dfn,dfd,loc=0,scale=1)	•(differential) entropy of the RV.
f.fit(data,dfn,dfd,loc=0,scale=1)	•Parameter estimates for f data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = f(dfn,dfd,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`foldnorm`

A folded normal continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = foldnorm.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = foldnorm(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = foldnorm.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-foldnorm.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = foldnorm.rvs(c,size=100)
```

Folded normal distribution

foldnormal.pdf(x,c) = sqrt(2/pi) * cosh(c*x) * exp(-(x**2+c**2)/2) for c >= 0.

Methods

foldnorm.rvs(c,loc=0,scale=1,size=1)	•random variates
foldnorm.pdf(x,c,loc=0,scale=1)	•probability density function
foldnorm.cdf(x,c,loc=0,scale=1)	•cumulative density function
foldnorm.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
foldnorm.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
foldnorm.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
foldnorm.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
foldnorm.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
foldnorm.fit(data,c,loc=0,scale=1)	•Parameter estimates for foldnorm data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = foldnorm(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

genlogistic

A generalized logistic continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = genlogistic.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = genlogistic(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = genlogistic.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-genlogistic.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = genlogistic.rvs(c,size=100)
```

Generalized logistic distribution

genlogistic.pdf(x,c) = c*exp(-x) / (1+exp(-x))**(c+1) for x > 0, c > 0.

Methods

genlogistic.rvs(c,loc=0,scale=1,size=1)	•random variates
genlogistic.pdf(x,c,loc=0,scale=1)	•probability density function
genlogistic.cdf(x,c,loc=0,scale=1)	•cumulative density function
genlogistic.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
genlogistic.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
genlogistic.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
genlogistic.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
genlogistic.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
genlogistic.fit(data,c,loc=0,scale=1)	•Parameter estimates for genlogistic data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = genlogistic(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

genpareto

A generalized Pareto continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = genpareto.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = genpareto(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = genpareto.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-genpareto.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = genpareto.rvs(c,size=100)
```

Generalized Pareto distribution

genpareto.pdf(x,c) = (1+c*x)**(-1-1/c) for c != 0, and for x >= 0 for all c, and x < 1/abs(c) for c < 0.

Methods

genpareto.rvs(c,loc=0,scale=1,size=1)	•random variates
genpareto.pdf(x,c,loc=0,scale=1)	•probability density function
genpareto.cdf(x,c,loc=0,scale=1)	•cumulative density function
genpareto.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
genpareto.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
genpareto.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
genpareto.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
genpareto.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
genpareto.fit(data,c,loc=0,scale=1)	•Parameter estimates for genpareto data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = genpareto(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

genexpon

A generalized exponential continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

a,b,c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

References

"The Exponential Distribution: Theory, Methods and Applications", N. Balakrishnan, Asit P. Basu

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = genexpon.numargs
>>> [ a,b,c ] = [0.9,]*numargs
>>> rv = genexpon(a,b,c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = genexpon.cdf(x,a,b,c)
>>> h=plt.semilogy(np.abs(x-genexpon.ppf(prb,a,b,c))+1e-20)
```

Random number generation

```
>>> R = genexpon.rvs(a,b,c,size=100)
```

Generalized exponential distribution (Ryu 1993)

f(x,a,b,c) = (a+b*(1-exp(-c*x))) * exp(-a*x-b*x+b/c*(1-exp(-c*x))) for x >= 0, a,b,c > 0.

a, b, c are the first, second and third shape parameters.

Methods

genexpon.rvs(a,b,c,loc=0,scale=1,size=1)	•random variates
genexpon.pdf(x,a,b,c,loc=0,scale=1)	•probability density function
genexpon.cdf(x,a,b,c,loc=0,scale=1)	•cumulative density function
genexpon.sf(x,a,b,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
genexpon.ppf(q,a,b,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
genexpon.isf(q,a,b,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
genexpon.stats(a,b,c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
genexpon.entropy(a,b,c,loc=0,scale=1)	•(differential) entropy of the RV.
genexpon.fit(data,a,b,c,loc=0,scale=1)	•Parameter estimates for genexpon data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = genexpon(a,b,c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

genextreme

A generalized extreme value continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = genextreme.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = genextreme(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = genextreme.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-genextreme.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = genextreme.rvs(c,size=100)
```

Generalized extreme value (see gumbel_r for c=0)

genextreme.pdf(x,c) = exp(-exp(-x))*exp(-x) for c==0 genextreme.pdf(x,c) = exp(-(1-c*x)**(1/c))*(1-c*x)**(1/c-1) for x <= 1/c, c > 0

Methods

genextreme.rvs(c,loc=0,scale=1,size=1)	•random variates
genextreme.pdf(x,c,loc=0,scale=1)	•probability density function
genextreme.cdf(x,c,loc=0,scale=1)	•cumulative density function
genextreme.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
genextreme.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
genextreme.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
genextreme.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
genextreme.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
genextreme.fit(data,c,loc=0,scale=1)	•Parameter estimates for genextreme data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = genextreme(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`gausshyper`

A Gauss hypergeometric continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

a,b,c,z : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = gausshyper.numargs
>>> [ a,b,c,z ] = [0.9,]*numargs
>>> rv = gausshyper(a,b,c,z)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = gausshyper.cdf(x,a,b,c,z)
>>> h=plt.semilogy(np.abs(x-gausshyper.ppf(prb,a,b,c,z))+1e-20)
```

Random number generation

```
>>> R = gausshyper.rvs(a,b,c,z,size=100)
```

Gauss hypergeometric distribution

gausshyper.pdf(x,a,b,c,z) = C * x**(a-1) * (1-x)**(b-1) * (1+z*x)**(-c) for 0 <= x <= 1, a > 0, b > 0, and C = 1/(B(a,b)F[2,1](c,a;a+b;-z))

Methods

gausshyper.rvs(a,b,c,z,loc=0,scale=1,size=1)	•random variates
gausshyper.pdf(x,a,b,c,z,loc=0,scale=1)	•probability density function
gausshyper.cdf(x,a,b,c,z,loc=0,scale=1)	•cumulative density function
gausshyper.sf(x,a,b,c,z,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
gausshyper.ppf(q,a,b,c,z,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
gausshyper.isf(q,a,b,c,z,loc=0,scale=1)	•inverse survival function (inverse of sf)
gausshyper.stats(a,b,c,z,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
gausshyper.entropy(a,b,c,z,loc=0,scale=1)	•(differential) entropy of the RV.
gausshyper.fit(data,a,b,c,z,loc=0,scale=1)	•Parameter estimates for gausshyper data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = gausshyper(a,b,c,z,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

gamma

A gamma continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

a : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = gamma.numargs
>>> [ a ] = [0.9,]*numargs
>>> rv = gamma(a)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = gamma.cdf(x,a)
>>> h=plt.semilogy(np.abs(x-gamma.ppf(prb,a))+1e-20)
```

Random number generation

```
>>> R = gamma.rvs(a,size=100)
```

Gamma distribution

For a = integer, this is the Erlang distribution, and for a=1 it is the exponential distribution.

gamma.pdf(x,a) = x**(a-1)*exp(-x)/gamma(a) for x >= 0, a > 0.

Methods

gamma.rvs(a,loc=0,scale=1,size=1)	•random variates
gamma.pdf(x,a,loc=0,scale=1)	•probability density function
gamma.cdf(x,a,loc=0,scale=1)	•cumulative density function
gamma.sf(x,a,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
gamma.ppf(q,a,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
gamma.isf(q,a,loc=0,scale=1)	•inverse survival function (inverse of sf)
gamma.stats(a,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
gamma.entropy(a,loc=0,scale=1)	•(differential) entropy of the RV.
gamma.fit(data,a,loc=0,scale=1)	•Parameter estimates for gamma data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = gamma(a,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

gengamma

A generalized gamma continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

a,c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = gengamma.numargs
>>> [ a,c ] = [0.9,]*numargs
>>> rv = gengamma(a,c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = gengamma.cdf(x,a,c)
>>> h=plt.semilogy(np.abs(x-gengamma.ppf(prb,a,c))+1e-20)
```

Random number generation

```
>>> R = gengamma.rvs(a,c,size=100)
```

Generalized gamma distribution

gengamma.pdf(x,a,c) = abs(c)*x**(c*a-1)*exp(-x**c)/gamma(a) for x > 0, a > 0, and c != 0.

Methods

gengamma.rvs(a,c,loc=0,scale=1,size=1)	•random variates
gengamma.pdf(x,a,c,loc=0,scale=1)	•probability density function
gengamma.cdf(x,a,c,loc=0,scale=1)	•cumulative density function
gengamma.sf(x,a,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
gengamma.ppf(q,a,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
gengamma.isf(q,a,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
gengamma.stats(a,c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
gengamma.entropy(a,c,loc=0,scale=1)	•(differential) entropy of the RV.
gengamma.fit(data,a,c,loc=0,scale=1)	•Parameter estimates for gengamma data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = gengamma(a,c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

genhalflogistic

A generalized half-logistic continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = genhalflogistic.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = genhalflogistic(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = genhalflogistic.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-genhalflogistic.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = genhalflogistic.rvs(c,size=100)
```

Generalized half-logistic

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.

Methods

genhalflogistic.rvs(c,loc=0,scale=1,size=1)	•random variates
genhalflogistic.pdf(x,c,loc=0,scale=1)	•probability density function
genhalflogistic.cdf(x,c,loc=0,scale=1)	•cumulative density function
genhalflogistic.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
genhalflogistic.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
genhalflogistic.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
genhalflogistic.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
genhalflogistic.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
genhalflogistic.fit(data,c,loc=0,scale=1)	•Parameter estimates for genhalflogistic data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = genhalflogistic(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

gompertz

A Gompertz (truncated Gumbel) distribution continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = gompertz.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = gompertz(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = gompertz.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-gompertz.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = gompertz.rvs(c,size=100)
```

Gompertz (truncated Gumbel) distribution

gompertz.pdf(x,c) = c*exp(x) * exp(-c*(exp(x)-1)) for x >= 0, c > 0.

Methods

gompertz.rvs(c,loc=0,scale=1,size=1)	•random variates
gompertz.pdf(x,c,loc=0,scale=1)	•probability density function
gompertz.cdf(x,c,loc=0,scale=1)	•cumulative density function
gompertz.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
gompertz.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
gompertz.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
gompertz.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
gompertz.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
gompertz.fit(data,c,loc=0,scale=1)	•Parameter estimates for gompertz data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = gompertz(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

gumbel_r

A (right-skewed) Gumbel continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = gumbel_r.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = gumbel_r(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = gumbel_r.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-gumbel_r.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = gumbel_r.rvs(size=100)
```

Right-skewed Gumbel (Log-Weibull, Fisher-Tippett, Gompertz) distribution

gumbel_r.pdf(x) = exp(-(x+exp(-x)))

Methods

gumbel_r.rvs(loc=0,scale=1,size=1)	•random variates
gumbel_r.pdf(x,loc=0,scale=1)	•probability density function
gumbel_r.cdf(x,loc=0,scale=1)	•cumulative density function
gumbel_r.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
gumbel_r.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
gumbel_r.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
gumbel_r.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
gumbel_r.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
gumbel_r.fit(data,loc=0,scale=1)	•Parameter estimates for gumbel_r data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = gumbel_r(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

gumbel_l

A left-skewed Gumbel continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = gumbel_l.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = gumbel_l(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = gumbel_l.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-gumbel_l.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = gumbel_l.rvs(size=100)
```

Left-skewed Gumbel distribution

gumbel_l.pdf(x) = exp(x - exp(x))

Methods

gumbel_l.rvs(loc=0,scale=1,size=1)	•random variates
gumbel_l.pdf(x,loc=0,scale=1)	•probability density function
gumbel_l.cdf(x,loc=0,scale=1)	•cumulative density function
gumbel_l.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
gumbel_l.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
gumbel_l.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
gumbel_l.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
gumbel_l.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
gumbel_l.fit(data,loc=0,scale=1)	•Parameter estimates for gumbel_l data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = gumbel_l(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`halfcauchy`

A Half-Cauchy continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = halfcauchy.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = halfcauchy(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = halfcauchy.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-halfcauchy.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = halfcauchy.rvs(size=100)
```

Half-Cauchy distribution

halfcauchy.pdf(x) = 2/(pi*(1+x**2)) for x >= 0.

Methods

halfcauchy.rvs(loc=0,scale=1,size=1)	•random variates
halfcauchy.pdf(x,loc=0,scale=1)	•probability density function
halfcauchy.cdf(x,loc=0,scale=1)	•cumulative density function
halfcauchy.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
halfcauchy.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
halfcauchy.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
halfcauchy.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
halfcauchy.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
halfcauchy.fit(data,loc=0,scale=1)	•Parameter estimates for halfcauchy data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = halfcauchy(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

halflogistic

A half-logistic continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = halflogistic.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = halflogistic(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = halflogistic.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-halflogistic.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = halflogistic.rvs(size=100)
```

Half-logistic distribution

halflogistic.pdf(x) = 2*exp(-x)/(1+exp(-x))**2 = 1/2*sech(x/2)**2 for x >= 0.

Methods

halflogistic.rvs(loc=0,scale=1,size=1)	•random variates
halflogistic.pdf(x,loc=0,scale=1)	•probability density function
halflogistic.cdf(x,loc=0,scale=1)	•cumulative density function
halflogistic.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
halflogistic.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
halflogistic.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
halflogistic.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
halflogistic.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
halflogistic.fit(data,loc=0,scale=1)	•Parameter estimates for halflogistic data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = halflogistic(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

halfnorm

A half-normal continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = halfnorm.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = halfnorm(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = halfnorm.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-halfnorm.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = halfnorm.rvs(size=100)
```

Half-normal distribution

halfnorm.pdf(x) = sqrt(2/pi) * exp(-x**2/2) for x > 0.

Methods

halfnorm.rvs(loc=0,scale=1,size=1)	•random variates
halfnorm.pdf(x,loc=0,scale=1)	•probability density function
halfnorm.cdf(x,loc=0,scale=1)	•cumulative density function
halfnorm.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
halfnorm.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
halfnorm.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
halfnorm.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
halfnorm.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
halfnorm.fit(data,loc=0,scale=1)	•Parameter estimates for halfnorm data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = halfnorm(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`hypsecant`

A hyperbolic secant continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = hypsecant.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = hypsecant(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = hypsecant.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-hypsecant.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = hypsecant.rvs(size=100)
```

Hyperbolic secant distribution

hypsecant.pdf(x) = 1/pi * sech(x)

Methods

hypsecant.rvs(loc=0,scale=1,size=1)	•random variates
hypsecant.pdf(x,loc=0,scale=1)	•probability density function
hypsecant.cdf(x,loc=0,scale=1)	•cumulative density function
hypsecant.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
hypsecant.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
hypsecant.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
hypsecant.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
hypsecant.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
hypsecant.fit(data,loc=0,scale=1)	•Parameter estimates for hypsecant data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = hypsecant(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`invgamma`

An inverted gamma continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

a : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = invgamma.numargs
>>> [ a ] = [0.9,]*numargs
>>> rv = invgamma(a)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = invgamma.cdf(x,a)
>>> h=plt.semilogy(np.abs(x-invgamma.ppf(prb,a))+1e-20)
```

Random number generation

```
>>> R = invgamma.rvs(a,size=100)
```

Inverted gamma distribution

invgamma.pdf(x,a) = x**(-a-1)/gamma(a) * exp(-1/x) for x > 0, a > 0.

Methods

invgamma.rvs(a,loc=0,scale=1,size=1)	•random variates
invgamma.pdf(x,a,loc=0,scale=1)	•probability density function
invgamma.cdf(x,a,loc=0,scale=1)	•cumulative density function
invgamma.sf(x,a,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
invgamma.ppf(q,a,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
invgamma.isf(q,a,loc=0,scale=1)	•inverse survival function (inverse of sf)
invgamma.stats(a,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
invgamma.entropy(a,loc=0,scale=1)	•(differential) entropy of the RV.
invgamma.fit(data,a,loc=0,scale=1)	•Parameter estimates for invgamma data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = invgamma(a,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

invnorm

An inverse normal continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

mu : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = invnorm.numargs
>>> [ mu ] = [0.9,]*numargs
>>> rv = invnorm(mu)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = invnorm.cdf(x,mu)
>>> h=plt.semilogy(np.abs(x-invnorm.ppf(prb,mu))+1e-20)
```

Random number generation

```
>>> R = invnorm.rvs(mu,size=100)
```

Inverse normal distribution

invnorm.pdf(x,mu) = 1/sqrt(2*pi*x**3) * exp(-(x-mu)**2/(2*x*mu**2)) for x > 0.

Methods

invnorm.rvs(mu,loc=0,scale=1,size=1)	•random variates
invnorm.pdf(x,mu,loc=0,scale=1)	•probability density function
invnorm.cdf(x,mu,loc=0,scale=1)	•cumulative density function
invnorm.sf(x,mu,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
invnorm.ppf(q,mu,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
invnorm.isf(q,mu,loc=0,scale=1)	•inverse survival function (inverse of sf)
invnorm.stats(mu,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
invnorm.entropy(mu,loc=0,scale=1)	•(differential) entropy of the RV.
invnorm.fit(data,mu,loc=0,scale=1)	•Parameter estimates for invnorm data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = invnorm(mu,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

invweibull

An inverted Weibull continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = invweibull.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = invweibull(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = invweibull.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-invweibull.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = invweibull.rvs(c,size=100)
```

Inverted Weibull distribution

invweibull.pdf(x,c) = c*x**(-c-1)*exp(-x**(-c)) for x > 0, c > 0.

Methods

invweibull.rvs(c,loc=0,scale=1,size=1)	•random variates
invweibull.pdf(x,c,loc=0,scale=1)	•probability density function
invweibull.cdf(x,c,loc=0,scale=1)	•cumulative density function
invweibull.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
invweibull.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
invweibull.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
invweibull.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
invweibull.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
invweibull.fit(data,c,loc=0,scale=1)	•Parameter estimates for invweibull data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = invweibull(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

johnsonsb

A Johnson SB continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

a,b : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = johnsonb.numargs
>>> [ a,b ] = [0.9,]*numargs
>>> rv = johnsonb(a,b)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = johnsonb.cdf(x,a,b)
>>> h=plt.semilogy(np.abs(x-johnsonb.ppf(prb,a,b))+1e-20)
```

Random number generation

```
>>> R = johnsonb.rvs(a,b,size=100)
```

Johnson SB distribution

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.

Methods

johnsonb.rvs(a,b,loc=0,scale=1,size=1)	•random variates
johnsonb.pdf(x,a,b,loc=0,scale=1)	•probability density function
johnsonb.cdf(x,a,b,loc=0,scale=1)	•cumulative density function
johnsonb.sf(x,a,b,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
johnsonb.ppf(q,a,b,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
johnsonb.isf(q,a,b,loc=0,scale=1)	•inverse survival function (inverse of sf)
johnsonb.stats(a,b,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
johnsonb.entropy(a,b,loc=0,scale=1)	•(differential) entropy of the RV.
johnsonb.fit(data,a,b,loc=0,scale=1)	•Parameter estimates for johnsonb data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = johnsonb(a,b,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

johnsonsu

A Johnson SU continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

a,b : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = johnsonsu.numargs
>>> [ a,b ] = [0.9,]*numargs
>>> rv = johnsonsu(a,b)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = johnsonsu.cdf(x,a,b)
>>> h=plt.semilogy(np.abs(x-johnsonsu.ppf(prb,a,b))+1e-20)
```

Random number generation

```
>>> R = johnsonsu.rvs(a,b,size=100)
```

Johnson SU distribution

johnsonsu.pdf(x,a,b) = b/sqrt(x**2+1) * phi(a + b*log(x+sqrt(x**2+1))) for all x, a,b > 0, and phi is the normal pdf.

Methods

johnsonsu.rvs(a,b,loc=0,scale=1,size=1)	•random variates
johnsonsu.pdf(x,a,b,loc=0,scale=1)	•probability density function
johnsonsu.cdf(x,a,b,loc=0,scale=1)	•cumulative density function
johnsonsu.sf(x,a,b,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
johnsonsu.ppf(q,a,b,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
johnsonsu.isf(q,a,b,loc=0,scale=1)	•inverse survival function (inverse of sf)
johnsonsu.stats(a,b,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
johnsonsu.entropy(a,b,loc=0,scale=1)	•(differential) entropy of the RV.
johnsonsu.fit(data,a,b,loc=0,scale=1)	•Parameter estimates for johnsonsu data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = johnsonsu(a,b,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

laplace

A Laplace continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = laplace.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = laplace(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = laplace.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-laplace.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = laplace.rvs(size=100)
```

Laplacian distribution

laplace.pdf(x) = 1/2*exp(-abs(x))

Methods

laplace.rvs(loc=0,scale=1,size=1)	•random variates
laplace.pdf(x,loc=0,scale=1)	•probability density function
laplace.cdf(x,loc=0,scale=1)	•cumulative density function
laplace.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
laplace.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
laplace.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
laplace.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
laplace.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
laplace.fit(data,loc=0,scale=1)	•Parameter estimates for laplace data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = laplace(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`logistic`

A logistic continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = logistic.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = logistic(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = logistic.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-logistic.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = logistic.rvs(size=100)
```

Logistic distribution

logistic.pdf(x) = exp(-x)/(1+exp(-x))**2

Methods

logistic.rvs(loc=0,scale=1,size=1)	•random variates
logistic.pdf(x,loc=0,scale=1)	•probability density function
logistic.cdf(x,loc=0,scale=1)	•cumulative density function
logistic.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
logistic.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
logistic.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
logistic.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
logistic.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
logistic.fit(data,loc=0,scale=1)	•Parameter estimates for logistic data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = logistic(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`loggamma`

A log gamma continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = loggamma.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = loggamma(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = loggamma.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-loggamma.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = loggamma.rvs(size=100)
```

Log gamma distribution

loggamma.pdf(x,c) = exp(c*x-exp(x)) / gamma(c) for all x, c > 0.

Methods

loggamma.rvs(loc=0,scale=1,size=1)	•random variates
loggamma.pdf(x,loc=0,scale=1)	•probability density function
loggamma.cdf(x,loc=0,scale=1)	•cumulative density function
loggamma.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
loggamma.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
loggamma.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
loggamma.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
loggamma.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
loggamma.fit(data,loc=0,scale=1)	•Parameter estimates for loggamma data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = loggamma(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`loglaplace`

A log-Laplace continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = loglaplace.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = loglaplace(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = loglaplace.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-loglaplace.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = loglaplace.rvs(c,size=100)
```

Log-Laplace distribution (Log Double Exponential)

loglaplace.pdf(x,c) = c/2*x(c-1) for 0 < x < 1**
= c/2*x**(-c-1) for x >= 1

for c > 0.

Methods

loglaplace.rvs(c,loc=0,scale=1,size=1)	•random variates
loglaplace.pdf(x,c,loc=0,scale=1)	•probability density function
loglaplace.cdf(x,c,loc=0,scale=1)	•cumulative density function
loglaplace.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
loglaplace.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
loglaplace.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
loglaplace.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
loglaplace.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
loglaplace.fit(data,c,loc=0,scale=1)	•Parameter estimates for loglaplace data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = loglaplace(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`lognorm`

A lognormal continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

s : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = lognorm.numargs
>>> [ s ] = [0.9,]*numargs
>>> rv = lognorm(s)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = lognorm.cdf(x,s)
>>> h=plt.semilogy(np.abs(x-lognorm.ppf(prb,s))+1e-20)
```

Random number generation

```
>>> R = lognorm.rvs(s,size=100)
```

Lognormal distribution

lognorm.pdf(x,s) = 1/(s*x*sqrt(2*pi)) * exp(-1/2*(log(x)/s)**2) for x > 0, s > 0.

If log x is normally distributed with mean mu and variance sigma**2, then x is log-normally distributed with shape paramter sigma and scale parameter exp(mu).

Methods

lognorm.rvs(s,loc=0,scale=1,size=1)	•random variates
lognorm.pdf(x,s,loc=0,scale=1)	•probability density function
lognorm.cdf(x,s,loc=0,scale=1)	•cumulative density function
lognorm.sf(x,s,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
lognorm.ppf(q,s,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
lognorm.isf(q,s,loc=0,scale=1)	•inverse survival function (inverse of sf)
lognorm.stats(s,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
lognorm.entropy(s,loc=0,scale=1)	•(differential) entropy of the RV.
lognorm.fit(data,s,loc=0,scale=1)	•Parameter estimates for lognorm data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = lognorm(s,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`gilbrat`

A Gilbrat continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = gilbrat.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = gilbrat(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = gilbrat.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-gilbrat.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = gilbrat.rvs(size=100)
```

Gilbrat distribution

gilbrat.pdf(x) = 1/(x*sqrt(2*pi)) * exp(-1/2*(log(x))**2)

Methods

gilbrat.rvs(loc=0,scale=1,size=1)	•random variates
gilbrat.pdf(x,loc=0,scale=1)	•probability density function
gilbrat.cdf(x,loc=0,scale=1)	•cumulative density function
gilbrat.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
gilbrat.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
gilbrat.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
gilbrat.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
gilbrat.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
gilbrat.fit(data,loc=0,scale=1)	•Parameter estimates for gilbrat data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = gilbrat(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

lomax

A Lomax (Pareto of the second kind) continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = lomax.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = lomax(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = lomax.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-lomax.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = lomax.rvs(c,size=100)
```

Lomax (Pareto of the second kind) distribution

lomax.pdf(x,c) = c / (1+x)**(c+1) for x >= 0, c > 0.

Methods

lomax.rvs(c,loc=0,scale=1,size=1)	•random variates
lomax.pdf(x,c,loc=0,scale=1)	•probability density function
lomax.cdf(x,c,loc=0,scale=1)	•cumulative density function
lomax.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
lomax.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
lomax.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
lomax.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
lomax.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
lomax.fit(data,c,loc=0,scale=1)	•Parameter estimates for lomax data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = lomax(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

maxwell

A Maxwell continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = maxwell.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = maxwell(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = maxwell.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-maxwell.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = maxwell.rvs(size=100)
```

Maxwell distribution

maxwell.pdf(x) = sqrt(2/pi) * x**2 * exp(-x**2/2) for x > 0.

Methods

maxwell.rvs(loc=0,scale=1,size=1)	•random variates
maxwell.pdf(x,loc=0,scale=1)	•probability density function
maxwell.cdf(x,loc=0,scale=1)	•cumulative density function
maxwell.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
maxwell.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
maxwell.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
maxwell.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
maxwell.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
maxwell.fit(data,loc=0,scale=1)	•Parameter estimates for maxwell data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = maxwell(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

mielke

A Mielke's Beta-Kappa continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

k,s : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = mielke.numargs
>>> [ k,s ] = [0.9,]*numargs
>>> rv = mielke(k,s)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = mielke.cdf(x,k,s)
>>> h=plt.semilogy(np.abs(x-mielke.ppf(prb,k,s))+1e-20)
```

Random number generation

```
>>> R = mielke.rvs(k,s,size=100)
```

Mielke's Beta-Kappa distribution

mielke.pdf(x,k,s) = k*x**(k-1) / (1+x**s)**(1+k/s) for x > 0.

Methods

mielke.rvs(k,s,loc=0,scale=1,size=1)	•random variates
mielke.pdf(x,k,s,loc=0,scale=1)	•probability density function
mielke.cdf(x,k,s,loc=0,scale=1)	•cumulative density function
mielke.sf(x,k,s,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
mielke.ppf(q,k,s,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
mielke.isf(q,k,s,loc=0,scale=1)	•inverse survival function (inverse of sf)
mielke.stats(k,s,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
mielke.entropy(k,s,loc=0,scale=1)	•(differential) entropy of the RV.
mielke.fit(data,k,s,loc=0,scale=1)	•Parameter estimates for mielke data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = mielke(k,s,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`nakagami`

A Nakagami continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

nu : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = nakagami.numargs
>>> [ nu ] = [0.9,]*numargs
>>> rv = nakagami(nu)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = nakagami.cdf(x,nu)
>>> h=plt.semilogy(np.abs(x-nakagami.ppf(prb,nu))+1e-20)
```

Random number generation

```
>>> R = nakagami.rvs(nu,size=100)
```

Nakagami distribution

nakagami.pdf(x,nu) = 2*nu**nu/gamma(nu) * x**(2*nu-1) * exp(-nu*x**2) for x > 0, nu > 0.

Methods

nakagami.rvs(nu,loc=0,scale=1,size=1)	•random variates
nakagami.pdf(x,nu,loc=0,scale=1)	•probability density function
nakagami.cdf(x,nu,loc=0,scale=1)	•cumulative density function
nakagami.sf(x,nu,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
nakagami.ppf(q,nu,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
nakagami.isf(q,nu,loc=0,scale=1)	•inverse survival function (inverse of sf)
nakagami.stats(nu,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
nakagami.entropy(nu,loc=0,scale=1)	•(differential) entropy of the RV.
nakagami.fit(data,nu,loc=0,scale=1)	•Parameter estimates for nakagami data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = nakagami(nu,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

ncx2

A non-central chi-squared continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

df,nc : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = ncx2.numargs
>>> [ df,nc ] = [0.9,]*numargs
>>> rv = ncx2(df,nc)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = ncx2.cdf(x,df,nc)
>>> h=plt.semilogy(np.abs(x-ncx2.ppf(prb,df,nc))+1e-20)
```

Random number generation

```
>>> R = ncx2.rvs(df,nc,size=100)
```

Non-central chi-squared distribution

ncx2.pdf(x,df,nc) = exp(-(nc+df)/2)*1/2*(x/nc)((df-2)/4)**

- I[(df-2)/2](sqrt(nc*x))

for x > 0.

Methods

ncx2.rvs(df,nc,loc=0,scale=1,size=1)	•random variates
ncx2.pdf(x,df,nc,loc=0,scale=1)	•probability density function
ncx2.cdf(x,df,nc,loc=0,scale=1)	•cumulative density function
ncx2.sf(x,df,nc,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
ncx2.ppf(q,df,nc,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
ncx2.isf(q,df,nc,loc=0,scale=1)	•inverse survival function (inverse of sf)
ncx2.stats(df,nc,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
ncx2.entropy(df,nc,loc=0,scale=1)	•(differential) entropy of the RV.
ncx2.fit(data,df,nc,loc=0,scale=1)	•Parameter estimates for ncx2 data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = ncx2(df,nc,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

ncf

A non-central F distribution continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

dfn,dfd,nc : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = ncf.numargs
>>> [ dfn,dfd,nc ] = [0.9,]*numargs
>>> rv = ncf(dfn,dfd,nc)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = ncf.cdf(x,dfn,dfd,nc)
>>> h=plt.semilogy(np.abs(x-ncf.ppf(prb,dfn,dfd,nc))+1e-20)
```

Random number generation

```
>>> R = ncf.rvs(dfn,dfd,nc,size=100)
```

Non-central F distribution

ncf.pdf(x,df1,df2,nc) = exp(nc/2 + nc*df1*x/(2*(df1*x+df2)))

- df1**(df1/2) * df2**(df2/2) * x**(df1/2-1)
- (df2+df1*x)**(-(df1+df2)/2)
- gamma(df1/2)*gamma(1+df2/2)
- L^{v1/2-1}^{v2/2}(-nc*v1*x/(2*(v1*x+v2)))

/ (B(v1/2, v2/2) * gamma((v1+v2)/2))

for df1, df2, nc > 0.

Methods

ncf.rvs(dfn,dfd,nc,loc=0,scale=1,size=1)	•random variates
ncf.pdf(x,dfn,dfd,nc,loc=0,scale=1)	•probability density function
ncf.cdf(x,dfn,dfd,nc,loc=0,scale=1)	•cumulative density function
ncf.sf(x,dfn,dfd,nc,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
ncf.ppf(q,dfn,dfd,nc,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
ncf.isf(q,dfn,dfd,nc,loc=0,scale=1)	•inverse survival function (inverse of sf)
ncf.stats(dfn,dfd,nc,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
ncf.entropy(dfn,dfd,nc,loc=0,scale=1)	•(differential) entropy of the RV.
ncf.fit(data,dfn,dfd,nc,loc=0,scale=1)	•Parameter estimates for ncf data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = ncf(dfn,dfd,nc,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

t

Student's T continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

df : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = t.numargs
>>> [ df ] = [0.9,]*numargs
>>> rv = t(df)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = t.cdf(x,df)
>>> h=plt.semilogy(np.abs(x-t.ppf(prb,df))+1e-20)
```

Random number generation

```
>>> R = t.rvs(df,size=100)
```

Student's T distribution

gamma((df+1)/2)

t.pdf(x,df) = ————————————————————————
sqrt(pi*df)*gamma(df/2)*(1+x**2/df)**((df+1)/2)

for df > 0.

Methods

t.rvs(df,loc=0,scale=1,size=1)	•random variates
t.pdf(x,df,loc=0,scale=1)	•probability density function
t.cdf(x,df,loc=0,scale=1)	•cumulative density function
t.sf(x,df,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
t.ppf(q,df,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
t.isf(q,df,loc=0,scale=1)	•inverse survival function (inverse of sf)
t.stats(df,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
t.entropy(df,loc=0,scale=1)	•(differential) entropy of the RV.
t.fit(data,df,loc=0,scale=1)	•Parameter estimates for t data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = t(df,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

nct

A Noncentral T continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

df,nc : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = nct.numargs
>>> [ df,nc ] = [0.9,]*numargs
>>> rv = nct(df,nc)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = nct.cdf(x,df,nc)
>>> h=plt.semilogy(np.abs(x-nct.ppf(prb,df,nc))+1e-20)
```

Random number generation

```
>>> R = nct.rvs(df,nc,size=100)
```

Non-central Student T distribution

df**(df/2) * gamma(df+1)

nct.pdf(x,df,nc) = ————————————————————————

2**df*exp(nc**2/2)*(df+x**2)**(df/2) * gamma(df/2)

for df > 0, nc > 0.

Methods

nct.rvs(df,nc,loc=0,scale=1,size=1)	•random variates
nct.pdf(x,df,nc,loc=0,scale=1)	•probability density function
nct.cdf(x,df,nc,loc=0,scale=1)	•cumulative density function
nct.sf(x,df,nc,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
nct.ppf(q,df,nc,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
nct.isf(q,df,nc,loc=0,scale=1)	•inverse survival function (inverse of sf)
nct.stats(df,nc,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
nct.entropy(df,nc,loc=0,scale=1)	•(differential) entropy of the RV.
nct.fit(data,df,nc,loc=0,scale=1)	•Parameter estimates for nct data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = nct(df,nc,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

pareto

A Pareto continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

b : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = pareto.numargs
>>> [ b ] = [0.9,]*numargs
>>> rv = pareto(b)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = pareto.cdf(x,b)
>>> h=plt.semilogy(np.abs(x-pareto.ppf(prb,b))+1e-20)
```

Random number generation

```
>>> R = pareto.rvs(b,size=100)
```

Pareto distribution

pareto.pdf(x,b) = b/x**(b+1) for x >= 1, b > 0.

Methods

pareto.rvs(b,loc=0,scale=1,size=1)	•random variates
pareto.pdf(x,b,loc=0,scale=1)	•probability density function
pareto.cdf(x,b,loc=0,scale=1)	•cumulative density function
pareto.sf(x,b,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
pareto.ppf(q,b,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
pareto.isf(q,b,loc=0,scale=1)	•inverse survival function (inverse of sf)
pareto.stats(b,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
pareto.entropy(b,loc=0,scale=1)	•(differential) entropy of the RV.
pareto.fit(data,b,loc=0,scale=1)	•Parameter estimates for pareto data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = pareto(b,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

powerlaw

A power-function continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

a : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = powerlaw.numargs
>>> [ a ] = [0.9,]*numargs
>>> rv = powerlaw(a)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = powerlaw.cdf(x,a)
>>> h=plt.semilogy(np.abs(x-powerlaw.ppf(prb,a))+1e-20)
```

Random number generation

```
>>> R = powerlaw.rvs(a,size=100)
```

Power-function distribution

powerlaw.pdf(x,a) = a*x**(a-1) for 0 <= x <= 1, a > 0.

Methods

powerlaw.rvs(a,loc=0,scale=1,size=1)	•random variates
powerlaw.pdf(x,a,loc=0,scale=1)	•probability density function
powerlaw.cdf(x,a,loc=0,scale=1)	•cumulative density function
powerlaw.sf(x,a,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
powerlaw.ppf(q,a,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
powerlaw.isf(q,a,loc=0,scale=1)	•inverse survival function (inverse of sf)
powerlaw.stats(a,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
powerlaw.entropy(a,loc=0,scale=1)	•(differential) entropy of the RV.
powerlaw.fit(data,a,loc=0,scale=1)	•Parameter estimates for powerlaw data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = powerlaw(a,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`powerlognorm`

A power log-normal continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c,s : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = powerlognorm.numargs
>>> [ c,s ] = [0.9,]*numargs
>>> rv = powerlognorm(c,s)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = powerlognorm.cdf(x,c,s)
>>> h=plt.semilogy(np.abs(x-powerlognorm.ppf(prb,c,s))+1e-20)
```

Random number generation

```
>>> R = powerlognorm.rvs(c,s,size=100)
```

Power log-normal distribution

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.

Methods

powerlognorm.rvs(c,s,loc=0,scale=1,size=1)	•random variates
powerlognorm.pdf(x,c,s,loc=0,scale=1)	•probability density function
powerlognorm.cdf(x,c,s,loc=0,scale=1)	•cumulative density function
powerlognorm.sf(x,c,s,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
powerlognorm.ppf(q,c,s,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
powerlognorm.isf(q,c,s,loc=0,scale=1)	•inverse survival function (inverse of sf)
powerlognorm.stats(c,s,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
powerlognorm.entropy(c,s,loc=0,scale=1)	•(differential) entropy of the RV.
powerlognorm.fit(data,c,s,loc=0,scale=1)	•Parameter estimates for powerlognorm data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = powerlognorm(c,s,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

powernorm

A power normal continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = powernorm.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = powernorm(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = powernorm.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-powernorm.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = powernorm.rvs(c,size=100)
```

Power normal distribution

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.

Methods

powernorm.rvs(c,loc=0,scale=1,size=1)	•random variates
powernorm.pdf(x,c,loc=0,scale=1)	•probability density function
powernorm.cdf(x,c,loc=0,scale=1)	•cumulative density function
powernorm.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
powernorm.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
powernorm.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
powernorm.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
powernorm.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
powernorm.fit(data,c,loc=0,scale=1)	•Parameter estimates for powernorm data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = powernorm(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

rdist

An R-distributed continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = rdist.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = rdist(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = rdist.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-rdist.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = rdist.rvs(c,size=100)
```

R-distribution

rdist.pdf(x,c) = (1-x**2)**(c/2-1) / B(1/2, c/2) for -1 <= x <= 1, c > 0.

Methods

rdist.rvs(c,loc=0,scale=1,size=1)	•random variates
rdist.pdf(x,c,loc=0,scale=1)	•probability density function
rdist.cdf(x,c,loc=0,scale=1)	•cumulative density function
rdist.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
rdist.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
rdist.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
rdist.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
rdist.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
rdist.fit(data,c,loc=0,scale=1)	•Parameter estimates for rdist data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = rdist(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`reciprocal`

A reciprocal continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

a,b : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = reciprocal.numargs
>>> [ a,b ] = [0.9,]*numargs
>>> rv = reciprocal(a,b)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = reciprocal.cdf(x,a,b)
>>> h=plt.semilogy(np.abs(x-reciprocal.ppf(prb,a,b))+1e-20)
```

Random number generation

```
>>> R = reciprocal.rvs(a,b,size=100)
```

Reciprocal distribution

reciprocal.pdf(x,a,b) = 1/(x*log(b/a)) for a <= x <= b, a,b > 0.

Methods

reciprocal.rvs(a,b,loc=0,scale=1,size=1)	•random variates
reciprocal.pdf(x,a,b,loc=0,scale=1)	•probability density function
reciprocal.cdf(x,a,b,loc=0,scale=1)	•cumulative density function
reciprocal.sf(x,a,b,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
reciprocal.ppf(q,a,b,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
reciprocal.isf(q,a,b,loc=0,scale=1)	•inverse survival function (inverse of sf)
reciprocal.stats(a,b,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
reciprocal.entropy(a,b,loc=0,scale=1)	•(differential) entropy of the RV.
reciprocal.fit(data,a,b,loc=0,scale=1)	•Parameter estimates for reciprocal data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = reciprocal(a,b,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`rayleigh`

A Rayleigh continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = rayleigh.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = rayleigh(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = rayleigh.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-rayleigh.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = rayleigh.rvs(size=100)
```

Rayleigh distribution

rayleigh.pdf(r) = r * exp(-r**2/2) for x >= 0.

Methods

rayleigh.rvs(loc=0,scale=1,size=1)	•random variates
rayleigh.pdf(x,loc=0,scale=1)	•probability density function
rayleigh.cdf(x,loc=0,scale=1)	•cumulative density function
rayleigh.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
rayleigh.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
rayleigh.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
rayleigh.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
rayleigh.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
rayleigh.fit(data,loc=0,scale=1)	•Parameter estimates for rayleigh data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = rayleigh(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

rice

A Rice continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

b : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = rice.numargs
>>> [ b ] = [0.9,]*numargs
>>> rv = rice(b)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = rice.cdf(x,b)
>>> h=plt.semilogy(np.abs(x-rice.ppf(prb,b))+1e-20)
```

Random number generation

```
>>> R = rice.rvs(b,size=100)
```

Rician distribution

rice.pdf(x,b) = x * exp(-(x**2+b**2)/2) * I[0](x*b) for x > 0, b > 0.

Methods

rice.rvs(b,loc=0,scale=1,size=1)	•random variates
rice.pdf(x,b,loc=0,scale=1)	•probability density function
rice.cdf(x,b,loc=0,scale=1)	•cumulative density function
rice.sf(x,b,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
rice.ppf(q,b,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
rice.isf(q,b,loc=0,scale=1)	•inverse survival function (inverse of sf)
rice.stats(b,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
rice.entropy(b,loc=0,scale=1)	•(differential) entropy of the RV.
rice.fit(data,b,loc=0,scale=1)	•Parameter estimates for rice data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = rice(b,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`recipinvgauss`

A reciprocal inverse Gaussian continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

mu : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = recipinvgauss.numargs
>>> [ mu ] = [0.9,]*numargs
>>> rv = recipinvgauss(mu)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = recipinvgauss.cdf(x,mu)
>>> h=plt.semilogy(np.abs(x-recipinvgauss.ppf(prb,mu))+1e-20)
```

Random number generation

```
>>> R = recipinvgauss.rvs(mu,size=100)
```

Reciprocal inverse Gaussian

recipinvgauss.pdf(x, mu) = 1/sqrt(2*pi*x) * exp(-(1-mu*x)**2/(2*x*mu**2)) for x >= 0.

Methods

recipinvgauss.rvs(mu,loc=0,scale=1,size=1)	•random variates
recipinvgauss.pdf(x,mu,loc=0,scale=1)	•probability density function
recipinvgauss.cdf(x,mu,loc=0,scale=1)	•cumulative density function
recipinvgauss.sf(x,mu,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
recipinvgauss.ppf(q,mu,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
recipinvgauss.isf(q,mu,loc=0,scale=1)	•inverse survival function (inverse of sf)
recipinvgauss.stats(mu,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
recipinvgauss.entropy(mu,loc=0,scale=1)	•(differential) entropy of the RV.
recipinvgauss.fit(data,mu,loc=0,scale=1)	•Parameter estimates for recipinvgauss data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = recipinvgauss(mu,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

semicircular

A semicircular continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = semicircular.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = semicircular(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = semicircular.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-semicircular.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = semicircular.rvs(size=100)
```

Semicircular distribution

semicircular.pdf(x) = 2/pi * sqrt(1-x**2) for -1 <= x <= 1.

Methods

semicircular.rvs(loc=0,scale=1,size=1)	•random variates
semicircular.pdf(x,loc=0,scale=1)	•probability density function
semicircular.cdf(x,loc=0,scale=1)	•cumulative density function
semicircular.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
semicircular.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
semicircular.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
semicircular.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
semicircular.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
semicircular.fit(data,loc=0,scale=1)	•Parameter estimates for semicircular data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = semicircular(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`triang`

A Triangular continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = triang.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = triang(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = triang.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-triang.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = triang.rvs(c,size=100)
```

Triangular distribution

up-sloping line from loc to (loc + c*scale) and then downsloping for (loc + c*scale) to (loc+scale).

•standard form is in the range [0,1] with c the mode.

•location parameter shifts the start to loc

•scale changes the width from 1 to scale

Methods

triang.rvs(c,loc=0,scale=1,size=1)	•random variates
triang.pdf(x,c,loc=0,scale=1)	•probability density function
triang.cdf(x,c,loc=0,scale=1)	•cumulative density function
triang.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
triang.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
triang.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
triang.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
triang.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
triang.fit(data,c,loc=0,scale=1)	•Parameter estimates for triang data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = triang(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

truncexpon

A truncated exponential continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

b : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = truncexpon.numargs
>>> [ b ] = [0.9,]*numargs
>>> rv = truncexpon(b)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = truncexpon.cdf(x,b)
>>> h=plt.semilogy(np.abs(x-truncexpon.ppf(prb,b))+1e-20)
```

Random number generation

```
>>> R = truncexpon.rvs(b,size=100)
```

Truncated exponential distribution

truncexpon.pdf(x,b) = exp(-x)/(1-exp(-b)) for 0 < x < b.

Methods

truncexpon.rvs(b,loc=0,scale=1,size=1)	•random variates
truncexpon.pdf(x,b,loc=0,scale=1)	•probability density function
truncexpon.cdf(x,b,loc=0,scale=1)	•cumulative density function
truncexpon.sf(x,b,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
truncexpon.ppf(q,b,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
truncexpon.isf(q,b,loc=0,scale=1)	•inverse survival function (inverse of sf)
truncexpon.stats(b,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
truncexpon.entropy(b,loc=0,scale=1)	•(differential) entropy of the RV.
truncexpon.fit(data,b,loc=0,scale=1)	•Parameter estimates for truncexpon data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = truncexpon(b,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`truncnorm`

A truncated normal continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

a,b : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = truncnorm.numargs
>>> [ a,b ] = [0.9,]*numargs
>>> rv = truncnorm(a,b)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = truncnorm.cdf(x,a,b)
>>> h=plt.semilogy(np.abs(x-truncnorm.ppf(prb,a,b))+1e-20)
```

Random number generation

```
>>> R = truncnorm.rvs(a,b,size=100)
```

Truncated Normal distribution.

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

Methods

truncnorm.rvs(a,b,loc=0,scale=1,size=1)	•random variates
truncnorm.pdf(x,a,b,loc=0,scale=1)	•probability density function
truncnorm.cdf(x,a,b,loc=0,scale=1)	•cumulative density function
truncnorm.sf(x,a,b,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
truncnorm.ppf(q,a,b,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
truncnorm.isf(q,a,b,loc=0,scale=1)	•inverse survival function (inverse of sf)
truncnorm.stats(a,b,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
truncnorm.entropy(a,b,loc=0,scale=1)	•(differential) entropy of the RV.
truncnorm.fit(data,a,b,loc=0,scale=1)	•Parameter estimates for truncnorm data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = truncnorm(a,b,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`tukeylambda`

A Tukey-Lambda continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

lam : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = tukeylambda.numargs
>>> [ lam ] = [0.9,]*numargs
>>> rv = tukeylambda(lam)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = tukeylambda.cdf(x,lam)
>>> h=plt.semilogy(np.abs(x-tukeylambda.ppf(prb,lam))+1e-20)
```

Random number generation

```
>>> R = tukeylambda.rvs(lam,size=100)
```

Tukey-Lambda distribution

A flexible distribution ranging from Cauchy (lam=-1) to logistic (lam=0.0) to approx Normal (lam=0.14) to u-shape (lam = 0.5) to Uniform from -1 to 1 (lam = 1)

Methods

tukeylambda.rvs(lam,loc=0,scale=1,size=1)	•random variates
tukeylambda.pdf(x,lam,loc=0,scale=1)	•probability density function
tukeylambda.cdf(x,lam,loc=0,scale=1)	•cumulative density function
tukeylambda.sf(x,lam,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
tukeylambda.ppf(q,lam,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
tukeylambda.isf(q,lam,loc=0,scale=1)	•inverse survival function (inverse of sf)
tukey-lambda.stats(lam,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
tukeylambda.entropy(lam,loc=0,scale=1)	•(differential) entropy of the RV.
tukeylambda.fit(data,lam,loc=0,scale=1)	•Parameter estimates for tukeylambda data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = tukeylambda(lam,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`uniform`

A uniform continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = uniform.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = uniform(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = uniform.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-uniform.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = uniform.rvs(size=100)
```

Uniform distribution

constant between loc and loc+scale

Methods

uniform.rvs(loc=0,scale=1,size=1)	•random variates
uniform.pdf(x,loc=0,scale=1)	•probability density function
uniform.cdf(x,loc=0,scale=1)	•cumulative density function
uniform.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
uniform.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
uniform.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
uniform.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
uniform.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
uniform.fit(data,loc=0,scale=1)	•Parameter estimates for uniform data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = uniform(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

wald

A Wald continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = wald.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = wald(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = wald.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-wald.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = wald.rvs(size=100)
```

Wald distribution

wald.pdf(x) = 1/sqrt(2*pi*x**3) * exp(-(x-1)**2/(2*x)) for x > 0.

Methods

wald.rvs(loc=0,scale=1,size=1)	•random variates
wald.pdf(x,loc=0,scale=1)	•probability density function
wald.cdf(x,loc=0,scale=1)	•cumulative density function
wald.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
wald.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
wald.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
wald.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
wald.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
wald.fit(data,loc=0,scale=1)	•Parameter estimates for wald data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = wald(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

`weibull_min`

A Weibull minimum continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = weibull_min.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = weibull_min(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = weibull_min.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-weibull_min.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = weibull_min.rvs(c,size=100)
```

A Weibull minimum distribution (also called a Frechet (right) distribution)

weibull_min.pdf(x,c) = c*x**(c-1)*exp(-x**c) for x > 0, c > 0.

Methods

weibull_min.rvs(c,loc=0,scale=1,size=1)	•random variates
weibull_min.pdf(x,c,loc=0,scale=1)	•probability density function
weibull_min.cdf(x,c,loc=0,scale=1)	•cumulative density function
weibull_min.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
weibull_min.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
weibull_min.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
weibull_min.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
weibull_min.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
weibull_min.fit(data,c,loc=0,scale=1)	•Parameter estimates for weibull_min data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = weibull_min(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

weibull_max

A Weibull maximum continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = weibull_max.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = weibull_max(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = weibull_max.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-weibull_max.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = weibull_max.rvs(c,size=100)
```

A Weibull maximum distribution (also called a Frechet (left) distribution)

weibull_max.pdf(x,c) = c * (-x)**(c-1) * exp(-(-x)**c) for x < 0, c > 0.

Methods

weibull_max.rvs(c,loc=0,scale=1,size=1)	•random variates
weibull_max.pdf(x,c,loc=0,scale=1)	•probability density function
weibull_max.cdf(x,c,loc=0,scale=1)	•cumulative density function
weibull_max.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
weibull_max.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
weibull_max.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
weibull_max.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
weibull_max.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
weibull_max.fit(data,c,loc=0,scale=1)	•Parameter estimates for weibull_max data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = weibull_max(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

wrapcauchy

A wrapped Cauchy continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

c : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = wrapcauchy.numargs
>>> [ c ] = [0.9,]*numargs
>>> rv = wrapcauchy(c)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = wrapcauchy.cdf(x,c)
>>> h=plt.semilogy(np.abs(x-wrapcauchy.ppf(prb,c))+1e-20)
```

Random number generation

```
>>> R = wrapcauchy.rvs(c,size=100)
```

Wrapped Cauchy distribution

wrapcauchy.pdf(x,c) = (1-c**2) / (2*pi*(1+c**2-2*c*cos(x))) for 0 <= x <= 2*pi, 0 < c < 1.

Methods

wrapcauchy.rvs(c,loc=0,scale=1,size=1)	•random variates
wrapcauchy.pdf(x,c,loc=0,scale=1)	•probability density function
wrapcauchy.cdf(x,c,loc=0,scale=1)	•cumulative density function
wrapcauchy.sf(x,c,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
wrapcauchy.ppf(q,c,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
wrapcauchy.isf(q,c,loc=0,scale=1)	•inverse survival function (inverse of sf)
wrapcauchy.stats(c,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
wrapcauchy.entropy(c,loc=0,scale=1)	•(differential) entropy of the RV.
wrapcauchy.fit(data,c,loc=0,scale=1)	•Parameter estimates for wrapcauchy data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = wrapcauchy(c,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

ksone

Kolmogorov-Smirnov A one-sided test statistic. continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

n : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = ksone.numargs
>>> [ n ] = [0.9,]*numargs
>>> rv = ksone(n)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = ksone.cdf(x,n)
>>> h=plt.semilogy(np.abs(x-ksone.ppf(prb,n))+1e-20)
```

Random number generation

```
>>> R = ksone.rvs(n,size=100)
```

General Kolmogorov-Smirnov one-sided test.

Methods

ksone.rvs(n,loc=0,scale=1,size=1)	•random variates
ksone.pdf(x,n,loc=0,scale=1)	•probability density function
ksone.cdf(x,n,loc=0,scale=1)	•cumulative density function
ksone.sf(x,n,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
ksone.ppf(q,n,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
ksone.isf(q,n,loc=0,scale=1)	•inverse survival function (inverse of sf)
ksone.stats(n,loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
ksone.entropy(n,loc=0,scale=1)	•(differential) entropy of the RV.
ksone.fit(data,n,loc=0,scale=1)	•Parameter estimates for ksone data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = ksone(n,loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

kstwobign

Kolmogorov-Smirnov two-sided (for large N) continuous random variable.

Continuous random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Parameters

x : array-like

quantiles

q : array-like

lower or upper tail probability

<shape(s)> : array-like

shape parameters

loc : array-like, optional

location parameter (default=0)

scale : array-like, optional

scale parameter (default=1)

size : int or tuple of ints, optional

shape of random variates (default computed from input arguments)

moments : string, optional

composed of letters ['mvsk'] specifying which moments to compute where 'm' = mean, 'v' = variance, 's' = (Fisher's) skew and 'k' = (Fisher's) kurtosis. (default='mv')

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = kstwobign.numargs
>>> [ <shape(s)> ] = [0.9,]*numargs
>>> rv = kstwobign(<shape(s)>)
```

Display frozen pdf

```
>>> x = np.linspace(0,np.minimum(rv.dist.b,3))
>>> h=plt.plot(x,rv.pdf(x))
```

Check accuracy of cdf and ppf

```
>>> prb = kstwobign.cdf(x,<shape(s)>)
>>> h=plt.semilogy(np.abs(x-kstwobign.ppf(prb,<shape(s)>))+1e-20)
```

Random number generation

```
>>> R = kstwobign.rvs(size=100)
```

Kolmogorov-Smirnov two-sided test for large N

Methods

kstwobign.rvs(loc=0,scale=1,size=1)	•random variates
kstwobign.pdf(x,loc=0,scale=1)	•probability density function
kstwobign.cdf(x,loc=0,scale=1)	•cumulative density function
kstwobign.sf(x,loc=0,scale=1)	•survival function (1-cdf — sometimes more accurate)
kstwobign.ppf(q,loc=0,scale=1)	•percent point function (inverse of cdf — percentiles)
kstwobign.isf(q,loc=0,scale=1)	•inverse survival function (inverse of sf)
kstwobign.stats(loc=0,scale=1,moments='mv')	•mean('m'), variance('v'), skew('s'), and/or kurtosis('k')
kstwobign.entropy(loc=0,scale=1)	•(differential) entropy of the RV.
kstwobign.fit(data,loc=0,scale=1)	•Parameter estimates for kstwobign data
Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object: rv = kstwobign(loc=0,scale=1)	•frozen RV object with the same methods but holding the given shape, location, and scale fixed

3.18.2 Discrete distributions

binom	A binom discrete random variable.
bernoulli	A bernoulli discrete random variable.
nbinom	A negative binomial discrete random variable.
geom	A geometric discrete random variable.
hypergeom	A hypergeometric discrete random variable.
logser	A logarithmic discrete random variable.
poisson	A Poisson discrete random variable.
planck	A discrete exponential discrete random variable.
boltzmann	A truncated discrete exponential discrete random variable.
randint	A discrete uniform (random integer) discrete random variable.
zipf	A Zipf discrete random variable.
dlaplace	A discrete Laplacian discrete random variable.

binom

A binom discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = binom.numargs
>>> [ n,pr ] = ['Replace with resonable value',]*numargs
```

Display frozen pmf:

```
>>> rv = binom(n,pr)
>>> x = np.arange(0,np.min(rv.dist.b,3)+1)
>>> h = plt.plot(x,rv.pmf(x))
```

Check accuracy of cdf and ppf:

```
>>> prb = binom.cdf(x,n,pr)
>>> h = plt.semilogy(np.abs(x-binom.ppf(prb,n,pr))+1e-20)
```

Random number generation:

```
>>> R = binom.rvs(n,pr,size=100)
```

Custom made discrete distribution:

```
>>> vals = [arange(7),(0.1,0.2,0.3,0.1,0.1,0.1,0.1)]
>>> custm = rv_discrete(name='custm',values=vals)
>>> h = plt.plot(vals[0],custm.pmf(vals[0]))
```

Binomial distribution

Counts the number of successes in *n* independent trials when the probability of success each time is *pr*.

binom.pmf(k,n,p) = choose(n,k)*p**k*(1-p)**(n-k) for k in {0,1,...,n}

Methods

binom.rvs(n,pr,loc=0,size=1)	•random variates
binom.pmf(x,n,pr,loc=0)	•probability mass function
binom.cdf(x,n,pr,loc=0)	•cumulative density function
binom.sf(x,n,pr,loc=0)	•survival function (1-cdf — sometimes more accurate)
binom.ppf(q,n,pr,loc=0)	•percent point function (inverse of cdf — percentiles)
binom.isf(q,n,pr,loc=0)	•inverse survival function (inverse of sf)
binom.stats(n,pr,loc=0,moments='mv')	•mean('m',axis=0), variance('v'), skew('s'), and/or kurtosis('k')
binom.entropy(n,pr,loc=0)	•entropy of the RV
Alternatively, the object may be called (as a function) to fix the shape and location parameters returning a "frozen" discrete RV object: myrv = binom(n,pr,loc=0)	•frozen RV object with the same methods but holding the given shape and location fixed.
You can construct an aribtrary discrete rv where P{X=xk} = pk by passing to the rv_discrete initialization method (through the values= keyword) a tuple of sequences (xk,pk) which describes only those values of X (xk) that occur with nonzero probability (pk).	

bernoulli

A bernoulli discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = bernoulli.numargs
>>> [ pr ] = ['Replace with resonable value',]*numargs
```

Display frozen pmf:

```
>>> rv = bernoulli(pr)
>>> x = np.arange(0,np.min(rv.dist.b,3)+1)
>>> h = plt.plot(x,rv.pmf(x))
```

Check accuracy of cdf and ppf:

```
>>> prb = bernoulli.cdf(x,pr)
>>> h = plt.semilogy(np.abs(x-bernoulli.ppf(prb,pr))+1e-20)
```

Random number generation:

```
>>> R = bernoulli.rvs(pr,size=100)
```

Custom made discrete distribution:

```
>>> vals = [arange(7),(0.1,0.2,0.3,0.1,0.1,0.1,0.1)]
>>> custm = rv_discrete(name='custm',values=vals)
>>> h = plt.plot(vals[0],custm.pmf(vals[0]))
```

Bernoulli distribution

1 if binary experiment succeeds, 0 otherwise. Experiment succeeds with probabilty *pr*.

bernoulli.pmf(k,p) = 1-p if k = 0
= p if k = 1

for k = 0,1

Methods

bernoulli.rvs(pr,loc=0,size=1)	•random variates
bernoulli.pmf(x,pr,loc=0)	•probability mass function
bernoulli.cdf(x,pr,loc=0)	•cumulative density function
bernoulli.sf(x,pr,loc=0)	•survival function (1-cdf — sometimes more accurate)
bernoulli.ppf(q,pr,loc=0)	•percent point function (inverse of cdf — percentiles)
bernoulli.isf(q,pr,loc=0)	•inverse survival function (inverse of sf)
bernoulli.stats(pr,loc=0,moments='mv')	•mean('m',axis=0), variance('v'), skew('s'), and/or kurtosis('k')
bernoulli.entropy(pr,loc=0)	•entropy of the RV
Alternatively, the object may be called (as a function) to fix the shape and location parameters returning a "frozen" discrete RV object: myrv = bernoulli(pr,loc=0)	•frozen RV object with the same methods but holding the given shape and location fixed.
You can construct an aribtrary discrete rv where P{X=xk} = pk by passing to the rv_discrete initialization method (through the values= keyword) a tuple of sequences (xk,pk) which describes only those values of X (xk) that occur with nonzero probability (pk).	

nbinom

A negative binomial discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = nbinom.numargs
>>> [ n,pr ] = ['Replace with resonable value',]*numargs
```

Display frozen pmf:

```
>>> rv = nbinom(n,pr)
>>> x = np.arange(0,np.min(rv.dist.b,3)+1)
>>> h = plt.plot(x,rv.pmf(x))
```

Check accuracy of cdf and ppf:

```
>>> prb = nbinom.cdf(x,n,pr)
>>> h = plt.semilogy(np.abs(x-nbinom.ppf(prb,n,pr))+1e-20)
```

Random number generation:

```
>>> R = nbinom.rvs(n,pr,size=100)
```

Custom made discrete distribution:

```
>>> vals = [arange(7),(0.1,0.2,0.3,0.1,0.1,0.1,0.1)]
>>> custm = rv_discrete(name='custm',values=vals)
>>> h = plt.plot(vals[0],custm.pmf(vals[0]))
```

Negative binomial distribution

nbinom.pmf(k,n,p) = choose(k+n-1,n-1) * p**n * (1-p)**k for k >= 0.

Methods

nbinom.rvs(n,pr,loc=0,size=1)	•random variates
nbinom.pmf(x,n,pr,loc=0)	•probability mass function
nbinom.cdf(x,n,pr,loc=0)	•cumulative density function
nbinom.sf(x,n,pr,loc=0)	•survival function (1-cdf — sometimes more accurate)
nbinom.ppf(q,n,pr,loc=0)	•percent point function (inverse of cdf — percentiles)
nbinom.isf(q,n,pr,loc=0)	•inverse survival function (inverse of sf)
nbinom.stats(n,pr,loc=0,moments='mv')	•mean('m',axis=0), variance('v'), skew('s'), and/or kurtosis('k')
nbinom.entropy(n,pr,loc=0)	•entropy of the RV
Alternatively, the object may be called (as a function) to fix the shape and location parameters returning a "frozen" discrete RV object: myrv = nbinom(n,pr,loc=0)	•frozen RV object with the same methods but holding the given shape and location fixed.
You can construct an aribtrary discrete rv where P{X=xk} = pk by passing to the rv_discrete initialization method (through the values= keyword) a tuple of sequences (xk,pk) which describes only those values of X (xk) that occur with nonzero probability (pk).	

geom

A geometric discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = geom.numargs
>>> [ pr ] = ['Replace with resonable value',]*numargs
```

Display frozen pmf:

```
>>> rv = geom(pr)
>>> x = np.arange(0,np.min(rv.dist.b,3)+1)
>>> h = plt.plot(x,rv.pmf(x))
```

Check accuracy of cdf and ppf:

```
>>> prb = geom.cdf(x,pr)
>>> h = plt.semilogy(np.abs(x-geom.ppf(prb,pr))+1e-20)
```

Random number generation:

```
>>> R = geom.rvs(pr,size=100)
```

Custom made discrete distribution:

```
>>> vals = [arange(7),(0.1,0.2,0.3,0.1,0.1,0.1,0.1)]
>>> custm = rv_discrete(name='custm',values=vals)
>>> h = plt.plot(vals[0],custm.pmf(vals[0]))
```

Geometric distribution

geom.pmf(k,p) = (1-p)**(k-1)*p for k >= 1

Methods

geom.rvs(pr,loc=0,size=1)	•random variates
geom.pmf(x,pr,loc=0)	•probability mass function
geom.cdf(x,pr,loc=0)	•cumulative density function
geom.sf(x,pr,loc=0)	•survival function (1-cdf — sometimes more accurate)
geom.ppf(q,pr,loc=0)	•percent point function (inverse of cdf — percentiles)
geom.isf(q,pr,loc=0)	•inverse survival function (inverse of sf)
geom.stats(pr,loc=0,moments='mv')	•mean('m',axis=0), variance('v'), skew('s'), and/or kurtosis('k')
geom.entropy(pr,loc=0)	•entropy of the RV
Alternatively, the object may be called (as a function) to fix the shape and location parameters returning a "frozen" discrete RV object: myrv = geom(pr,loc=0)	•frozen RV object with the same methods but holding the given shape and location fixed.
You can construct an aribtrary discrete rv where P{X=xk} = pk by passing to the rv_discrete initialization method (through the values= keyword) a tuple of sequences (xk,pk) which describes only those values of X (xk) that occur with nonzero probability (pk).	

hypergeom

A hypergeometric discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = hypergeom.numargs
>>> [ M,n,N ] = ['Replace with resonable value',]*numargs
```

Display frozen pmf:

```
>>> rv = hypergeom(M,n,N)
>>> x = np.arange(0,np.min(rv.dist.b,3)+1)
>>> h = plt.plot(x,rv.pmf(x))
```

Check accuracy of cdf and ppf:

```
>>> prb = hypergeom.cdf(x,M,n,N)
>>> h = plt.semilogy(np.abs(x-hypergeom.ppf(prb,M,n,N))+1e-20)
```

Random number generation:

```
>>> R = hypergeom.rvs(M,n,N,size=100)
```

Custom made discrete distribution:

```
>>> vals = [arange(7),(0.1,0.2,0.3,0.1,0.1,0.1,0.1)]
>>> custm = rv_discrete(name='custm',values=vals)
>>> h = plt.plot(vals[0],custm.pmf(vals[0]))
```

Hypergeometric distribution

Models drawing objects from a bin. M is total number of objects, n is total number of Type I objects. RV counts number of Type I objects in N drawn without replacement from population.

hypergeom.pmf(k, M, n, N) = choose(n,k)*choose(M-n,N-k)/choose(M,N) for N - (M-n) <= k <= min(m,N)

Methods

hypergeom.rvs(M,n,N,loc=0,size=1)	•random variates
hypergeom.pmf(x,M,n,N,loc=0)	•probability mass function
hypergeom.cdf(x,M,n,N,loc=0)	•cumulative density function
hypergeom.sf(x,M,n,N,loc=0)	•survival function (1-cdf — sometimes more accurate)
hypergeom.ppf(q,M,n,N,loc=0)	•percent point function (inverse of cdf — percentiles)
hypergeom.isf(q,M,n,N,loc=0)	•inverse survival function (inverse of sf)
hypergeom.stats(M,n,N,loc=0,moments='mv')	•mean('m',axis=0), variance('v'), skew('s'), and/or kurtosis('k')
hypergeom.entropy(M,n,N,loc=0)	•entropy of the RV
Alternatively, the object may be called (as a function) to fix the shape and location parameters returning a "frozen" discrete RV object: myrv = hypergeom(M,n,N,loc=0)	•frozen RV object with the same methods but holding the given shape and location fixed.
You can construct an aribtrary discrete rv where P{X=xk} = pk by passing to the rv_discrete initialization method (through the values= keyword) a tuple of sequences (xk,pk) which describes only those values of X (xk) that occur with nonzero probability (pk).	

logser

A logarithmic discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = logser.numargs
>>> [ pr ] = ['Replace with resonable value',]*numargs
```

Display frozen pmf:

```
>>> rv = logser(pr)
>>> x = np.arange(0,np.min(rv.dist.b,3)+1)
>>> h = plt.plot(x,rv.pmf(x))
```

Check accuracy of cdf and ppf:

```
>>> prb = logser.cdf(x,pr)
>>> h = plt.semilogy(np.abs(x-logser.ppf(prb,pr))+1e-20)
```

Random number generation:

```
>>> R = logser.rvs(pr,size=100)
```

Custom made discrete distribution:

```
>>> vals = [arange(7),(0.1,0.2,0.3,0.1,0.1,0.1,0.1)]
>>> custm = rv_discrete(name='custm',values=vals)
>>> h = plt.plot(vals[0],custm.pmf(vals[0]))
```

Logarithmic (Log-Series, Series) distribution

logser.pmf(k,p) = - p**k / (k*log(1-p)) for k >= 1

Methods

logser.rvs(pr,loc=0,size=1)	•random variates
logser.pmf(x,pr,loc=0)	•probability mass function
logser.cdf(x,pr,loc=0)	•cumulative density function
logser.sf(x,pr,loc=0)	•survival function (1-cdf — sometimes more accurate)
logser.ppf(q,pr,loc=0)	•percent point function (inverse of cdf — percentiles)
logser.isf(q,pr,loc=0)	•inverse survival function (inverse of sf)
logser.stats(pr,loc=0,moments='mv')	•mean('m',axis=0), variance('v'), skew('s'), and/or kurtosis('k')
logser.entropy(pr,loc=0)	•entropy of the RV
Alternatively, the object may be called (as a function) to fix the shape and location parameters returning a "frozen" discrete RV object: myrv = logser(pr,loc=0)	•frozen RV object with the same methods but holding the given shape and location fixed.
You can construct an aribtrary discrete rv where P{X=xk} = pk by passing to the rv_discrete initialization method (through the values= keyword) a tuple of sequences (xk,pk) which describes only those values of X (xk) that occur with nonzero probability (pk).	

poisson

A Poisson discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = poisson.numargs
>>> [ mu ] = ['Replace with resonable value',]*numargs
```

Display frozen pmf:

```
>>> rv = poisson(mu)
>>> x = np.arange(0,np.min(rv.dist.b,3)+1)
>>> h = plt.plot(x,rv.pmf(x))
```

Check accuracy of cdf and ppf:

```
>>> prb = poisson.cdf(x,mu)
>>> h = plt.semilogy(np.abs(x-poisson.ppf(prb,mu))+1e-20)
```

Random number generation:

```
>>> R = poisson.rvs(mu,size=100)
```

Custom made discrete distribution:

```
>>> vals = [arange(7),(0.1,0.2,0.3,0.1,0.1,0.1,0.1)]
>>> custm = rv_discrete(name='custm',values=vals)
>>> h = plt.plot(vals[0],custm.pmf(vals[0]))
```

Poisson distribution

poisson.pmf(k, mu) = exp(-mu) * mu**k / k! for k >= 0

Methods

poisson.rvs(mu,loc=0,size=1)	•random variates
poisson.pmf(x,mu,loc=0)	•probability mass function
poisson.cdf(x,mu,loc=0)	•cumulative density function
poisson.sf(x,mu,loc=0)	•survival function (1-cdf — sometimes more accurate)
poisson.ppf(q,mu,loc=0)	•percent point function (inverse of cdf — percentiles)
poisson.isf(q,mu,loc=0)	•inverse survival function (inverse of sf)
poisson.stats(mu,loc=0,moments='mv')	•mean('m',axis=0), variance('v'), skew('s'), and/or kurtosis('k')
poisson.entropy(mu,loc=0)	•entropy of the RV
Alternatively, the object may be called (as a function) to fix the shape and location parameters returning a "frozen" discrete RV object: myrv = poisson(mu,loc=0)	•frozen RV object with the same methods but holding the given shape and location fixed.
You can construct an aribtrary discrete rv where P{X=xk} = pk by passing to the rv_discrete initialization method (through the values= keyword) a tuple of sequences (xk,pk) which describes only those values of X (xk) that occur with nonzero probability (pk).	

planck

A discrete exponential discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = planck.numargs
>>> [ lambda_ ] = ['Replace with resonable value',]*numargs
```

Display frozen pmf:

```
>>> rv = planck(lambda_)
>>> x = np.arange(0,np.min(rv.dist.b,3)+1)
>>> h = plt.plot(x,rv.pmf(x))
```

Check accuracy of cdf and ppf:

```
>>> prb = planck.cdf(x,lambda_)
>>> h = plt.semilogy(np.abs(x-planck.ppf(prb,lambda_))+1e-20)
```

Random number generation:

```
>>> R = planck.rvs(lambda_,size=100)
```

Custom made discrete distribution:

```
>>> vals = [arange(7),(0.1,0.2,0.3,0.1,0.1,0.1,0.1)]
>>> custm = rv_discrete(name='custm',values=vals)
>>> h = plt.plot(vals[0],custm.pmf(vals[0]))
```

Planck (Discrete Exponential)

planck.pmf(k,b) = (1-exp(-b))*exp(-b*k) for k*b >= 0

Methods

planck.rvs(**lambda_**,loc=0,size=1)	•random variates
planck.pmf(x,lambda_,loc=0)	•probability mass function
planck.cdf(x,lambda_,loc=0)	•cumulative density function
planck.sf(x,lambda_,loc=0)	•survival function (1-cdf — sometimes more accurate)
planck.ppf(q,lambda_,loc=0)	•percent point function (inverse of cdf — percentiles)
planck.isf(q,lambda_,loc=0)	•inverse survival function (inverse of sf)
planck.stats(**lambda_**,loc=0,moments='mv')	•mean('m',axis=0), variance('v'), skew('s'), and/or kurtosis('k')
planck.entropy(**lambda_**,loc=0)	•entropy of the RV
Alternatively, the object may be called (as a function) to fix the shape and location parameters returning a "frozen" discrete RV object: myrv = planck(**lambda_**,loc=0)	•frozen RV object with the same methods but holding the given shape and location fixed.
You can construct an aribtrary discrete rv where P{X=xk} = pk by passing to the rv_discrete initialization method (through the values= keyword) a tuple of sequences (xk,pk) which describes only those values of X (xk) that occur with nonzero probability (pk).	

boltzmann

A truncated discrete exponential discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = boltzmann.numargs
>>> [ lambda_,N ] = ['Replace with resonable value',]*numargs
```

Display frozen pmf:

```
>>> rv = boltzmann(lambda_,N)
>>> x = np.arange(0,np.min(rv.dist.b,3)+1)
>>> h = plt.plot(x,rv.pmf(x))
```

Check accuracy of cdf and ppf:

```
>>> prb = boltzmann.cdf(x,lambda_,N)
>>> h = plt.semilogy(np.abs(x-boltzmann.ppf(prb,lambda_,N))+1e-20)
```

Random number generation:

```
>>> R = boltzmann.rvs(lambda_,N,size=100)
```

Custom made discrete distribution:

```
>>> vals = [arange(7),(0.1,0.2,0.3,0.1,0.1,0.1,0.1)]
>>> custm = rv_discrete(name='custm',values=vals)
>>> h = plt.plot(vals[0],custm.pmf(vals[0]))
```

Boltzmann (Truncated Discrete Exponential)

boltzmann.pmf(k,b,N) = (1-exp(-b))*exp(-b*k)/(1-exp(-b*N)) for k=0,..,N-1

Methods

boltzmann.rvs(**lambda_**,N,loc=0,size=1)	•random variates
boltzmann.pmf(x,lambda_,N,loc=0)	•probability mass function
boltzmann.cdf(x,lambda_,N,loc=0)	•cumulative density function
boltzmann.sf(x,lambda_,N,loc=0)	•survival function (1-cdf — sometimes more accurate)
boltzmann.ppf(q,lambda_,N,loc=0)	•percent point function (inverse of cdf — percentiles)
boltzmann.isf(q,lambda_,N,loc=0)	•inverse survival function (inverse of sf)
boltzmann.stats(**lambda_**,N,loc=0,moments='mv')	•mean('m',axis=0), variance('v'), skew('s'), and/or kurtosis('k')
boltzmann.entropy(**lambda_**,N,loc=0)	•entropy of the RV
Alternatively, the object may be called (as a function) to fix the shape and location parameters returning a "frozen" discrete RV object: myrv = boltzmann(**lambda_**,N,loc=0)	•frozen RV object with the same methods but holding the given shape and location fixed.
You can construct an aribtrary discrete rv where P{X=xk} = pk by passing to the rv_discrete initialization method (through the values= keyword) a tuple of sequences (xk,pk) which describes only those values of X (xk) that occur with nonzero probability (pk).	

randint

A discrete uniform (random integer) discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = randint.numargs
>>> [ min,max ] = ['Replace with resonable value',]*numargs
```

Display frozen pmf:

```
>>> rv = randint(min,max)
>>> x = np.arange(0,np.min(rv.dist.b,3)+1)
>>> h = plt.plot(x,rv.pmf(x))
```

Check accuracy of cdf and ppf:

```
>>> prb = randint.cdf(x,min,max)
>>> h = plt.semilogy(np.abs(x-randint.ppf(prb,min,max))+1e-20)
```

Random number generation:

```
>>> R = randint.rvs(min,max,size=100)
```

Custom made discrete distribution:

```
>>> vals = [arange(7),(0.1,0.2,0.3,0.1,0.1,0.1,0.1)]
>>> custm = rv_discrete(name='custm',values=vals)
>>> h = plt.plot(vals[0],custm.pmf(vals[0]))
```

Discrete Uniform

Random integers >=min and <max.

randint.pmf(k,min, max) = 1/(max-min) for min <= k < max.

Methods

randint.rvs(min,max,loc=0,size=1)	•random variates
randint.pmf(x,min,max,loc=0)	•probability mass function
randint.cdf(x,min,max,loc=0)	•cumulative density function
randint.sf(x,min,max,loc=0)	•survival function (1-cdf — sometimes more accurate)
randint.ppf(q,min,max,loc=0)	•percent point function (inverse of cdf — percentiles)
randint.isf(q,min,max,loc=0)	•inverse survival function (inverse of sf)
randint.stats(min,max,loc=0,moments='mv')	•mean('m',axis=0), variance('v'), skew('s'), and/or kurtosis('k')
randint.entropy(min,max,loc=0)	•entropy of the RV
Alternatively, the object may be called (as a function) to fix the shape and location parameters returning a "frozen" discrete RV object: myrv = randint(min,max,loc=0)	•frozen RV object with the same methods but holding the given shape and location fixed.
You can construct an aribtrary discrete rv where P{X=xk} = pk by passing to the rv_discrete initialization method (through the values= keyword) a tuple of sequences (xk,pk) which describes only those values of X (xk) that occur with nonzero probability (pk).	

zipf

A Zipf discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = zipf.numargs
>>> [ a ] = ['Replace with resonable value',]*numargs
```

Display frozen pmf:

```
>>> rv = zipf(a)
>>> x = np.arange(0,np.min(rv.dist.b,3)+1)
>>> h = plt.plot(x,rv.pmf(x))
```

Check accuracy of cdf and ppf:

```
>>> prb = zipf.cdf(x,a)
>>> h = plt.semilogy(np.abs(x-zipf.ppf(prb,a))+1e-20)
```

Random number generation:

```
>>> R = zipf.rvs(a,size=100)
```

Custom made discrete distribution:

```
>>> vals = [arange(7),(0.1,0.2,0.3,0.1,0.1,0.1,0.1)]
>>> custm = rv_discrete(name='custm',values=vals)
>>> h = plt.plot(vals[0],custm.pmf(vals[0]))
```

Zipf distribution

zipf.pmf(k,a) = 1/(zeta(a)*k**a) for k >= 1

Methods

zipf.rvs(a,loc=0,size=1)	•random variates
zipf.pmf(x,a,loc=0)	•probability mass function
zipf.cdf(x,a,loc=0)	•cumulative density function
zipf.sf(x,a,loc=0)	•survival function (1-cdf — sometimes more accurate)
zipf.ppf(q,a,loc=0)	•percent point function (inverse of cdf — percentiles)
zipf.isf(q,a,loc=0)	•inverse survival function (inverse of sf)
zipf.stats(a,loc=0,moments='mv')	•mean('m',axis=0), variance('v'), skew('s'), and/or kurtosis('k')
zipf.entropy(a,loc=0)	•entropy of the RV
Alternatively, the object may be called (as a function) to fix the shape and location parameters returning a "frozen" discrete RV object: myrv = zipf(a,loc=0)	•frozen RV object with the same methods but holding the given shape and location fixed.
You can construct an aribtrary discrete rv where P{X=xk} = pk by passing to the rv_discrete initialization method (through the values= keyword) a tuple of sequences (xk,pk) which describes only those values of X (xk) that occur with nonzero probability (pk).	

dlaplace

A discrete Laplacian discrete random variable.

Discrete random variables are defined from a standard form and may require some shape parameters to complete its specification. Any optional keyword parameters can be passed to the methods of the RV object as given below:

Examples

```
>>> import matplotlib.pyplot as plt
>>> numargs = dlaplace.numargs
>>> [ a ] = ['Replace with resonable value',]*numargs
```

Display frozen pmf:

```
>>> rv = dlaplace(a)
>>> x = np.arange(0,np.min(rv.dist.b,3)+1)
>>> h = plt.plot(x,rv.pmf(x))
```

Check accuracy of cdf and ppf:

```
>>> prb = dlaplace.cdf(x,a)
>>> h = plt.semilogy(np.abs(x-dlaplace.ppf(prb,a))+1e-20)
```

Random number generation:

```
>>> R = dlaplace.rvs(a,size=100)
```

Custom made discrete distribution:

```
>>> vals = [arange(7),(0.1,0.2,0.3,0.1,0.1,0.1,0.1)]
>>> custm = rv_discrete(name='custm',values=vals)
>>> h = plt.plot(vals[0],custm.pmf(vals[0]))
```

Discrete Laplacian distribution.

dlapacle.pmf(k,a) = tanh(a/2) * exp(-a*abs(k)) for a > 0.

Methods

dlaplace.rvs(a,loc=0,size=1)	•random variates
dlaplace.pmf(x,a,loc=0)	•probability mass function
dlaplace.cdf(x,a,loc=0)	•cumulative density function
dlaplace.sf(x,a,loc=0)	•survival function (1-cdf — sometimes more accurate)
dlaplace.ppf(q,a,loc=0)	•percent point function (inverse of cdf — percentiles)
dlaplace.isf(q,a,loc=0)	•inverse survival function (inverse of sf)
dlaplace.stats(a,loc=0,moments='mv')	•mean('m',axis=0), variance('v'), skew('s'), and/or kurtosis('k')
dlaplace.entropy(a,loc=0)	•entropy of the RV
Alternatively, the object may be called (as a function) to fix the shape and location parameters returning a "frozen" discrete RV object: myrv = dlaplace(a,loc=0)	•frozen RV object with the same methods but holding the given shape and location fixed.
You can construct an aribtrary discrete rv where P{X=xk} = pk by passing to the rv_discrete initialization method (through the values= keyword) a tuple of sequences (xk,pk) which describes only those values of X (xk) that occur with nonzero probability (pk).	

3.18.3 Statistical functions

Several of these functions have a similar version in scipy.stats.mstats which work for masked arrays.

gmean(a[, axis, dtype])	Compute the geometric mean along the specified axis.
hmean(a[, axis, dtype])	Calculates the harmonic mean along the specified axis.
mean(a[, axis])	Returns the arithmetic mean of m along the given dimension.
cmedian(a[, numbins])	Returns the computed median value of an array.
median(a[, axis])	Returns the median of the passed array along the given axis.
mode(a[, axis])	Returns an array of the modal (most common) value in the passed array.
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
tstd(a[, limits, inclusive])	Compute the trimmed sample standard deviation
tsem(a[, limits, inclusive])	Compute the trimmed standard error of the mean
moment(a[, moment, axis])	Calculates the nth moment about the mean for a sample.
variation(a[, axis])	Computes the coefficient of variation, the ratio of the biased standard deviation to the mean.
skew(a[, axis, bias])	Computes the skewness of a data set.
kurtosis(a[, axis, fisher, bias])	Computes the kurtosis (Fisher or Pearson) of a dataset.
describe(a[, axis])	Computes several descriptive statistics of the passed array.
skewtest(a[, axis])	Tests whether the skew is different from the normal distribution.
kurtosistest(a[, axis])	Tests whether a dataset has normal kurtosis
normaltest(a[, axis])	Tests whether a sample differs from a normal distribution

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, optional, default axis=0

Axis along which the geometric mean is computed.

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.

hmean(*a, axis=0, dtype=None*)

Calculates the harmonic mean along the specified axis.

That is: n / (1/x1 + 1/x2 + ... + 1/xn)

Parameters

a : array_like

Input array, masked array or object that can be converted to an array.

axis : int, optional, default axis=0

Axis along which the harmonic mean is computed.

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.

mean(*a, axis=0*)

Returns the arithmetic mean of m along the given dimension.

That is: (x1 + x2 + .. + xn) / n

Parameters

a : array

axis : int or None

Returns

The arithmetic mean computed over a single dimension of the input array or :

all values in the array if axis=None. The return value will have a floating :

point dtype even if the input data are integers. :

cmedian (*a, numbins=1000*)

Returns the computed median value of an array.

All of the values in the input array are used. The input array is first histogrammed using numbins bins. The bin containing the median is selected by searching for the halfway point in the cumulative histogram. The median value is then computed by linearly interpolating across that bin.

Parameters

a : array

numbins : int

The number of bins used to histogram the data. More bins give greater accuracy to the approximation of the median.

Returns

A floating point value approximating the median. :

References

[CRCProbStat2000] Section 2.2.6

[CRCProbStat2000]

median (*a, axis=0*)

Returns the median of the passed array along the given axis.

If there is an even number of entries, the mean of the 2 middle values is returned.

Parameters

a : array

axis=0 : int

Returns

The median of each remaining axis, or of all of the values in the array :

if axis is None. :

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

axis=0 : int

Returns

(array of modal values, array of counts for each mode) :

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, 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

tmean : float

tvar(*a, limits=None, inclusive=(1, 1)*)

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

tmin(*a, lowerlimit=None, axis=0, inclusive=True*)

Compute the trimmed minimum

This function finds the miminum 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 : None or int, optional

Operate along this axis. None means to use the flattened array and the default is zero

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 :

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 : None or int, optional

Operate along this axis. None means to use the flattened array and the default is zero.

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

tstd(*a, limits=None, inclusive=(1, 1)*)
Compute the trimmed sample standard deviation

This function finds the sample standard deviation of given values, ignoring values outside the given *limits*.

Parameters
a : array_like

array of values

limits : None or (lower limit, upper limit), optional

Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None, then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval. The default value is None.

inclusive : (bool, bool), optional

A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).

Returns
tstd : float

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

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

moment : int

axis : int or None

Returns

The appropriate moment along the given axis or over all values if axis is :

None. :

variation(*a, axis=0*)

Computes the coefficient of variation, the ratio of the biased standard deviation to the mean.

Parameters

a : array

axis : int or None

References

[CRCProbStat2000] Section 2.2.20

[CRCProbStat2000]

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 : array

axis : int or None

bias : bool

If False, then the calculations are corrected for statistical bias.

Returns

The skewness of values along an axis, returning 0 where all values are :

equal. :

References

[CRCProbStat2000] Section 2.2.24.1

[CRCProbStat2000]

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 comming from biased moment estimators

Use kurtosistest() to see if result is close enough to normal.

Parameters
a : array

axis : int or None

fisher : bool

If True, Fisher's definition is used (normal ==> 0.0). If False, Pearson's definition is used (normal ==> 3.0).

bias : bool

If False, then the calculations are corrected for statistical bias.

Returns
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

[CRCProbStat2000] Section 2.2.25

[CRCProbStat2000]

describe(*a, axis=0*)
Computes several descriptive statistics of the passed array.

Parameters
a : array

axis : int or None

Returns
(size of the data, :

(min, max), arithmetic mean, unbiased variance, biased skewness, biased kurtosis)

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

axis : int or None

Returns
p-value : float

a 2-sided p-value for the hypothesis test

Notes

The sample size should be at least 8.

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

the axis to operate along, or None to work on the whole array. The default is the first axis.

Returns
p-value : 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.

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 [R30], [R31] test that combines skew and kurtosis to produce an omnibus test of normality.

Parameters
a : array

axis : int or None

Returns
p-value : float

A 2-sided chi squared probability for the hypothesis test

References

[R30], [R31]

itemfreq(a)	Returns a 2D array of item frequencies.
scoreatpercentile(a, per[, limit])	Calculate the score at the given 'per' percentile of the sequence a.
percentileofscore(a, score[, kind])	The percentile rank of a score relative to a list of scores.
histogram2(a, bins)	histogram2(a,bins) – Compute histogram of a using divisions in bins
histogram(a[, numbins, defaultlimits, ...])	Separates the range into several bins and returns the number of instances of a in each bin.
cumfreq(a[, numbins, defaultreallimits, weights])	Returns a cumulative frequency histogram, using the histogram function.
relfreq(a[, numbins, defaultreallimits, weights])	Returns a relative frequency histogram, using the histogram function.

itemfreq(*a*)

Returns a 2D array of item frequencies.

Column 1 contains item values, column 2 contains their respective counts. Assumes a 1D array is passed.

Parameters

a : array

Returns

A 2D frequency table (col [0:n-1]=scores, col n=frequencies) :

scoreatpercentile(*a, per, limit=()*)

Calculate the score at the given 'per' percentile of the sequence a. For example, the score at per=50 is the median.

If the desired quantile lies between two data points, we interpolate between them.

If the parameter 'limit' is provided, it should be a tuple (lower, upper) of two values. Values of 'a' outside this (closed) interval will be ignored.

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*.

Examples

Three-quarters of the given values lie below a given score:

```
>>> 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:

```
>>> percentileofscore([1, 2, 3, 3, 4], 3)
70.0
```

Only 2/5 values are strictly less than 3:

```
>>> percentileofscore([1, 2, 3, 3, 4], 3, kind='strict')
40.0
```

But 4/5 values are less than or equal to 3:

```
>>> percentileofscore([1, 2, 3, 3, 4], 3, kind='weak')
80.0
```

The average between the weak and the strict scores is

```
>>> percentileofscore([1, 2, 3, 3, 4], 3, kind='mean')
60.0
```

histogram2 (*a, bins*)

histogram2(a,bins) – Compute histogram of a using divisions in bins

Description:

Count the number of times values from array a fall into numerical ranges defined by bins. Range x is given by bins[x] <= 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] <= range_N < infinity. Values less than bins[0] are not included in the histogram.

Arguments:

a – 1D array. The array of values to be divied into bins bins – 1D array. Defines the ranges of values to use during

histogramming.

Returns:

1D array. Each value represents the occurences for a given bin (range) of values.

Caveat:

This should probably have an axis argument that would histogram along a specific axis (kinda like matlab)

histogram (*a, numbins=10, defaultlimits=None, weights=None, printextras=False*)

Separates the range into several bins and returns the number of instances of a in each bin. This histogram is based on numpy's histogram but has a larger range by default if defaultlimits is not set.

Parameters

a: array like :

Array of scores which will be put into bins.

numbins: integer, 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 then the range of the values in a is used. Specifically (a.min() - s, a.max() + s),

where s is (1/2)(a.max() - a.min()) / (numbins - 1)

weights: array like, same length as a, optional :

The weights for each value in a. Default is None, which gives each value a weight of 1.0

printextras: boolean, optional :

If True, the number of extra points is printed to standard output. Default is False

Returns

histogram: array :

Number of points (or sum of weights) in each bin

low_range: 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: integer :

The number of points outside the range of the histogram

See Also:

`numpy.histogram`

cumfreq(*a, numbins=10, defaultreallimits=None, weights=None*)

Returns a cumulative frequency histogram, using the histogram function. Defaultreallimits can be None (use all data), or a 2-sequence containing lower and upper limits on values to include.

Returns: array of cumfreq bin values, lowerreallimit, binsize, extrapoints

relfreq(*a, numbins=10, defaultreallimits=None, weights=None*)

Returns a relative frequency histogram, using the histogram function. Defaultreallimits can be None (use all data), or a 2-sequence containing lower and upper limits on values to include.

Returns: array of cumfreq bin values, lowerreallimit, binsize, extrapoints

obrientransform(*args)	Computes a transform on input data (any number of columns).
samplevar(*args, **kwds)	*samplevar* is deprecated!
samplestd(*args, **kwds)	*samplestd* is deprecated!
signaltonoise(a[, axis, ddof])	Calculates the signal-to-noise ratio, defined as the ratio between the mean and the standard deviation.
bayes_mvs(data[, alpha])	Return Bayesian confidence intervals for the mean, var, and std.
var(a[, axis, bias])	Returns the estimated population variance of the values in the passed
std(a[, axis, bias])	Returns the estimated population standard deviation of the values in
stderr(*args, **kwds)	*stderr* is deprecated!
sem(a[, axis, ddof])	Calculates the standard error of the mean (or standard error of measurement) of the values in the passed array.
z(*args, **kwds)	*z* is deprecated!
zs(*args, **kwds)	*zs* is deprecated!
zmap(scores, compare[, axis])	Returns an array of z-scores the shape of scores (e.g., [x,y]), compared to array passed to compare (e.g., [time,x,y]).

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

samplevar(**args, **kwds*)

samplevar is deprecated!

scipy.stats.samplevar is deprecated; please update your code to use numpy.var.

Please note that `numpy.var` axis argument defaults to None, not 0.

Returns the sample standard deviation of the values in the passed array (i.e., using N). Axis can equal None (ravel array first), an integer (the axis over which to operate)

samplestd(**args, **kwds*)

samplestd is deprecated!

scipy.stats.samplestd is deprecated; please update your code to use numpy.std.

Please note that `numpy.std` axis argument defaults to None, not 0.

Returns the sample standard deviation of the values in the passed array (i.e., using N). Axis can equal None (ravel array first), an integer (the axis over which to operate).

signaltonoise(*a, axis=0, ddof=0*)

Calculates the signal-to-noise ratio, defined as the ratio between the mean and the standard deviation.

Parameters

a: array-like :

An array like object containing the sample data

axis: int or None, optional :

If axis is equal to None, the array is first ravel'd. If axis is an integer, this is the axis over which to operate. Defaults to None???0

ddof : integer, optional, default 0

degrees of freedom correction for standard deviation

Returns

array containing the value of the ratio of the mean to the standard :

deviation along axis, or 0, when the standard deviation is equal to 0 :

bayes_mvs(*data, alpha=0.90000000000000002*)

Return Bayesian confidence intervals for the mean, var, and std.

Assumes 1-d data all has same mean and variance and uses Jeffrey's prior for variance and std.

alpha gives the probability that the returned confidence interval contains the true parameter.

Uses mean of conditional pdf as center estimate (but centers confidence interval on the median)

Returns (center, (a, b)) for each of mean, variance and standard deviation. Requires 2 or more data-points.

var(*a, axis=0, bias=False*)

Returns the estimated population variance of the values in the passed array (i.e., N-1). Axis can equal None (ravel array first), or an integer (the axis over which to operate).

std(*a, axis=0, bias=False*)

Returns the estimated population standard deviation of the values in the passed array (i.e., N-1). Axis can equal None (ravel array first), or an integer (the axis over which to operate).

stderr(**args, **kwds*)

stderr is deprecated!

scipy.stats.stderr is deprecated; please update your code to use scipy.stats.sem.

Returns the estimated population standard error of the values in the passed array (i.e., N-1). Axis can equal None (ravel array first), or an integer (the axis over which to operate).

sem(*a, axis=0, ddof=1*)

Calculates the standard error of the mean (or standard error of measurement) of the values in the passed array.

Parameters

a: array like :

An array containing the values for which

axis: int or None, optional. :

if equal None, ravel array first. If equal to an integer, this will be the axis over which to operate. Defaults to 0.

ddof: int :

Delta degrees-of-freedom. How many degrees of freedom to adjust for bias in limited samples relative to the population estimate of variance

Returns

The standard error of the mean in the sample(s), along the input axis :

z(**args, **kwds*)

z is deprecated!

scipy.stats.z is deprecated; please update your code to use scipy.stats.zscore_compare.

Returns the z-score of a given input score, given thearray from which that score came. Not appropriate for population calculations, nor for arrays > 1D.

zs(**args, **kwds*)

zs is deprecated!

scipy.stats.zs is deprecated; please update your code to use scipy.stats.zscore.

Returns a 1D array of z-scores, one for each score in the passed array, computed relative to the passed array.

zmap (*scores, compare, axis=0*)
Returns an array of z-scores the shape of scores (e.g., [x,y]), compared to array passed to compare (e.g., [time,x,y]). Assumes collapsing over dim 0 of the compare array.

threshold(a[, threshmin, threshmax, newval])	Clip array to a given value.
trimboth(a, proportiontocut)	Slices off the passed proportion of items from BOTH ends of the passed
trim1(a, proportiontocut[, tail])	Slices off the passed proportion of items from ONE end of the passed
cov(m[, y, rowvar, bias])	Estimate the covariance matrix.
corrcoef(x[, y, rowvar, bias])	The correlation coefficients formed from 2-d array x, where the rows are the observations, and the columns are variables.

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.

Returns: a, with values less than threshmin or greater than threshmax
replaced with newval

trimboth (*a, proportiontocut*)
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).

Returns: trimmed version of array a

trim1 (*a, proportiontocut, tail='right'*)
Slices off the passed proportion of items from ONE end of the passed array (i.e., 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).

Returns: trimmed version of array a

cov (*m, y=None, rowvar=False, bias=False*)
Estimate the covariance matrix.

If m is a vector, return the variance. For matrices where each row is an observation, and each column a variable, return the covariance matrix. Note that in this case diag(cov(m)) is a vector of variances for each column.

cov(m) is the same as cov(m, m)

Normalization is by (N-1) where N is the number of observations (unbiased estimate). If bias is True then normalization is by N.

If rowvar is False, then each row is a variable with observations in the columns.

corrcoef (*x, y=None, rowvar=False, bias=True*)
The correlation coefficients formed from 2-d array x, where the rows are the observations, and the columns are variables.

corrcoef(x,y) where x and y are 1d arrays is the same as corrcoef(transpose([x,y]))

If rowvar is True, then each row is a variables with observations in the columns.

f_oneway(*args)	Performs a 1-way ANOVA.
pearsonr(x, y)	Calculates a Pearson correlation coefficient and the p-value for testing
spearmanr(x, y)	Calculates a Spearman rank-order correlation coefficient and the p-value
pointbiserialr(x, y)	Calculates a point biserial correlation coefficient and the associated p-value.
kendalltau(x, y)	Calculates Kendall's tau, a correlation measure for ordinal data
linregress(*args)	Calculate a regression line

f_oneway (**args*)

Performs a 1-way ANOVA.

The on-way ANOVA tests the null hypothesis that 2 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 should be given as arguments.

Returns

F-value : float

The computed F-value of the test

p-value : 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 homocedasticity.

If these assumptions are not true for a given set of data, it may still be possible to use the Kruskal-Wallis H-test (**'stats.kruskal'_**) although with some loss of power

The algorithm is from Heiman[2], pp.394-7.

References

[R17], [R18]

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 : 1D array

y : 1D array the same length as x

Returns
(Pearson's correlation coefficient, :

2-tailed p-value)

References

http://www.statsoft.com/textbook/glosp.html#Pearson%20Correlation

spearmanr (*x, y*)
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.

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 : 1D array

Must have length > 2

y : 1D array

Must have the same length as x.

Returns
r : float

The Spearman correlation coefficient

p-value : float

The two-sided p-value for a hypothesis test whose null hypothesis is that the two sets of data are uncorrelated.

References

[CRCProbStat2000] Section 14.7

[CRCProbStat2000]

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.

Parameters
x : array of bools

y : array of floats

Returns
(point-biserial r, :

2-tailed p-value)

References

http://www.childrens-mercy.org/stats/definitions/biserial.htm

kendalltau (*x, y*)

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.

Parameters

x : array_like

array of rankings

y : array_like

second array of rankings, must be the same length as x

Returns

Kendall's tau : float

The tau statistic

p-value : float

The two-sided p-value for a hypothesis test whose null hypothesis is an absence of association, tau = 0.

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, 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

p-value : 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

ttest_1samp(a, popmean[, axis])	Calculates the T-test for the mean of ONE group of scores *a*.
ttest_ind(a, b[, axis])	Calculates the T-test for the means of TWO INDEPENDENT samples of scores.
ttest_rel(a, b[, axis])	Calculates the T-test on TWO RELATED samples of scores, a and b.
kstest(rvs, cdf, **kwds[, args, N, ...])	Perform the Kolmogorov-Smirnov test for goodness of fit
chisquare(f_obs[, f_exp, ddof])	Calculates a one-way chi square test.
ks_2samp(data1, data2)	Computes the Kolmogorov-Smirnof statistic on 2 samples.
mannwhitneyu(x, y[, use_continuity])	Computes the Mann-Whitney rank test on samples x and y.
tiecorrect(rankvals)	Tie-corrector for ties in Mann Whitney U and Kruskal Wallis H tests.
ranksums(x, y)	Compute the Wilcoxon rank-sum statistic for two samples.
wilcoxon(x[, y])	Calculate the Wilcoxon signed-rank test
kruskal(*args)	Compute the Kruskal-Wallis H-test for independent samples
friedmanchisquare(*args)	Computes the Friedman test for repeated measurements

ttest_1samp(*a, popmean, axis=0*)

Calculates the T-test for the mean of ONE group of scores *a*.

This is a two-sided test for the null hypothesis that the expected value (mean) of a sample of independent observations 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, optional, (default axis=0)

Axis can equal None (ravel array first), or an integer (the axis over which to operate on a).

Returns

t : float or array

t-statistic

prob : float or array

two-tailed p-value

Examples

```
>>> from scipy import stats
>>> import numpy as np


>>> #fix seed to get the same result
>>> np.random.seed(7654567)
>>> 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]])
(array([[-0.68014479, -0.04323899],
       [ 2.77025808,  4.11038784]]), array([[  4.99613833e-01,   9.65686743e-01],
       [  7.89094663e-03,   1.49986458e-04]]))
```

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.

Parameters

a, b : sequence of ndarrays

The arrays must have the same shape, except in the dimension corresponding to *axis* (the first, by default).

axis : int, optional

Axis can equal None (ravel array first), or an integer (the axis over which to operate on a and b).

Returns

t : float or array

t-statistic

prob : float or array

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.

Examples

```
>>> from scipy import stats
>>> import numpy as np


>>> #fix seed to get the same result
>>> np.random.seed(12345678)
```

test with sample with identical means

```
>>> rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> rvs2 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> stats.ttest_ind(rvs1,rvs2)
(0.26833823296239279, 0.78849443369564765)
```

test with sample with different means

```
>>> rvs3 = stats.norm.rvs(loc=8,scale=10,size=500)
>>> stats.ttest_ind(rvs1,rvs3)
(-5.0434013458585092, 5.4302979468623391e-007)
```

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 : sequence of ndarrays

The arrays must have the same shape.

axis : int, optional, (default axis=0)

Axis can equal None (ravel array first), or an integer (the axis over which to operate on a and b).

Returns

t : float or array

t-statistic

prob : 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.

Examples

```
>>> 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)
```

kstest (*rvs, cdf, args=(), N=20, alternative='two_sided', mode='approx', **kwds*)

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 : string or array or callable

string: name of a distribution in scipy.stats

array: 1-D observations of random variables

callable: function to generate random variables, requires keyword argument *size*

cdf : string or callable

string: name of a distribution in scipy.stats, if rvs is a string then cdf can evaluate to *False* or be the same as rvs callable: function to evaluate cdf

args : tuple, sequence

distribution parameters, used if rvs or cdf are strings

N : int

sample size if rvs is string or callable

alternative : 'two_sided' (default), 'less' or 'greater'

defines the alternative hypothesis (see explanation)

mode : 'approx' (default) or 'asymp'

defines the distribution used for calculating p-value

'approx' : use approximation to exact distribution of test statistic

'asymp' : use asymptotic distribution of test statistic

Returns

D : float

KS test statistic, either D, D+ or D-

p-value : 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)<=F(x), resp. G(x)>=F(x).

Examples

```
>>> from scipy import stats
>>> import numpy as np
>>> from scipy.stats import kstest


>>> x = np.linspace(-15,15,9)
>>> kstest(x,'norm')
(0.44435602715924361, 0.038850142705171065)
```

```
>>> np.random.seed(987654321) # set random seed to get the same result
>>> kstest('norm','',N=100)
(0.058352892479417884, 0.88531190944151261)
```

is equivalent to this

```
>>> np.random.seed(987654321)
>>> kstest(stats.norm.rvs(size=100),'norm')
(0.058352892479417884, 0.88531190944151261)
```

Test against one-sided alternative hypothesis:

```
>>> np.random.seed(987654321)
```

Shift distribution to larger values, so that cdf_dgp(x)< norm.cdf(x):

```
>>> x = stats.norm.rvs(loc=0.2, size=100)
>>> kstest(x,'norm', alternative = 'less')
(0.12464329735846891, 0.040989164077641749)
```

Reject equal distribution against alternative hypothesis: less

```
>>> kstest(x,'norm', alternative = 'greater')
(0.0072115233216311081, 0.98531158590396395)
```

Don't reject equal distribution against alternative hypothesis: greater

```
>>> kstest(x,'norm', mode='asymp')
(0.12464329735846891, 0.08944488871182088)
```

Testing t distributed random variables against normal distribution:

With 100 degrees of freedom the t distribution looks close to the normal distribution, and the kstest does not reject the hypothesis that the sample came from the normal distribution

```
>>> np.random.seed(987654321)
>>> stats.kstest(stats.t.rvs(100,size=100),'norm')
(0.072018929165471257, 0.67630062862479168)
```

With 3 degrees of freedom the t distribution looks sufficiently different from the normal distribution, that we can reject the hypothesis that the sample came from the normal distribution at a alpha=10% level

```
>>> np.random.seed(987654321)
>>> stats.kstest(stats.t.rvs(3,size=100),'norm')
(0.131016895759829, 0.058826222555312224)
```

chisquare (*f_obs, f_exp=None, ddof=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

observed frequencies in each category

f_exp : array, optional

expected frequencies in each category. By default the categories are assumed to be equally likely.

ddof : int, optional

adjustment to the degrees of freedom for the p-value

Returns

chisquare statistic : float

The chisquare test statistic

p : float

The p-value of the test.

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 then the dof can be between k-1-p and k-1. However, it is also possible that the asymptotic distributions is not a chisquare, in which case this test is notappropriate.

References

[R16]

ks_2samp(*data1, data2*)

Computes the Kolmogorov-Smirnof 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

a, b : sequence of 1-D ndarrays

two arrays of sample observations assumed to be drawn from a continuous distribution, sample sizes can be different

Returns

D : float

KS statistic

p-value : 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

```
>>> from scipy import stats
>>> import numpy as np
>>> from scipy.stats import ks_2samp

>>> #fix random seed to get the same result
>>> np.random.seed(12345678);

>>> n1 = 200  # size of first sample
>>> n2 = 300  # size of second sample
```

different distribution we can reject the null hypothesis since the pvalue is below 1%

```
>>> rvs1 = stats.norm.rvs(size=n1,loc=0.,scale=1);
>>> rvs2 = stats.norm.rvs(size=n2,loc=0.5,scale=1.5)
>>> ks_2samp(rvs1,rvs2)
(0.20833333333333337, 4.6674975515806989e-005)
```

slightly different distribution we cannot reject the null hypothesis at a 10% or lower alpha since the pvalue at 0.144 is higher than 10%

```
>>> rvs3 = stats.norm.rvs(size=n2,loc=0.01,scale=1.0)
>>> ks_2samp(rvs1,rvs3)
(0.10333333333333333, 0.14498781825751686)
```

identical distribution we cannot reject the null hypothesis since the pvalue is high, 41%

```
>>> rvs4 = stats.norm.rvs(size=n2,loc=0.0,scale=1.0)
>>> ks_2samp(rvs1,rvs4)
(0.07999999999999996, 0.41126949729859719)
```

mannwhitneyu(*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

u : float

The Mann-Whitney statistics.

prob : 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.

tiecorrect (*rankvals*)
Tie-corrector for ties in Mann Whitney U and Kruskal Wallis H tests. See Siegel, S. (1956) Nonparametric Statistics for the Behavioral Sciences. New York: McGraw-Hill. Code adapted from |Stat rankind.c code.

Returns: T correction factor for U or H

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 **'stats.mannwhitneyu'_**

Parameters
x,y : array_like

The data from the two samples

Returns
z-statistic : float

The test statistic under the large-sample approximation that the rank sum statistic is normally distributed

p-value : float

The two-sided p-value of the test

References

[R32]

wilcoxon (*x, y=None*)
Calculate the Wilcoxon signed-rank test

The Wilcoxon signed-rank test tests the null hypothesis that two related samples come from the same distribution. It is a a non-parametric version of the paired T-test.

Parameters
x : array_like

The first set of measurements

y : array_like, optional, default None

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.

Returns
z-statistic : float

The test statistic under the large-sample approximation that the signed-rank statistic is normally distributed.

p-value : 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

[R34]

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

H-statistic : float

The Kruskal-Wallis H statistic, corrected for ties

p-value : 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

[R22]

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

friedman chi-square statistic : float

the test statistic, correcting for ties

p-value : 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-vale is only reliable for n > 10 and more than 6 repeated measurements.

References

[R21]

ansari(x, y)	Perform the Ansari-Bradley test for equal scale parameters
bartlett(*args)	Perform Bartlett's test for equal variances
levene(*args, **kwds)	Perform Levene test for equal variances
shapiro(x[, a, reta])	Perform the Shapiro-Wilk test for normality.
anderson(x[, dist])	Anderson-Darling test for data coming from a particular distribution
binom_test(x[, n, p])	Perform a test that the probability of success is p.
fligner(*args, **kwds)	Perform Fligner's test for equal variances
mood(x, y)	Perform Mood's test for equal scale parameters
oneway(*args, **kwds)	Test for equal means in two or more samples from the normal distribution.

ansari (*x, y*)

Perform the Ansari-Bradley test for equal scale parameters

The Ansari-Bradley test is a non-parametric test for the equality of the scale parameter of the distributions from which two samples were drawn.

Parameters

x, y : array_like

arrays of sample data

Returns

p-value : float

The p-value of the hypothesis test

See Also:

fligner

A non-parametric test for the equality of k variances

mood

A non-parametric test for the equality of two scale parameters

Notes

The p-value given is exact when the sample sizes are both less than 55 and there are no ties, otherwise a normal approximation for the p-value is used.

References

[R12]

bartlett (**args*)

Perform Bartlett's test for equal variances

Bartlett's test tests the null hypothesis that all input samples are from populations with equal variances. For samples from significantly non-normal populations, Levene's test **'levene'_** is more robust.

Parameters

sample1, sample2,... : array_like

arrays of sample data. May be different lengths.

Returns

T : float

the test statistic

p-value : float

the p-value of the test

References

[R13], [R14]

levene (**args, **kwds*)

Perform Levene test for equal variances

The Levene test tests the null hypothesis that all input samples are from populations with equal variances. Levene's test is an alternative to Bartlett's test **'bartlett'_** in the case where there are significant deviations from normality.

Parameters

sample1, sample2, ... : array_like

The sample data, possibly with different lengths

center : {'mean', 'median', 'trimmed'}, optional

Which function of the data to use in the test. The default is 'median'.

Returns

W : float

the test statistic

p-value : 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

[R23], [R24], [R25]

shapiro (*x, a=None, reta=0*)

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 : {True, False}

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

[R33]

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

A2 : float

The Anderson-Darling test statistic

critical : list

The critical values for this distribution

sig : 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/exponenential
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

[R6], [R7], [R8], [R9], [R10], [R11]

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

[R15]

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'.

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

[R19], [R20]

mood(*x, y*)

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

Returns

p-value : float

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.

oneway(**args, **kwds*)

Test for equal means in two or more samples from the normal distribution.

If the keyword parameter <equal_var> is true then the variances are assumed to be equal, otherwise they are not assumed to be equal (default).

Return test statistic and the p-value giving the probability of error if the null hypothesis (equal means) is rejected at this value.

glm(data, para)	Calculates a linear model fit ...
anova	

glm(*data, para*)

Calculates a linear model fit ... anova/ancova/lin-regress/t-test/etc. Taken from:

Peterson et al. Statistical limitations in functional neuroimaging I. Non-inferential methods and statistical models. Phil Trans Royal Soc Lond B 354: 1239-1260.

Returns: statistic, p-value ???

3.18.4 Plot-tests

probplot(x[, sparams, dist, fit, plot])	Return (osm, osr){,(scale,loc,r)} where (osm, osr) are order statistic medians and ordered response data respectively so that plot(osm, osr) is a probability plot.
ppcc_max(x[, brack, dist])	Returns the shape parameter that maximizes the probability plot correlation coefficient for the given data to a one-parameter family of distributions.
ppcc_plot(x, a, b[, dist, plot, N])	Returns (shape, ppcc), and optionally plots shape vs.

probplot (*x, sparams=(), dist='norm', fit=1, plot=None*)

Return (osm, osr){,(scale,loc,r)} where (osm, osr) are order statistic medians and ordered response data respectively so that plot(osm, osr) is a probability plot. If fit==1, then do a regression fit and compute the slope (scale), intercept (loc), and correlation coefficient (r), of the best straight line through the points. If fit==0, only (osm, osr) is returned.

sparams is a tuple of shape parameter arguments for the distribution.

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

ppcc_plot (*x, a, b, dist='tukeylambda', plot=None, N=80*)

Returns (shape, ppcc), and optionally plots shape vs. ppcc (probability plot correlation coefficient) as a function of shape parameter for a one-parameter family of distributions from shape value a to b.

See also ppcc_max

3.18.5 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.

argstoarray(*args)	Constructs a 2D array from
betai(a, b, x)	Returns the incomplete
chisquare(f_obs[, f_exp])	Calculates a one-way
count_tied_groups(x[, use_missing])	Counts the number of tied values in
describe(a[, axis])	Computes several descriptive
f_oneway(*args)	Performs a 1-way ANOVA,
f_value_wilks_lambda(ER, EF, dfnum, dfden, a, b)	Calculation of Wilks lambda
find_repeats(arr)	Find repeats in arr and
friedmanchisquare(*args)	Friedman Chi-Square is a
gmean(a[, axis])	Compute the geometric mean
hmean(a[, axis])	Calculates the harmonic mean
kendalltau(x, y[, use_ties, use_missing])	Computes Kendall's rank correlation
kendalltau_seasonal(x)	Computes a multivariate extensi
kruskalwallis(*args)	Compute the Kruskal-Wallis
kruskalwallis(*args)	Compute the Kruskal-Wallis
ks_twosamp(data1, data2[, alternative])	Computes the Kolmogorov-Smirnov

Table 3.11 – continued from

ks_twosamp(data1, data2[, alternative])	Computes the Kolmogorov-Smirnov
kurtosis(a[, axis, fisher, bias])	Computes the kurtosis (Fisher
kurtosistest(a[, axis])	Tests whether a
linregress(*args)	Calculate a
mannwhitneyu(x, y[, use_continuity])	Computes the Mann-Whitney
plotting_positions(data[, alpha, beta])	Returns the plotting positions (or
mode(a[, axis])	Returns an array of the modal
moment(a[, moment, axis])	Calculates the nth moment
mquantiles(a, 5[, prob, alphap, betap, ...])	Computes empirical quantiles
msign(x)	Returns the sign of x,
normaltest(a[, axis])	Tests whether a sample
obrientransform(*args)	Computes a transform on i
pearsonr(x, y)	Calculates a Pearson correlation
plotting_positions(data[, alpha, beta])	Returns the plotting positions (or
pointbiserialr(x, y)	Calculates a point biserial corre
rankdata(data[, axis, use_missing])	Returns the rank (also known as orc
samplestd(data[, axis])	Returns a biased estimate of the standard deviation
samplevar(data[, axis])	Returns a biased estimate of the variance of
scoreatpercentile(data, per[, limit, ...])	Calculate the score at the
sem(a[, axis])	Calculates the standard error of the mean (
signaltonoise(data[, axis])	Calculates the signal-to-noise ratio, as the
skew(a[, axis, bias])	Computes the skewness
skewtest(a[, axis])	Tests whether the skew is
spearmanr(x, y[, use_ties])	Calculates a Spearman rank-o
std(a[, axis])	Returns the estimated population
stderr(a[, axis])	*stderr* is
theilslopes(y[, x, alpha])	Computes the Theil slope over
threshold(a[, threshmin, threshmax, newval])	Clip array to
tmax(a, upperlimit[, axis, inclusive])	Compute the
tmean(a[, limits, inclusive])	Compute the
tmin(a[, lowerlimit, axis, inclusive])	Compute the
trim(a[, limits, inclusive, relative, axis])	Trims an array by masking
trima(a[, limits, inclusive])	Trims an array by masking
trimboth(data[, proportiontocut, inclusive, ...])	Trims the data by masking the int(proportiontocut*n) smallest and int(
trimmed_stde(a[, limits, inclusive, axis])	Returns the standard error of the
trimr(a[, limits, inclusive, axis])	Trims an array by masking sc
trimtail(data[, proportiontocut, tail, ...])	Trims the data by masking
tsem(a[, limits, inclusive])	Compute the trimmed
ttest_onesamp(a, popmean)	Calculates the T-test for the
ttest_ind(a, b[, axis])	Calculates the T-test for the m
ttest_onesamp(a, popmean)	Calculates the T-test for the
ttest_rel(a, b[, axis])	Calculates the T-test on TWO
tvar(a[, limits, inclusive])	Compute the
var(a[, axis])	Returns the estimated population
variation(a[, axis])	Computes the coefficient of variation, th
winsorize(a[, limits, inclusive, inplace, axis])	Returns a Winsorized versi
z(a, score)	*z* is
zmap(scores, compare[, axis])	Returns an array of z-scores the shape of s
zs(a)	*zs* is

argstoarray(**args*)

Constructs a 2D array from a sequence of sequences. Sequences are filled with missing values to match the

length of the longest sequence.

Returns

output : MaskedArray

a (mxn) masked array, where m is the number of arguments and n the length of the longest argument.

betai (*a, b, x*)

Returns the incomplete beta function.

I_x(a,b) = 1/B(a,b)*(Integral(0,x) of 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 or float > 0

b : array or float > 0

x : array or float

x will be clipped to be no greater than 1.0 .

chisquare (*f_obs, f_exp=None*)

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

observed frequencies in each category

f_exp : array, optional

expected frequencies in each category. By default the categories are assumed to be equally likely.

ddof : int, optional

adjustment to the degrees of freedom for the p-value

Returns

chisquare statistic : float

The chisquare test statistic

p : float

The p-value of the test.

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 then the dof can be between k-1-p and k-1. However, it is also possible that the asymptotic distributions is not a chisquare, in which case this test is notappropriate.

References

[R26]

count_tied_groups(*x, use_missing=False*)

Counts the number of tied values in x, and returns a dictionary
(nb of ties: nb of groups).

Parameters

x : sequence

Sequence of data on which to counts the ties

use_missing : boolean

Whether to consider missing values as tied.

Examples

```
>>> z = [0, 0, 0, 2, 2, 2, 3, 3, 4, 5, 6]
>>> count_tied_groups(z)
>>> {2:1, 3:2}
>>> # The ties were 0 (3x), 2 (3x) and 3 (2x)
>>> z = ma.array([0, 0, 1, 2, 2, 2, 3, 3, 4, 5, 6])
>>> count_tied_groups(z)
>>> {2:2, 3:1}
>>> # The ties were 0 (2x), 2 (3x) and 3 (2x)
>>> z[[1,-1]] = masked
>>> count_tied_groups(z, use_missing=True)
>>> {2:2, 3:1}
>>> # The ties were 2 (3x), 3 (2x) and masked (2x)
```

describe(*a, axis=0*)
Computes several descriptive statistics of the passed array.

Parameters

a : array

axis : int or None

Returns

(size of the data (discarding missing values), :

(min, max), arithmetic mean, unbiased variance, biased skewness, biased kurtosis)

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: f-value, probability

f_value_wilks_lambda(*ER, EF, dfnum, dfden, a, b*)
Calculation of Wilks lambda F-statistic for multivarite data, per Maxwell & Delaney p.657.

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.

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: chi-square statistic, associated p-value

gmean(*a, axis=0*)
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, optional, default axis=0

Axis along which the geometric mean is computed.

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.

hmean (*a, axis=0*)
Calculates the harmonic mean along the specified axis.

That is: n / (1/x1 + 1/x2 + ... + 1/xn)

Parameters
a : array_like

Input array, masked array or object that can be converted to an array.

axis : int, optional, default axis=0

Axis along which the harmonic mean is computed.

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.

kendalltau (*x, y, use_ties=True, use_missing=False*)
Computes Kendall's rank correlation tau on two variables *x* and *y*.

Parameters
xdata: sequence :

First data list (for example, time).

ydata: 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

tau : float

Kendall tau

prob

[float] Approximate 2-side p-value.

kendalltau_seasonal (*x*)

Computes a multivariate extension Kendall's rank correlation tau, designed for seasonal data.

Parameters

x: 2D array :

Array of seasonal data, with seasons in columns.

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

H-statistic : float

The Kruskal-Wallis H statistic, corrected for ties

p-value : 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

[R27]

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
H-statistic : float

The Kruskal-Wallis H statistic, corrected for ties

p-value : 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

[R27]

ks_twosamp(*data1, data2, alternative='two_sided'*)
Computes the Kolmogorov-Smirnov test on two samples. Missing values are discarded.

Parameters
data1 : sequence

First data set

data2
[sequence] Second data set

alternative
[{'two_sided', 'less', 'greater'} optional] Indicates the alternative hypothesis.

Returns
d : float

Value of the Kolmogorov Smirnov test

p
[float] Corresponding p-value.

ks_twosamp(*data1, data2, alternative='two_sided'*)
Computes the Kolmogorov-Smirnov test on two samples. Missing values are discarded.

Parameters
data1 : sequence

First data set

data2
[sequence] Second data set

alternative
[{'two_sided', 'less', 'greater'} optional] Indicates the alternative hypothesis.

Returns
d : float

Value of the Kolmogorov Smirnov test

p
[float] Corresponding p-value.

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 comming from biased moment estimators

Use kurtosistest() to see if result is close enough to normal.

Parameters
a : array

axis : int or None

fisher : bool

If True, Fisher's definition is used (normal ==> 0.0). If False, Pearson's definition is used (normal ==> 3.0).

bias : bool

If False, then the calculations are corrected for statistical bias.

Returns
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

[CRCProbStat2000] Section 2.2.25

[CRCProbStat2000]

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

the axis to operate along, or None to work on the whole array. The default is the first axis.

Returns

p-value : 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.

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, 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

p-value

[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.

mannwhitneyu(*x, y, use_continuity=True*)

Computes the Mann-Whitney on samples x and y. Missing values in x and/or y are discarded.

Parameters

x : sequence

y : sequence use_continuity : {True, False} optional

Whether a continuity correction (1/2.) should be taken into account.

Returns

u : float

The Mann-Whitney statistics

prob

[float] Approximate p-value assuming a normal distribution.

plotting_positions(*data, alpha=0.40000000000000002, beta=0.40000000000000002*)

Returns the plotting positions (or empirical percentile points) for the
data. Plotting positions are defined as (i-alpha)/(n-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

Parameters
x : sequence

Input data, as a sequence or array of dimension at most 2.

prob
[sequence] List of quantiles to compute.

alpha
[{0.4, float} optional] Plotting positions parameter.

beta
[{0.4, float} optional] Plotting positions parameter.

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

axis=0 : int

Returns
(array of modal values, array of counts for each mode) :

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

moment : int

axis : int or None

Returns

The appropriate moment along the given axis or over all values if axis is :

None. :

mquantiles(*a, prob=, [0.25, 0.5, 0.75], alphap=0.40000000000000002, betap=0.40000000000000002, axis=None, limit=()*)

Computes empirical quantiles for a data array.

Samples quantile are defined by $Q(p) = (1-g).x[i] + g.x[i+1]$, where $x[j]$ is the *j*th order statistic, and *i = (floor(n*p+m))*, *m=alpha+p*(1-alpha-beta)* and *g = n*p + m - i*.

Typical values of (alpha,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)* : (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

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.

alpha : float, optional

Plotting positions parameter, default is 0.4.

beta : 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

Tuple of (lower, upper) values. Values of *a* outside this closed interval are ignored.

Returns

quants : MaskedArray

An array containing the calculated quantiles.

Examples

```
>>> 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.

```
>>> 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.  ,  37.5 ,   2.5 ],
       [ 42.8 ,  40.05,   3.55]])


>>> 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)
```

msign(*x*)

Returns the sign of x, or 0 if x is masked.

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 [R28], [R29] test that combines skew and kurtosis to produce an omnibus test of normality.

Parameters

a : array

axis : int or None

Returns

p-value : float

A 2-sided chi squared probability for the hypothesis test

References

[R28], [R29]

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

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 : 1D array

y : 1D array the same length as x

Returns

(Pearson's correlation coefficient, :

2-tailed p-value)

References

http://www.statsoft.com/textbook/glosp.html#Pearson%20Correlation

plotting_positions(*data, alpha=0.40000000000000002, beta=0.40000000000000002*)

Returns the plotting positions (or empirical percentile points) for the

data. Plotting positions are defined as (i-alpha)/(n-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

Parameters

x : sequence

Input data, as a sequence or array of dimension at most 2.

prob

[sequence] List of quantiles to compute.

alpha

[{0.4, float} optional] Plotting positions parameter.

beta

[{0.4, float} optional] Plotting positions parameter.

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.

Parameters

x : array of bools

y : array of floats

Returns

(point-biserial r, :

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.

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
[{boolean} optional] Whether the masked values have a rank of 0 (False) or equal to the average rank of the unmasked values (True).

samplestd(*data, axis=0*)
Returns a biased estimate of the standard deviation of the data, as the square root of the average squared deviations from the mean.

Parameters
data : sequence

Input data

axis
[{0,int} optional] Axis along which to compute. If None, the computation is performed on a flat version of the array.

Notes

samplestd(a) is equivalent to a.std(ddof=0)

samplevar(*data, axis=0*)
Returns a biased estimate of the variance of the data, as the average of the squared deviations from the mean.

Parameters
data : sequence

Input data

axis
[{0, int} optional] Axis along which to compute. If None, the computation is performed on a flat version of the array.

scoreatpercentile(*data, per, limit=(), alphap=0.40000000000000002, betap=0.40000000000000002*)
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

sem(*a, axis=0*)
Calculates the standard error of the mean (or standard error of measurement) of the values in the passed array.

Parameters
a: array like :

An array containing the values for which

axis: int or None, optional. :

if equal None, ravel array first. If equal to an integer, this will be the axis over which to operate. Defaults to 0.

ddof: int :

Delta degrees-of-freedom. How many degrees of freedom to adjust for bias in limited samples relative to the population estimate of variance

Returns
The standard error of the mean in the sample(s), along the input axis :

signaltonoise(*data, axis=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

[{0, int} optional] Axis along which to compute. If None, the computation is performed on a flat version of the array.

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 : array

axis : int or None

bias : bool

If False, then the calculations are corrected for statistical bias.

Returns

The skewness of values along an axis, returning 0 where all values are :

equal. :

References

[CRCProbStat2000] Section 2.2.24.1

[CRCProbStat2000]

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

axis : int or None

Returns

p-value : float

a 2-sided p-value for the hypothesis test

Notes

The sample size should be at least 8.

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 : 1D array

y
[1D array the same length as x] The lengths of both arrays must be > 2.

use_ties
[{True, False} optional] Whether the correction for ties should be computed.

Returns

(Spearman correlation coefficient, :

2-tailed p-value)

std(*a, axis=None*)

Returns the estimated population standard deviation of the values in the passed array (i.e., N-1). Axis can equal None (ravel array first), or an integer (the axis over which to operate).

stderr(*a, axis=0*)

stderr is deprecated!

scipy.stats.stderr is deprecated; please update your code to use scipy.stats.sem.

Returns the estimated population standard error of the values in the passed array (i.e., N-1). Axis can equal None (ravel array first), or an integer (the axis over which to operate).

theilslopes(*y, x=None, alpha=0.050000000000000003*)

Computes the Theil slope over the dataset (x,y), as the median of all slopes between paired values.

Parameters

y : sequence

Dependent variable.

x
[{None, sequence} optional] Independent variable. If None, use arange(len(y)) instead.

alpha
[float] Confidence degree.

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

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
a, with values less (greater) than threshmin (threshmax) replaced with newval. :

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 : None or int, optional

Operate along this axis. None means to use the flattened array and the default is zero.

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

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, 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

tmean : float

tmin(*a, lowerlimit=None, axis=0, inclusive=True*)

Compute the trimmed minimum

This function finds the miminum 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 : None or int, optional

Operate along this axis. None means to use the flattened array and the default is zero

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 :

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 == 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 == True, tuple (lower percentage, upper percentage) to cut on each side of the array, with respect to the number of unmasked data. Noting n the number of unmasked data before trimming, the (n*limits[0])th smallest data and the (n*limits[1])th largest data are masked, and the total number of unmasked data after trimming is n*(1.-sum(limits)) In each case, the value of one limit can be set to None to indicate an open interval. If limits is None, no trimming is performed

inclusive : {(True, True) tuple} optional

If relative==False, tuple indicating whether values exactly equal to the absolute limits are allowed. If relative==True, tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

relative : {False, True} optional

Whether to consider the limits as absolute values (False) or proportions to cut (True).

axis : {None, integer}, 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,–,–]

trima (*a, limits=None, inclusive=(True, True)*)

Trims an array by masking the data outside some given limits. Returns a masked version of the input array.

Parameters

a : sequence

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 : {(True,True) tuple} optional

Tuple of (lower flag, upper flag), indicating whether values exactly equal to the lower (upper) limit are allowed.

trimboth (*data, proportiontocut=0.20000000000000001, inclusive=(True, True), axis=None*)

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
[{0.2, 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.

inclusive
[{(True, True) tuple} optional] Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

axis
[{None, integer}, optional] Axis along which to perform the trimming. If None, the input array is first flattened.

trimmed_stde(*a, limits=(0.10000000000000001, 0.10000000000000001), inclusive=(1, 1), axis=None*)

Returns the standard error of the trimmed mean of the data 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. 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

[{(True, True) tuple} optional] Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

axis

[{None, integer}, optional] Axis along which to trim.

trimr(*a, limits=None, inclusive=(True, True), axis=None*)

Trims an array by masking some proportion of the data on each end. Returns a masked version of the input array.

Parameters

a : sequence

Input array.

limits : {None, tuple} optional

Tuple of the percentages to cut on each side of the array, with respect to the number of unmasked data, as floats between 0. and 1. Noting n the number of unmasked data before trimming, the (n*limits[0])th smallest data and the (n*limits[1])th largest data are masked, and the total number of unmasked data after trimming is n*(1.-sum(limits)) The value of one limit can be set to None to indicate an open interval.

inclusive : {(True,True) tuple} optional

Tuple of flags indicating whether the number of data being masked on the left (right) end should be truncated (True) or rounded (False) to integers.

axis : {None,int} optional

Axis along which to trim. If None, the whole array is trimmed, but its shape is maintained.

trimtail(*data, proportiontocut=0.20000000000000001, tail='left', inclusive=(True, True), axis=None*)

Trims the data by masking int(trim*n) values from ONE tail of the

data along the given axis, where n is the number of unmasked values.

Parameters

data : {ndarray}

Data to trim.

proportiontocut

[{0.2, float} optional] Percentage of trimming. If n is the number of un-

masked values before trimming, the number of values after trimming is (1-proportiontocut)*n.

tail
[{'left','right'} optional] If left (right), the `proportiontocut` lowest (greatest) values will be masked.

inclusive
[{(True, True) tuple} optional] Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

axis
[{None, integer}, optional] Axis along which to perform the trimming. If None, the input array is first flattened.

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

ttest_onesamp(*a, popmean*)
Calculates the T-test for the mean of ONE group of scores *a*.

This is a two-sided test for the null hypothesis that the expected value (mean) of a sample of independent observations 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, optional, (default axis=0)

Axis can equal None (ravel array first), or an integer (the axis over which to operate on a).

Returns
t : float or array

t-statistic

prob : float or array

two-tailed p-value

Examples

```
>>> from scipy import stats
>>> import numpy as np


>>> #fix seed to get the same result
>>> np.random.seed(7654567)
>>> 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]])
(array([[-0.68014479, -0.04323899],
       [ 2.77025808,  4.11038784]]), array([[  4.99613833e-01,   9.65686743e-01],
       [  7.89094663e-03,   1.49986458e-04]]))
```

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.

Parameters

a, b : sequence of ndarrays

The arrays must have the same shape, except in the dimension corresponding to *axis* (the first, by default).

axis : int, optional

Axis can equal None (ravel array first), or an integer (the axis over which to operate on a and b).

Returns

t : float or array

t-statistic

prob : float or array

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.

Examples

```
>>> from scipy import stats
>>> import numpy as np


>>> #fix seed to get the same result
>>> np.random.seed(12345678)
```

test with sample with identical means

```
>>> rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> rvs2 = stats.norm.rvs(loc=5,scale=10,size=500)
>>> stats.ttest_ind(rvs1,rvs2)
(0.26833823296239279, 0.78849443369564765)
```

test with sample with different means

```
>>> rvs3 = stats.norm.rvs(loc=8,scale=10,size=500)
>>> stats.ttest_ind(rvs1,rvs3)
(-5.0434013458585092, 5.4302979468623391e-007)
```

ttest_onesamp(*a, popmean*)

Calculates the T-test for the mean of ONE group of scores *a*.

This is a two-sided test for the null hypothesis that the expected value (mean) of a sample of independent observations 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, optional, (default axis=0)

Axis can equal None (ravel array first), or an integer (the axis over which to operate on a).

Returns

t : float or array

t-statistic

prob : float or array

two-tailed p-value

Examples

```
>>> from scipy import stats
>>> import numpy as np


>>> #fix seed to get the same result
>>> np.random.seed(7654567)
>>> 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]])
(array([[-0.68014479, -0.04323899],
       [ 2.77025808,  4.11038784]]), array([[  4.99613833e-01,   9.65686743e-01],
       [  7.89094663e-03,   1.49986458e-04]]))
```

ttest_rel(*a, b, axis=None*)

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 : sequence of ndarrays

The arrays must have the same shape.

axis : int, optional, (default axis=0)

Axis can equal None (ravel array first), or an integer (the axis over which to operate on a and b).

Returns

t : float or array

t-statistic

prob : 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.

Examples

```
>>> 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)
```

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

var (*a, axis=None*)

Returns the estimated population variance of the values in the passed array (i.e., N-1). Axis can equal None (ravel array first), or an integer (the axis over which to operate).

variation (*a, axis=0*)

Computes the coefficient of variation, the ratio of the biased standard deviation to the mean.

Parameters

a : array

axis : int or None

References

[CRCProbStat2000] Section 2.2.20

[CRCProbStat2000]

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 (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.

z (*a, score*)

z is deprecated!

scipy.stats.z is deprecated; please update your code to use scipy.stats.zscore_compare.

Returns the z-score of a given input score, given thearray from which that score came. Not appropriate for population calculations, nor for arrays > 1D.

zmap (*scores, compare, axis=0*)

Returns an array of z-scores the shape of scores (e.g., [x,y]), compared to array passed to compare (e.g., [time,x,y]). Assumes collapsing over dim 0 of the compare array.

zs (*a*)

zs is deprecated!

scipy.stats.zs is deprecated; please update your code to use scipy.stats.zscore.

Returns a 1D array of z-scores, one for each score in the passed array, computed relative to the passed array.

3.18.6 Univariate and multivariate kernel density estimation (`scipy.stats.kde`)

gaussian_kde(dataset)	Representation of a kernel-density estimate using Gaussian kernels.

class gaussian_kde (*dataset*)

Representation of a kernel-density estimate using Gaussian kernels.

Parameters

dataset : (# of dims, # of data)-array

datapoints to estimate from

Attributes

d	int	number of dimensions
n	int	number of datapoints

Methods

kde.evaluate(points)	array	evaluate the estimated pdf on a provided set of points
kde(points)	array	same as kde.evaluate(points)
kde.integrate_gaussian(mean, cov)	float	multiply pdf with a specified Gaussian and integrate over the whole domain
kde.integrate_box_1d(low, high)	float	integrate pdf (1D only) between two bounds
kde.integrate_box(low_bounds, high_bounds)	float	integrate pdf over a rectangular space between low_bounds and high_bounds
kde.integrate_kde(other_kde)	float	integrate two kernel density estimates multiplied together

For many more stat related functions install the software R and the interface package rpy.

3.19 Image Array Manipulation and Convolution (`scipy.stsci`)

3.19.1 Image Array manipulation Functions (`scipy.stsci.image`)

```
average
combine
median
minimum
threshhold
translate
```

3.19.2 Image Array Convolution Functions (`scipy.stsci.convolve`)

```
boxcar
convolution_modes
convolve
convolve2d
correlate
correlate2d
cross_correlate
dft
iraf_frame
pix_modes
```

3.20 C/C++ integration (`scipy.weave`)

Warning: This documentation is work-in-progress and unorganized.

3.20.1 C/C++ integration

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

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