HAllA: Hierarchical All-against All Documentation

Release 0.0.1

Yo Sup Moon, Curtis Huttenhower

November 27, 2013

CONTENTS

1 Version 0.0.1 **1**

1.1 Chapter 0 Getting Started . . . 1
1.2 Chapter 1 Basics . . . 2
1.3 Frequently Asked Questions . . . 3
1.4 Functions . . . 3
1.5 Indices and tables . . . 29
1.6 License . . . 29

Bibliography **31**

Python Module Index **33**

Python Module Index **35**

Index **37**

CHAPTER

ONE

VERSION 0.0.1

Authors Yo Sup Moon, Curtis Huttenhower

Google Group halla-users: https://groups.google.com/forum/#!forum/halla-users

URL http://huttenhower.sph.harvard.edu/halla

Citation Yo Sup Moon, Curtis Huttenhower, "Retrieving Signal from Noise in Big Data: An Information-Theoretic Approach to Hierarchical Exploratory Data Analysis" (In Preparation)

1.1 Chapter 0 Getting Started

1.1.1 Operating System

- **Supported**
  - Ubuntu Linux (>= 12.04)
  - Mac OS X (>= 10.7)
- **Unsupported**
  - Windows (>= XP)

1.1.2 Dependencies

- **Required**
  - Python (>= 2.7)
  - Numpy (>= 1.7.1)
  - Scipy (>= 0.12)
  - Scikit-learn (>=0.13)
  - rpy (>=2.0)
  - sampledoc-master
- **Recommended Tools for documentation**
  - Docutils
  - itex2MML

1.1.3 Getting HAllA

HAllA can be downloaded from its bitbucket repository: http://bitbucket.org/chuttenh/halla.

1.2 Chapter 1 Basics

1.2.1 Introduction

HAllA: is a programmatic tool for performing multiple association testing between two or more heterogeneous datasets, each containing a mixture of discrete, binary, or continuous data. HAllA is a robust and efficient alternative to traditional all-against-all association testing of variables. Its robustness relies on the usage of mutual information-based measures to calculate the degree to which two variables are related. Mutual-information is well-suited to serve as an all-purpose measure since it is well-behaved even when comparing two variables of different data types. Its efficiency relies on a hierarchical clustering scheme to reduce the number of tests necessary to discover interesting associations in datasets that contain potentially millions of genotypic and phenotypic data. In a traditional all-against-all association-testing scheme, the number of pairwise tests scale quadratically with the number of features in the data (O(N^2)). The sheer number of association tests dramatically reduces the power of standard hypothesis tests to discover relationships among variables. We introduce a hierarchical hypothesis-testing scheme to perform tiered testing on clusters of data to reduce computational time for comparisons. Hierarchical false discovery rate correction is implemented to curb discoveries of associations due to noise in the data.

1.2.2 Input

HAlLA by default takes a tab-delimited text file as an input, where each row describes feature (data/metadata) and each column represents an instance. In other words, input *X* is a *D x N* matrix where *D* is the number of dimensions in each instance of the data and *N* is the number of instances (samples). The "edges" of the matrix should contain labels of the data, if desired. The following is an example input

```
+-------+---------+---------+--------+
|       | Sample1 | Sample2 | Sample3|
+-------+---------+---------+--------+
| Data1 | 0       | 1       | 2      |
+-------+---------+---------+--------+
| Data2 | 1.5     | 100.2   | -30.7  |
+-------+---------+---------+--------+
```

1.2.3 Output

HAllA by default prints a tab-delimited text file as output

```
+------+------+-------+------+------+
| One  | Two  | MID   | Pperm| Pboot|
+------+------+-------+------+------+
| Data1| Data2| 0.64  | 0.02 | 0.008|
+------+------+-------+------+------+
```

MID stands for "mutual information distance", which is an information-theoretic measure of association between two random variables. *Pperm* and *Pboot* corresponds to the p-values of the permutation and bootstrap tests used to assess the statistical significance of the mutual information distance (i.e. lower p-values signify that the association between two variables is not likely to be caused by the noise in the data).

1.2.4 Advanced

The following is a list of all available arguments that can be passed into halla:

```
usage: halla.py [-h] [-o output.txt] [-p p_value] [-P p_mi] [-b bootstraps] [-v verbosity] [input.txt

Hierarchical All-against-All significance association testing.

positional arguments:
  input.txt      Tab-delimited text input file, one row per feature, one
                 column per measurement

optional arguments:
  -h, --help     show this help message and exit
  -o output.txt  Optional output file for association significance tests
  -p p_value     P-value for overall significance tests
  -P p_mi        P-value for permutation equivalence of MI clusters
  -b bootstraps  Number of bootstraps for significance testing
  -v verbosity   Debug logging level; increase for greater verbosity
```

1.2.5 Mini-tutorial

Suppose you have a tab-delimited file containing the dataset you wish to run halla on. We will call this file *in.txt*. We will call the output file *out.txt*. In the root directory of halla, one can type:

```
$ python halla.py in.txt > out.txt
```

To obtain the output in *out.txt*.

1.3 Frequently Asked Questions

NB: Direct all questions to the halla-users google group.

1.4 Functions

1.4.1 HAllA: Hiearchical All-against All

Description An object-oriented halla implementation Aim to be as self-contained as possible

Global namespace conventions:

- *m()* <- map for arrays
- *r()* <- reduce for arrays
- *rd()* <- generic reduce-dimension method

halla.**multinomial**(*n*, *pvals*, *size=None*)

Draw samples from a multinomial distribution.

The multinomial distribution is a multivariate generalisation of the binomial distribution. Take an experiment with one of `p` possible outcomes. An example of such an experiment is throwing a dice, where the outcome can be 1 through 6. Each sample drawn from the distribution represents *n* such experiments. Its values, `X_i = [X_0, X_1, ..., X_p]`, represent the number of times the outcome was `i`.

Parameters **n** : int

Number of experiments.

pvals : sequence of floats, length p

Probabilities of each of the `p` different outcomes. These should sum to 1 (however, the last element is always assumed to account for the remaining probability, as long as `sum(pvals[:-1]) <= 1)`.

size : tuple of ints

Given a *size* of `(M, N, K)`, then `M*N*K` samples are drawn, and the output shape becomes `(M, N, K, p)`, since each sample has shape `(p,)`.

Examples

Throw a dice 20 times:

```
>>> np.random.multinomial(20, [1/6.]*6, size=1)
array([[4, 1, 7, 5, 2, 1]])
```

It landed 4 times on 1, once on 2, etc.

Now, throw the dice 20 times, and 20 times again:

```
>>> np.random.multinomial(20, [1/6.]*6, size=2)
array([[3, 4, 3, 3, 4, 3],
       [2, 4, 3, 4, 0, 7]])
```

For the first run, we threw 3 times 1, 4 times 2, etc. For the second, we threw 2 times 1, 4 times 2, etc.

A loaded dice is more likely to land on number 6:

```
>>> np.random.multinomial(100, [1/7.]*5)
array([13, 16, 13, 16, 42])
```

halla.**normal**(*loc=0.0*, *scale=1.0*, *size=None*)

Draw random samples from a normal (Gaussian) distribution.

The probability density function of the normal distribution, first derived by De Moivre and 200 years later by both Gauss and Laplace independently [R2], is often called the bell curve because of its characteristic shape (see the example below).

The normal distributions occurs often in nature. For example, it describes the commonly occurring distribution of samples influenced by a large number of tiny, random disturbances, each with its own unique distribution [R2].

Parameters **loc** : float

Mean ("centre") of the distribution.

scale : float

Standard deviation (spread or "width") of the distribution.

size : tuple of ints

Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn.

See also:

scipy.stats.distributions.norm probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Gaussian distribution is

$$p(x) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x-\mu)^2}{2\sigma^2}}, \tag{1.1}$$

where μ is the mean and σ the standard deviation. The square of the standard deviation, σ^2, is called the variance.

The function has its peak at the mean, and its "spread" increases with the standard deviation (the function reaches 0.607 times its maximum at $x + \sigma$ and $x - \sigma$ [R2]). This implies that *numpy.random.normal* is more likely to return samples lying close to the mean, rather than those far away.

References

[R1], [R2]

Examples

Draw samples from the distribution:

```
>>> mu, sigma = 0, 0.1 # mean and standard deviation
>>> s = np.random.normal(mu, sigma, 1000)
```

Verify the mean and the variance:

```
>>> abs(mu - np.mean(s)) < 0.01
True

>>> abs(sigma - np.std(s, ddof=1)) < 0.01
True
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt
>>> count, bins, ignored = plt.hist(s, 30, normed=True)
>>> plt.plot(bins, 1/(sigma * np.sqrt(2 * np.pi)) *
...                np.exp( - (bins - mu)**2 / (2 * sigma**2) ),
...          linewidth=2, color='r')
>>> plt.show()
```

unified statistics module

halla.stats.**IBP_cut**(*cake_length*)
random cut generated by Indian Buffet Process prior

halla.stats.**PY_cut**(*cake_length*)
random cut generated by pitman-yor process prior

halla.stats.**bh**(*afPVAL*, *fQ=1.0*)
Implement the benjamini-hochberg hierarchical hypothesis testing criterion In practice, used for implementing Yekutieli criterion *per layer*.

When BH is performed per layer, FDR is approximately

$$FDR = q \cdot \delta^* \cdot (m_0 + m_1)/(m_0 + 1) \tag{1.2}$$

where m_0 is the observed number of discoveries and m_1 is the observed number of families tested.

Universal bound: the full tree FDR is $< q \cdot \delta^* \cdot 2$

afPVAL list of p-values

abOUT boolean vector corresponding to which hypothesis test rejected, corresponding to p-value

halla.stats.**binomial**(*n*, *p*, *size=None*)

Draw samples from a binomial distribution.

Samples are drawn from a Binomial distribution with specified parameters, n trials and p probability of success where n an integer > 0 and p is in the interval [0,1]. (n may be input as a float, but it is truncated to an integer in use)

Parameters **n** : float (but truncated to an integer)

parameter, > 0.

p : float

parameter, >= 0 and <=1.

size : {tuple, int}

Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn.

Returns **samples** : {ndarray, scalar}

where the values are all integers in [0, n].

See also:

scipy.stats.distributions.binom probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Binomial distribution is

$$P(N) = \binom{n}{N} p^N (1-p)^{n-N}, \tag{1.3}$$

where n is the number of trials, p is the probability of success, and N is the number of successes.

When estimating the standard error of a proportion in a population by using a random sample, the normal distribution works well unless the product p*n <=5, where p = population proportion estimate, and n = number of samples, in which case the binomial distribution is used instead. For example, a sample of 15 people shows 4 who are left handed, and 11 who are right handed. Then p = 4/15 = 27%. 0.27*15 = 4, so the binomial distribution should be used in this case.

References

[R3], [R4], [R5], [R6], [R7]

Examples

Draw samples from the distribution:

```
>>> n, p = 10, .5 # number of trials, probability of each trial
>>> s = np.random.binomial(n, p, 1000)
# result of flipping a coin 10 times, tested 1000 times.
```

A real world example. A company drills 9 wild-cat oil exploration wells, each with an estimated probability of success of 0.1. All nine wells fail. What is the probability of that happening?

Let's do 20,000 trials of the model, and count the number that generate zero positive results.

```
>>> sum(np.random.binomial(9,0.1,20000)==0)/20000.
answer = 0.38885, or 38%.
```

halla.stats.**cumulative_log_cut**(*cake_length*, *iBase=2*)

Input: cake_length <- length of array, iBase <- base of logarithm

Output: array of indices corresponding to the slice

Note: Probably don't want size-1 cake slices, but for proof-of-concept, this should be okay. Avoid the "all" case

halla.stats.**discretize**(*pArray*, *iN=None*, *method=None*, *aiSkip=[]*)

```
>>> discretize( [0.1, 0.2, 0.3, 0.4] )
[0, 0, 1, 1]

>>> discretize( [0.01, 0.04, 0.09, 0.16] )
[0, 0, 1, 1]

>>> discretize( [-0.1, -0.2, -0.3, -0.4] )
[1, 1, 0, 0]

>>> discretize( [0.25, 0.5, 0.75, 1.00] )
[0, 0, 1, 1]

>>> discretize( [0.015625, 0.125, 0.421875, 1] )
[0, 0, 1, 1]

>>> discretize( [0] )
[0]

>>> discretize( [0, 1] )
[0, 0]

>>> discretize( [0, 1], 2 )
[0, 1]

>>> discretize( [1, 0], 2 )
[1, 0]

>>> discretize( [0.2, 0.1, 0.3], 3 )
[1, 0, 2]

>>> discretize( [0.2, 0.1, 0.3], 1 )
[0, 0, 0]
```

```
>>> discretize( [0.2, 0.1, 0.3], 2 )
[0, 0, 1]

>>> discretize( [0.4, 0.2, 0.1, 0.3], 2 )
[1, 0, 0, 1]

>>> discretize( [4, 0.2, 0.1, 0.3], 2 )
[1, 0, 0, 1]

>>> discretize( [0.4, 0.2, 0.1, 0.3, 0.5] )
[1, 0, 0, 0, 1]

>>> discretize( [0.4, 0.2, 0.1, 0.3, 0.5], 3 )
[1, 0, 0, 1, 2]

>>> discretize( [0.4, 0.2, 0.6, 0.1, 0.3, 0.5] )
[1, 0, 1, 0, 0, 1]

>>> discretize( [0.4, 0.2, 0.6, 0.1, 0.3, 0.5], 3 )
[1, 0, 2, 0, 1, 2]

>>> discretize( [0.4, 0.2, 0.6, 0.1, 0.3, 0.5], 0 )
[3, 1, 5, 0, 2, 4]

>>> discretize( [0.4, 0.2, 0.6, 0.1, 0.3, 0.5], 6 )
[3, 1, 5, 0, 2, 4]

>>> discretize( [0.4, 0.2, 0.6, 0.1, 0.3, 0.5], 60 )
[3, 1, 5, 0, 2, 4]

>>> discretize( [0, 0, 0, 0, 0, 0, 1, 2], 2 )
[0, 0, 0, 0, 0, 0, 1, 1]

>>> discretize( [0, 0, 0, 0, 1, 2, 2, 2, 2, 3], 3 )
[0, 0, 0, 0, 1, 1, 1, 1, 1, 2]

>>> discretize( [0.1, 0, 0, 0, 0, 0, 0, 0, 0] )
[1, 0, 0, 0, 0, 0, 0, 0, 0]

>>> discretize( [0.992299, 1, 1, 0.999696, 0.999605, 0.663081, 0.978293, 0.987621, 0.997237, 0.9
[3, 6, 6, 5, 5, 0, 2, 2, 3, 5, 2, 4, 4, 2, 3, 5, 0, 4, 0, 6, 0, 1, 6, 1, 5, 3, 0, 3, 2, 1, 3, 0,

>>> x = array([[0.1,0.2,0.3,0.4],[1,1,1,0],[0.01,0.04,0.09,0.16],[0,0,0,1]])
>>> y = array([[-0.1,-0.2,-0.3,-0.4],[1,1,0,0],[0.25,0.5,0.75,1.0],[0.015625,0.125,0.421875,1.0]
>>> dx = discretize( x, iN = None, method = None, aiSkip = [1,3] )
>>> dx
array([[ 0.,  0.,  1.,  1.],
       [ 1.,  1.,  1.,  0.],
       [ 0.,  0.,  1.,  1.],
       [ 0.,  0.,  0.,  1.]])
>>> dy = discretize( y, iN = None, method = None, aiSkip = [1] )
>>> dy
array([[ 1.,  1.,  0.,  0.],
       [ 1.,  1.,  0.,  0.],
       [ 0.,  0.,  1.,  1.],
       [ 0.,  0.,  1.,  1.]])
```

halla.stats.**get_medoid**(*pArray*, *iAxis=0*, *pMetric=<function l2 at 0x7313f50>*)

Input: numpy array Output: float

For lack of better way, compute centroid, then compute medoid by looking at an element that is closest to the centroid.

Can define arbitrary metric passed in as a function to pMetric

halla.stats.**log_cut**(*cake_length*, *iBase=2*)
Input: cake_length <- length of array, iBase <- base of logarithm

Output: array of indices corresponding to the slice

Note: Probably don't want size-1 cake slices, but for proof-of-concept, this should be okay. Avoid the "all" case

halla.stats.**mca**(*pArray*, *iComponents=1*)
Input: D x N STRING DISCRETIZED matrix #Caution! must pass in strings Output: D x N FLOAT matrix

halla.stats.**multinomial**(*n*, *pvals*, *size=None*)
Draw samples from a multinomial distribution.

The multinomial distribution is a multivariate generalisation of the binomial distribution. Take an experiment with one of `p` possible outcomes. An example of such an experiment is throwing a dice, where the outcome can be 1 through 6. Each sample drawn from the distribution represents *n* such experiments. Its values, `X_i = [X_0, X_1, ..., X_p]`, represent the number of times the outcome was `i`.

Parameters **n** : int

Number of experiments.

pvals : sequence of floats, length p

Probabilities of each of the `p` different outcomes. These should sum to 1 (however, the last element is always assumed to account for the remaining probability, as long as `sum(pvals[:-1]) <= 1)`.

size : tuple of ints

Given a *size* of `(M, N, K)`, then `M*N*K` samples are drawn, and the output shape becomes `(M, N, K, p)`, since each sample has shape `(p,)`.

Examples

Throw a dice 20 times:

```
>>> np.random.multinomial(20, [1/6.]*6, size=1)
array([[4, 1, 7, 5, 2, 1]])
```

It landed 4 times on 1, once on 2, etc.

Now, throw the dice 20 times, and 20 times again:

```
>>> np.random.multinomial(20, [1/6.]*6, size=2)
array([[3, 4, 3, 3, 4, 3],
       [2, 4, 3, 4, 0, 7]])
```

For the first run, we threw 3 times 1, 4 times 2, etc. For the second, we threw 2 times 1, 4 times 2, etc.

A loaded dice is more likely to land on number 6:

```
>>> np.random.multinomial(100, [1/7.]*5)
array([13, 16, 13, 16, 42])
```

halla.stats.**normal**(*loc=0.0*, *scale=1.0*, *size=None*)
Draw random samples from a normal (Gaussian) distribution.

The probability density function of the normal distribution, first derived by De Moivre and 200 years later by both Gauss and Laplace independently [R9], is often called the bell curve because of its characteristic shape (see the example below).

The normal distributions occurs often in nature. For example, it describes the commonly occurring distribution of samples influenced by a large number of tiny, random disturbances, each with its own unique distribution [R9].

Parameters **loc** : float

Mean ("centre") of the distribution.

scale : float

Standard deviation (spread or "width") of the distribution.

size : tuple of ints

Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn.

See also:

`scipy.stats.distributions.norm` probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Gaussian distribution is

$$p(x) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x-\mu)^2}{2\sigma^2}}, \tag{1.4}$$

where μ is the mean and σ the standard deviation. The square of the standard deviation, σ^2, is called the variance.

The function has its peak at the mean, and its "spread" increases with the standard deviation (the function reaches 0.607 times its maximum at $x + \sigma$ and $x - \sigma$ [R9]). This implies that *numpy.random.normal* is more likely to return samples lying close to the mean, rather than those far away.

References

[R8], [R9]

Examples

Draw samples from the distribution:

```
>>> mu, sigma = 0, 0.1 # mean and standard deviation
>>> s = np.random.normal(mu, sigma, 1000)
```

Verify the mean and the variance:

```
>>> abs(mu - np.mean(s)) < 0.01
True
```

```
>>> abs(sigma - np.std(s, ddof=1)) < 0.01
True
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt
>>> count, bins, ignored = plt.hist(s, 30, normed=True)
>>> plt.plot(bins, 1/(sigma * np.sqrt(2 * np.pi)) *
...                np.exp( - (bins - mu)**2 / (2 * sigma**2) ),
...          linewidth=2, color='r')
>>> plt.show()
```

halla.stats.**p_val_plot**(*pArray1*, *pArray2*, *pCut=<function log_cut at 0x7316848>*, *iIter=100*)
Returns p value plot of combinatorial cuts

In practice, works best when arrays are of similar size, since I implement the minimum ... For future think about implementing the correct step function

halla.stats.**pca**(*pArray*, *iComponents=1*)
Input: N x D matrix Output: D x N matrix

halla.stats.**permutation_test_by_representative**(*pArray1*, *pArray2*, *metric='mi'*, *decomposition='pca'*, *iIter=100*)
Input: pArray1, pArray2, metric = "mi", decomposition = "pca", iIter = 100

metric = {"mca": mca, "pca": pca}

halla.stats.**shuffle**(*x*)
Modify a sequence in-place by shuffling its contents.

Parameters **x** : array_like

The array or list to be shuffled.

Returns **None** :

Examples

```
>>> arr = np.arange(10)
>>> np.random.shuffle(arr)
>>> arr
[1 7 5 2 9 4 3 6 0 8]
```

This function only shuffles the array along the first index of a multi-dimensional array:

```
>>> arr = np.arange(9).reshape((3, 3))
>>> np.random.shuffle(arr)
>>> arr
array([[3, 4, 5],
       [6, 7, 8],
       [0, 1, 2]])
```

halla.stats.**uniform_cut**(*cake_length*, *iCuts=10*)
Cut cake uniformly

Abstract distance module providing different notions of distance

class halla.distance.**AdjustedMutualInformation**(*c_array1*, *c_array2*)
adjusted for chance

Methods

class halla.distance.**Distance**(*c_array1*, *c_array2*)
abstract distance, handles numpy arrays (probably should support lists for compatibility issues)

Methods

class halla.distance.**MutualInformation**(*c_array1*, *c_array2*, *bSym=False*)
Scikit-learn uses the convention log = ln Adjust multiplicative factor of log(e,2)

Methods

class halla.distance.**NormalizedMutualInformation**(*c_array1*, *c_array2*)
normalized by sqrt(H1*H2) so the range is [0,1]

Methods

halla.distance.**adj_mi**(*pData1*, *pData2*)
Static implementation of adjusted distance

Examples

```
>>> x = array([[0.1,0.2,0.3,0.4],[1,1,1,0],[0.01,0.04,0.09,0.16],[0,0,0,1]])
>>> y = array([[-0.1,-0.2,-0.3,-0.4],[1,1,0,0],[0.25,0.5,0.75,1.0],[0.015625,0.125,0.421875,1.0]
>>> dx = halla.stats.discretize( x, iN = None, method = None, aiSkip = [1,3] )
>>> dy = halla.stats.discretize( y, iN = None, method = None, aiSkip = [1] )
>>> p = itertools.product( range(len(x)), range(len(y)) )
>>> for item in p: i,j = item; print (i,j), adj_mi( dx[i], dy[j] )
(0, 0) 1.0
(0, 1) 1.0
(0, 2) 1.0
(0, 3) 1.0
(1, 0) 2.51758394487e-08
(1, 1) 2.51758394487e-08
(1, 2) 2.51758394487e-08
(1, 3) 2.51758394487e-08
(2, 0) 1.0
(2, 1) 1.0
(2, 2) 1.0
(2, 3) 1.0
(3, 0) -3.72523550982e-08
(3, 1) -3.72523550982e-08
(3, 2) -3.72523550982e-08
(3, 3) -3.72523550982e-08
```

halla.distance.**adj_mid**(*pData1*, *pData2*)
Static implementation of adjusted distance

Examples

```
>>> x = array([[0.1,0.2,0.3,0.4],[1,1,1,0],[0.01,0.04,0.09,0.16],[0,0,0,1]])
>>> y = array([[-0.1,-0.2,-0.3,-0.4],[1,1,0,0],[0.25,0.5,0.75,1.0],[0.015625,0.125,0.421875,1.0]
>>> dx = halla.stats.discretize( x, iN = None, method = None, aiSkip = [1,3] )
>>> dy = halla.stats.discretize( y, iN = None, method = None, aiSkip = [1] )
>>> p = itertools.product( range(len(x)), range(len(y)) )
>>> for item in p: i,j = item; print (i,j), adj_mid( dx[i], dy[j] )
(0, 0) 0.0
(0, 1) 0.0
(0, 2) 0.0
(0, 3) 0.0
(1, 0) 0.999999974824
(1, 1) 0.999999974824
(1, 2) 0.999999974824
(1, 3) 0.999999974824
(2, 0) 0.0
(2, 1) 0.0
(2, 2) 0.0
(2, 3) 0.0
(3, 0) 1.00000003725
(3, 1) 1.00000003725
(3, 2) 1.00000003725
(3, 3) 1.00000003725
```

halla.distance.**cor**(*pData1*, *pData2*, *method='pearson'*, *pval=False*)

Get correlation coefficient and corresponding parametric p-value (t-test)

Parameters **pData1, pData2** : numpy arrays

data matrices

method : str

{“pearson”, “spearman”} “abs”

pval : bool

True if parametric estimate of p-value requested

Returns **rho: float** :

correlation coefficient

p: float :

p-value

Examples

View pairwise correlation measures (pearson,spearman) between two datasets *x* and *y*:

```
>>> x = array([[0.1,0.2,0.3,0.4],[1,1,1,0],[0.01,0.04,0.09,0.16],[0,0,0,1]])
>>> y = array([[-0.1,-0.2,-0.3,-0.4],[1,1,0,0],[0.25,0.5,0.75,1.0],[0.015625,0.125,0.421875,1.0]
>>> p = [_ for _ in itertools.product( range(len(x)), range(len(y)) )]
>>> for item in p: i,j = item; print (i,j),cor(x[i],y[j], method="pearson"),cor(x[i],y[j], metho
(0, 0) -1.0 -1.0
(0, 1) -0.894427191 -0.894427191
(0, 2) 1.0 1.0
(0, 3) 0.951369855792 1.0
```

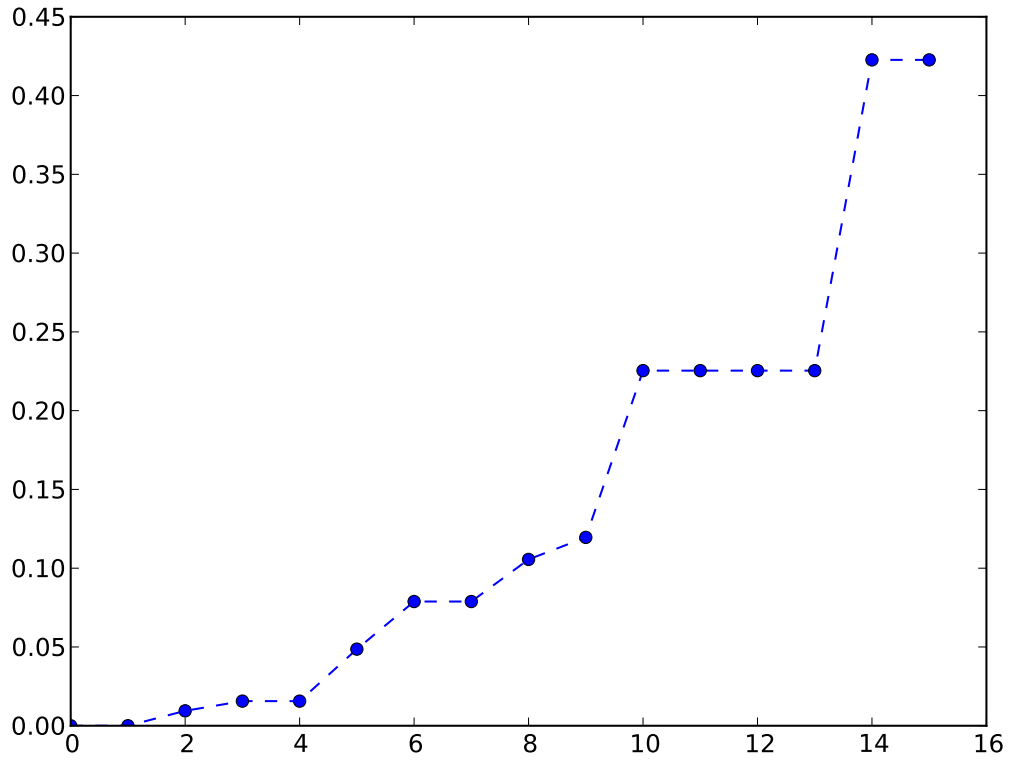
```
(1, 0) 0.774596669241 0.774596669241
(1, 1) 0.57735026919 0.57735026919
(1, 2) -0.774596669241 -0.774596669241
(1, 3) -0.921159901892 -0.774596669241
(2, 0) -0.984374038698 -1.0
(2, 1) -0.880450906326 -0.894427191
(2, 2) 0.984374038698 1.0
(2, 3) 0.99053285189 1.0
(3, 0) -0.774596669241 -0.774596669241
(3, 1) -0.57735026919 -0.57735026919
(3, 2) 0.774596669241 0.774596669241
(3, 3) 0.921159901892 0.774596669241
```

Generate p-values for pearson correlation:

```
>>> pval_pearson = sorted( [cor(x[i],y[j], method="pearson", pval=True)[1] for i,j in p] )
>>> pval_pearson
[0.0, 0.0, 0.0094671481098304033, 0.01562596130230276, 0.015625961302302867, 0.04863014420759581
```

View plot:

```
plt.plot( pval_pearson )
plt.show()
```

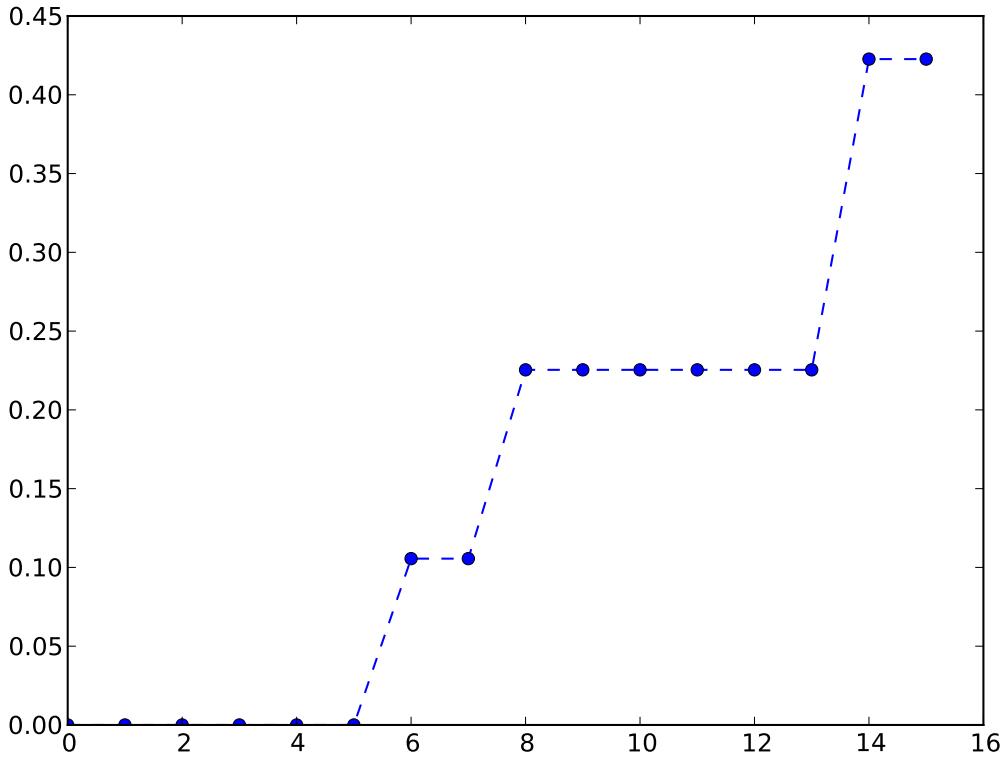


Generate p-values for spearman correlation:

```
>>> pval_spearman = sorted( [cor(x[i],y[j], method="spearman", pval=True)[1] for i,j in p] )
>>> pval_spearman
[0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.10557280900008413, 0.10557280900008413, 0.22540333075851657, 0.
```

View plot:

```
plt.plot(pval_pearson)
plt.show()
```



halla.distance.**cord**(*pData*, *pData2*, *method='pearson'*, *inversion_method='abs'*, *pval=False*)

Get correlation divergence

Parameters **pData1, pData2** : numpy arrays

data matrices

method : str

{"pearson", "spearman"}

inversion_method : str

"abs"

pval : bool

True if parametric estimate of p-value requested

Returns **rho: float** :

correlation coefficient

p: float :

p-value

Examples

```
>>> x = [0.1,0.2,0.3,0.4]
>>> y = [-0.1,-0.2,-0.3,-0.4]
>>> cord( x,y )
0.0
```

halla.distance.**l2**(*pData1*, *pData2*)

Returns the l2 distance

```
>>> x = numpy.array([1,2,3]); y = numpy.array([4,5,6])
>>> l2(x,y)
5.196152422706632
```

halla.distance.**mi**(*pData1*, *pData2*)

Static implementation of mutual information, returns bits

Parameters **pData1, pData2** : Numpy arrays

Returns **mi** : float

Examples

```
>>> x = array([[0.1,0.2,0.3,0.4],[1,1,1,0],[0.01,0.04,0.09,0.16],[0,0,0,1]])
>>> y = array([[-0.1,-0.2,-0.3,-0.4],[1,1,0,0],[0.25,0.5,0.75,1.0],[0.015625,0.125,0.421875,1.0]
>>> dx = halla.stats.discretize( x, iN = None, method = None, aiSkip = [1,3] )
>>> dy = halla.stats.discretize( y, iN = None, method = None, aiSkip = [1] )
>>> p = itertools.product( range(len(x)), range(len(y)) )
>>> for item in p: i,j = item; print (i,j), mi( dx[i], dy[j] )
(0, 0) 1.0
(0, 1) 1.0
(0, 2) 1.0
(0, 3) 1.0
(1, 0) 0.311278124459
(1, 1) 0.311278124459
(1, 2) 0.311278124459
(1, 3) 0.311278124459
(2, 0) 1.0
(2, 1) 1.0
(2, 2) 1.0
(2, 3) 1.0
(3, 0) 0.311278124459
(3, 1) 0.311278124459
(3, 2) 0.311278124459
(3, 3) 0.311278124459
```

halla.distance.**mid**(*pData1*, *pData2*)

Static implementation of mutual information,

Examples

```
>>> x = array([[0.1,0.2,0.3,0.4],[1,1,1,0],[0.01,0.04,0.09,0.16],[0,0,0,1]])
>>> y = array([[-0.1,-0.2,-0.3,-0.4],[1,1,0,0],[0.25,0.5,0.75,1.0],[0.015625,0.125,0.421875,1.0]
>>> dx = halla.stats.discretize( x, iN = None, method = None, aiSkip = [1,3] )
>>> dy = halla.stats.discretize( y, iN = None, method = None, aiSkip = [1] )
>>> p = itertools.product( range(len(x)), range(len(y)) )
```

```
>>> for item in p: i,j = item; print (i,j), mid( dx[i], dy[j] )
(0, 0) 0.0
(0, 1) 0.0
(0, 2) 0.0
(0, 3) 0.0
(1, 0) 0.688721875541
(1, 1) 0.688721875541
(1, 2) 0.688721875541
(1, 3) 0.688721875541
(2, 0) 0.0
(2, 1) 0.0
(2, 2) 0.0
(2, 3) 0.0
(3, 0) 0.688721875541
(3, 1) 0.688721875541
(3, 2) 0.688721875541
(3, 3) 0.688721875541
```

halla.distance.**norm_mi**(*pData1*, *pData2*)

Static implementation of normalized mutual information

Examples

```
>>> x = array([[0.1,0.2,0.3,0.4],[1,1,1,0],[0.01,0.04,0.09,0.16],[0,0,0,1]])
>>> y = array([[-0.1,-0.2,-0.3,-0.4],[1,1,0,0],[0.25,0.5,0.75,1.0],[0.015625,0.125,0.421875,1.0]
>>> dx = halla.stats.discretize( x, iN = None, method = None, aiSkip = [1,3] )
>>> dy = halla.stats.discretize( y, iN = None, method = None, aiSkip = [1] )
>>> p = itertools.product( range(len(x)), range(len(y)) )
>>> for item in p: i,j = item; print (i,j), norm_mi( dx[i], dy[j] )
(0, 0) 1.0
(0, 1) 1.0
(0, 2) 1.0
(0, 3) 1.0
(1, 0) 0.345592029944
(1, 1) 0.345592029944
(1, 2) 0.345592029944
(1, 3) 0.345592029944
(2, 0) 1.0
(2, 1) 1.0
(2, 2) 1.0
(2, 3) 1.0
(3, 0) 0.345592029944
(3, 1) 0.345592029944
(3, 2) 0.345592029944
(3, 3) 0.345592029944
```

halla.distance.**norm_mid**(*pData1*, *pData2*)

Static implementation of normalized mutual information

Examples

```
>>> x = array([[0.1,0.2,0.3,0.4],[1,1,1,0],[0.01,0.04,0.09,0.16],[0,0,0,1]])
>>> y = array([[-0.1,-0.2,-0.3,-0.4],[1,1,0,0],[0.25,0.5,0.75,1.0],[0.015625,0.125,0.421875,1.0]
>>> dx = halla.stats.discretize( x, iN = None, method = None, aiSkip = [1,3] )
>>> dy = halla.stats.discretize( y, iN = None, method = None, aiSkip = [1] )
```

```
>>> p = itertools.product( range(len(x)), range(len(y)) )
>>> for item in p: i,j = item; print (i,j), norm_mid( dx[i], dy[j] )
(0, 0) 0.0
(0, 1) 0.0
(0, 2) 0.0
(0, 3) 0.0
(1, 0) 0.654407970056
(1, 1) 0.654407970056
(1, 2) 0.654407970056
(1, 3) 0.654407970056
(2, 0) 0.0
(2, 1) 0.0
(2, 2) 0.0
(2, 3) 0.0
(3, 0) 0.654407970056
(3, 1) 0.654407970056
(3, 2) 0.654407970056
(3, 3) 0.654407970056
```

halla.distance.**pdist**(*pArray*, *metric='euclidean'*)

Performs pairwise distance computation

Parameters **pArray** : numpy array

metric : str

Returns **D** : redundancy-checked distance matrix (flat)

Examples

```
>>> x = array([[0.1,0.2,0.3,0.4],[1,1,1,0],[0.01,0.04,0.09,0.16],[0,0,0,1]])
>>> y = array([[-0.1,-0.2,-0.3,-0.4],[1,1,0,0],[0.25,0.5,0.75,1.0],[0.015625,0.125,0.421875,1.0]
>>> dx = halla.stats.discretize( x, iN = None, method = None, aiSkip = [1,3] )
>>> dy = halla.stats.discretize( y, iN = None, method = None, aiSkip = [1] )
>>> list( halla.distance.pdist( x, halla.distance.cord ) )
[0.22540333075851648, 0.015625961302302871, 0.22540333075851648, 0.1358414347819068, 0.0, 0.1358
>>> list( halla.distance.pdist( y, halla.distance.cord ) )
[0.10557280900008403, 0.0, 0.048630144207595816, 0.10557280900008414, 0.16134197652754312, 0.048
>>> list( halla.distance.pdist( x, lambda u,v: halla.distance.cord(u,v, method="spearman") ) )
[0.2254033307585166, 0.0, 0.2254033307585166, 0.2254033307585166, 0.0, 0.2254033307585166]
>>> list( halla.distance.pdist( y, lambda u,v: halla.distance.cord(u,v, method="spearman") ) )
[0.10557280900008414, 0.0, 0.0, 0.10557280900008414, 0.10557280900008414, 0.0]
>>> list( halla.distance.pdist( dx, halla.distance.norm_mid ) )
[0.65440797005578877, 0.0, 0.65440797005578877, 0.65440797005578877, 0.0, 0.65440797005578877]
>>> list( halla.distance.pdist( dy, halla.distance.norm_mid ) )
[0.0, 0.0, 0.0, 0.0, 0.0, 0.0]
```

halla.distance.**squareform**(*pArray*)

Switches back and forth between square and flat distance matrices

Parses input/output formats, manages transformations

class halla.parser.**Input**(*strFileName1*, *strFileName2=None*, *var_names=True*, *headers=False*)

Methods

class halla.parser.**Output**

Wrappers for testing procedures, random data generation, etc

halla.test.**multinomial**(*n*, *pvals*, *size=None*)

Draw samples from a multinomial distribution.

The multinomial distribution is a multivariate generalisation of the binomial distribution. Take an experiment with one of `p` possible outcomes. An example of such an experiment is throwing a dice, where the outcome can be 1 through 6. Each sample drawn from the distribution represents *n* such experiments. Its values, `X_i = [X_0, X_1, ..., X_p]`, represent the number of times the outcome was `i`.

Parameters **n** : int

Number of experiments.

pvals : sequence of floats, length p

Probabilities of each of the `p` different outcomes. These should sum to 1 (however, the last element is always assumed to account for the remaining probability, as long as `sum(pvals[:-1]) <= 1)`.

size : tuple of ints

Given a *size* of `(M, N, K)`, then `M*N*K` samples are drawn, and the output shape becomes `(M, N, K, p)`, since each sample has shape `(p,)`.

Examples

Throw a dice 20 times:

```
>>> np.random.multinomial(20, [1/6.]*6, size=1)
array([[4, 1, 7, 5, 2, 1]])
```

It landed 4 times on 1, once on 2, etc.

Now, throw the dice 20 times, and 20 times again:

```
>>> np.random.multinomial(20, [1/6.]*6, size=2)
array([[3, 4, 3, 3, 4, 3],
       [2, 4, 3, 4, 0, 7]])
```

For the first run, we threw 3 times 1, 4 times 2, etc. For the second, we threw 2 times 1, 4 times 2, etc.

A loaded dice is more likely to land on number 6:

```
>>> np.random.multinomial(100, [1/7.]*5)
array([13, 16, 13, 16, 42])
```

halla.test.**normal**(*loc=0.0*, *scale=1.0*, *size=None*)

Draw random samples from a normal (Gaussian) distribution.

The probability density function of the normal distribution, first derived by De Moivre and 200 years later by both Gauss and Laplace independently [R11], is often called the bell curve because of its characteristic shape (see the example below).

The normal distributions occurs often in nature. For example, it describes the commonly occurring distribution of samples influenced by a large number of tiny, random disturbances, each with its own unique distribution [R11].

Parameters **loc** : float

Mean ("centre") of the distribution.

scale : float

Standard deviation (spread or "width") of the distribution.

size : tuple of ints

Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn.

See also:

scipy.stats.distributions.norm probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Gaussian distribution is

$$p(x) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x-\mu)^2}{2\sigma^2}}, \tag{1.5}$$

where μ is the mean and σ the standard deviation. The square of the standard deviation, σ^2, is called the variance.

The function has its peak at the mean, and its "spread" increases with the standard deviation (the function reaches 0.607 times its maximum at $x + \sigma$ and $x - \sigma$ [R11]). This implies that *numpy.random.normal* is more likely to return samples lying close to the mean, rather than those far away.

References

[R10], [R11]

Examples

Draw samples from the distribution:

```
>>> mu, sigma = 0, 0.1 # mean and standard deviation
>>> s = np.random.normal(mu, sigma, 1000)
```

Verify the mean and the variance:

```
>>> abs(mu - np.mean(s)) < 0.01
True

>>> abs(sigma - np.std(s, ddof=1)) < 0.01
True
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt
>>> count, bins, ignored = plt.hist(s, 30, normed=True)
>>> plt.plot(bins, 1/(sigma * np.sqrt(2 * np.pi)) *
...                np.exp( - (bins - mu)**2 / (2 * sigma**2) ),
...          linewidth=2, color='r')
>>> plt.show()
```

halla.test.**randmat**(*tShape=(10, 10)*, *pDist=<built-in method normal of mtrand.RandomState object at 0x3815b10>*)

Returns a tShape-dimensional matrix given by base distribution pDist Order: Row, Col

halla.test.**randmix**(*N*, *pDist*, *atParam*, *tPi*)
Returns N copies drawn from a mixture distribution H Input: N <- number of components

pDist <- pointer to base distribution H atParam <- length k parameters to distribution pDist, $ heta$ tPi <- length k tuple (vector) to categorical rv Z_n

Output: N copies from mixture distribution $sum_{k=1}^{K} pi_k H(.| heta)$

halla.test.**uniformly_spaced_gaussian**(*N*, *K=4*, *fD=2.0*, *tPi=(0.25*, *0.25*, *0.25*, *0.25)*)
Generate uniformly spaced Gaussian, with spacing fD in the mean. Constant 1.0 variance

Hiearchy module, used to build trees and other data structures. Handles clustering and other organization schemes.

class halla.hierarchy.**Gardener**
A gardener object is a handler for the different types of hierarchical data structures ("trees") Can collapse and manipulate data structures and wrap them in different objects, depending on the context.

Methods

static PlantTree()
Input: halla.Dataset object Output: halla.hierarchy.Tree object

next()
return the data of the tree, layer by layer input: None output: a list of data pointers

class halla.hierarchy.**Tree**
A hierarchically nested structure containing nodes as a basic core unit

Methods

halla.hierarchy.**all_against_all**(*apClusterNode1*, *apClusterNode2*, *pArray1*, *pArray2*)
Perform all-against-all per layer

Input: apClusterNode1, apClusterNode2, pArray1, pArray2

Output: a list of ((i,j), (aiIndex1, aiIndex2, pVal))

halla.hierarchy.**couple_tree**(*pClusterNode1*, *pClusterNode2*, *method='unif'*)
Couples two data trees to produce a hypothesis tree

Examples

```
>>> depth1 = depth_tree( pClusterNode1 )
>>> depth2 = depth_tree( pClusterNode2 )
```

halla.hierarchy.**depth_tree**(*pClusterNode*)
Get the depth of a tree

halla.hierarchy.**get_layer**(*atData*, *iLayer*)
Get output from *reduce_tree_by_layer* and parse

Input: atData = a list of (iLevel, list_of_nodes_at_iLevel), iLayer = zero-indexed layer number

halla.hierarchy.**hclust**(*pArray*, *pdist_metric=<function norm_mid at 0x73162a8>*, *cluster_method='single'*, *bTree=False*)
Performs hierarchical clustering on an numpy array

Parameters **pArray** : numpy array

pdist_metric : str cluster_method : str bTree : boolean

Returns **Z** : numpy array or ClusterNode object

Notes

This hclust function is not quite right for the MI case. Need a generic MI function that can take in clusters of RV's, not just single ones Use the "grouping property" as discussed by Kraskov paper.

Examples

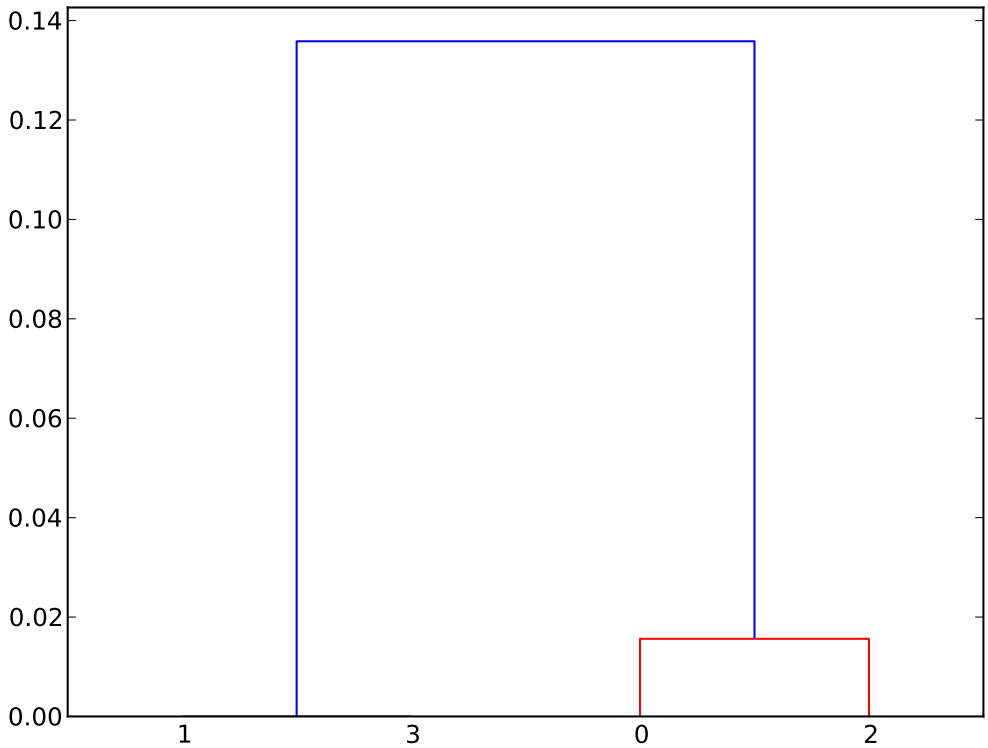
•Pearson correlation 1:

```
from numpy import array
from scipy.cluster.hierarchy import dendrogram, linkage
import scipy.cluster.hierarchy
import halla

x = array([[0.1,0.2,0.3,0.4],[1,1,1,0],[0.01,0.04,0.09,0.16],[0,0,0,1]])

lxpearson = halla.hierarchy.hclust( x, pdist_metric = halla.distance.cord )

dendrogram(lxpearson)
```



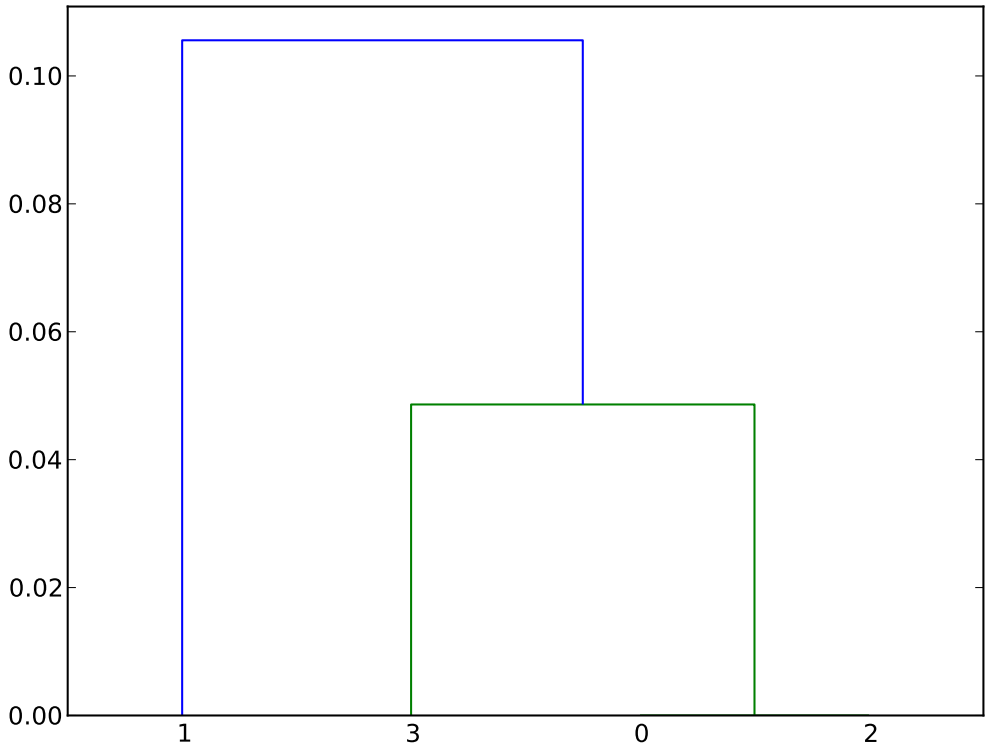
•Pearson correlation 2:

```
from numpy import array
from scipy.cluster.hierarchy import dendrogram, linkage
import scipy.cluster.hierarchy
import halla

y = array([[-0.1,-0.2,-0.3,-0.4],[1,1,0,0],[0.25,0.5,0.75,1.0], [0.015625,0.125,0.421875,1.0

lypearson = halla.hierarchy.hclust( y, pdist_metric = halla.distance.cord )

dendrogram(lypearson)
```



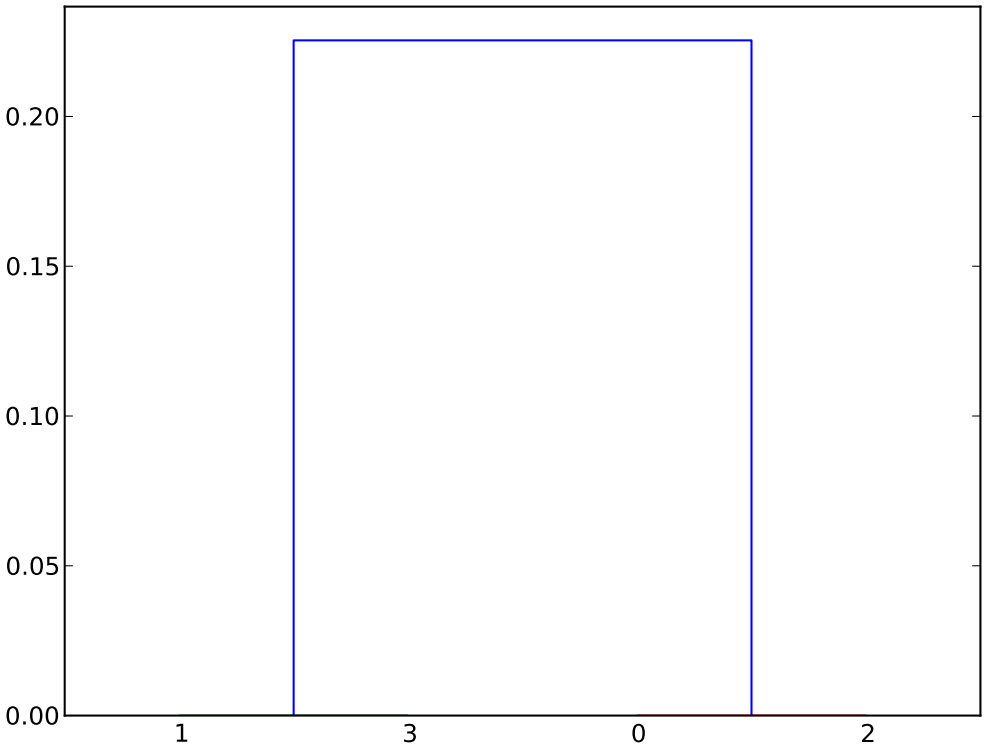
•Spearman correlation 1:

```
from numpy import array
from scipy.cluster.hierarchy import dendrogram, linkage
import scipy.cluster.hierarchy
import halla

x = array([[0.1,0.2,0.3,0.4],[1,1,1,0],[0.01,0.04,0.09,0.16],[0,0,0,1]])

lxspearman = halla.hierarchy.hclust( x, pdist_metric = lambda u,v: halla.distance.cord(u,v,m

dendrogram(lxspearman)
```



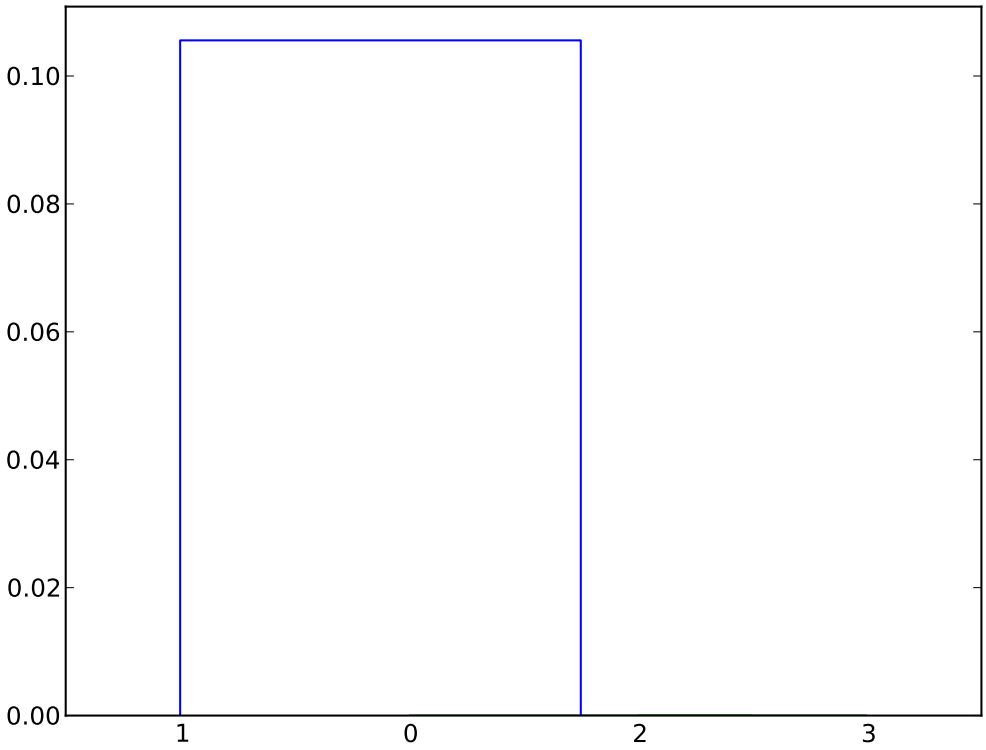
•Spearman correlation 2:

```
from numpy import array
from scipy.cluster.hierarchy import dendrogram, linkage
import scipy.cluster.hierarchy
import halla

y = array([[-0.1,-0.2,-0.3,-0.4],[1,1,0,0],[0.25,0.5,0.75,1.0], [0.015625,0.125,0.421875,1.0

lyspearman = halla.hierarchy.hclust( y, pdist_metric = lambda u,v: halla.distance.cord(u,v,m

dendrogram(lyspearman)
```



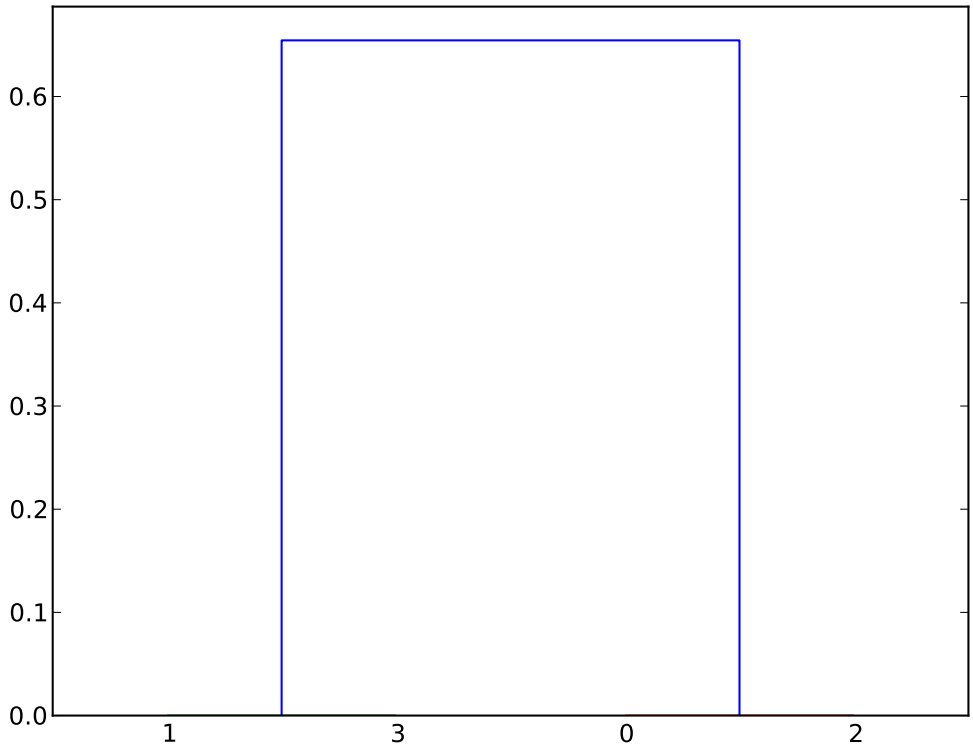
•Mutual Information 1:

```
from numpy import array
from scipy.cluster.hierarchy import dendrogram, linkage
import scipy.cluster.hierarchy
import halla

x = array([[0.1,0.2,0.3,0.4],[1,1,1,0],[0.01,0.04,0.09,0.16],[0,0,0,1]])
dx = halla.stats.discretize( x, iN = None, method = None, aiSkip = [1,3] )

lxmi = halla.hierarchy.hclust( dx, pdist_metric = halla.distance.norm_mid )

dendrogram(lxmi)
```



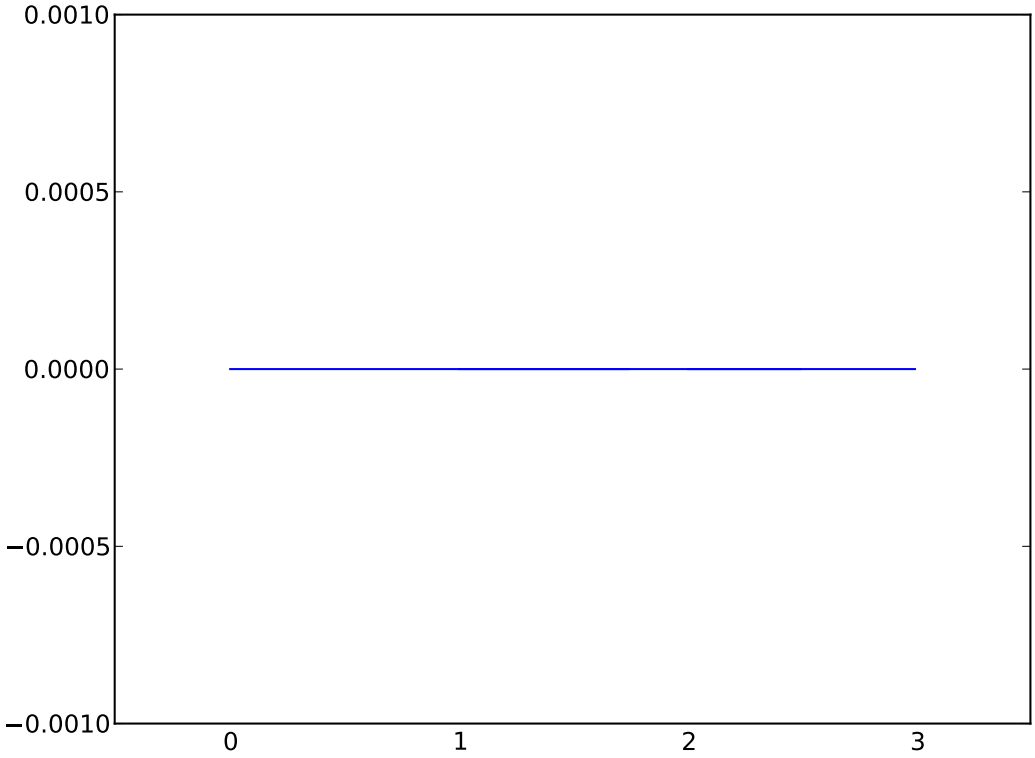
•Mutual Information 2:

```
from numpy import array
from scipy.cluster.hierarchy import dendrogram
import halla

y = array([[-0.1,-0.2,-0.3,-0.4],[1,1,0,0],[0.25,0.5,0.75,1.0], [0.015625,0.125,0.421875,1.0
dy = halla.stats.discretize( y, iN = None, method = None, aiSkip = [1] )

lymi = halla.hierarchy.hclust( dy, pdist_metric = halla.distance.norm_mid )

dendrogram( lymi )
```



halla.hierarchy.**normal**(*loc=0.0*, *scale=1.0*, *size=None*)

Draw random samples from a normal (Gaussian) distribution.

The probability density function of the normal distribution, first derived by De Moivre and 200 years later by both Gauss and Laplace independently [R13], is often called the bell curve because of its characteristic shape (see the example below).

The normal distributions occurs often in nature. For example, it describes the commonly occurring distribution of samples influenced by a large number of tiny, random disturbances, each with its own unique distribution [R13].

Parameters **loc** : float

Mean ("centre") of the distribution.

scale : float

Standard deviation (spread or "width") of the distribution.

size : tuple of ints

Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn.

See also:

scipy.stats.distributions.norm probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Gaussian distribution is

$$p(x) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x-\mu)^2}{2\sigma^2}}, \tag{1.6}$$

where μ is the mean and σ the standard deviation. The square of the standard deviation, σ^2, is called the variance.

The function has its peak at the mean, and its "spread" increases with the standard deviation (the function reaches 0.607 times its maximum at $x + \sigma$ and $x - \sigma$ [R13]). This implies that *numpy.random.normal* is more likely to return samples lying close to the mean, rather than those far away.

References

[R12], [R13]

Examples

Draw samples from the distribution:

```
>>> mu, sigma = 0, 0.1 # mean and standard deviation
>>> s = np.random.normal(mu, sigma, 1000)
```

Verify the mean and the variance:

```
>>> abs(mu - np.mean(s)) < 0.01
True

>>> abs(sigma - np.std(s, ddof=1)) < 0.01
True
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt
>>> count, bins, ignored = plt.hist(s, 30, normed=True)
>>> plt.plot(bins, 1/(sigma * np.sqrt(2 * np.pi)) *
...                np.exp( - (bins - mu)**2 / (2 * sigma**2) ),
...          linewidth=2, color='r')
>>> plt.show()
```

halla.hierarchy.**one_against_one**(*pClusterNode1*, *pClusterNode2*, *pArray1*, *pArray2*)

one_against_one hypothesis testing for a particular layer

Input: pClusterNode1, pClusterNode2, pArray1, pArray2

Output: aiIndex1, aiIndex2, pVal

halla.hierarchy.**recursive_all_against_all**(*apClusterNode1*, *apClusterNode2*, *pArray1*, *pArray2*, *pOut=[]*, *pFDR=<function bh at 0x7316cf8>*)

Performs recursive all-against-all (the default HAllA routine) with fdr correction

Input: apClusterNode1, apClusterNode2, pArray1, pArray2, pFDR

Output: a list of ((aiIndex1, pBag1), (aiIndex2, pBag2))

halla.hierarchy.**reduce_tree**(*pClusterNode*, *pFunction=<function <lambda> at 0x7bd4c08>*, *aOut=[]*)

Recursive

Input: pClusterNode, pFunction = lambda x: x.id, aOut = []

Output: a list of pFunction calls (node ids by default)

halla.hierarchy.**reduce_tree_by_layer**(*apParents*, *iLevel=0*, *iStop=None*)

Traverse one tree.

Input: apParents, iLevel = 0, iStop = None

Output: a list of (iLevel, list_of_nodes_at_iLevel)

halla.hierarchy.**traverse_by_layer**(*pClusterNode1*, *pClusterNode2*, *pArray1*, *pArray2*, *pFunction*)

Useful function for doing all-against-all comparison between nodes in each layer

traverse two trees at once, applying function *pFunction* to each layer pair

latex: $pFunction: data1 imes data2

ightarrow mathbb{R}^k, $ for k the size of the cross-product set per layer

Input: pClusterNode1, pClusterNode2, pArray1, pArray2, pFunction Output: (i,j), pFunction(pArray[:,i], pArray2[:,j])

halla.hierarchy.**truncate_tree**(*apClusterNode*, *iSkip*, *iLevel=0*)

Chop tree from root, returning smaller tree towards the leaves

Input: pClusterNode, iLevel

Output: list of ClusterNodes

1.5 Indices and tables

- *genindex*
- *modindex*
- *search*

1.6 License

[R1] Wikipedia, “Normal distribution”, http://en.wikipedia.org/wiki/Normal_distribution

[R2] P. R. Peebles Jr., “Central Limit Theorem” in “Probability, Random Variables and Random Signal Principles”, 4th ed., 2001, pp. 51, 51, 125.

[R3] Dalgaard, Peter, “Introductory Statistics with R”, Springer-Verlag, 2002.

[R4] Glantz, Stanton A. “Primer of Biostatistics.”, McGraw-Hill, Fifth Edition, 2002.

[R5] Lentner, Marvin, “Elementary Applied Statistics”, Bogden and Quigley, 1972.

[R6] Weisstein, Eric W. “Binomial Distribution.” From MathWorld–A Wolfram Web Resource. http://mathworld.wolfram.com/BinomialDistribution.html

[R7] Wikipedia, “Binomial-distribution”, http://en.wikipedia.org/wiki/Binomial_distribution

[R8] Wikipedia, “Normal distribution”, http://en.wikipedia.org/wiki/Normal_distribution

[R9] P. R. Peebles Jr., “Central Limit Theorem” in “Probability, Random Variables and Random Signal Principles”, 4th ed., 2001, pp. 51, 51, 125.

[R10] Wikipedia, “Normal distribution”, http://en.wikipedia.org/wiki/Normal_distribution

[R11] P. R. Peebles Jr., “Central Limit Theorem” in “Probability, Random Variables and Random Signal Principles”, 4th ed., 2001, pp. 51, 51, 125.

[R12] Wikipedia, “Normal distribution”, http://en.wikipedia.org/wiki/Normal_distribution

[R13] P. R. Peebles Jr., “Central Limit Theorem” in “Probability, Random Variables and Random Signal Principles”, 4th ed., 2001, pp. 51, 51, 125.

h

halla.distance, 11
halla.hierarchy, 21
halla.logger, 19
halla.parser, 18
halla.stats, 5
halla.test, 19

h

halla.distance, 11
halla.hierarchy, 21
halla.logger, 19
halla.parser, 18
halla.stats, 5
halla.test, 19

A

adj_mi() (in module halla.distance), 12
adj_mid() (in module halla.distance), 12
AdjustedMutualInformation (class in halla.distance), 11
all_against_all() (in module halla.hierarchy), 21

B

bh() (in module halla.stats), 5
binomial() (in module halla.stats), 6

C

cor() (in module halla.distance), 13
cord() (in module halla.distance), 15
couple_tree() (in module halla.hierarchy), 21
cumulative_log_cut() (in module halla.stats), 7

D

depth_tree() (in module halla.hierarchy), 21
discretize() (in module halla.stats), 7
Distance (class in halla.distance), 12

G

Gardener (class in halla.hierarchy), 21
get_layer() (in module halla.hierarchy), 21
get_medoid() (in module halla.stats), 8

H

halla (module), 3
halla.distance (module), 11
halla.hierarchy (module), 21
halla.logger (module), 19
halla.parser (module), 18
halla.stats (module), 5
halla.test (module), 19
hclust() (in module halla.hierarchy), 21

I

IBP_cut() (in module halla.stats), 5
Input (class in halla.parser), 18

L

l2() (in module halla.distance), 16
log_cut() (in module halla.stats), 9

M

mca() (in module halla.stats), 9
mi() (in module halla.distance), 16
mid() (in module halla.distance), 16
multinomial() (in module halla), 3
multinomial() (in module halla.stats), 9
multinomial() (in module halla.test), 19
MutualInformation (class in halla.distance), 12

N

next() (halla.hierarchy.Gardener method), 21
norm_mi() (in module halla.distance), 17
norm_mid() (in module halla.distance), 17
normal() (in module halla), 4
normal() (in module halla.hierarchy), 27
normal() (in module halla.stats), 9
normal() (in module halla.test), 19
NormalizedMutualInformation (class in halla.distance), 12

O

one_against_one() (in module halla.hierarchy), 28
Output (class in halla.parser), 18

P

p_val_plot() (in module halla.stats), 11
pca() (in module halla.stats), 11
pdist() (in module halla.distance), 18
permutation_test_by_representative() (in module halla.stats), 11
PlantTree() (halla.hierarchy.Gardener static method), 21
PY_cut() (in module halla.stats), 5

R

randmat() (in module halla.test), 20
randmix() (in module halla.test), 20
recursive_all_against_all() (in module halla.hierarchy), 28
reduce_tree() (in module halla.hierarchy), 28
reduce_tree_by_layer() (in module halla.hierarchy), 29

S

shuffle() (in module halla.stats), 11
squareform() (in module halla.distance), 18

T

traverse_by_layer() (in module halla.hierarchy), 29
Tree (class in halla.hierarchy), 21
truncate_tree() (in module halla.hierarchy), 29

U

uniform_cut() (in module halla.stats), 11
uniformly_spaced_gaussian() (in module halla.test), 21