

# Package ‘bioDist’

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**Title** Different distance measures

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**Description** A collection of software tools for calculating distance measures.

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**Depends** R (>= 2.0), methods, Biobase, KernSmooth

**Suggests** locfit

**biocViews** Bioinformatics

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closest.top

*Find the closest genes.*

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**Description**

Find the closest genes to the supplied target gene based on the supplied distances.

**Usage**

```
closest.top(x, dist.mat, top)
```

**Arguments**

x	the name of the gene (feature) to use.
dist.mat	either a dist object or a matrix of distances.
top	the number of closest genes desired.

**Details**

The feature named x must be in the supplied distances. If so, then the top closest other features are returned.

**Value**

A vector of names of the top closest features.

**Author(s)**

Beiyong Ding

**See Also**

[cor.dist](#), [spearman.dist](#), [tau.dist](#), [euc](#), [man](#), [KLdist.matrix](#), [KLD.matrix](#), [mutualInfo](#)

**Examples**

```
data(sample.ExpressionSet)
sE <- sample.ExpressionSet[1:100,]
d1 <- KLdist.matrix(sE, sample = FALSE)
closest.top(featureNames(sE)[1], d1, 5)
```

---

cor.dist	<i>Pearson correlational distance</i>
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**Description**

Calculate pairwise Pearson correlational distances, i.e. 1-COR or 1-|COR|, and saves as a 'dist' object

**Usage**

```
cor.dist(x, ...)
```

**Arguments**

- |     |  |
|-----|--|
| x   | n by p matrix or ExpressionSet; if x is an ExpressionSet, then the function uses its 'exprs' slot.   |
| ... | arguments passed to cor.dist: <ul style="list-style-type: none"><li>• absif TRUE, then 1- COR  else 1-COR, default is TRUE.</li><li>• diagif TRUE, then the diagonal of the distance matrix will be displayed, default is FALSE.</li><li>• upperif TRUE, then the upper triangle of the distance matrix will be displayed, default is FALSE.</li><li>• samplefor objects of classes that extend eSet: if TRUE, then distances are computed between samples(columns) , otherwise, they are computed between features(rows).</li></ul> |

**Details**

The cor function is used to compute the pairwise distances between rows of an input matrix, except if the input is an object of a class that extends eSet and sample is TRUE.

**Value**

Pairwise Pearson correlational distance object

**Author(s)**

Beiyong Ding

**See Also**

[spearman.dist](#), [tau.dist](#), [euc](#), [man](#), [KLdist.matrix](#), [KLD.matrix](#), [mutualInfo](#)

**Examples**

```
x <- matrix(rnorm(200), nrow = 5)
cor.dist(x)
```

---

`euc`*Euclidean distance*

---

**Description**

Calculate pairwise Euclidean distances and saves the result as a 'dist' object

**Usage**

```
euc(x, ...)
```

**Arguments**

`x` n by p matrix or an object of a class that extends `eSet`; if `x` is a matrix, pairwise distances are calculated between the rows of a matrix. If `x` is an object of a class that extends `eSet`, the method makes use of the 'exprs' method and pairwise distances are calculated between samples(columns) if `sample` is `TRUE`

`...` arguments passed to `euc`:

- `diagif` `TRUE`, then the diagonal of the distance matrix will be displayed; default is `FALSE`.
- `upperif` `TRUE`, then the upper triangle of the distance matrix will be displayed; default is `FALSE`.
- `sample` For objects of classes that extends `eSet`, pairwise distances are calculated between samples(columns) if `sample` is `TRUE` ; default value is `TRUE`

**Details**

The method calculates pairwise euclidean distances, assuming that all samples have the same number of observations

**Value**

An object of class `dist` with the pairwise Euclidean distance between rows except in case of objects of class that extend `eSet` when `sample` is `TRUE`

**Author(s)**

Beiyong Ding

**See Also**

[spearman.dist](#), [tau.dist](#), [man,KLdist.matrix,KLD.matrix](#), [mutualInfo](#)

**Examples**

```
x <- matrix(rnorm(200), nrow = 5)
euc(x)
```

---

`KLD.matrix`*Continuous version of Kullback-Leibler Distance (KLD)*

---

**Description**

Calculate KLD by estimating by smoothing  $\log(f(x)/g(x)) * f(x)$  and then integrating.

**Usage**

```
KLD.matrix(x, ...)
```

**Arguments**

- |                  |   |
|------------------|---|
| <code>x</code>   | n by p matrix or list or an object of a class that extends eSet; if x is an object of a class that extends eSet (eg ExpressionSet), then the function works against its 'exprs' slot.   |
| <code>...</code> | arguments passed to <code>KLD.matrix</code> : <ul style="list-style-type: none"><li>• <code>method</code> use <code>locfit</code> or <code>density</code> to estimate integrand; default is <code>c("locfit", "density")</code> (i.e. both methods).</li><li>• <code>supp</code> upper and lower limits of the integral; default is <code>NULL</code> in which case the limits of the integral are calculated from the range of the data.</li><li>• <code>subdivisions</code> subdivisions for the integration; default is 1000.</li><li>• <code>diag</code> if <code>TRUE</code>, then the diagonal of the distance matrix will be displayed; default is <code>FALSE</code>.</li><li>• <code>upper</code> if <code>TRUE</code>, then the upper triangle of the distance matrix will be displayed; default is <code>FALSE</code>.</li><li>• <code>sample</code> for ExpressionSet methods: if <code>TRUE</code>, then distances are computed between samples, otherwise, they are computed between genes.</li></ul> |

**Details**

The distance is computed between rows of the input matrix (except if the input is an object of a class that extends eSet and `sample` is `TRUE`).

The presumption is that all samples have the same number of observations. The list method is meant for use when samples sizes are unequal.

**Value**

An object of class `dist` with the pairwise, between rows, Kullback-Leibler distances.

**Author(s)**

Beiyong Ding, Vincent Carey

**See Also**

[cor.dist](#), [spearman.dist](#), [tau.dist](#), [dist](#), [Kldist.matrix](#), [mutualInfo](#)

**Examples**

```
x <- matrix(rnorm(100), nrow = 5)
KLD.matrix(x, method = "locfit", supp = range(x))
```

---

KLdist.matriX

*Discrete version of Kullback-Leibler Distance (KLD)*


---

**Description**

Calculate the KLD by binning continuous data.

KL distance is calculated using the formula

$$KLD(f_1(x), f_2(x)) = \sum_{i=1}^N f_1(x_i) * \log \frac{f_1(x_i)}{f_2(x_i)}$$

**Usage**

```
KLdist.matrix(x, ...)
```

**Arguments**

**x** n by p matrix or a list or an object of a class that extends eSet. If x is an object of a class derived from eSet (ExpressionSet, SnpSet etc), then the values returned by the exprs function are used.

**...** arguments passed to KLdist.matrix:

- gridsize** the number of grid points used to select the optimal bin width of the histogram used to estimate density. If no value is supplied, the grid size is calculated internally; default is NULL.
- symmetrize** if TRUE, then symmetrize; the default is FALSE.
- diag** if TRUE, then the diagonal of the distance matrix will be displayed; the default is FALSE.
- upper** if TRUE, then the upper triangle of the distance matrix will be displayed; default is FALSE.
- sample** for eSet methods: if TRUE, then the distances are computed between samples, otherwise, between features; the default is TRUE.

**Details**

The data are binned, and then the KL distance between the two discrete distributions is computed and used. The distance is computed between rows of the input matrix (except if the input is an object of a class that extends eSet and sample is TRUE).

The presumption is that all samples have the same number of observations. The list method is meant for use when samples sizes are unequal.

**Value**

An object of class `dist` is returned.

**Author(s)**

Beiyong Ding

**See Also**

[cor.dist](#), [spearman.dist](#), [tau.dist](#), [euc](#), [man](#), [KLD.matrix](#), [mutualInfo](#)

**Examples**

```
x <- matrix(rnorm(100), nrow = 5)
KLdist.matrix(x, symmetrize = TRUE)
```

---

man

*Manhattan distance*


---

**Description**

Calculate pairwise Manhattan distances and saves as a `dist` object.

**Usage**

```
man(x, ...)
```

**Arguments**

`x` n by p matrix or an object of class that extends `eSet`. If `x` is an object of class that extends `eSet`, (eg `ExpressionSet`) then the function uses its `'exprs'` slot.

`...` arguments passed to `man`:

- `diagif TRUE`, then the diagonal of the distance matrix will be displayed; default is `FALSE`.
- `upperif TRUE`, then the upper triangle of the distance matrix will be displayed; default is `FALSE`.

**Details**

This is just an interface to `dist` with the right parameters set.

**Value**

An instance of the `dist` class with the pairwise Manhattan distances between the rows of `x` in case of a matrix or between the features (rows) in case of a class that extends `eSet`.

**Author(s)**

Beiyong Ding

**See Also**[cor.dist](#), [spearman.dist](#), [tau.dist](#), [euc](#), [KLdist.matrix](#), [KLD.matrix](#), [mutualInfo](#)**Examples**

```
x <- matrix(rnorm(200), nrow = 5)
man(x)
```

mutualInfo

*Mutual Information***Description**

Calculate mutual information via binning

**Usage**

```
mutualInfo(x, ...)
MIdist(x, ...)
```

**Arguments**

- |     |  |
|-----|--|
| x   | an n by p matrix or ExpressionSet; if x is an ExpressionSet, then the function uses its 'exprs' slot.  |
| ... | arguments passed to mutualInfo and MIdist: <ul style="list-style-type: none"> <li>• nbnumber of bins to calculate discrete probabilities; default is 10.</li> <li>• diagif TRUE, then the diagonal of the distance matrix will be displayed; default is FALSE.</li> <li>• upperif TRUE, then the upper triangle of the distance matrix will be displayed; default is FALSE.</li> <li>• samplefor ExpressionSet methods, if TRUE, then distances are computed between samples, otherwise, between genes.</li> </ul> |

**Details**

For mutualInfo each row of x is divided into nbin groups and then the mutual information is computed, treating the data as if they were discrete.

For MIdist we use the transformation proposed by Joe (1989),  $\delta^* = (1 - \exp(-2\delta))^{1/2}$  where  $\delta$  is the mutual information. The MIdist is then  $1 = \delta^*$ . Joe argues that this measure is then similar to Kendall's tau, [tau.dist](#).



**Value**

An object of class `dist` which contains the pairwise distances.

**Author(s)**

Robert Gentleman

**References**

H. Joe, Relative Entropy Measures of Multivariate Dependence, JASA, 1989, 157-164.

**See Also**

[dist](#), [Kldist.matrix](#), [cor.dist](#), [KLD.matrix](#)

**Examples**

```
x <- matrix(rnorm(100), nrow = 5)
mutualInfo(x, nbin = 3)
```

---

spearman.dist

*Spearman correlational distance*

---

**Description**

Calculate pairwise Spearman correlational distances, i.e. 1-SPEAR or 1-ISPEAR, for all rows of a matrix and return a `dist` object.

**Usage**

```
spearman.dist(x, ...)
```

**Arguments**

- |                  |  |
|------------------|--|
| <code>x</code>   | <code>n</code> by <code>p</code> matrix or <code>ExpressionSet</code> ; if <code>x</code> is an <code>ExpressionSet</code> , then the function uses its <code>'exprs'</code> slot.   |
| <code>...</code> | arguments passed to <code>spearman.dist</code> : <ul style="list-style-type: none"> <li>• <code>absif</code> TRUE, then 1-ISPEAR else 1-SPEAR; default is TRUE.</li> <li>• <code>diagif</code> TRUE, then the diagonal of the distance matrix will be displayed; default is FALSE.</li> <li>• <code>upperif</code> TRUE, then the upper triangle of the distance matrix will be displayed; default is FALSE.</li> <li>• <code>samplefor</code> the <code>ExpressionSet</code> method: if TRUE (the default), then distances are computed between samples.</li> </ul> |

**Details**

We call `cor` with the appropriate arguments to compute the row-wise correlations.

**Value**

One minus the Spearman correlation, between rows of `x`, are returned, as an instance of the `dist` class.

**Author(s)**

Beiyong Ding

**See Also**

[cor.dist](#), [tau.dist](#), [euc](#), [man](#), [Kldist.matrix](#), [KLD.matrix](#), [mutualInfo](#), [dist](#)

**Examples**

```
x <- matrix(rnorm(200), nrow = 5)
spearman.dist(x)
```

---

tau.dist

*Kendall's tau correlational distance*

---

**Description**

Calculate pairwise Kendall's tau correlational distances, i.e.  $1-\text{TAU}$  or  $1-|\text{TAU}|$ , for all rows of the input matrix and return an instance of the `dist` class.

**Usage**

```
tau.dist(x, ...)
```

**Arguments**

- |                  |  |
|------------------|--|
| <code>x</code>   | <code>n</code> by <code>p</code> matrix or <code>ExpressionSet</code> ; if <code>x</code> is an <code>ExpressionSet</code> , then the function uses its <code>'exprs'</code> slot.   |
| <code>...</code> | arguments passed to <code>tau.dist</code> : <ul style="list-style-type: none"> <li>• <code>absif</code> TRUE, then <math>1- \text{TAU} </math> else <math>1-\text{TAU}</math>; default is TRUE.</li> <li>• <code>diagif</code> TRUE, then the diagonal of the distance matrix will be displayed; default is FALSE.</li> <li>• <code>upperif</code> TRUE, then the upper triangle of the distance matrix will be displayed; default is FALSE.</li> <li>• <code>samplefor</code> the <code>ExpressionSet</code> method: if TRUE (the default), then distances are computed between samples.</li> </ul> |

**Details**

Row-wise correlations are computed by calling the `cor` function with the appropriate arguments.

**Value**

One minus the row-wise Kendall's tau correlations are returned as an instance of the `dist` class. Note that this can be extremely slow for large data sets.

**Author(s)**

Beiyong Ding

**See Also**

[cor.dist](#), [spearman.dist](#), [euc](#), [man](#), [KLdist.matrix](#), [KLD.matrix](#), [mutualInfo](#)

**Examples**

```
x <- matrix(rnorm(200), nrow = 5)
tau.dist(x)
```

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