bioDist

October 25, 2011

`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

`x`	n by p matrix or list or an object of a class that extends eSet; if x is an an object of a class that extends eSet (eg ExpressionSet), then the function works against its 'exprs' slot.
`...`	arguments passed to `KLD.matrix`:

- methoduse `locfit` or `density` to estimate integrand; default is c("locfit", "density")(i.e. both methods).
- suppupper and lower limits of the integral; default is NULL in which case the limits of the integral are calculated from the range of the data.
- subdivisionssubdivisions for the integration; default is 1000.
- 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.
- samplefor ExpressionSet methods: if TRUE, then distances are computed between samples, otherwise, they are computed between genes.

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)

Beiying 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)

Beiying 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)
```

`closest.top` *Find the closest genes.*

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)

Beiying 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 *Pearson correlational distance*

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: • absif TRUE, then 1-|COR| else 1-COR, default is TRUE. • 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. • samplefor objects of classes that extend eSet: if TRUE, then distances are computed between samples(columns) , otherwise, they are computed between features(rows).

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)

Beiying 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. • sampleFor 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)

Beiying Ding

See Also

spearman.dist, tau.dist, man,KLdist.matrix,KLD.matrix, mutualInfo

Examples

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

`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)

Beiying 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:

- nbinnumber of bins to calculate discrete probabilities; default is 10.
- 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.
- samplefor ExpressionSet methods, if TRUE, then distances are computed between samples, otherwise, between genes.

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 δ 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-|SPEAR|, for all rows of a matrix and return a `dist` object.

Usage

```
spearman.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 `spearman.dist`:

- absif `TRUE`, then 1-|SPEAR| else 1-SPEAR; default is TRUE.
- 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.
- samplefor the ExpressionSet method: if TRUE (the default), then distances are computed between samples.

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)

Beiying 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-TAU or 1-|TAU|, for all rows of the input matrix and return an instance of the `dist` class.

Usage

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

Usage

```
tau.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 `tau.dist`: • absif TRUE, then 1-|TAU| else 1-TAU; default is TRUE. • 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. • samplefor the ExpressionSet method: if TRUE (the default), then distances are computed between samples.

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)

Beiying Ding

See Also

`cor.dist`, `spearman.dist`, `euc`, `man`, `KLdist.matrix`, `KLD.matrix`, `mutualInfo`

Examples

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

Index