Package 'ksia'

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Type Package

Title k-Strong Inference, Gene Network Inference Algorithm

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Description Information theory based gene network inference algorithm.

Depends R (>= 3.5.0), c3net, minet

License GPL (>=2)

Encoding UTF-8

LazyData true

R topics documented:

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concatenateZscore   *Concatenate different z-scores*

Description

concatenateZscore combines Spearman and Pearson based mutual information values

Usage

```
concatenateZscore(data,method="ssos")
```

Arguments

data	Example data; rows correspond to variables (e.g. genes) and columns to samples.
method	It refers how to integrate z-score. This parameters takes three values, these are: "ssos" means square root sum of squares of z-scores, "average" takes average of z-scores and "mul" refers multiplication of z-scores.

Value

concatenateZscore integrates Spearman and Pearson based mutual information values and returns integrated z-scores .

See Also

dataset, kStrongInference, zscore

Examples

```
data(dataset)
mim= concatenateZscore(dataset)
```

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dataset   *Example data set*

Description

dataset Synthetic Escherichia coli data from SynTReN

Usage

```
data(dataset)
```

Arguments

dataset   Example data; rows correspond to variables (e.g. genes) and columns to samples.

Details

Synthetic Escherichia coli data from SynTReN which consists of 200 genes from 100 samples

Value

dataset returns an example data set where rows are variables (e.g. genes) and columns are samples. It consists of 200 genes from 100 samples.

References

Van den Bulcke, Tim, et al. "SynTReN: a generator of synthetic gene expression data for design and analysis of structure learning algorithms." BMC bioinformatics 7.1 (2006): 1-12.

See Also

kStrongInference, concatenateZscore, zscore

Examples

```
data(dataset)
```

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kStrongInference   *k-Strong Inference Algorithm,ksia*

Description

kStrongInference takes a mutual information matrix and computes the inferred network using k-Strong Inference Algorithm.

Usage

```
kStrongInference(mim, sym = TRUE,k=3)
```

Arguments

mim	Mutual Information Matrix
sym	Indicates the final matrix is symetric or not. It takes TRUE or FALSE for symetric and unsymetric respectively.
k	It refers the number of neighbors for each gene.

Value

kStrongInference returns boolean matrix that presents relations between genes and these relations are inferred by k-Strong Inference Algorithm.

See Also

[dataset](), [concatenateZscore](), [zscore]()

Examples

```
data(dataset)
mim= concatenateZscore(dataset)
ksiNetwork= kStrongInference(mim, sym = TRUE,k=3)
```

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zscore   *Calculate z-scores of matrix*

Description

zscore calculate z-scores of matrix

Usage

```
zscore(datam)
```

Arguments

datam	Example data; rows correspond to variables (e.g. genes) and columns to samples.

Value

zscore returns z-scores of matrix .

See Also

[dataset](#), [kStrongInference](#), [concatenateZscore](#)

Examples

```
data(dataset)
zScoreVals= zscore(dataset)
```

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