

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

RoxygenNote 7.1.1

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concatenateZscore	<i>Concatenate PCC and SCC based z-scores</i>
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Description

concatenateZscore combines Spearman and Pearson based mutual information values

Usage

```
concatenateZscore(data)
```

Arguments

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

concatenateZscore Integrates Spearman and Pearson based mutual information values using square root sum of squares of z-scores. It returns integrated z-scores .

See Also

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

Examples

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

dataset	<i>Example data set</i>
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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.
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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)
```

kStrongInference	<i>k-Strong Inference Algorithm,ksia</i>
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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 symmetric or not. It takes TRUE or FALSE for symmetric and unsymmetric 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)
```

zscore	<i>Calculate z-scores of matrix</i>
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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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