

Package ‘GNIAP’

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Type Package

Title Gene Network Inference and Analysis Package

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Description Gene Co-expression Network Inference and Evaluation Package

Depends c3net, GAnet, minet, ProNet, igraph, gProfileR, WGCNA

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LazyData true

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annotation	<i>Annotations of the RAS pathway related to dataset</i>
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Description

annotation Subset annotation data of Affymetrix HG-U95AV2 GeneChip.

Usage

```
data(annotation)
```

Arguments

annotation Consist of two columns, first refers gene symbols and second refers gene symbol.

Details

The microarray platform used in the prostate cancer study is the Affymetrix HG-U95AV2 GeneChip.

Value

annotation returns annotation data.

Examples

```
data(annotation)
```

calculateRSquare	<i>Return R-Squared value</i>
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Description

calculateRSquare Return R-Squared value

Usage

```
calculateRSquare(graph)
```

Arguments

graph Igraph object refers gene coexpression network

Value

calculateRSquare Return R-Squared value, goodness of fitness value

See Also

[networkInference](#), [calculateTopologicalFitness](#), [literatureOverlapAnalysis](#), [topologicalBiologicalEvaluation](#)

Examples

```
g = erdos.renyi.game(500, 350, type = "gnm")
rsquareValue= calculateRSquare(g)
```

`calculateTopologicalFitness`*This function measures how well gene networks follows scale free network topology*

Description

`calculateTopologicalFitness` measures how well gene networks follows scale free network topology.

Usage

```
calculateTopologicalFitness(temp_dataset)
```

Arguments

`temp_dataset` co-expression network sample

Value

`calculateTopologicalFitness` Return Kolmogorov-Smirnov Goodness of fit values and R-squared value which displays how gene networks follows scale free network topology

See Also

[calculateRSquare](#), [literatureOverlapAnalysis](#), [networkInference](#), [topologicalBiologicalEvaluation](#)

Examples

```
data(networkExample)

topologyFitnessValues <- calculateTopologicalFitness(networkExample)
```

`dataset`*Example data set*

Description

`dataset` This dataset contains (part of) the gene expression, annotations and clinical data as published by Jorissen and colleagues in 2009. Genes related to KRAS mutations were retrieved from Bild et al, Nature, 2006. Only genes with known gene symbols were selected resulting in a dataset of 290 human colon tumors and 259 RAS-related genes.

Usage

```
data(dataset)
```

Arguments

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

Value

dataset returns mRNA expression dataset

References

<http://www.ncbi.nlm.nih.gov/projects/geo/query/acc.cgi?acc=GSE14333>

Examples

```
data(dataset)
```

```
literatureOverlapAnalysis
```

Validating the inferred network using literature data<PPI data>

Description

literatureOverlapAnalysis Overlap analysis of gene networks via literature data.

Usage

```
literatureOverlapAnalysis(ppi, anno, temp_dataset)
```

Arguments

ppi Protein- protein interaction data , literature data, which is utilized as validation data in overlap analysis

anno Annotation data for getting all possible interaction space.

temp_dataset co-expression network sample

Value

literatureOverlapAnalysis Return performance evaluation metrics of gene coexpression networks.

See Also

[calculateRSquare](#), [calculateTopologicalFitness](#), [networkInference](#), [topologicalBiologicalEvaluation](#)

Examples

```
data(ppi)
data(annotation)
data(networkExample)
```

```
overlapAnalysisResult <- literatureOverlapAnalysis(ppi, annotation, networkExample)
```

networkExample	<i>networkExample co-expression network sample</i>
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Description

networkExample networkExample contains gene- gene relations as undirectional pairs

Usage

```
data(networkExample)
```

Arguments

networkExample co-expression network sample

Details

networkExample co-expression network sample.

Value

networkExample returns co-expression network sample.

Examples

```
data(networkExample)
```

networkInference	<i>Gene coexpression network inference</i>
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Description

networkInference Gene coexpression network inference step

Usage

```
networkInference(dataset, anno, gnimethod)
```

Arguments

dataset	mRNA,RNA-Seq or any other biological expression dataset file
anno	Annotation data for getting all possible interaction space.
gnimethod	We used information theory based algorithms. It string value must be any of these values which show popular inference algorithms: c3net, aracne, clr, mrnet or wgna

Value

networkInference Return gene- gene interactions which forms gene coexpression network

See Also

[calculateRSquare](#), [calculateTopologicalFitness](#), [literatureOverlapAnalysis](#), [topologicalBiologicalEvaluation](#)

Examples

```
data(dataset)
data(annotation)

geneNetwork <- networkInference(dataset,annotation,gnimethod="c3net")
```

omim	<i>OMIM diseases gene list which contains breast cancer related data</i>
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Description

omim OMIM diseases gene list which contains breast cancer related data. It was obtained via Enrichr tool

Usage

```
data(omim)
```

Arguments

omim Gene list

Details

OMIM diseases gene list which contains breast cancer related data

Value

omim returns omim gene list.

Examples

```
data(omim)
```

ppi	<i>Example literature dataset</i>
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Description

ppi This ppi is utilized as literature data in overlap analysis. It contains more than 1.5 million protein protein interactions which can be access by GAnet R package.

Usage

```
data(ppi)
```

Arguments

ppi	Protein protein interactions
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Value

ppi returns protein protein interactions

Examples

```
data(ppi)
```

topologicalBiologicalEvaluation	<i>Assessment of gene networks via topological and biological features</i>
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Description

topologicalBiologicalEvaluation Returns topological and biological analyses results of gene coexpression network

Usage

```
topologicalBiologicalEvaluation(temp_dataset,omim)
```

Arguments

temp_dataset	co-expression network sample
omim	OMIM disease gene list

Value

topologicalBiologicalEvaluation return environment res that returns biological analysis results using GO- terms as res\$biolEval and topological features as res\$topological.

See Also

[calculateRSquare](#), [calculateTopologicalFitness](#), [networkInference](#), [literatureOverlapAnalysis](#)

Examples

```
data(omim)
data(networkExample)

res <- topologicalBiologicalEvaluation(networkExample,omim)

topologicalResults= res$topological
biologicalAnalysisResults=res$biolEval
```


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