

Package ‘FunctionalNetworks’

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Type Package

Title An algorithm for gene and gene set network inference

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Description R package providing functions to perform gene and gene set network inference.

Depends R (>= 2.10), breastCancerVDX, Biobase

License Artistic-2.0

Collate data.generation.R bic.generation.R network.estimate.R

LazyLoad yes

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FunctionalNetworks-package

An Algorithm for Gene and Gene Set Network Inference.

Description

Functions to perform gene and gene set network inferences. This method is described in detail in the paper soon to be published. This work is done by Alejandro Quiroz-Zarate in collaboration with Benjamin Haibe-Kains and John Quackenbush.

Details

Package:	FunctionalNetworks
Type:	Package
Version:	1.0
Date:	2013-09-03
License:	Artistics-2.0
LazyLoad:	yes

For a detailed example on the use and manipulation of the functions provided on this package please see the package Vignette.

Author(s)

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References

Quiroz-Zarate, A., Haibe-Kains, B. and Quackenbush, J. Manuscript in preparation (2013).

Examples

```
# vignette("FunctionalNetworks")
```

bic.4.toy.network

List containing the results from the application of the function bic.generation for a toy dataset based on the breastCancerVDX dataset

Description

This dataset contains a list with the results from the application of the function bic.generation for a toy dataset based on the breastCancerVDX dataset. It is based on the results from the application of the function data.generation. See the package Vignette for a detailed usage.

Usage

```
data(bic.4.toy.network)
```

Format

A list containing the information in the following way:

- BIC.Gene.0.Pred A vector with the BIC calculations were genes are set as objective nodes in the network with no source gene.
- BIC.Gene.1.Pred A matrix with the BIC calculations were genes are set as objective nodes in the network with one source gene.
- BIC.Set.0.Pred A vector with the BIC calculations were gene sets are set as objective nodes in the network with no source gene sets.
- BIC.Set.1.Pred A matrix with the BIC calculations were gene sets are set as objective nodes in the network with one source gene set.

Details

This data set is calculated for the particular case were it is of interest to obtain the Functional Network for a toy dataset based on the breastCancerVDX dataset and the annotation system chosen is the MF from GO. The phenotype chose are the samples with Estrogen receptor negative (ER-) and the minimum number of genes on each MF is at least 5.

Author(s)

A. Quiroz-Zarate. <aquiroz@jimmy.harvard.edu>

References

Quiroz-Zarate A, Haibe-Kains, B and Quackenbush J (2013). "Manuscript in preparation".

Examples

```
# See Package Vignette for a detailed example of the usage of this dataset  
# vignette("FunctionalNetworks")
```

data.4.toy.network	<i>List containing the results from the application of the function data.generation for a toy dataset based on the breastCancerVDX dataset</i>
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Description

This dataset contains a list with the results from the application of the function `data.generation` for a toy dataset based on the breastCancerVDX dataset. It is based on the Molecular Functions ontology from GO by the MSigBD. Only MF with at least 5 genes were considered. See the package Vignette for a detailed usage.

Usage

```
data(data.4.toy.network)
```

Format

A list containing the information in the following way:

- `gene.data` A matrix with gene expression data. Rows are genes (HUGO ids) and columns are samples.
- `set.data` A matrix with expression data for the gene sets. Rows are gene sets and columns are samples.
- `affy.loc` A vector that contains the row numbers corresponding to the genes that are reported in the annotation system chosen
- `gene2set.mat` A matrix that where each row represents a gene and each column contains the gene set to which this gene is reported based on the annotation system chosen.
- `set2gene.mat` A matrix that where each row represents a gene set and each column contains the genes reported to be in the set based on the annotation system chosen.
- `Set.obj` A vector with the gene sets set as objective nodes in the network.
- `Set.src` A vector with the gene sets set as source nodes in the network.
- `G.obj` A vector with the genes set as objective nodes in the network.
- `G.src` A vector with the genes set as source nodes in the network.

Details

This data set is calculated for the particular case were it is of interest to obtain the Functional Network for a toy dataset based on the breastCancerVDX dataset and the annotation system chosen is the MF from GO. The phenotype chose are the samples with Estrogen receptor negative (ER-).

Author(s)

A. Quiroz-Zarate. <aquiroz@jimmy.harvard.edu>

References

Quiroz-Zarate A, Haibe-Kains, B and Quackenbush J (2013). "Manuscript in preparation".

Examples

```
# See Package Vignette for a detailed example of the usage of this dataset  
# vignette("FunctionalNetworks")
```

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