Package 'grndata'

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Type Package

Title Synthetic Expression Data for Gene Regulatory Network Inference

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Description Simulated expression data for five large Gene Regulatory Networks from different simulators

LazyLoad yes

LazyData yes

License GPL-3

Suggests RUnit, BiocGenerics, knitr

VignetteBuilder knitr

biocViews ExperimentData, NetworkInference, GeneExpression, Microarray, GeneRegulation, Network

Depends R (>= 2.10)

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`Availabledata` *Available datasources*

Description

Availabledata contains a character vector with the names of the datasources that the package contains.

Usage

```
data("Availabledata")
```

Format

A character vector with the names of the datasources.

Value

`character vector` with the names of the datasources.

Examples

```
data(Availabledata)
cat(Availabledata)
```

getData *Datasource and underlying network loading*

Description

Function to load a gene expression datasource and the network that have generate it.

Usage

```
getData(datasource.name=NULL,getNet=TRUE)
```

Arguments

datasource.name	A character containing the name of network datasources to (default: NULL).
getNet	Logical specifying if the true underlying network should be returned (default: TRUE).

Details

If getNet is TRUE the function will return a list with two components:

1. A data.frame with the specified datasoruce.
2. A matrix with the true underlying network.

Value

The function getData loads the specified datasource by datasource.name and its true underlying network if it is specified by getNet.

Examples

```
# Get only datasource
data <- getData(datasource.name="syntren300",getNet=FALSE)
# Get the datasource and network in a list
mydata <- getData(datasource.name="syntren1000")
data <- mydata[[1]]
net <- mydata[[2]]
```

gnw1565.data *Simulated Gene Expression Data*

Description

Dataset containing 1565 samples and 1565 genes generated by the publicly available GNW generator using an ecoli source network with no added noise.

Usage

```
data(gnw1565.data)
```

Format

gnw1565.data is a data frame containing 1565 rows and 1565 columns. Each row contains a simulated microarray experiment and each column contains a gene. The dataset was generated with GNW generator which relies on ODEs for modeling gene regulation.

Value

data.frame containg the data.

Source

GNW v3.1 with source network : Ecoli

References

Schaffter, Thomas, Daniel Marbach, and Dario Floreano. "GeneNetWeaver: in silico benchmark generation and performance profiling of network inference methods." Bioinformatics 27.16 (2011): 2263-2270.

See Also

gnw1565.net, gnw2000.data, rogers1000.data, syntren300.data, syntren1000.data

Examples

```
data(gnw1565.data)
# Print size
print(dim(gnw1565.data))
```

gnw1565.net *Simulated Gene Expression Data*

Description

True underlying network used to generate the dataset at gnw1565.data.

Usage

```
data(gnw1565.net)
```

Format

true.net is the true underlying network used to generate the dataset loaded at gnw1565.data.

Value

matrix containg underlying network.

Source

GNW v3.1 with source network : Ecoli

References

Schaffter, Thomas, Daniel Marbach, and Dario Floreano. "GeneNetWeaver: in silico benchmark generation and performance profiling of network inference methods." Bioinformatics 27.16 (2011): 2263-2270.

See Also

gnw1565.data, gnw2000.data, rogers1000.data, syntren300.data, syntren1000.data

Examples

```
data(gnw1565.net)
# Number of directed edges
nEdges<- sum(gnw1565.net)
```

gnw2000.data *Simulated Gene Expression Data*

Description

Dataset containing 2000 samples and 2000 genes generated by the publicly available GNW generator using a yeast source network with no added noise.

Usage

```
data(gnw2000.data)
```

Format

gnw2000.data is a data frame containing 2000 rows and 2000 columns. Each row contains a simulated microarray experiment and each column contains a gene. The dataset was generated with GNW generator which relies on ODEs for modeling gene regulation.

Value

data.frame containg the data.

Source

GNW v3.1 with source network : Yeast

References

Schaffter, Thomas, Daniel Marbach, and Dario Floreano. "GeneNetWeaver: in silico benchmark generation and performance profiling of network inference methods." Bioinformatics 27.16 (2011): 2263-2270.

See Also

gnw2000.net, gnw1565.data, rogers1000.data, syntren300.data, syntren1000.data

Examples

```
data(gnw2000.data)
# Print size
print(dim(gnw2000.data))
```

gnw2000.net *Simulated Gene Expression Data*

Description

True underlying network used to generate the dataset at gnw2000.data.

Usage

```
data(gnw2000.net)
```

Format

true.net is the true underlying network used to generate the dataset loaded at gnw2000.data.

Value

matrix containg underlying network.

Source

GNW v3.1 with source network : Yeast

References

Schaffter, Thomas, Daniel Marbach, and Dario Floreano. "GeneNetWeaver: in silico benchmark generation and performance profiling of network inference methods." Bioinformatics 27.16 (2011): 2263-2270.

See Also

gnw2000.data, gnw1565.data, rogers1000.data, syntren300.data, syntren1000.data

Examples

```
data(gnw2000.net)
# Number of directed edges
nEdges<- sum(gnw2000.net)
```

rogers1000.data *Simulated Gene Expression Data*

Description

Dataset containing 1000 samples and 1000 genes generated by the publicly available generator using a power-law tail topology network with no added noise.

Usage

```
data(rogers1000.data)
```

Format

rogers1000.data is a data frame containing 1000 rows and 1000 columns. Each row contains a simulated microarray experiment and each column contains a gene.

Value

data.frame containg the data.

Source

sRogers with Power-law tail topology

References

Rogers, Simon, and Mark Girolami. "A Bayesian regression approach to the inference of regulatory networks from gene expression data." Bioinformatics 21.14 (2005): 3131-3137.

See Also

rogers1000.net, gnw1565.data, gnw2000.data, syntren300.data, syntren1000.data

Examples

```
data(rogers1000.data)
# Print size
print(dim(rogers1000.data))
```

rogers1000.net *Simulated Gene Expression Data*

Description

True underlying network used to generate the dataset at rogers1000.data.

Usage

```
data(rogers1000.net)
```

Format

true.net is the true underlying network used to generate the dataset loaded at rogers1000.data.

Value

matrix containg underlying network.

Source

sRogers with Power-law tail topology

References

Rogers, Simon, and Mark Girolami. "A Bayesian regression approach to the inference of regulatory networks from gene expression data." Bioinformatics 21.14 (2005): 3131-3137.

See Also

rogers1000.data, gnw1565.data, gnw2000.data, syntren300.data, syntren1000.data

Examples

```
data(rogers1000.net)
# Number of directed edges
nEdges<- sum(rogers1000.net)
```

syntren1000.data *Simulated Gene Expression Data*

Description

Dataset containing 1000 samples and 1000 genes generated by the publicly available SynTReN generator using an ecoli source network.

Usage

```
data(syntren1000.data)
```

Format

syntren1000.data is a data frame containing 1000 rows and 1000 columns. Each row contains a simulated microarray experiment and each column contains a gene.

Value

data.frame containg the data.

Source

SynTReN 1.1.3 with source network : ecoli_nn.sif

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): 43.

See Also

gnw1565.data, gnw2000.data, rogers1000.data, syntren300.data

Examples

```
data(syntren1000.data)
# Print size
print(dim(syntren1000.data))
```

syntren1000.net *Simulated Gene Expression Data*

Description

True underlying network used to generate the dataset at syntren1000.data.

Usage

```
data(syntren1000.net)
```

Format

syntren1000.net is the true underlying network used to generate the dataset loaded at syntren1000.data.

Value

matrix containg underlying network.

Source

SynTReN 1.1.3 with source network : ecoli_nn.sif

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): 43.

See Also

syntren1000.data,gnw1565.data, gnw2000.data, rogers1000.data, syntren300.data

Examples

```
data(syntren1000.net)
# Number of directed edges
nEdges<- sum(syntren1000.net)
```

syntren300.data *Simulated Gene Expression Data*

Description

Dataset containing 800 samples and 300 genes generated by the publicly available SynTReN generator using an ecoli source network.

Usage

```
data(syntren300.data)
```

Format

syntren300.data is a data frame containing 800 rows and 300 columns. Each row contains a simulated microarray experiment and each column contains a gene.

Value

data.frame containg the data.

Source

SynTReN 1.1.3 with source network : ecoli_nn.sif

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): 43.

See Also

syntren300.net, syntren1000.data, rogers1000.data, gnw1565.data, gnw2000.data

Examples

```
data(syntren300.data)
# Print size
print(dim(syntren300.data))
```

syntren300.net *Simulated Gene Expression Data*

Description

True underlying network used to generate the dataset at syntren300.data.

Usage

```
data(syntren300.net)
```

Format

true.net is the true underlying network used to generate the dataset loaded at syntren300.data.

Value

matrix containg underlying network.

Source

SynTReN 1.1.3 with source network : ecoli_nn.sif

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): 43.

See Also

syntren300.data, syntren1000.data, rogers1000.data, gnw1565.data, gnw2000.data

Examples

```
data(syntren300.net)
# Number of directed edges
nEdges<-sum(syntren300.net)
```

toy.data *Simulated Toy example of Gene Expression Data*

Description

Dataset containing 64 samples and 64 genes generated by the publicly available GNW generator using an ecoli source network.

Usage

```
data(toy.data)
```

Format

`toy.data` is a data frame containing 64 rows and 64 columns. Each row contains a simulated microarray experiment and each column contains a gene.

Value

`data.frame` containg the data.

Source

GNW v3.1 with source network : Example (Ecoli)

References

Schaffter, Thomas, Daniel Marbach, and Dario Floreano. "GeneNetWeaver: in silico benchmark generation and performance profiling of network inference methods." Bioinformatics 27.16 (2011): 2263-2270.

See Also

`toy.net`

Examples

```
data(toy.data)
# Print size
print(dim(toy.data))
```

toy.net *Simulated Toy example of Gene Expression Data*

Description

True underlying network used to generate the dataset at toy.data.

Usage

```
data(toy.net)
```

Format

toy.net is the true underlying network used to generate the dataset loaded at toy.data.

Value

matrix containg underlying network.

Source

GNW v3.1 with source network : Example (Ecoli)

References

Schaffter, Thomas, Daniel Marbach, and Dario Floreano. "GeneNetWeaver: in silico benchmark generation and performance profiling of network inference methods." Bioinformatics 27.16 (2011): 2263-2270.

See Also

toy.data

Examples

```
data(toy.net)
# Print size
nEdges<- sum(toy.net)
```

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