

Package ‘grndata’

February 18, 2025

Type Package

Title Synthetic Expression Data for Gene Regulatory Network Inference

Version 1.39.0

Date 2014-12-01

Author Pau Bellot, Catharina Olsen, Patrick E Meyer

Maintainer Pau Bellot <pau.bellot@upc.edu>

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)

git_url <https://git.bioconductor.org/packages/grndata>

git_branch devel

git_last_commit be59265

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2025-02-18

Contents

Availabledata	2
getData	3
gnw1565.data	4
gnw1565.net	5

gnw2000.data	6
gnw2000.net	7
rogers1000.data	8
rogers1000.net	9
syntren1000.data	10
syntren1000.net	11
syntren300.data	12
syntren300.net	13
toy.data	14
toy.net	15
Index	16

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	<i>Datasource and underlying network loading</i>
---------	--

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 containing 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 containing 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 containing 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 containing 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 containing 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	<i>Simulated Gene Expression Data</i>
----------------	---------------------------------------

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 containing 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	<i>Simulated Gene Expression Data</i>
-----------------	---------------------------------------

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 containing 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	<i>Simulated Gene Expression Data</i>
----------------	---------------------------------------

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 containing 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)
```

Index

* datasets

Availabledata, 2
gnw1565.data, 4
gnw1565.net, 5
gnw2000.data, 6
gnw2000.net, 7
rogers1000.data, 8
rogers1000.net, 9
syntren1000.data, 10
syntren1000.net, 11
syntren300.data, 12
syntren300.net, 13
toy.data, 14
toy.net, 15

* misc

getData, 3

Availabledata, 2

getData, 3

gnw1565.data, 4, 5–13

gnw1565.net, 4, 5

gnw2000.data, 4, 5, 6, 7–13

gnw2000.net, 6, 7

rogers1000.data, 4–7, 8, 9–13

rogers1000.net, 8, 9

syntren1000.data, 4–9, 10, 11–13

syntren1000.net, 11

syntren300.data, 4–11, 12, 13

syntren300.net, 12, 13

toy.data, 14, 15

toy.net, 14, 15