

Package ‘grndata’

October 7, 2025

Type Package

Title Synthetic Expression Data for Gene Regulatory Network Inference

Version 1.41.0

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 1ef7035

git_last_commit_date 2025-04-15

Repository Bioconductor 3.22

Date/Publication 2025-10-07

Contents

Availabledata	2
getData	2
gnw1565.data	3
gnw1565.net	4
gnw2000.data	5
gnw2000.net	6
rogers1000.data	6
rogers1000.net	7

syntren1000.data	8
syntren1000.net	9
syntren300.data	9
syntren300.net	10
toy.data	11
toy.net	12

Index	13
--------------	-----------

Availabledata	<i>Available datasources</i>
---------------	------------------------------

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 `datasource`.
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 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 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 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 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

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 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*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 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

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	<i>Simulated Toy example of Gene Expression Data</i>
----------	--

Description

Dataset containing 64 samples and 64 genes generated by the publicly available GNW generator using an ecol 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, [3](#)
gnw1565.net, [4](#)
gnw2000.data, [5](#)
gnw2000.net, [6](#)
rogers1000.data, [6](#)
rogers1000.net, [7](#)
syntren1000.data, [8](#)
syntren1000.net, [9](#)
syntren300.data, [9](#)
syntren300.net, [10](#)
toy.data, [11](#)
toy.net, [12](#)

* misc

getData, [2](#)

Availabledata, [2](#)

getData, [2](#)

gnw1565.data, [3](#), [4–11](#)

gnw1565.net, [4](#), [4](#)

gnw2000.data, [4](#), [5](#), [6–11](#)

gnw2000.net, [5](#), [6](#)

rogers1000.data, [4–6](#), [6](#), [7–11](#)

rogers1000.net, [7](#), [7](#)

syntren1000.data, [4–8](#), [8](#), [9–11](#)

syntren1000.net, [9](#)

syntren300.data, [4–9](#), [9](#), [10](#), [11](#)

syntren300.net, [10](#), [10](#)

toy.data, [11](#), [12](#)

toy.net, [11](#), [12](#)