

# Package ‘BoolNet’

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**Type** Package

**Title** Generation, reconstruction, simulation and analysis of  
synchronous, asynchronous, and probabilistic Boolean networks

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**Suggests** igraph, XML

**Description** Provides methods to reconstruct and generate synchronous, asynchronous, and probabilistic Boolean networks, and to analyze and visualize attractors in Boolean networks

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**LazyLoad** yes

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BoolNet-package	<i>Analyze Boolean networks</i>
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**Description**

Tools for reconstruction, analysis and visualization of synchronous, asynchronous, and probabilistic Boolean networks, in particular for the identification of attractors in gene-regulatory networks

**Details**

Package:	BoolNet
Type:	Package
Version:	1.50
Date:	2012-04-10

License: Artistic-2.0  
LazyLoad: yes

This package provides useful methods for the construction and generation of Boolean networks and for their analysis. In particular, it is designed for the analysis of gene-regulatory networks. The software supports three types of networks:

**Synchronous Boolean networks** These networks consist of a set of Boolean variables (genes)  $X$  and a set of transition functions, one for each variable. These transition functions map an input from the set  $X$  to a Boolean value. A state is a vector of values for each of the variables in  $X$ . Then, the next state of the network is calculated by applying *all* transition functions to the state.

**Asynchronous Boolean networks** Asynchronous networks have the same structure as synchronous Boolean networks. Yet, the next state of the network is calculating by choosing only *one* of the transition functions at random and updating the corresponding Boolean variable (gene). This corresponds to the assumption that in a genetic network, gene expression levels are likely to change at different points of time.

**Probabilistic Boolean networks** Probabilistic networks allow for specifying more than one transition function per variable/gene. Each of these functions has a probability to be chosen, where the probabilities of all functions for one variable sum up to 1. Transitions are performed synchronously by choosing one transition function for each gene according to their probabilities and applying them to the current state.

Networks can be assembled in several ways using **BoolNet**: The `reconstructNetwork` function infers Boolean networks from time series of measurements using several popular reconstruction algorithms. `binarizeTimeSeries` provides a means of binarizing real-valued time series for these reconstruction algorithms. Boolean networks (synchronous, asynchronous, and probabilistic networks) can also be expressed in a description language and loaded from files using `loadNetwork`. Furthermore, networks can be imported from BioTapestry using `loadBioTapestry`. Via `generateRandomNKNetwork` and `perturbNetwork`, the package supports various methods of generating random networks and perturbing existing networks for robustness analysis.

The `getAttractors` function identifies attractor cycles in a synchronous or asynchronous Boolean network. Attractors can be identified by exhaustive search or heuristic methods.

The `markovSimulation` function identifies relevant states in probabilistic Boolean networks by performing a Markov chain simulation.

The package also provides methods to visualize state transitions and basins of attraction (`plotPBNTransitions`, `plotStateGraph`), to plot the wiring of a network (`plotNetworkWiring`), to plot attractor state tables (`plotAttractors`) and sequences of states (`plotSequence`), and to export them to LaTeX (`attractorsToLaTeX` and `sequenceToLaTeX`) and Pajek (`toPajek`).

Transition tables of the network can be analyzed using `getTransitionTable`. Paths from start states to their corresponding attractors are identified using `getPathToAttractor`.

#### Author(s)

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## References

S. A. Kauffman (1969), Metabolic stability and epigenesis in randomly constructed nets. *J. Theor. Biol.* 22:437–467.

S. A. Kauffman (1993), *The Origins of Order*. Oxford University Press.

Further references are listed in the corresponding help sections.

## Examples

```
#####
# Example 1: identify attractors #
#####

# load example data
data(cellcycle)

# get all synchronous attractors by exhaustive search
attractors <- getAttractors(cellcycle)

# plot attractors side by side
par(mfrow=c(2,length(attractors$attractors)))
plotAttractors(attractors)

# identifies asynchronous attractors
attractors <- getAttractors(cellcycle,
                             type="asynchronous", startStates=100)
plotAttractors(attractors, mode="graph")

#####
# Example 2: reconstruct a network #
#####

# load example data
data(yeastTimeSeries)

# perform binarization with k-means
bin <- binarizeTimeSeries(yeastTimeSeries)

# reconstruct networks from transition table
net <- reconstructNetwork(bin$binarizedMeasurements,
                           method="bestfit", maxK=3)

# analyze the network using a Markov chain simulation
print(markovSimulation(net, returnTable=FALSE))
```

## Description

Exports state tables of attractors (corresponding to the plot generated by `plotAttractors` with `mode="table"`) to a LaTeX document.

## Usage

```
attractorsToLaTeX(attractorInfo,
                  subset,
                  title = "",
                  grouping = list(),
                  plotFixed = TRUE,
                  onColor = "[gray]{0.9}",
                  offColor = "[gray]{0.6}",
                  file = "attractors.tex")
```

## Arguments

<code>attractorInfo</code>	An object of class <code>AttractorInfo</code> , as returned by <code>getAttractors</code>
<code>subset</code>	An subset of attractors to be exported. This is a vector of attractor indices in <code>attractorInfo</code> .
<code>grouping</code>	An optional structure to form groups of genes in the plot. This is a list with the following elements:  <b>class</b> A vector of names for the groups. These names will be printed in the region belonging to the group in the table. <b>index</b> A list with the same length as <code>class</code> . Each element is a vector of gene indices belonging to the group.
<code>title</code>	An optional title for the plot
<code>plotFixed</code>	If this is true, genes with fixed values are included in the plot. Otherwise, these genes are not shown.
<code>onColor</code>	An optional color value for the 1/ON values in the table. Defaults to dark grey.
<code>offColor</code>	An optional color value for the 0/OFF values in the table. Defaults to light grey.
<code>file</code>	The file to which the LaTeX document is written. Defaults to "attractors.tex".

## Details

This function creates LaTeX tables that visualize the states of synchronous attractors. Asynchronous attractors are ignored. Attractors in `attractorInfo` are first grouped by length. Then, a LaTeX table environment is created for each attractor length (i.e. one plot with all attractors consisting of 1 state, one plot with all attractors consisting of 2 states, etc.). The output file does not contain a document header and requires the inclusion of the packages `tabularx` and `colortbl`. The tables have the genes in the rows and the states of the attractors in the columns. If not specified otherwise, cells of the table are light grey for 0/OFF values and dark grey for 1/ON values. If `grouping` is set, the genes are rearranged according to the indices in the group, horizontal separation lines are plotted between the groups, and the group names are printed.

**Value**

A list of matrices corresponding to the plots is returned. Each of these matrices has the genes in the rows and the states of the attractors in the columns.

**See Also**

[getAttractors](#), [plotAttractors](#), [sequenceToLaTeX](#), [plotSequence](#)

**Examples**

```
# load example data
data(cellcycle)

# get attractors
attractors <- getAttractors(cellcycle)

# output LaTeX document
attractorsToLaTeX(attractors, file="attractors.tex")
```

---

binarizeTimeSeries      *Binarize a set of real-valued time series*

---

**Description**

Binarizes a set of real-valued time series using k-means clustering, edge detection, or scan statistics.

**Usage**

```
binarizeTimeSeries(measurements,
                   method = c("kmeans", "edgeDetector", "scanStatistic"),
                   nstart = 100,
                   iter.max = 1000,
                   edge = c("firstEdge", "maxEdge"),
                   scaling = 1,
                   windowSize = 0.25,
                   sign.level = 0.1,
                   dropInsignificant = FALSE)
```

**Arguments**

measurements	A list of matrices, each corresponding to one time series. Each row of these matrices contains real-valued measurements for one gene on a time line, i. e. column $i+1$ contains the successor states of column $i$ . The genes must be the same for all matrices in the list.
method	The employed binarization technique. "kmeans" uses k-means clustering for binarization. "edgeDetector" searches for a large gradient in the sorted measurements. "scanStatistic" searches for accumulations in the measurements. See Details for descriptions of the techniques.

nstart	If method="kmeans", this is the number of restarts for k-means. See <a href="#">kmeans</a> for details.
iter.max	If method="kmeans", the maximum number of iterations for k-means. See <a href="#">kmeans</a> for details.
edge	If method="edgeDetector", this decides which of the edges is used as a threshold for binarization. If set to "firstEdge", the binarization threshold is the first combination of two successive sorted values whose difference exceeds a predefined value (average gradient * scaling). The parameter scaling can be used to adjust this value.  If set to "maxEdge", the binarization threshold is the position of the edge with the overall highest gradient.
scaling	If method="edgeDetector" and edge="firstEdge", this holds the scaling factor used for adjustment of the average gradient.
windowSize	If method="scanStatistic", this specifies the size of the scanning window (see Details). The size is given as a fraction of the whole range of input values for a gene. Default is 0.25.
sign.level	If method="scanStatistic", the significance level used for the scan statistic (see Details).
dropInsignificant	If this is set to true, genes whose binarizations are insignificant in the scan statistic (see Details) are removed from the binarized time series. Otherwise, a warning is printed if such genes exist.

## Details

This method supports three binarization techniques:

**k-means clustering** For each gene, k-means clusterings are performed to determine a good separation of groups. The values belonging to the cluster with the smaller centroid are set to 0, and the values belonging to the greater centroid are set to 1.

**Edge detector** This approach first sorts the measurements for each gene. In the sorted measurements, the algorithm searches for differences of two successive values that satisfy a predefined condition: If the "firstEdge" method was chosen, the pair of values whose difference exceeds the scaled average gradient of all values is chosen and used as maximum and minimum value of the two groups. If the "maxEdge" method was chosen, the largest difference between two successive values is taken. For details, see Shmulevich et al.

**Scan statistic** The scan statistic assumes that the measurements for each gene are uniformly and independently distributed independently over a certain range. The scan statistic shifts a scanning window across the data and decides for each window position whether there is an unusual accumulation of data points based on an approximated test statistic (see Glaz et al.). The window with the smallest p-value is remembered. The boundaries of this window form two thresholds, from which the value that results in more balanced groups is taken for binarization. Depending on the supplied significance level, gene binarizations are rated according to the p-value of the chosen window.

**Value**

Returns a list with the following elements:

binarizedMeasurements	A list of matrices with the same structure as measurements containing the binarized time series measurements
reject	If method="scanStatistic", a Boolean vector indicating for each gene whether the scan statistic algorithm was able to find a significant binarization window (FALSE) or not (TRUE). Rejected genes should probably be excluded from the data.
thresholds	The thresholds used for binarization

**References**

I. Shmulevich and W. Zhang (2002), Binary analysis and optimization-based normalization of gene expression data. *Bioinformatics* 18(4):555–565.

J. Glaz, J. Naus, S. Wallenstein (2001), *Scan Statistics*. New York: Springer.

**See Also**

[reconstructNetwork](#)

**Examples**

```
# load test data
data(yeastTimeSeries)

# perform binarization with k-means
bin <- binarizeTimeSeries(yeastTimeSeries)
print(bin)

# perform binarization with scan statistic
# - will find and remove 2 insignificant genes!
bin <- binarizeTimeSeries(yeastTimeSeries, method="scanStatistic",
                          dropInsignificant=TRUE, sign.level=0.2)
print(bin)

# perform binarization with edge detector
bin <- binarizeTimeSeries(yeastTimeSeries, method="edgeDetector")
print(bin)

# reconstruct a network from the data
reconstructed <- reconstructNetwork(bin$binarizedMeasurements,
                                   method="bestfit", maxK=4)
print(reconstructed)
```

---

cellcycle	<i>Mammalian cell cycle network</i>
-----------	-------------------------------------

---

**Description**

The mammalian cell cycle network as described by Faure et al.

**Usage**

```
data(cellcycle)
```

**Details**

The data consists of a variable `cellcycle` of class `BooleanNetwork` with 10 genes describing the four phases of the mammalian cell cycle. The network has one steady-state attractor. Furthermore, it has one synchronous attractor with 7 states and one asynchronous complex/loose attractor with 112 states. The class `BooleanNetwork` is described in more detail in [loadNetwork](#).

**Source**

A. Faure, A. Naldi, C. Chaouiya and D. Thieffry (2006), Dynamical analysis of a generic Boolean model for the control of the mammalian cell cycle. *Bioinformatics* 22(14):e124–e131.

**Examples**

```
data(cellcycle)

# the network is stored in a variable called 'cellcycle'
print(cellcycle)
```

---

chooseNetwork	<i>Extract a single Boolean network from a probabilistic Boolean network</i>
---------------	--

---

**Description**

Creates a `BooleanNetwork` object with exactly one function per gene by extracting a specified set of transition functions from a `ProbabilisticBooleanNetwork` object.

**Usage**

```
chooseNetwork(probabilisticNetwork, functionIndices)
```

**Arguments**

`probabilisticNetwork`  
A ProbabilisticBooleanNetwork object as returned by [reconstructNetwork](#) or [loadNetwork](#)

`functionIndices`  
A vector of function indices with one entry for each gene

**Value**

Returns an object of class `BooleanNetwork` consisting of the transition functions whose indices were specified in `functionIndices`. The class `BooleanNetwork` is described in more detail in [loadNetwork](#).

Constant genes are automatically fixed (e.g. knocked-out or over-expressed). This means that they are always set to the constant value, and states with the complementary value are not considered in transition tables etc. If you would like to change this behaviour, use [fixGenes](#) to reset the fixing.

**See Also**

[reconstructNetwork](#), [loadNetwork](#)

**Examples**

```
# load example data
data(examplePBN)

# extract a unique network
# - always use the first function
net <- chooseNetwork(examplePBN, rep(1, length(examplePBN$genes)))

# get attractors from this network
print(getAttractors(net))
```

---

examplePBN

*An artificial probabilistic Boolean network*

---

**Description**

An artificial probabilistic Boolean network example introduced by Shmulevich et al.

**Usage**

```
data(examplePBN)
```

**Details**

This artificial network is introduced by Shmulevich et al. for a step-by-step description of their Markov chain algorithm. It is included as a general example for a probabilistic Boolean network. The network consists of 3 genes, where gene 1 and gene 3 have two alternative transition functions, and gene 2 has a unique transition function.

**Source**

I. Shmulevich, E. R. Dougherty, S. Kim, W. Zhang (2002), Probabilistic Boolean networks: a rule-based uncertainty model for gene regulatory networks. *Bioinformatics* 18(2):261–274.

**Examples**

```
data(examplePBN)

# the network is stored in a variable called 'examplePBN'
print(examplePBN)
```

---

 fixGenes

---

*Simulate knocked-out or over-expressed genes*


---

**Description**

Simulates knocked-out or over-expressed genes by fixing the values of genes to 0 or 1, or turn off knock-out or over-expression of genes.

**Usage**

```
fixGenes(network, fixIndices, values)
```

**Arguments**

network	The original network of class BooleanNetwork or ProbabilisticBooleanNetwork containing the genes to be fixed
fixIndices	A vector of names or indices of the genes to be fixed
values	Either one single value, or a vector with the same length as fixIndices. For each gene, a value of 1 means that the gene is always turned on (over-expressed), a value of 0 means that the gene is always turned off (knocked-out), and a value of -1 means that the gene is not fixed.

**Value**

Depending on the input, an object of class BooleanNetwork or ProbabilisticBooleanNetwork containing the fixed genes is returned. The classes BooleanNetwork and ProbabilisticBooleanNetwork is described in more detail in [loadNetwork](#).

**See Also**[loadNetwork](#)**Examples**

```
# load example data
data(cellcycle)

# knock out gene CycD (index 1)
net <- fixGenes(cellcycle, 1, 0)
# or
net <- fixGenes(cellcycle, "CycD", 0)

# get attractors by exhaustive search
attractors <- getAttractors(net)

print(attractors)
```

---

```
generateRandomNKNetwork
```

*Generate a random N-K Boolean network*

---

**Description**

Generates a random N-K Boolean network (see Kauffman, 1969) using different configurations for the topology, the linkage, and the functions.

**Usage**

```
generateRandomNKNetwork(n, k,
                        topology = c("fixed", "homogeneous", "scale_free"),
                        linkage = c("uniform", "lattice"),
                        functionGeneration = c("uniform", "biased"),
                        validationFunction, failureIterations=10000,
                        simplify = FALSE, noIrrelevantGenes=TRUE,
                        readableFunctions = FALSE,
                        d_lattice = 1, zeroBias = 0.5,
                        gamma = 2.5, approx_cutoff = 100)
```

**Arguments**

n	The total number of genes in the network
k	If this is a single number, this is either the maximum number of genes in the input of a transition function (for topology="fixed" and topology="scale_free") or the mean number of genes in the input of a function (for topology="homogeneous"). If topology="fixed", this can also be a vector with n elements specifying the number of input genes for each gene separately.

topology	<p>If set to "fixed", all transition functions of the network depend on exactly k input genes (unless there are irrelevant input genes to be removed if simplify=TRUE and noIrrelevantGenes=FALSE).</p> <p>If set to "homogeneous", the number of input genes is drawn independently at random from a Poisson distribution with <math>\lambda = k</math>.</p> <p>If set to "scale_free", the number of input genes of each function is drawn from a Zeta distribution with parameter <math>\gamma</math>.</p>
linkage	<p>If this parameter is "uniform", the actual input genes are drawn uniformly at random from the total k genes.</p> <p>If set to "lattice", only genes from the neighbourhood <math>(i - d\_lattice * k\_i):(i + d\_lattice * k\_i)</math> are taken, which means that all genes are dependent from other genes in the direct neighbourhood.</p>
functionGeneration	<p>If set to "uniform", the truth table result column of the function is filled uniformly at random with 0 and 1. If set to "biased", a bias is introduced, where the probability of drawing a 0 is determined by the parameter zeroBias.</p>
validationFunction	<p>An optional function that restricts the generated Boolean functions to certain classes. The function should have two input parameter input and func that receive a candidate function. input is a matrix of 0/1 integer values specifying the input part of the truth table of the candidate function, with the input genes in the columns. Each of the <math>2^k</math> rows of input (where k is the number of input genes) corresponds to one entry of func, which is an integer vector of 0/1 values corresponding to the output of the candidate function. The validation function should return TRUE if the candidate function is accepted or FALSE if it is rejected.</p>
failureIterations	<p>The maximum number of iterations the generator tries to generate a function that is accepted by validationFunction before it gives up and throws an error. Defaults to 10000.</p>
simplify	<p>If this is true, <a href="#">simplifyNetwork</a> is called to simplify the gene transition functions after the perturbation. This removes irrelevant input genes. Should not be used together with noIrrelevantGenes=TRUE, as this automatically generates a network that cannot be simplified any further. Defaults to FALSE.</p>
noIrrelevantGenes	<p>If set to true, gene transition functions are not allowed to contain irrelevant genes, i.e. the functions have exactly the number of input genes determined by the topology method. This means that the network cannot be simplified any further, and simplify should be turned off. The default value is TRUE.</p>
readableFunctions	<p>If this is true, readable DNF representations of the truth tables of the functions are generated. These DNF are displayed when the network is printed. The DNF representations are not minimized and can thus be very long. If set to FALSE, the truth table result column is displayed.</p>
d_lattice	<p>The dimension parameter for the lattice if linkage="lattice". Defaults to 1.</p>
zeroBias	<p>The bias parameter for biased functions for functionGeneration="biased". Defaults to 0.5 (no bias).</p>

gamma	The Gamma parameter of the Zeta distribution for topology="scale_free". Default is 2.5.
approx_cutoff	This parameter is only used with topology="scale_free". It sets the number of iterations in the sum used to approximate the Riemann Zeta function. Defaults to 100.

## Details

The function supports a high number of different configurations to generate random networks. Several of the parameters are only needed for special configurations. The generated networks have different structural properties. Refer to the literature for more details.

Constant genes are automatically fixed (e.g. knocked-out or over-expressed). This means that they are always set to the constant value, and states with the complementary value are not considered in transition tables etc. If you would like to change this behaviour, use [fixGenes](#) to reset the fixing.

## Value

An object of class `BooleanNetwork` containing the generated random network. The class `BooleanNetwork` is described in more detail in [loadNetwork](#).

## References

- S. A. Kauffman (1969), Metabolic stability and epigenesis in randomly constructed nets. *J. Theor. Biol.* 22:437–467.
- S. A. Kauffman (1993), *The Origins of Order*. Oxford University Press.
- M. Aldana (2003), Boolean dynamics of networks with scale-free topology. *Physica D* 185: 45–66.
- M. Aldana and S. Coppersmith and L. P. Kadanoff (2003), Boolean dynamics with random coupling. In E. Kaplan, J. E. Marsden and K. R. Sreenivasan (editors): *Perspectives and Problems in Nonlinear Science*, Springer.

## See Also

[perturbNetwork](#), [loadNetwork](#), [simplifyNetwork](#), [fixGenes](#)

## Examples

```
# generate different random networks
net1 <- generateRandomNKNetwork(n=10, k=10,
                                topology="scale_free",
                                linkage="uniform",
                                functionGeneration="uniform",
                                noIrrelevantGenes=FALSE,
                                simplify=TRUE)

net2 <- generateRandomNKNetwork(n=10, k=3,
                                topology="homogeneous",
                                linkage="lattice",
                                functionGeneration="uniform",
                                d_lattice=1.5,
```

```
                                simplify=TRUE)

net3 <- generateRandomNKNetwork(n=10, k=2,
                                topology="fixed",
                                linkage="uniform",
                                functionGeneration="biased",
                                noIrrelevantGenes=FALSE,
                                zeroBias=0.6)

# get attractors
print(getAttractors(net1))
print(getAttractors(net2))
print(getAttractors(net3))
```

---

generateState	<i>Generate a state vector from single gene values</i>
---------------	--

---

### Description

This function provides a simple interface to generate full state vectors by specifying only the genes of interest. For example, only those genes that are active can be specified, while the others are set to a default value.

### Usage

```
generateState(network,
              specs,
              default = 0)
```

### Arguments

network	An network of class BooleanNetwork or ProbabilisticBooleanNetwork for which a state is generated.
specs	A named vector specifying the genes to be set. Here, the names of the elements correspond to the gene names, and the elements correspond to the gene values.
default	The default value used for the unspecified genes (usually 0).

### Value

Returns a full state vector with one entry for each gene of the network.

### See Also

[getAttractors](#), [stateTransition](#)

**Examples**

```
# load cell cycle network
data(cellcycle)

# generate a state in which only CycD and CycA are active
state <- generateState(cellcycle, c("CycD"=1, "CycA"=1))
print(state)

# use the state as a start state for attractor search
print(getAttractors(cellcycle, startStates=list(state)))
```

---

generateTimeSeries      *Generate time series from a network*

---

**Description**

Generates time series by simulating successive state transitions from random start states. In addition, the resulting matrices can be perturbed by Gaussian noise.

**Usage**

```
generateTimeSeries(network,
                   numSeries,
                   numMeasurements,
                   type = c("synchronous", "asynchronous", "probabilistic"),
                   geneProbabilities,
                   noiseLevel = 0)
```

**Arguments**

network	An object of class BooleanNetwork that contains the network for which time series are generated
numSeries	The number of random start states used to generate successive series of states, that is, the number of time series matrices to generate
numMeasurements	The number of states in each of the time series matrices. The first state of each time series is the randomly generated start state. The remaining numMeasurements - 1 states are obtained by successive state transitions.
type	The type of state transitions to be performed (see <a href="#">stateTransition</a> )
geneProbabilities	An optional vector of probabilities for the genes if type="asynchronous". By default, each gene has the same probability to be chosen for the next state transition. These probabilities can be modified by supplying a vector of probabilities for the genes which sums up to one.
noiseLevel	If this is non-zero, it specifies the standard deviation of the Gaussian noise which is added to all entries of the time series matrices. By default, no noise is added to the time series.

**Value**

A list of matrices, each corresponding to one time series. Each row of these matrices contains measurements for one gene on a time line, i. e. column  $i+1$  contains the successor states of column  $i$ . If `noiseLevel` is non-zero, the matrices contain real values, otherwise they contain only 0 and 1.

The result format is compatible with the input parameters of [binarizeTimeSeries](#) and [reconstructNetwork](#).

**See Also**

[stateTransition](#), [binarizeTimeSeries](#), [reconstructNetwork](#)

**Examples**

```
# generate noisy time series from the cell cycle network
data(cellcycle)
ts <- generateTimeSeries(cellcycle, numSeries=50, numMeasurements=10, noiseLevel=0.1)

# binarize the noisy time series
bin <- binarizeTimeSeries(ts, method="kmeans")$binarizedMeasurements

# reconstruct the network
print(reconstructNetwork(bin, method="bestfit"))
```

---

getAttractors

*Identify attractors in a Boolean network*

---

**Description**

Identifies attractors (cycles) in a supplied Boolean network using synchronous or asynchronous state transitions

**Usage**

```
getAttractors(network,
               type = c("synchronous", "asynchronous"),
               method = c("exhaustive", "random", "chosen"),
               startStates = list(),
               genesON = c(), genesOFF = c(),
               canonical = TRUE,
               randomChainLength = 10000,
               avoidSelfLoops = TRUE,
               geneProbabilities = NULL,
               returnTable = TRUE)
```

**Arguments**

network	A network structure of class BooleanNetwork. These networks can be read from files by <code>loadNetwork</code> , generated by <code>generateRandomNKNetwork</code> , or reconstructed by <code>reconstructNetwork</code> .
type	<p>If type="synchronous", synchronous state transitions are used, i.e. all genes are updated at the same time. Synchronous attractor search can be performed in an exhaustive manner or using a heuristic that starts from predefined states.</p> <p>If type="asynchronous", asynchronous state transitions are performed, i.e. one (randomly chosen) gene is updated in each transition. Steady-state attractors are the same in asynchronous and synchronous networks, but the asynchronous search is also able to identify complex/loose attractors. Asynchronous search relies on a heuristic algorithm that starts from predefined states.</p> <p>See Details for more information on the algorithms.</p>
method	<p>The search method to be used. If "exhaustive", attractors are identified by exhaustive search of all <math>2^n</math> states (where n is the number of genes that are not set to a fixed value). This kind of search is only available for synchronous attractor search, and the maximum number of genes allowed for exhaustive search is 29, as R cannot allocate memory for larger state tables.</p> <p>If method is "random", startStates is interpreted as an integer value specifying the number of states to be generated randomly. The algorithm is then initialized with these random states and identifies the attractors to which these states lead.</p> <p>If method is "chosen", startStates is interpreted as a list of binary vectors, each specifying one input state. Each vector must have length(network\$genes) elements with 0 or 1 values. The algorithm identifies the attractors to which the supplied states lead.</p> <p>If method is not supplied, the desired method is inferred from the type of startStates. By default, if neither method nor startStates are provided, an exhaustive search is performed.</p>
startStates	The value of startStates depends on the chosen method. See method for more details.
genesON	A vector of genes whose values are fixed to 1, which reduces the complexity of the search. This is equivalent to a preceding call of <code>fixGenes</code> .
genesOFF	A vector of genes whose values are fixed to 0, which reduces the complexity of the search. This is equivalent to a preceding call of <code>fixGenes</code> .
canonical	If set to true, the states in the attractors are rearranged such that the state whose binary encoding makes up the smallest number is the first element of the vector. This ensures that attractors found by different heuristic runs of <code>getAttractors</code> are comparable, as the cycles may have been entered at different states in different runs of the algorithm.
randomChainLength	If type="asynchronous", this parameter specifies the number of random transitions performed by the search to enter a potential attractor (see Details). Defaults to 10000.

avoidSelfLoops	If type="asynchronous" and avoidSelfLoops=TRUE, the asynchronous attractor search only enters self loops (i.e. transitions that result in the same state) if none of the possible transitions can leave the state. This results in attractors with fewer edges. Otherwise, self loops are included in the attractors. By default, self loops are avoided.
geneProbabilities	If type="asynchronous", this allows to specify probabilities for the genes. By default, each gene has the same probability to be chosen for the next state transition. You can supply a vector of probabilities for each of the genes which sums up to one.
returnTable	Specifies whether a transition table is included in the returned AttractorInfo structure. If type="asynchronous", this parameter is ignored, as the asynchronous search never returns a transition table due to the large size.

## Details

There are three different modes of attractor search:

**Exhaustive synchronous search** In this mode, synchronous state transitions are carried out from each of the possible states until an attractor is reached. This identifies all synchronous attractors.

**Heuristic synchronous search** In contrast to exhaustive synchronous search, only a subset of the possible states is used. From these states, synchronous transitions are carried out until an attractor is reached. This subset is specified in startStates.

**Heuristic asynchronous search** This algorithm uses asynchronous state transitions and is able to identify steady-state and complex/loose attractors (see Harvey and Bossomaier, Garg et al.). These attractors are sets of states from which all possible asynchronous transitions lead into a state that is member of the set as well. The heuristic algorithm does the following for each of the input state specified by startStates:

1. Perform randomChainLength random asynchronous transitions. After these transitions, the network state is expected to be located in an attractor with a high probability.
2. Calculate the forward reachable set of the current state. Then, compare this set to the forward reachable set of all states in the set. If all sets are equal, a complex attractor is found.

Printing the return value of getAttractors using `print` visualizes the identified attractors.

## Value

A list of class AttractorInfo with components

attractors	A list of attractors. Each element is a 2-element list with the following components: <ul style="list-style-type: none"> <li><b>involvedStates</b> A matrix containing the states that make up the attractor. Each column represents one state. The entries are decimal numbers that internally represent the states of the genes. The number of rows depends on the number of genes in the network: The first 32 genes are encoded in the first row, genes 33-64 are encoded in the second row, etc.</li> </ul>
------------	--

	<p><b>initialStates</b> This element is only available if an asynchronous search was carried out and this is a complex attractor. In this case, it holds the encoded start states of the transitions in the complex attractor</p> <p><b>nextStates</b> This element is only available if an asynchronous search was carried out and this is a complex attractor. In this case, it holds the encoded successor states of the transitions in the complex attractor</p> <p><b>basinSize</b> The number of states in the basin of attraction. Details on the states in the basin can be retrieved via <a href="#">getBasinOfAttraction</a>.</p>
stateInfo	<p>A summary structure of class BooleanStateInfo containing information on the transition table. It has the following components:</p> <p><b>initialStates</b> This element is only available if type="synchronous", method is "random" or "chosen", and returnTable=TRUE. This is a matrix describing the initial states that lead to the states in table after a state transition. If method is "exhaustive", this component is NULL. In this case, the initial states can be inferred, as all states are used. The format of the matrix is described in involvedStates.</p> <p><b>table</b> This element is only available if type="synchronous" and returnTable=TRUE. It holds result vector of the transition table as a matrix with one column for each state. These are encoded bit vectors in decimal numbers as described above.</p> <p><b>attractorAssignment</b> This element is only available if type="synchronous" and returnTable=TRUE. It contains a vector that corresponds to the entries in table and describes the attractor index in attractors to which successive transitions from the described state finally lead.</p> <p><b>stepsToAttractor</b> This element is only available if type="synchronous" and returnTable=TRUE. Referring to attractorAssignment, this is the number of transitions needed to reach the attractor.</p> <p><b>genes</b> A list of names of the genes in network.</p> <p><b>fixedGenes</b> Specifies the fixed genes as in the fixed component of network.</p> <p>The structure supports pretty printing using the <a href="#">print</a> method.</p>

## References

- S. A. Kauffman (1969), Metabolic stability and epigenesis in randomly constructed nets. *J. Theor. Biol.* 22:437–467.
- S. A. Kauffman (1993), *The Origins of Order*. Oxford University Press.
- I. Harvey, T. Bossomaier (1997), Time out of joint: Attractors in asynchronous random Boolean networks. *Proc. of the Fourth European Conference on Artificial Life*, 67–75.
- A. Garg, A. Di Cara, I. Xenarios, L. Mendoza, G. De Micheli (2008): Synchronous versus asynchronous modeling of gene regulatory networks. *Bioinformatics* 24(17):1917–1925.

## See Also

[loadNetwork](#), [generateRandomNKNetwork](#), [plotAttractors](#), [attractorsToLaTeX](#), [getTransitionTable](#), [getBasinOfAttraction](#), [getAttractorSequence](#), [getStateSummary](#), [getPathToAttractor](#), [fixGenes](#), [generateState](#)

## Examples

```
# load example data
data(cellcycle)

# get all synchronous attractors by exhaustive search
attractors <- getAttractors(cellcycle)

# plot attractors side by side
par(mfrow=c(2, length(attractors$attractors)))
plotAttractors(attractors)

# finds the synchronous attractor with 7 states
attractors <- getAttractors(cellcycle, method="chosen",
                           startStates=list(rep(1, length(cellcycle$genes))))
plotAttractors(attractors)

# finds the attractor with 1 state
attractors <- getAttractors(cellcycle, method="chosen",
                           startStates=list(rep(0, length(cellcycle$genes))))
plotAttractors(attractors)

# identifies asynchronous attractors
attractors <- getAttractors(cellcycle, type="asynchronous", startStates=100)
plotAttractors(attractors, mode="graph")
```

---

getAttractorSequence *Decode the state sequence of a synchronous attractor*

---

## Description

Obtains the sequence of states belonging to a single synchronous attractor from the encoded data in an `AttractorInfo` structure.

## Usage

```
getAttractorSequence(attractorInfo, attractorNo)
```

## Arguments

<code>attractorInfo</code>	An object of class <code>AttractorInfo</code> , as returned by <code>getAttractors</code> . <code>getAttractors</code> must be called in synchronous mode.
<code>attractorNo</code>	The index of the attractor in <code>attractorInfo</code> whose state sequence should be obtained

## Value

Returns a data frame with the genes in the columns. The rows are the successive states of the attractor. The successor state of the last state (i.e. the last row) is the first state (i.e. the first row).

**See Also**

[getAttractors](#), [getPathToAttractor](#), [plotSequence](#), [sequenceToLaTeX](#)

**Examples**

```
# load example data
data(cellcycle)

# get attractors
attractors <- getAttractors(cellcycle)

# print basin of 7-state attractor
print(getAttractorSequence(attractors, 2))
```

---

getBasinOfAttraction    *Get states in basin of attraction*

---

**Description**

Extracts information on all states in the basin of a supplied attractor

**Usage**

```
getBasinOfAttraction(attractorInfo, attractorNo)
```

**Arguments**

**attractorInfo**    An object of class `AttractorInfo`, as returned by [getAttractors](#). As the transition table information in this structure is required, `getAttractors` must be called in synchronous mode and with `returnTable` set to `TRUE`.

**attractorNo**    The index of the attractor in `attractorInfo` whose basin should be identified

**Details**

The function outputs a transition table containing only the states that are contained in the basin of attraction, and displays additional information on these states. If `attractorInfo` is the result of an exhaustive synchronous attractor search, the complete basin of attraction is returned. If `attractorInfo` is the result of a heuristic synchronous search, there is no guarantee that the complete basin of attraction is returned, as only the calculated states are included. Asynchronous search results are not supported, as no transition table is calculated.

**Value**

Returns a generic dataframe of the class `TransitionTable`. For  $n$  genes, the first  $n$  columns code for the original state, i.e. each column represents the value of one gene. The next  $n$  columns code for the successive state after a transition. The column `attractorAssignment` indicates the attractor to the state is assigned (in this case, `attractorNo`), and the column `stepsToAttractor` indicates how many transitions are needed from the original state to the attractor. The `TransitionTable` class supports pretty printing using the `print` method.

**See Also**

[getStateSummary](#), [getTransitionTable](#), [getAttractors](#)

**Examples**

```
# load example data
data(cellcycle)

# get attractors
attractors <- getAttractors(cellcycle)

# print basin of first attractor
print(getBasinOfAttraction(attractors, 1))
```

---

`getPathToAttractor`      *Get state transitions between a state and its attractor*

---

**Description**

Lists the states in the path from a specified state to the corresponding synchronous attractor.

**Usage**

```
getPathToAttractor(network,
                   state,
                   includeAttractorStates = c("all", "first", "none"))
```

**Arguments**

<code>network</code>	Either a structure of class <code>BooleanNetwork</code> , or a structure of class <code>AttractorInfo</code> . In the former case, a synchronous attractor search starting from <code>state</code> is conducted. In the latter case, <code>network</code> must be the result of a call to <a href="#">getAttractors</a> with <code>returnTable=TRUE</code> , and its transition table must include <code>state</code> .
<code>state</code>	A binary vector with exactly one entry per gene in the network.
<code>includeAttractorStates</code>	Specifies whether the actual attractor states are included in the resulting table or not. If <code>includeAttractorStates = "all"</code> (which is the default behaviour), the sequence ends when the attractor was traversed once. If <code>includeAttractorStates</code>

= "first", only the first state of attractor is added to the sequence. This corresponds to the behaviour prior to **BoolNet** version 1.5. If includeAttractorStates = "none", the sequence ends with the last non-attractor state. In this case, the sequence can be empty if the start state is an attractor state.

### Value

Returns a data frame with the genes in the columns. The rows are the successive states from state to the the corresponding attractor. Depending on includeAttractorStates, attractor states are included or not.

### See Also

[getAttractors](#), [getTransitionTable](#), [getBasinOfAttraction](#)

### Examples

```
# load example network
data(cellcycle)

# get path from a state to its attractor
# include all attractor states
path <- getPathToAttractor(cellcycle, rep(1,10),
                           includeAttractorStates="all")
print(path)

# include only the first attractor state
path <- getPathToAttractor(cellcycle, rep(1,10),
                           includeAttractorStates="first")
print(path)

# exclude attractor states
path <- getPathToAttractor(cellcycle, rep(1,10),
                           includeAttractorStates="none")
print(path)
```

---

getStateSummary	<i>Retrieve summary information on a state</i>
-----------------	--

---

### Description

Returns information on the supplied state, i.e. the successive state after a transition, the (synchronous) attractor to which the state leads, and the distance to this attractor.

### Usage

```
getStateSummary(attractorInfo, state)
```

### Arguments

- `attractorInfo` An object of class `AttractorInfo`, as returned by [getAttractors](#). As the transition table information in this structure is required, `getAttractors` must be called in synchronous mode and with `returnTable` set to `TRUE`.
- `state` A 0-1 vector with `n` elements (where `n` is the number of genes in the underlying networks) describing the state.

### Value

Returns a generic dataframe of the class `TransitionTable`. For `n` genes, the first `n` columns code for the original state (in this case, the `state` parameter), i.e. each column represents the value of one gene. The next `n` columns code for the successive state after a transition. The column `attractorAssignment` indicates the attractor to the state is assigned, and the column `stepsToAttractor` indicates how many transitions are needed from the original state to the attractor. In this case, the table has only one row describing the supplied state. The `TransitionTable` class supports pretty printing using the [print](#) method.

### See Also

[getBasinOfAttraction](#), [getTransitionTable](#), [getAttractors](#)

### Examples

```
# load example data
data(cellcycle)

# get attractors
attractors <- getAttractors(cellcycle)

# print information for an arbitrary state
print(getStateSummary(attractors, c(1,1,1,1,1,1,1,1,1,1)))
```

---

`getTransitionProbabilities`

*Get a matrix of transitions and their probabilities in probabilistic Boolean networks*

---

### Description

Retrieves the state transitions and their probabilities in a probabilistic Boolean network. This takes the transition table information calculated by the [markovSimulation](#) method.

### Usage

```
getTransitionProbabilities(markovSimulation)
```

**Arguments**

markovSimulation

An object of class MarkovSimulation, as returned by [markovSimulation](#). As the transition table information in this structure is required, [markovSimulation](#) must be called with `returnTable` set to TRUE.

**Value**

Returns a data frame with the first `n` columns describing the values of the genes before the transition, the next `n` columns describing the values of the genes after the transition, and the last column containing the probability of the transition. Here, `n` is the number of genes in the underlying network. Only transitions with non-zero probability are included.

**See Also**

[markovSimulation](#)

**Examples**

```
# load example network
data(examplePBN)

# perform a Markov chain simulation
sim <- markovSimulation(examplePBN)

# print out the probability table
print(getTransitionProbabilities(sim))
```

---

getTransitionTable      *Retrieve the transition table of a network*

---

**Description**

Retrieves the transition table and additional attractor information of a network.

**Usage**

```
getTransitionTable(attractorInfo)
```

**Arguments**

attractorInfo      An object of class AttractorInfo, as returned by [getAttractors](#). As the transition table information in this structure is required, [getAttractors](#) must be called in synchronous mode and with `returnTable` set to TRUE.

## Details

Depending on the configuration of the call to `getAttractors` that returned `attractorInfo`, this function either returns the complete transition table (for exhaustive synchronous search) or the part of the transition table calculated in a heuristic synchronous search. Asynchronous search is not supported, as no transition table is calculated.

## Value

Returns a generic dataframe of the class `TransitionTable`. For  $n$  genes, the first  $n$  columns code for the original state (in this case, the `state` parameter), i.e. each column represents the value of one gene. The next  $n$  columns code for the successive state after a transition. The column `attractorAssignment` indicates the attractor to the state is assigned, and the column `stepsToAttractor` indicates how many transitions are needed from the original state to the attractor. The table has a row for each possible input state. The `TransitionTable` class supports pretty printing using the `print` method.

## See Also

[getStateSummary](#), [getBasinOfAttraction](#), [getAttractors](#)

## Examples

```
# load example data
data(cellcycle)

# get attractors
attractors <- getAttractors(cellcycle)

# print the transition table
print(getTransitionTable(attractors))
```

---

loadBioTapestry	<i>Import a network from BioTapestry</i>
-----------------	--

---

## Description

Imports a Boolean network from a BioTapestry file (\*.btp). BioTapestry is an interactive tool for building, visualizing, and simulating gene-regulatory networks, and can be accessed at <http://www.biotapestry.org>.

## Usage

```
loadBioTapestry(file)
```

## Arguments

`file` The name of the file to import. This must be a BioTapestry XML file (\*.btp).

**Details**

The function builds up a Boolean network by importing the nodes, the links between these nodes, and the simulation parameters of the top-level plot of a BioTapestry file. The BioTapestry network should have the following properties:

- All links should be either enhancers or repressors. Unspecified ("neutral") links are ignored.
- In the simulation parameters, each node should specify the correct logical function (AND, OR, XOR) for its inputs.
- Constant genes can be generated by modeling a gene without any input link and setting the simulation parameter `initVal` to 0 or 1.

**Value**

A network of class `BooleanNetwork`, as described in [loadNetwork](#).

**References**

W. J. R. Longabaugh, E. H. Davidson, H. Bolour (2005), Computational representation of developmental genetic regulatory networks. *Developmental Biology* 283(1):1–16.

**See Also**

[loadNetwork](#)

**Examples**

```
# import the example BioTapestry file
# included in the package vignette
exampleFile <- system.file("doc/example.btp",
                           package="BoolNet")
net <- loadBioTapestry(exampleFile)

# print the imported network
print(net)
```

---

loadNetwork

*Load a Boolean network from a file*

---

**Description**

Loads a Boolean network or probabilistic Boolean network from a file and converts it to an internal transition table representation.

**Usage**

```
loadNetwork(file,
            bodySeparator = ",",
            lowercaseGenes = FALSE)
```

## Arguments

file	The name of the file to be read
bodySeparator	An optional separation character to divide the target factors and the formulas. Default is ",".
lowercaseGenes	If set to TRUE, all gene names are converted to lower case, i.e. the gene names are case-insensitive. This corresponds to the behaviour of <b>BoolNet</b> versions prior to 1.5. Defaults to FALSE.

## Details

The routine supports a description language based on the Boolean operators AND (&), or (|), and NOT (!). The first line contains a header. In case of a Boolean network with only one function per gene, the header is "targets, functions"; in a probabilistic network, there is an optional third column "probabilities". All subsequent lines contain Boolean rules. A rule consists of a target gene, a separator, a Boolean expression to calculate a transition step for the target gene, and an optional probability for the rule (for probabilistic Boolean networks only – see below). The EBNF description of the rule format is as follows:

```
Rule = GeneName Separator BooleanExpression [Separator Probability];
BooleanExpression = GeneName
                  | "!" BooleanExpression
                  | "(" BooleanExpression ")"
                  | BooleanExpression " & " BooleanExpression
                  | BooleanExpression " | " BooleanExpression;
GeneName = ? A gene name from the list of involved genes ?;
Separator = ? The field <bodySeparator>, usually "," ?;
Probability = ? A floating-point number ?;
```

If there is exactly one rule for each gene, a Boolean network of class `BooleanNetwork` is created. In these networks, constant genes are automatically fixed (e.g. knocked-out or over-expressed). This means that they are always set to the constant value, and states with the complementary value are not considered in transition tables etc. If you would like to change this behaviour, use [fixGenes](#) to reset the fixing.

If two or more rules exist for the same gene, the function returns a probabilistic network of class `ProbabilisticBooleanNetwork`. In this case, alternative rules may be annotated with probabilities, which must sum up to 1 for all rules that belong to the same gene. If no probabilities are supplied, uniform distribution is assumed.

## Value

If only one function per gene is specified, a structure of class `BooleanNetwork` representing the network is returned. It has the following components:

genes	A vector of gene names involved in the network. This list determines the indices of genes in inputs of functions or in state bit vectors.
interactions	A list with <code>length(genes)</code> elements, where the <i>i</i> -th element describes the transition function for the <i>i</i> -th gene. Each element has the following sub-components:

	<p><b>input</b> A vector of indices of the genes that serve as the input of the Boolean transition function. If the function has no input (i.e. the gene is constant), the vector consists of a zero element.</p> <p><b>func</b> The transition function in truth table representation. This vector has <math>2^{\text{length}(\text{input})}</math> entries, one for each combination of input variables. If the gene is constant, the function is 1 or 0.</p> <p><b>expression</b> A string representation of the Boolean expression from which the truth table was generated</p>
fixed	A vector specifying which genes are knocked-out or over-expressed. For each gene, there is one element which is set to 0 if the gene is knocked-out, to 1 if the gene is over-expressed, and to -1 if the gene is not fixed at all, i. e. can change its value according to the supplied transition function. Constant genes are automatically set to fixed values.

If there is at least one gene with two or more alternative transition functions, a structure of class `ProbabilisticBooleanNetwork` is returned. This structure is similar to `BooleanNetwork`, but allows for storing more than one function in an interaction. It consists of the following components:

genes	A vector of gene names involved in the network. This list determines the indices of genes in inputs of functions or in state bit vectors.
interactions	A list with <code>length(genes)</code> elements, where the <i>i</i> -th element describes the alternative transition functions for the <i>i</i> -th gene. Each element is a list of transition functions. In this second-level list, each element has the the following sub-components: <p><b>input</b> A vector of indices of the genes that serve as the input of the Boolean transition function. If the function has no input (i.e. the gene is constant), the vector consists of a zero element.</p> <p><b>func</b> The transition function in truth table representation. This vector has <math>2^{\text{length}(\text{input})}</math> entries, one for each combination of input variables. If the gene is constant, the function is -1.</p> <p><b>expression</b> A string representation of the underlying Boolean expression</p> <p><b>probability</b> The probability that the corresponding transition function is chosen</p>
fixed	A vector specifying which genes are knocked-out or over-expressed. For each gene, there is one element which is set to 0 if the gene is knocked-out, to 1 if the gene is over-expressed, and to -1 if the gene is not fixed at all, i. e. can change its value according to the supplied transition function. You can knock-out and over-express genes using <code>fixGenes</code> .

### See Also

[getAttractors](#), [markovSimulation](#), [toPajek](#), [stateTransition](#), [fixGenes](#)

### Examples

```
# write example network to file
sink("testNet.bn")
cat("targets, functions\n")
cat("Gene1, !Gene2 | !Gene3\n")
```

```

cat("Gene2, Gene3 & Gene4\n")
cat("Gene3, Gene2 & !Gene1\n")
cat("Gene4, 1\n")
sink()

# read file
net <- loadNetwork("testNet.bn")
print(net)

```

---

markovSimulation      *Identify important states in probabilistic Boolean networks*

---

### Description

Identifies important states in probabilistic Boolean networks (PBN) using a Markov chain simulation

### Usage

```

markovSimulation(network,
                 numIterations = 1000,
                 startStates = list(),
                 cutoff = 0.001,
                 returnTable = TRUE)

```

### Arguments

network	An object of class <code>ProbabilisticBooleanNetwork</code> or <code>BooleanNetwork</code> whose transitions are simulated
numIterations	The number of iterations for the matrix multiplication, which corresponds to the number of state transitions to simulate
startStates	An optional list of start states. Each entry of the list must be a vector with a 0/1 value for each gene. If specified, the simulation is restricted to the states reachable from the supplied start states. Otherwise, all states are considered.
cutoff	The cutoff value used to determine if a probability is 0. All output probabilities less than or equal to this value are set to 0.
returnTable	If set to true, a transition table annotated with the probabilities for the transitions is included in the results. This is required by <a href="#">plotPBNTransitions</a> and <a href="#">getTransitionProbabilities</a> .

### Details

The algorithm identifies important states by performing the following steps: First, a Markov matrix is calculated from the set of transition functions, where each entry of the matrix specifies the probability of a state transition from the state belonging to the corresponding row to the state belonging to the corresponding column. A vector is initialized with uniform probability for all states (or – if specified – uniform probability for all start states) and repeatedly multiplied with the Markov matrix. The method returns all states with non-zero probability in this vector. See the references for more details.

**Value**

An object of class MarkovSimulation with the following components:

reachedStates	A data frame with one state in each row. The first columns specify the gene values of the state, and the last column holds the probability that the corresponding state is reached after numIterations transitions. Only states with a probability greater than cutoff are included in this table.
genes	A vector of gene names of the input network
table	If returnTable=TRUE, this structure holds a table of transitions with the corresponding probabilities that transitions are chosen. This is a list with the following components: <b>initialStates</b> A matrix of encoded start states of the transitions <b>nextStates</b> The encoded successor states of the transitions <b>probabilities</b> The probabilities that the transitions are chosen in a single step

**References**

I. Shmulevich, E. R. Dougherty, S. Kim, W. Zhang (2002), Probabilistic Boolean networks: a rule-based uncertainty model for gene regulatory networks. *Bioinformatics* 18(2):261–274.

**See Also**

[reconstructNetwork](#), [plotPBNTransitions](#), [getTransitionProbabilities](#)

**Examples**

```
# load example network
data(examplePBN)

# perform a Markov chain simulation
sim <- markovSimulation(examplePBN)

# print the relevant states and transition probabilities
print(sim)

# plot the transitions and their probabilities
plotPBNTransitions(sim)
```

---

perturbNetwork

*Perturb a Boolean network randomly*

---

**Description**

Modifies a synchronous, asynchronous, or probabilistic Boolean network by randomly perturbing either the functions for single genes or the state transitions. Random perturbations can be employed to assess the stability of the network.

**Usage**

```

perturbNetwork(network,
  perturb = c("functions", "states"),
  method = c("bitflip", "shuffle"),
  simplify = (perturb[1]=="states"),
  readableFunctions = FALSE,
  excludeFixed = TRUE,
  maxNumBits = 1,
  numStates = max(1, 2^length(network$genes)/100))

```

**Arguments**

network	A network structure of class <code>BooleanNetwork</code> or <code>ProbabilisticBooleanNetwork</code> . These networks can be read from files by <a href="#">loadNetwork</a> , generated by <a href="#">generateRandomNKNetwork</a> , or reconstructed by <a href="#">reconstructNetwork</a> .
perturb	If set to "functions", a transition function of a single gene is chosen at random and perturbed directly. This is the default mode. If set to "states", the transition table is generated, one or several state transitions are perturbed randomly, and the gene transition functions are rebuilt from the modified transition table. <code>perturb="states"</code> is only allowed for non-probabilistic networks of class <code>BooleanNetworks</code> .
method	The perturbation method to be applied to the functions or transitions. "bitflip" randomly inverts one or several bits (depending on the value of <code>maxNumBits</code> ). "shuffle" generates a random permutation of the positions in the function or state and rearranges the bits according to this permutation.
simplify	If this is true, <a href="#">simplifyNetwork</a> is called to simplify the gene transition functions after the perturbation. This removes irrelevant input genes. Defaults to TRUE if <code>perturb</code> is "states", and to FALSE otherwise.
readableFunctions	If this is true, readable DNF representations of the truth tables of the functions are generated. These DNF are displayed when the network is printed. The DNF representations are not minimized and can thus be very long. If set to FALSE, the truth table result column is displayed.
excludeFixed	Determines whether fixed variables can also be perturbed (if set to FALSE) or if they are excluded from the perturbation (if set to TRUE). Default is TRUE.
maxNumBits	The maximum number of bits to be perturbed in one function or state. Defaults to 1.
numStates	The number of states to be perturbed if <code>perturb</code> is "states". Defaults to 1

**Value**

Depending on the input, an object of class `BooleanNetwork` or `ProbabilisticBooleanNetwork` containing the perturbed copy of the original network is returned. The classes `BooleanNetwork` and `ProbabilisticBooleanNetwork` are described in more detail in [loadNetwork](#).

## References

Y. Xiao and E. R. Dougherty (2007), The impact of function perturbations in Boolean networks. *Bioinformatics* 23(10):1265–1273.

I. Shmulevich, E. R. Dougherty, W. Zhang (2002), Control of stationary behavior in probabilistic Boolean networks by means of structural intervention. *Journal of Biological Systems* 10(4):431–445.

## See Also

[loadNetwork](#), [generateRandomNKNetwork](#), [reconstructNetwork](#), [simplifyNetwork](#)

## Examples

```
# load example data
data(cellcycle)

# perturb the network
perturbedNet1 <- perturbNetwork(cellcycle, perturb="functions", method="shuffle")
perturbedNet2 <- perturbNetwork(cellcycle, perturb="states", method="bitflip")

# get attractors
print(getAttractors(perturbedNet1))
print(getAttractors(perturbedNet2))
```

---

plotAttractors

*Plot state tables or transition graphs of attractors*

---

## Description

Visualizes attractors, either by drawing a table of the involved states in two colors, or by drawing a graph of transitions between the states of the attractor.

## Usage

```
plotAttractors(attractorInfo,
               subset,
               title = "",
               mode = c("table", "graph"),
               grouping = list(),
               plotFixed = TRUE,
               onColor = "green",
               offColor = "red",
               layout = layout.circle,
               drawLabels = TRUE,
               drawLegend = TRUE,
               ...)
```

**Arguments**

attractorInfo	An object of class AttractorInfo, as returned by <a href="#">getAttractors</a>
subset	An subset of attractors to be plotted. This is a vector of attractor indices in attractorInfo.
title	An optional title for the plot
mode	Switches between two kinds of attractor plots. See Details for more information. Default is "table".
grouping	This optional parameter is only used if mode="table" and specifies a structure to form groups of genes in the plot. This is a list with the following elements: <b>class</b> A vector of names for the groups. These names will be printed in the region belonging to the group in the plot. <b>index</b> A list with the same length as class. Each element is a vector of gene names or gene indices belonging to the group.
plotFixed	This optional parameter is only used if mode="table". If this is true, genes with fixed values are included in the plot. Otherwise, these genes are not drawn.
onColor	This optional parameter is only used if mode="table" and specifies the color value for the 1/ON values in the table. Defaults to green.
offColor	This optional parameter is only used if mode="table" and specifies the color value for the 0/OFF values in the table. Defaults to red.
layout	If mode="graph", this parameter specifies a layouting function that determines the placement of the nodes in the graph. Please refer to the <a href="#">layout</a> manual entry in the <b>igraph</b> package for further details. By default, the circle layout is used.
drawLabels	This parameter is only relevant if mode="graph". It determines whether the nodes of the graph are annotated with the corresponding values of the genes in the attractor states.
drawLegend	Specifies whether a color key for the ON/OFF states is drawn if mode="table". Defaults to TRUE.
...	Further graphical parameters to be passed to <a href="#">plot.igraph</a> if mode="graph".

**Details**

This function comprises two different types of plots:

The "table" mode visualizes the gene values of the states in the attractor and is only suited for synchronous or steady-state attractors. Complex asynchronous attractors are omitted in this mode. Attractors in attractorInfo are first grouped by length. Then, a figure is plotted to the currently selected device for each attractor length (i.e. one plot with all attractors consisting of 1 state, one plot with all attractors consisting of 2 states, etc.). This means that on the standard X11 output device, only the last plot is displayed unless you set `par(mfrow=c(...))` accordingly. The figure is a table with the genes in the rows and the states of the attractors in the columns. Cells of the table are (by default) red for 0/OFF values and green for 1/ON values. If grouping is set, the genes are rearranged according to the indices in the group, horizontal separation lines are plotted between the groups, and the group names are printed.

The "graph" mode visualizes the transitions between different states. It creates a graph in which the vertices are the states in the attractor and the edges are state transitions among these states. This

mode can visualize all kinds of attractors, including complex/loose attractors. One plot is drawn for each attractor. As before, this means that on the standard output device, only the last plot is displayed unless you set `par(mfrow=c(...))` accordingly.

### Value

If `mode="table"`, a list of matrices corresponding to the tables is returned. Each of these matrices has the genes in the rows and the states of the attractors in the columns.

If `mode="graph"`, a list of objects of class `igraph` is returned. Each of these objects describes the graph for one attractor.

### See Also

[getAttractors](#), [attractorsToLaTeX](#), [plotSequence](#), [sequenceToLaTeX](#)

### Examples

```
# load example data
data(cellcycle)

# get attractors
attractors <- getAttractors(cellcycle)

# calculate number of different attractor lengths,
# and plot attractors side by side in "table" mode
par(mfrow=c(1, length(table(sapply(attractors$attractors,
                                   function(attractor)
                                   {
                                     length(attractor$involvedStates)
                                   }))))))
plotAttractors(attractors)

# plot attractors in "graph" mode
par(mfrow=c(1, length(attractors$attractors)))
plotAttractors(attractors, mode="graph")

# identify asynchronous attractors
attractors <- getAttractors(cellcycle, type="asynchronous")

# plot attractors in "graph" mode
par(mfrow=c(1, length(attractors$attractors)))
plotAttractors(attractors, mode="graph")
```

## Description

Plots the wiring of genes (i.e. the gene dependencies) of a synchronous or probabilistic Boolean network. The nodes of the graph are the genes, and the directed edges show the dependencies of the genes. This requires the **igraph** package.

## Usage

```
plotNetworkWiring(network,  
                  layout = layout.fruchterman.reingold,  
                  plotIt = TRUE, ...)
```

## Arguments

network	A network structure of class <code>BooleanNetwork</code> or <code>ProbabilisticBooleanNetwork</code> . These networks can be read from files by <code>loadNetwork</code> , generated by <code>generateRandomNKNetwork</code> , or reconstructed by <code>reconstructNetwork</code> .
layout	A layouting function that determines the placement of the nodes in the graph. Please refer to the <code>layout</code> manual entry in the <b>igraph</b> package for further details. By default, the Fruchterman-Reingold algorithm is used.
plotIt	If this is true, a plot is generated. Otherwise, only an object of class <code>igraph</code> is returned, but no plot is drawn.
...	Further graphical parameters to be passed to <code>plot.igraph</code> .

## Details

This function uses the `plot.igraph` function from the **igraph** package. The plots are customizable using the `...` argument. For details on possible parameters, please refer to `igraph.plotting`.

## Value

Returns an invisible object of class `igraph` containing the wiring graph.

## See Also

`loadNetwork`, `generateRandomNKNetwork`, `reconstructNetwork`, `plotStateGraph`, `igraph.plotting`

## Examples

```
# load example data  
data(cellcycle)  
  
# plot wiring graph  
plotNetworkWiring(cellcycle)
```

---

plotPBNTransitions      *Visualize the transitions in a probabilistic Boolean network*

---

### Description

Visualizes the state transitions and their probabilities in a probabilistic Boolean network. This takes the transition table information calculated by the [markovSimulation](#) method. Only transitions with non-zero probability are included in the plot. The function requires the **igraph** package.

### Usage

```
plotPBNTransitions(markovSimulation,
                   stateSubset,
                   drawProbabilities = TRUE,
                   drawStateLabels = TRUE,
                   layout = layout.fruchterman.reingold,
                   plotIt = TRUE, ...)
```

### Arguments

markovSimulation	An object of class MarkovSimulation, as returned by <a href="#">markovSimulation</a> . As the transition table information in this structure is required, <a href="#">markovSimulation</a> must be called with returnTable set to TRUE.
stateSubset	An optional list of states, where each element of the list must be a vector with a 0/1 entry for each gene. If this argument is supplied, the graph only contains the specified states and transitions between these states.
drawProbabilities	If set to true, the edges of the graph are annotated with the probabilities of the corresponding transitions. Default is TRUE.
drawStateLabels	If set to true, the vertices of the graph are annotated with the gene values of the corresponding states. Defaults to TRUE.
layout	A layouting function that determines the placement of the nodes in the graph. Please refer to the <a href="#">layout</a> manual entry in the <b>igraph</b> package for further details. By default, the Fruchterman-Reingold algorithm is used.
plotIt	If this is true, a plot is generated. Otherwise, only an object of class igraph is returned, but no plot is drawn.
...	Further graphical parameters to be passed to <a href="#">plot.igraph</a> .

### Details

This function uses the [plot.igraph](#) function from the **igraph** package. The plots are customizable using the ... argument. For details on possible parameters, please refer to [igraph.plotting](#).

**Value**

Returns an invisible object of class `igraph` containing the wiring graph.

**See Also**

[markovSimulation](#)

**Examples**

```
# load example network
data(examplePBN)

# perform a Markov chain simulation
sim <- markovSimulation(examplePBN)

# plot the transitions and their probabilities
plotPBNTransitions(sim)
```

---

plotSequence

*Plot a sequence of states*

---

**Description**

Visualizes sequences of states in synchronous Boolean networks, either by drawing a table of the involved states in two colors, or by drawing a graph of transitions between the successive states.

**Usage**

```
plotSequence(network,
             startState,
             includeAttractorStates = c("all", "first", "none"),
             sequence,
             title = "",
             mode=c("table", "graph"),
             plotFixed = TRUE, grouping = list(),
             onColor="green",
             offColor="red",
             layout,
             drawLabels=TRUE,
             drawLegend=TRUE,
             ...)
```

**Usage**

```

plotSequence(network,
             startState,
             includeAttractorStates = c("all", "first", "none"),
             title = "",
             mode=c("table", "graph"),
             plotFixed = TRUE, grouping = list(),
             onColor="green",
             offColor="red",
             layout,
             drawLabels=TRUE,
             drawLegend=TRUE,
             ...)

plotSequence(sequence,
             title = "",
             mode=c("table", "graph"),
             plotFixed = TRUE, grouping = list(),
             onColor="green",
             offColor="red",
             layout,
             drawLabels=TRUE,
             drawLegend=TRUE,
             ...)

```

**Arguments**

network	An object of class <code>BooleanNetwork</code> for which a sequence of state transitions is calculated
startState	The start state of the sequence
includeAttractorStates	Specifies whether the actual attractor states are included in the plot or not (see also <a href="#">getPathToAttractor</a> ). If <code>includeAttractorStates = "all"</code> (which is the default behaviour), the sequence ends when the attractor was traversed once. If <code>includeAttractorStates = "first"</code> , only the first state of attractor is added to the sequence. If <code>includeAttractorStates = "none"</code> , the sequence ends with the last non-attractor state.
sequence	The alternative call to <code>plotSequence</code> requires the specification of the sequence itself instead of the network and the start state. The sequence must be provided as a data frame with the genes in the columns and the successive states in the rows. For example, sequences can be obtained using <a href="#">getPathToAttractor</a> or <a href="#">getAttractorSequence</a> (however, the specialized plot <a href="#">plotAttractors</a> exists for attractors).
title	An optional title for the plot
mode	Switches between two kinds of attractor plots. See Details for more information. Default is "table".

plotFixed	This optional parameter is only used if mode="table". If this is true, genes with fixed values are included in the plot. Otherwise, these genes are not drawn.
grouping	This optional parameter is only used if mode="table" and specifies a structure to form groups of genes in the plot. This is a list with the following elements: <b>class</b> A vector of names for the groups. These names will be printed in the region belonging to the group in the plot. <b>index</b> A list with the same length as class. Each element is a vector of gene names or gene indices belonging to the group.
onColor	This optional parameter is only used if mode="table" and specifies the color value for the 1/ON values in the table. Defaults to green.
offColor	This optional parameter is only used if mode="table" and specifies the color value for the 0/OFF values in the table. Defaults to red.
layout	If mode="graph", this parameter specifies a layouting function that determines the placement of the nodes in the graph. Please refer to the <a href="#">layout</a> manual entry in the <b>igraph</b> package for further details. By default, the nodes are placed in a horizontal line.
drawLabels	This parameter is only relevant if mode="graph". It determines whether the nodes of the graph are annotated with the corresponding values of the genes in the attractor states.
drawLegend	Specifies whether a color key for the ON/OFF states is drawn if mode="table". Defaults to TRUE.
...	Further graphical parameters to be passed to <code>plot.igraph</code> if mode="graph".

## Details

This function comprises two different types of plots:

The "table" mode visualizes the gene values of the states in the sequence. The figure is a table with the genes in the rows and the successive states of the sequence in the columns. Cells of the table are (by default) red for 0/OFF values and green for 1/ON values. If grouping is set, the genes are rearranged according to the indices in the group, horizontal separation lines are plotted between the groups, and the group names are printed.

The "graph" mode visualizes the transitions between different states. It creates a graph in which the vertices are the states in the sequence and the edges are state transitions among these states.

The function can be called with different types of inputs: The user can specify the parameters network, startState and includeAttractorStates), in which case `getPathToAttractor` is called to obtain the sequence. Alternatively, the sequence can be supplied directly as a data frame in the sequence parameter.

## Value

If mode="table", a matrix corresponding to the table is returned. The matrix has the genes in the rows and the states of the attractors in the columns. If sequence was supplied, this corresponds to the transposed input whose rows may be rearranged if grouping was set.

If mode="graph", an object of class `igraph` describing the graph for the sequence is returned.

**See Also**

[sequenceToLaTeX](#), [plotAttractors](#), [attractorsToLaTeX](#), [getPathToAttractor](#), [getAttractorSequence](#)

**Examples**

```
# load example data
data(cellcycle)

# alternative 1: supply network and start state
# and plot sequence as a table
plotSequence(network=cellcycle,
             startState=rep(1,10),
             includeAttractorStates="all")

# alternative 2: calculate sequence in advance
sequence <- getPathToAttractor(cellcycle,
                              state=rep(1,10),
                              includeAttractorStates="all")

# plot sequence as a graph
plotSequence(sequence=sequence,
             mode="graph")
```

---

plotStateGraph

*Visualize state transitions and attractor basins*

---

**Description**

Plots a graph containing all states visited in `attractorInfo`, and optionally highlights attractors and basins of attraction. This requires the **igraph** package.

**Usage**

```
plotStateGraph(attractorInfo, highlightAttractors = TRUE,
              colorBasins = TRUE, colorSet,
              drawLegend = TRUE, drawLabels = FALSE,
              layout = layout.fruchterman.reingold,
              piecewise = FALSE,
              basin.lty = 2, attractor.lty = 1,
              plotIt = TRUE, ...)
```

**Arguments**

`attractorInfo` An object of class `AttractorInfo`, as returned by [getAttractors](#). As the transition table information in this structure is required, [getAttractors](#) must be called in synchronous mode and with `returnTable` set to `TRUE`.

`highlightAttractors`

If this parameter is true, edges in attractors are drawn bold and with a different line type (which can be specified in `attractor.lty`). Defaults to `TRUE`.

colorBasins	If set to true, each basin of attraction is drawn in a different color. Colors can be specified in colorSet. Defaults to TRUE.
colorSet	An optional vector specifying the colors to be used for the different attractor basins. If not supplied, a default color set is used.
drawLegend	If set to true and colorBasins is true, a legend for the colors of the basins of attraction is drawn. Defaults to TRUE.
drawLabels	If set to true, the binary encodings of the states are drawn beside the vertices of the graph. As this can be confusing for large graphs, the default value is FALSE.
layout	A layouting function that determines the placement of the nodes in the graph. Please refer to the <a href="#">layout</a> manual entry in the <b>igraph</b> package for further details. By default, the Fruchterman-Reingold algorithm is used.
piecewise	If set to true, a piecewise layout is used, i.e. the subgraphs corresponding to different basins of attraction are separated and layouted separately.
basin.lty	The line type used for edges in a basin of attraction. Defaults to 2 (dashed).
attractor.lty	If highlightAttractors is true, this specifies the line type for edges in an attractor. Defaults to 1 (straight).
plotIt	If this is true, a plot is generated. Otherwise, only an object of class igraph is returned, but no plot is drawn.
...	Further graphical parameters to be passed to <a href="#">plot.igraph</a> .

### Details

This function uses the [plot.igraph](#) function from the **igraph** package. The plots are customizable using the ... argument. For details on possible parameters, please refer to [igraph.plotting](#).

### Value

Returns an invisible object of class igraph containing the state graph, including color and line attributes.

### See Also

[getAttractors](#), [plotNetworkWiring](#), [igraph.plotting](#)

### Examples

```
# load example data
data(cellcycle)

# get attractors
attractors <- getAttractors(cellcycle)

# plot state graph
plotStateGraph(attractors, main="Cell cycle network")
```

---

```
print.AttractorInfo    Print attractor cycles
```

---

### Description

Specialized print method to print the attractor cycles stored in an `AttractorInfo` object. For simple or steady-state attractors, the states of the attractors are printed in binary encoding in the order they are reached. For asynchronous complex/loose attractors, the possible transitions of the states in the attractor are printed. The method can print either the full states, or only the active genes of the states.

### Usage

```
## S3 method for class 'AttractorInfo'
print(x,
      activeOnly = FALSE,
      ...)
```

### Arguments

<code>x</code>	An object of class <code>AttractorInfo</code> to be printed
<code>activeOnly</code>	If set to true, a state is represented by a list of active genes (i.e., genes which are set to 1). If set to false, a state is represented by a binary vector with one entry for each gene, specifying whether the gene is active or not. Defaults to FALSE.
<code>...</code>	Further parameters for the <code>print</code> method. Currently not used.

### Value

Invisibly returns the printed object

### See Also

[print](#), [getAttractors](#)

---

```
print.BooleanNetwork    Print a Boolean network
```

---

### Description

A specialized method to print an object of class `BooleanNetwork`. This prints the transition functions of all genes. If genes are knocked-out or over-expressed, these genes are listed below the functions.

**Usage**

```
## S3 method for class 'BooleanNetwork'  
print(x, ...)
```

**Arguments**

x                    An object of class BooleanNetwork to be printed  
...                  Further parameters for the `print` method. Currently not used.

**Value**

Invisibly returns the printed object

**See Also**

[print](#), [loadNetwork](#)

---

print.MarkovSimulation

*Print the results of a Markov chain simulation*

---

**Description**

A specialized method to print an object of class MarkovSimulation. This prints all states that have a non-zero probability to be reached after the number of iterations in the Markov simulation. If the simulation was run with `returnTable=TRUE`, it also prints a table of state transitions and their probabilities to be chosen in a single step.

**Usage**

```
## S3 method for class 'MarkovSimulation'  
print(x,  
      activeOnly = FALSE,  
      ...)
```

**Arguments**

x                    An object of class MarkovSimulation to be printed  
activeOnly          If set to true, a state is represented by a list of active genes (i.e., genes which are set to 1). If set to false, a state is represented by a binary vector with one entry for each gene, specifying whether the gene is active or not. Defaults to FALSE.  
...                  Further parameters for the `print` method. Currently not used.

**Value**

Invisibly returns the printed object

**See Also**

[print, markovSimulation](#)

---

`print.ProbabilisticBooleanNetwork`

*Print a probabilistic Boolean network*

---

**Description**

A specialized method to print an object of class `ProbabilisticBooleanNetwork`. For backward compatibility, this method also prints objects of class `BooleanNetworkCollection`, which have been replaced by `ProbabilisticBooleanNetwork`. This prints all alternative transition functions and their probabilities. If the network is the result of a reconstruction from time series measurements, it also outputs the error the functions make on the time series. If genes are knocked-out or over-expressed, these genes are listed below the functions.

**Usage**

```
## S3 method for class 'ProbabilisticBooleanNetwork'  
print(x, ...)
```

```
## S3 method for class 'BooleanNetworkCollection'  
print(x, ...)
```

**Arguments**

<code>x</code>	An object of class <code>ProbabilisticBooleanNetwork</code> or <code>BooleanNetworkCollection</code> to be printed
<code>...</code>	Further parameters for the <code>print</code> method. Currently not used.

**Value**

Invisibly returns the printed object

**See Also**

[print, reconstructNetwork, loadNetwork](#)

---

print.TransitionTable *Print a transition table*

---

### Description

Specialized print method to print a transition table with the initial state in the first column, the successor state in the second column, the basin of attraction to which the state leads in the third column, and the number of transitions to the attractor in the fourth column.

### Usage

```
## S3 method for class 'TransitionTable'
print(x,
      activeOnly = FALSE,
      ...)

## S3 method for class 'BooleanStateInfo'
print(x,
      activeOnly=FALSE,
      ...)
```

### Arguments

x	An object of class TransitionTable or BooleanStateInfo to be printed
activeOnly	If set to true, a state is represented by a list of active genes (i.e., genes which are set to 1). If set to false, a state is represented by a binary vector with one entry for each gene, specifying whether the gene is active or not. Defaults to FALSE.
...	Further parameters for the <code>print</code> method. Currently not used.

### Value

Invisibly returns the printed object

### See Also

[print](#), [getTransitionTable](#), [getBasinOfAttraction](#), [getStateSummary](#)

---

reconstructNetwork	<i>Reconstruct a Boolean network from time series of measurements</i>
--------------------	---

---

### Description

Reconstructs a Boolean network from a set of time series or from a transition table using the best-fit extension algorithm or the REVEAL algorithm.

### Usage

```
reconstructNetwork(measurements,
                  method = c("bestfit", "reveal"),
                  maxK = 5,
                  readableFunctions = FALSE,
                  allSolutions = FALSE)
```

### Arguments

measurements	This can either be an object of class <code>TransitionTable</code> as returned by <a href="#">getTransitionTable</a> , or a set of time series of measurements. In this case, measurements must be a list of matrices, each corresponding to one time series. Each row of these matrices contains measurements for one gene on a time line, i. e. column $i+1$ contains the successor states of column $i$ . The genes must be the same for all matrices in the list. Real-valued time series can be binarized using <a href="#">binarizeTimeSeries</a> .
method	This specifies the reconstruction algorithm to be used. If set to "bestfit", Laehdesmaeki's Best-Fit Extension algorithm is employed. This algorithm is an improvement of the algorithm by Akutsu et al. with a lower runtime complexity. It determines the functions with a minimal error for each gene. If set to "reveal", Liang's REVEAL algorithm is used. This algorithm searches for relevant input genes using the mutual information between the input genes and the output gene.
maxK	The maximum number of input genes for one gene to be tested. Defaults to 5.
readableFunctions	If this is true, readable DNF representations of the truth tables of the functions are generated. These DNF are displayed when the network is printed. The DNF representations are not minimized and can thus be very long. If set to FALSE, the truth table result column is displayed.
allSolutions	If this is true, all solutions with the minimum error and up to maxK inputs are returned. By default, allSolutions=FALSE, which means that only the solutions with both minimum error and minimum k are returned.

### Details

Both algorithms iterate over all possible input combinations. While Best-Fit Extension is capable of returning functions that do not perfectly explain the measurements (for example, if there are

inconsistent measurements or if maxK was specified too small), REVEAL only finds functions that explain all measurements. For more information, please refer to the cited publications.

### Value

Returns an object of class `ProbabilisticBooleanNetwork`, with each alternative function of a gene having the same probability. The structure is described in detail in `loadNetwork`. In addition to the standard components, each alternative transition function has a component error which stores the error of the function on the input time series data. If a non-probabilistic network of class `BooleanNetwork` is required, a specific Boolean network can be extracted using `chooseNetwork`.

### References

- H. Laehdesmaeki, I. Shmulevich and O. Yli-Harja (2003), On Learning Gene-Regulatory Networks Under the Boolean Network Model. *Machine Learning* 52:147–167.
- T. Akutsu, S. Miyano and S. Kuhara (2000). Inferring qualitative relations in genetic networks and metabolic pathways. *Bioinformatics* 16(8):727–734.
- S. Liang, S. Fuhrman and R. Somogyi (1998), REVEAL, a general reverse engineering algorithm for inference of genetic network architectures. *Pacific Symposium on Biocomputing* 3:18–29.

### See Also

`binarizeTimeSeries`, `chooseNetwork`

### Examples

```
# load example data
data(yeastTimeSeries)

# perform binarization with k-means
bin <- binarizeTimeSeries(yeastTimeSeries)

# reconstruct networks from transition table
net <- reconstructNetwork(bin$binarizedMeasurements, method="bestfit", maxK=3)

# print reconstructed net
print(net)

# plot reconstructed net
plotNetworkWiring(net)
```

---

sequenceToLaTeX

*Create LaTeX table of state sequences*

---

### Description

Exports tables of state sequences (corresponding to the plot generated by `plotSequence` with `mode="table"`) to a LaTeX document.

**Usage**

```
sequenceToLaTeX(network,
                 startState,
                 includeAttractorStates = c("all", "first", "none"),
                 sequence,
                 title = "",
                 grouping = list(),
                 plotFixed = TRUE,
                 onColor="[gray]\\{0.9\\}",
                 offColor="[gray]\\{0.6\\}",
                 file="sequence.tex")
```

**Usage**

```
sequenceToLaTeX(network,
                 startState,
                 includeAttractorStates = c("all", "first", "none"),
                 title = "",
                 grouping = list(),
                 plotFixed = TRUE,
                 onColor="[gray]{0.9}",
                 offColor="[gray]{0.6}",
                 file="sequence.tex")
```

```
sequenceToLaTeX(sequence,
                 title = "",
                 grouping = list(),
                 onColor="[gray]{0.9}",
                 offColor="[gray]{0.6}",
                 file="sequence.tex")
```

**Arguments**

network	An object of class <code>BooleanNetwork</code> for which a sequence of state transitions is calculated
startState	The start state of the sequence
includeAttractorStates	Specifies whether the actual attractor states are included in the table or not (see also <a href="#">getPathToAttractor</a> ). If <code>includeAttractorStates = "all"</code> (which is the default behaviour), the sequence ends when the attractor was traversed once. If <code>includeAttractorStates = "first"</code> , only the first state of attractor is added to the sequence. If <code>includeAttractorStates = "none"</code> , the sequence ends with the last non-attractor state.
sequence	The alternative call to <code>sequenceToLaTeX</code> requires the specification of the sequence itself instead of the network and the start state. The sequence must be provided as a data frame with the genes in the columns and the successive states in the rows. For example, sequences can be obtained using <a href="#">getPathToAttractor</a>

	or <a href="#">getAttractorSequence</a> (however, the specialized function <a href="#">attractorsToLaTeX</a> exists for attractors).
title	An optional title for the table
plotFixed	If this is true, genes with fixed values are included in the plot. Otherwise, these genes are not shown.
grouping	This optional parameter specifies a structure to form groups of genes in the table. This is a list with the following elements: <ul style="list-style-type: none"> <li><b>class</b> A vector of names for the groups. These names will be printed in the region belonging to the group in the table.</li> <li><b>index</b> A list with the same length as <b>class</b>. Each element is a vector of gene names or gene indices belonging to the group.</li> </ul>
onColor	An optional color value for the 1/ON values in the table. Defaults to dark grey.
offColor	An optional color value for the 0/OFF values in the table. Defaults to light grey.
file	The file to which the LaTeX document is written. Defaults to "sequence.tex".

### Details

This function creates a LaTeX table that visualizes a sequence of states in a synchronous network. The output file does not contain a document header and requires the inclusion of the packages `tabularx` and `colortbl`. The tables have the genes in the rows and the successive states of the sequence in the columns. If not specified otherwise, cells of the table are light grey for 0/OFF values and dark grey for 1/ON values. If grouping is set, the genes are rearranged according to the indices in the group, horizontal separation lines are plotted between the groups, and the group names are printed.

The function can be called with different types of inputs: The user can specify the parameters `network`, `startState` and `includeAttractorStates`), in which case [getPathToAttractor](#) is called to obtain the sequence. Alternatively, the sequence can be supplied directly as a data frame in the `sequence` parameter.

### Value

Returns a matrix corresponding to the table. The matrix has the genes in the rows and the states of the attractors in the columns. If `sequence` was supplied, this corresponds to the transposed input whose rows may be rearranged if grouping was set.

### See Also

[attractorsToLaTeX](#), [plotSequence](#), [plotAttractors](#), [getPathToAttractor](#), [getAttractorSequence](#).

### Examples

```
# load example data
data(cellcycle)

# alternative 1: supply network and start state
# and export sequence to LaTeX
sequenceToLaTeX(network=cellcycle,
```

```

startState=rep(1,10),
includeAttractorStates="all",
file="sequence.txt")

# alternative 2: calculate sequence in advance
sequence <- getPathToAttractor(cellcycle,
                             state=rep(1,10),
                             includeAttractorStates="all")

sequenceToLaTeX(sequence=sequence,
                file="sequence.txt")

```

---

simplifyNetwork	<i>Simplify the functions of a synchronous, asynchronous, or probabilistic Boolean network</i>
-----------------	--

---

## Description

Eliminates irrelevant variables from the inputs of the gene transition functions. This can be useful if the network was generated randomly via [generateRandomNKNetwork](#) or if it was perturbed via [perturbNetwork](#).

## Usage

```
simplifyNetwork(network, readableFunctions = FALSE)
```

## Arguments

**network** A network structure of class `BooleanNetwork` or `ProbabilisticBooleanNetwork`. These networks can be read from files by [loadNetwork](#), generated by [generateRandomNKNetwork](#), or reconstructed by [reconstructNetwork](#).

**readableFunctions** If this is true, readable DNF representations of the truth tables of the functions are generated. These DNF are displayed when the network is printed. The DNF representations are not minimized and can thus be very long. If set to `FALSE`, the truth table result column is displayed.

## Details

The function checks whether the output of a gene transition function is independent from the states of any of the input variables. If this is the case, these input variables are dropped, and the transition function is shortened accordingly.

In non-probabilistic Boolean networks (class `BooleanNetwork`), constant genes are automatically fixed (e.g. knocked-out or over-expressed). This means that they are always set to the constant value, and states with the complementary value are not considered in transition tables etc. If you would like to change this behaviour, use [fixGenes](#) to reset the fixing.

**Value**

The simplified network of class `BooleanNetwork` or `ProbabilisticBooleanNetwork`. These classes are described in more detail in [loadNetwork](#).

**See Also**

[loadNetwork](#), [generateRandomNKNetwork](#), [perturbNetwork](#), [reconstructNetwork](#), [fixGenes](#)

**Examples**

```
# load example data
data(cellcycle)

# perturb the network
perturbedNet <- perturbNetwork(cellcycle, perturb="functions", method="shuffle")
print(perturbedNet$interactions)

# simplify the network
perturbedNet <- simplifyNetwork(perturbedNet)
print(perturbedNet$interactions)
```

---

<code>stateTransition</code>	<i>Perform a transition to the next state</i>
------------------------------	---

---

**Description**

Calculates the next state in a supplied network for a given current state

**Usage**

```
stateTransition(network,
               state,
               type = c("synchronous", "asynchronous", "probabilistic"),
               geneProbabilities,
               chosenGene,
               chosenFunctions)
```

**Arguments**

<code>network</code>	A network structure of class <code>BooleanNetwork</code> or <code>ProbabilisticBooleanNetwork</code> . These networks can be read from files by <a href="#">loadNetwork</a> , generated by <a href="#">generateRandomNKNetwork</a> , or reconstructed by <a href="#">reconstructNetwork</a> .
<code>state</code>	The current state of the network, encoded as a vector with one 0-1 element for each gene.

type	<p>The type of transition to be performed.</p> <p>If set to "synchronous", all genes are updated using the corresponding transition functions.</p> <p>If set to "asynchronous", only one gene is updated. This gene is either chosen randomly or supplied in parameter chosenGene.</p> <p>If set to "probabilistic", one transition function is chosen for each gene, and the genes are updated synchronously. The functions are either chosen randomly depending on their probabilities, or they are supplied in parameter chosenFunctions.</p> <p>Default is "synchronous" for objects of class BooleanNetwork and "probabilistic" for objects of class ProbabilisticBooleanNetwork.</p>
geneProbabilities	<p>An optional vector of probabilities for the genes if type="asynchronous". By default, each gene has the same probability to be chosen for the next state transition. These probabilities can be modified by supplying a vector of probabilities for the genes which sums up to one.</p>
chosenGene	<p>If type="asynchronous" and this parameter is supplied, no random update is performed. Instead, the gene with the supplied name or index is chosen for the next transition.</p>
chosenFunctions	<p>If type="probabilistic", this parameter can contain a set of function indices for each gene. In this case, transition functions are not chosen randomly, but the provided functions are used in the state transition.</p>

### Value

The subsequent state of the network, encoded as a vector with one 0-1 element for each gene.

### See Also

[loadNetwork](#), [generateRandomNKNetwork](#), [generateState](#)

### Examples

```
# load example network
data(cellcycle)

# calculate a synchronous state transition
print(stateTransition(cellcycle, c(1,1,1,1,1,1,1,1,1,1)))

# calculate an asynchronous state transition of gene CycA
print(stateTransition(cellcycle, c(1,1,1,1,1,1,1,1,1,1),
                      type="asynchronous", chosenGene="CycA"))

# load probabilistic network
data(examplePBN)

# perform a probabilistic state transition
print(stateTransition(examplePBN, c(0,1,1),
                      type="probabilistic"))
```

---

testNetworkProperties *Test properties of networks by comparing them to random networks*

---

### Description

This is a general function designed to determine unique properties of biological networks by comparing them to a set of randomly generated networks with similar structure.

### Usage

```
testNetworkProperties(network,
                     numRandomNets = 100,
                     testFunction = "testIndegree",
                     testFunctionParams = list(),
                     accumulation = c("characteristic", "kullback_leibler"),
                     sign.level = 0.05,
                     drawSignificanceLevel = TRUE,
                     klBins,
                     klMinVal = 1e-05,
                     linkage = c("uniform", "lattice"),
                     functionGeneration = c("uniform", "biased"),
                     simplify = FALSE,
                     noIrrelevantGenes = TRUE,
                     d_lattice = 1,
                     zeroBias = 0.5,
                     title = "",
                     xlab,
                     xlim,
                     breaks = 30,
                     ...)
```

### Arguments

network	A network structure of class BooleanNetwork
numRandomNets	The number of random networks to generate for comparison
testFunction	The name of a function that calculates characteristic values that describe properties of the network. There are two built-in functions: "testIndegree" calculates the in-degrees of states in the network, and "testAttractorRobustness" counts the occurrences of attractors in perturbed copies. It is possible to supply user-defined functions here. See Details.
testFunctionParams	A list of parameters to testFunction. The elements of the list depend on the chosen function.
accumulation	If "characteristic" is chosen, the test function is required to return a single value that describes the network. In this case, a histogram of these values in random

networks is plotted, and the value of the original network is inserted as a vertical line.

If "kullback\_leibler" is chosen, the test function can return a vector of values which is regarded as a sample from a probability distribution. In this case, the Kullback-Leibler distances of the distributions from the original network and each of the random networks are calculated and plotted in a histogram. The Kullback-Leibler distance measures the difference between two probability distributions. In this case, the resulting histogram shows the distribution of differences between the original network and randomly generated networks.

sign.level	if accumulation="characteristic", this specifies a significance level for a computer-intensive test. The test is significant if the characteristic value is greater than at least $(1-\text{sign.level}) \times 100\%$ of the characteristic values of the random networks
drawSignificanceLevel	If accumulation="characteristic" and this is true, a vertical line is plotted for the significance level in the histogram.
linkage, functionGeneration, simplify, noIrrelevantGenes, d_lattice, zeroBias	The corresponding parameters of <a href="#">generateRandomNKNetwork</a> used to generate the random networks. This allows for customization of the network generation process. The three remaining parameters of <a href="#">generateRandomNKNetwork</a> are set to values that ensure structural similarity to the original network: The parameters n and k are set to the corresponding values of the original network, and topology="fixed".
k1Bins	If accumulation="kullback_leibler", the number of bins used to discretize the samples for the Kullback-Leibler distance calculations. By default, each unique value in the samples has its own bin, i.e. no further discretization is performed. The influence of discretization on the resulting histogram may be high.
k1MinVal	If accumulation="kullback_leibler", this defines the minimum probability for the calculation of the Kullback-Leibler distance to ensure stability of the results.
title	The title of the plots. This is empty by default.
xlab	Customizes label of the x axis of the histogram. For the built-in test functions, the x axis label is set automatically.
xlim	Customizes the limits of the x axis of the histogram. For the built-in test functions, suitable values are chosen automatically.
breaks	Customizes the number of breaks in the
...	Further graphical parameters for <a href="#">hist</a>

### Details

This function generically compares properties of biological networks to a set of random networks. It can be extended by supplying custom functions to the parameter testFunction. Such a function must have the signature

```
function(network, accumulate=TRUE, params)
```

**network** This is the network to test. In the process of the comparison, both the original network and the random networks are passed to the function

**accumulate** If `accumulate=TRUE`, the function must return a single value quantifying the examined property of the network. If `accumulate=FALSE`, the function can return a vector of values (e.g., one value for each gene/state etc.)

**params** A list of further parameters for the function supplied by the user in `testFunctionParams` (see above). This can contain any type of information your test function needs.

Two built-in functions for synchronous Boolean networks already exist:

**testIndegree** This function is based on the observation that, often, in biological networks, many state transitions lead to the same states. In other words, there is a small number of "hub" states. In the state graph, this means that the in-degree of some states (i.e., the number of transitions leading to it) is high, while the in-degree of many other states is 0. We observed that random networks do not show this behaviour, thus it may be a distinct property of biological networks.

The function does not require any parameter entries in `params`. If `accumulate=FALSE`, it returns the in-degrees of all synchronous states in the network. If `accumulate=TRUE`, the Gini index of the in-degrees is returned as a characteristic value of the network. The Gini index is a measure of inequality. If all states have an in-degree of 1, the Gini index is 0. If all state transitions lead to one single state, the Gini index is 1.

This function requires the **igraph** package for the analysis of the in-degrees.

**testAttractorRobustness** This function tests the robustness of attractors in a network to noise. We expect attractors in a real network to be less susceptible to noise than attractors in randomly generated networks, as biological processes can be assumed to be comparatively stable. The function generates a number of perturbed copies of the network and checks whether the original attractors can still be found in the network.

`params` can hold a number of parameters:

**copies** The number of perturbed copies to generate

**perturb, method, simplify, readableFunctions, excludeFixed, maxNumBits, numStates** The corresponding parameters of `perturbNetwork` that influence the way the network is perturbed.

If `accumulate=FALSE`, the function returns a vector of percentages of original attractors found in each of the perturbed copies of the original network. If `accumulate=TRUE`, the function returns the overall percentage of original attractors found in all perturbed copies.

## Value

The function returns a list with the following elements

<code>hist</code>	The histogram that was plotted. The type of histogram depends on the parameter <code>accumulation</code> .
<code>pval</code>	If <code>accumulation="characteristic"</code> , a p-value for the alternative hypothesis that the test statistic value of the supplied network is greater than the value of a randomly generated network is supplied.
<code>significant</code>	If <code>accumulation="characteristic"</code> , this is true for <code>pval &lt; sign.level</code> .

**See Also**

[generateRandomNKNetwork](#), [perturbNetwork](#), [plotStateGraph](#), [getAttractors](#)

**Examples**

```
# load mammalian cell cycle network
data(cellcycle)

# compare the in-degrees of the states in the
# cell cycle network to random networks
testNetworkProperties(cellcycle, testFunction="testIndegree")

# compare the in-degrees of the states in the
# cell cycle network to random networks,
# and plot the Kullback-Leibler distances of the 100 experiments
testNetworkProperties(cellcycle, testFunction="testIndegree",
                      accumulation = "kullback_leibler")

# compare the robustness of attractors in the cell cycle network
# to random networks
testNetworkProperties(cellcycle, testFunction="testAttractorRobustness",
                      testFunctionParams=list(copies=10))
```

---

toPajek

*Export a network to the Pajek file format*


---

**Description**

Exports a network to the Pajek file format to visualize transition trajectories. For more information on Pajek, please refer to <http://pajek.imfm.si/doku.php>

**Usage**

```
toPajek(attractorInfo, file = "boolean.net", includeLabels=FALSE)
```

**Arguments**

attractorInfo	An object of class <code>AttractorInfo</code> , as returned by <a href="#">getAttractors</a> . As the transition table information in this structure is required, <code>getAttractors</code> must be called in synchronous mode and with <code>returnTable</code> set to <code>TRUE</code> .
file	The name of the output file for Pajek. Defaults to "boolean.net".
includeLabels	If set to true, the vertices of the graph in the output file are labeled with the binary encodings of the states. Defaults to <code>FALSE</code> .

**Value**

This function has no return value.

**See Also**[loadNetwork](#)**Examples**

```
# load example data
data(cellcycle)

# get attractors
attractors <- getAttractors(cellcycle)

# export to Pajek
toPajek(attractors, file="pajek_export.net")
```

---

yeastTimeSeries	<i>Yeast cell cycle time series data</i>
-----------------	--

---

**Description**

Preprocessed time series measurements of four genes from the yeast cell cycle data by Spellman et al.

**Usage**

```
data(yeastTimeSeries)
```

**Format**

A matrix with 14 measurements for the genes Fhk2, Swi5, Sic1, and Clb1. Each gene is a row of the matrix, and each column is a measurement.

**Details**

The data were obtained from the web site of the yeast cell cycle analysis project at <http://genome-www.stanford.edu/cellcycle>. The time series synchronized with the elutriation method were extracted for the genes Fhk2, Swi5, SIC1, and Clb1. In a preprocessing step, missing values were imputed by taking the means of the measurements of the same genes at neighbouring time points.

**Source**

P. T. Spellman, G. Sherlock, M. Q. Zhang, V. R. Iyer, K. Anders, M. B. Eisen, P. O. Brown, D. Botstein, B. Futcher (1998), Comprehensive Identification of Cell Cycle-regulated Genes of the Yeast *Saccharomyces cerevisiae* by Microarray Hybridization. *Molecular Biology of the Cell* 9(12):3273–3297.

Yeast cell cycle analysis project web site: <http://genome-www.stanford.edu/cellcycle>

**Examples**

```
data(yeastTimeSeries)
```

```
# the data set is stored in a variable called 'yeastTimeSeries'  
print(yeastTimeSeries)
```

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