

# Package ‘bnem’

May 15, 2024

**Type** Package

**Title** Training of logical models from indirect measurements of  
perturbation experiments

**Version** 1.13.0

**Description** bnem combines the use of indirect measurements of Nested Effects  
Models (package mnem) with the Boolean networks of CellNOptR. Perturbation  
experiments of signalling nodes in cells are analysed for their effect  
on the global gene expression profile. Those profiles give evidence  
for the Boolean regulation of down-stream nodes in the network,  
e.g., whether two parents activate their child independently  
(OR-gate) or jointly (AND-gate).

**Depends** R (>= 4.1)

**License** GPL-3

**Encoding** UTF-8

**biocViews** Pathways, SystemsBiology, NetworkInference, Network,  
GeneExpression, GeneRegulation, Preprocessing

**Imports** CellNOptR, matrixStats, snowfall, Rgraphviz, cluster,  
flexclust, stats, RColorBrewer, epiNEM, mnem, Biobase, methods,  
utils, graphics, graph, affy, binom, limma, sva, vsn, rmarkdown

**VignetteBuilder** knitr

**Suggests** knitr, BiocGenerics, MatrixGenerics, BiocStyle, RUnit

**BugReports** <https://github.com/MartinFXP/bnem/issues>

**URL** <https://github.com/MartinFXP/bnem/>

**RoxygenNote** 7.1.1

**git\_url** <https://git.bioconductor.org/packages/bnem>

**git\_branch** devel

**git\_last\_commit** 3ac5d3e

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.20

**Date/Publication** 2024-05-15

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absorption	<i>Absorption</i>
------------	-------------------

---

**Description**

applies absorption law to a disjunctive normal form

**Usage**

absorption(bString, model = NULL)

**Arguments**

- |         |  |
|---------|--|
| bString | a disjunctive normal form or binary vector according to model                        |
| model   | Model object including the search space, if available. See CellNOptR::preprocessing. |

**Value**

bString after absorption law

**Author(s)**

Martin PirkI

**Examples**

```
graph <- c("A+B=C", "A=C")
absorption(graph)
```

---

absorptionII

*Inverse absorption*

---

**Description**

applies "inverse" absorption law to a disjunctive normal form

**Usage**

```
absorptionII(bString, model = NULL)
```

**Arguments**

bString	a disjunctive normal form or binary vector according to model
model	Model object including the search space, if available. See CellNOptR::preprocessing.

**Value**

bString after "inverse" absorption law

**Author(s)**

Martin PirkI

**Examples**

```
graph <- c("A+B=C", "A=C")
absorptionII(graph)
```

---

addNoise	<i>Add noise</i>
----------	------------------

---

### Description

Adds noise to simulated data

### Usage

```
addNoise(sim, sd = 1)
```

### Arguments

sim	bnemsim object from simBoolGtn
sd	standard deviation for the rnorm function

### Value

noisy fold-change matrix

### Author(s)

Martin Pirkel

### Examples

```
sim <- simBoolGtn(Sgenes = 10, maxEdges = 10, negation=0.1, layer=1)
fc <- addNoise(sim, sd=1)
```

---

bcr	<i>B-Cell receptor signalling perturbations</i>
-----	---

---

### Description

Processed data from experiments with a stimulated B-Cell receptor (bcr) and perturbed signalling genes. The raw data is available at <https://www.ncbi.nlm.nih.gov/geo/> with accession id GSE68761. For the process steps we refer to the publication Martin Pirkel, Elisabeth Hand, Dieter Kube, Rainer Spang, Analyzing synergistic and non-synergistic interactions in signalling pathways using Boolean Nested Effect Models, Bioinformatics, Volume 32, Issue 6, 15 March 2016, Pages 893–900, <https://doi.org/10.1093/bioinformatics/btw088>. Alternatively see also the function processDataBCR for details and for reproduction.

### Usage

```
bcr
```

## References

Martin Pirkel, Elisabeth Hand, Dieter Kube, Rainer Spang, Analyzing synergistic and non-synergistic interactions in signalling pathways using Boolean Nested Effect Models, Bioinformatics, Volume 32, Issue 6, 15 March 2016, Pages 893–900, <https://doi.org/10.1093/bioinformatics/btv680>

## Examples

```
data(bcr)
```

---

bnem

*Boolean Nested Effects Model main function*


---

## Description

This function takes a prior network and normalized perturbation data as input and trains logical functions on that prior network

## Usage

```
bnem(
  search = "greedy",
  fc = NULL,
  expression = NULL,
  egenes = NULL,
  pkn = NULL,
  design = NULL,
  stimuli = NULL,
  inhibitors = NULL,
  signals = NULL,
  CNOList = NULL,
  model = NULL,
  sizeFac = 10^-10,
  NAFac = 1,
  parameters = list(cutOffs = c(0, 1, 0), scoring = c(0.1, 0.2, 0.9)),
  parallel = NULL,
  method = "cosine",
  relFit = FALSE,
  verbose = TRUE,
  reduce = TRUE,
  parallel2 = 1,
  initBstring = NULL,
  popSize = 100,
  pMutation = 0.5,
  maxTime = Inf,
  maxGens = Inf,
  stallGenMax = 10,
  relTol = 0.01,
```

```

priorBitString = NULL,
selPress = c(1.2, 1e-04),
fit = "linear",
targetBstring = "none",
elitism = NULL,
inversion = NULL,
selection = c("t"),
type = "SOCK",
exhaustive = FALSE,
delcyc = FALSE,
seeds = 1,
maxSteps = Inf,
node = NULL,
absorpII = TRUE,
draw = TRUE,
prior = NULL,
maxInputsPerGate = 2
)

```

## Arguments

search	Type of search heuristic. Either "greedy", "genetic" or "exhaustive". "greedy" uses a greedy algorithm to move through the local neighbourhood of a initial hyper-graph. "genetic" uses a genetic algorithm. "exhaustive" searches through the complete search space and is not recommended.
fc	m x l matrix of foldchanges of gene expression values or equivalent input (normalized pvalues, logodds, ...) for m E-genes and l contrasts. If left NULL, the gene expression data is used to calculate naive foldchanges.
expression	Optional normalized m x l matrix of gene expression data for m E-genes and l experiments.
egenes	list object; each list entry is named after an S-gene and contains the names of egenes which are potential children
pkn	Prior knowledge network as output by CellNOptR::readSIF.
design	Optional n x l design matrix with n S-genes and l experiments. If available. If kept NULL, bnem needs either stimuli, inhibitors or a CNolist object.
stimuli	Character vector of stimuli names.
inhibitors	Character vector of inhibitors.
signals	Optional character vector of signals. Signals are S-genes, which can directly regulate E-genes. If left NULL, all stimuli and inhibitors are defined as signals.
CNolist	CNolist object (see package CellNOptR), if available.
model	Model object including the search space, if available. See CellNOptR::preprocessing.
sizeFac	Size factor penelizing the hyper-graph size.
NAFac	factor penelizing NAs in the data.

parameters	parameters for discrete case (not recommended); has to be a list with entries cutOffs and scoring: cutOffs = c(a,b,c) with a (cutoff for real zeros), b (cutoff for real effects), c = -1 for normal scoring, c between 0 and 1 for keeping only relevant between -1 and 0 for keeping only a specific quantile of E-genes, and c > 1 for keeping the top c E-genes; scoring = c(a,b,c) with a (weight for real effects), c (weight for real zeros), b (multiplier for effects/zeros between a and c);
parallel	Parallelize the search. An integer value specifies the number of threads on the local machine or a list object as in list(c(1,2,3), c("machine1", "machine2", "machine3")) specifies the threads distributed on different machines (local or others).
method	Scoring method can be "cosine", a correlation, or a distance measure. See ?cor and ?dist for details.
relFit	if TRUE a relative fit for each E-gene is computed (not recommended)
verbose	TRUE for verbose output
reduce	if TRUE reduces the search space for exhaustive search
parallel2	if TRUE parallelises the starts and not the search itself
initBstring	Binary vector for the initial hyper-graph.
popSize	Population size (only "genetic").
pMutation	Probability between 0 and 1 for mutation (only "genetic").
maxTime	Define a maximal time (seconds) for the search.
maxGens	Maximal number of generations (only "genetic").
stallGenMax	Maximum number of stall generations (only "genetic").
relTol	Score tolerance for networks defined as optimal but with a lower score as the real optimum (only "genetic").
priorBitString	Binary vector defining hyper-edges which are added to every hyper-graph. E.g. if you know hyper-edge 55 is definitely there and to fix that, set priorBitString[55] <- 1 (only "genetic").
selPress	Selection pressure between 1 and 2 (if fit="linear") and greater 2 (for fit "non-linear") for the stochastic universal sampling (only "genetic").
fit	"linear" or "nonlinear fit for stochastic universal sampling
targetBstring	define a binary vector representing a network; if this network is found, the computation stops
elitism	Number of best hyper-graphs transferred to the next generation (only "genetic").
inversion	Number of worst hyper-graphs for which their binary strings are inversed (only "genetic").
selection	"t" for tournament selection and "s" for stochastic universal sampling (only "genetic").
type	type of the parallelisation on multiple machines (default: "SOCK")
exhaustive	If TRUE an exhaustive search is conducted if the genetic algorithm would take longer (only "genetic").
delcyc	If TRUE deletes cycles in all hyper-graphs (not recommended).

seeds	how many starts for the greedy search? (default: 1); uses the n-dimensional cube (n = number of S-genes) to maximize search space coverage
maxSteps	Maximal number of steps (only "greedy").
node	vector of S-gene names, which are used in the greedy search; if node = NULL all nodes are considered
absorpII	Use inverse absorption (default: TRUE).
draw	If TRUE draws the network evolution.
prior	Binary vector. A 1 specifies hyper-edges which should not be optimized (only "greedy").
maxInputsPerGate	If no model is supplied, one is created with maxInputsPerGate as maximum number of parents for each hyper-edge.

### Value

List object including the optimized hyper-graph, its corresponding binary vector for full hyper-graph and optimized scores.

### Author(s)

Martin Pirkel

### See Also

nem

### Examples

```
sifMatrix <- rbind(c("A", 1, "B"), c("A", 1, "C"), c("B", 1, "D"),
c("C", 1, "D"))
temp.file <- tempfile(pattern="interaction",fileext=".sif")
write.table(sifMatrix, file = temp.file, sep = "\t",
row.names = FALSE, col.names = FALSE,
quote = FALSE)
PKN <- CellNOptR::readSIF(temp.file)
CNolist <- dummyCNolist("A", c("B","C","D"), maxStim = 1,
maxInhibit = 2, signals = c("A", "B","C","D"))
model <- CellNOptR::preprocessing(CNolist, PKN, maxInputsPerGate = 100)
expression <- matrix(rnorm(nrow(slot(CNolist, "cues"))*10), 10,
nrow(slot(CNolist, "cues")))
fc <- computeFc(CNolist, expression)
initBstring <- rep(0, length(model$reacID))
res <- bnem(search = "greedy", model = model, CNolist = CNolist,
fc = fc, pkn = PKN, stimuli = "A", inhibitors = c("B","C","D"),
parallel = NULL, initBstring = initBstring, draw = FALSE, verbose = FALSE,
maxSteps = Inf)
```



---

bnemBs	<i>Bootstraped Network</i>
--------	----------------------------

---

## Description

Runs Bootstraps on the data

## Usage

```
bnemBs(fc, x = 10, f = 0.5, replace = TRUE, startString = NULL, ...)
```

## Arguments

fc	m x l matrix of foldchanges of gene expression values or equivalent input (normalized pvalues, logodds, ...) for m E-genes and l contrasts. If left NULL, the gene expression data is used to calculate naive foldchanges.
x	number of bootstraps
f	percentage to sample, e.g. f = 0.5 samples only 50 the amount of E-genes as the original data
replace	if TRUE classical bootstrap, if FALSE sub-sampling without replacement
startString	matrix with each row being a string denoting a network to start inference several times with a specific network
...	additional parameters for the bnem function

## Value

list with the accumulation of edges in x and the number of bootstraps in n

## Author(s)

Martin Pirkl

## Examples

```
sifMatrix <- rbind(c("A", 1, "B"), c("A", 1, "C"), c("B", 1, "D"),
c("C", 1, "D"))
temp.file <- tempfile(pattern="interaction",fileext=".sif")
write.table(sifMatrix, file = temp.file, sep = "\t",
row.names = FALSE, col.names = FALSE,
quote = FALSE)
PKN <- CellNOptR::readSIF(temp.file)
CN0list <- dummyCN0list("A", c("B","C","D"), maxStim = 1,
maxInhibit = 2, signals = c("A", "B","C","D"))
model <- CellNOptR::preprocessing(CN0list, PKN, maxInputsPerGate = 100)
expression <- matrix(rnorm(nrow(slot(CN0list, "cues"))*10), 10,
nrow(slot(CN0list, "cues")))
fc <- computeFc(CN0list, expression)
```

```

initBstring <- rep(0, length(model$reacID))
res <- bnemBs(search = "greedy", model = model, CNolist = CNolist,
fc = fc, pk = PKN, stimuli = "A", inhibitors = c("B","C","D"),
parallel = NULL, initBstring = initBstring, draw = FALSE, verbose = FALSE,
maxSteps = Inf)

```

---

computeFc

---

*Compute differential effects*


---

## Description

computes differential effects given an activation pattern (absolute gene expression or truth table)

## Usage

```
computeFc(CNolist, y)
```

## Arguments

CNolist	CNolist object (see package CellNOptR), if available.
y	activation pattern according to the annotation in CNolist

## Value

numeric matrix with annotated response scheme

## Author(s)

Martin Pirkel

## Examples

```

sifMatrix <- rbind(c("A", 1, "B"), c("A", 1, "C"), c("B", 1, "D"),
c("C", 1, "D"))
temp.file <- tempfile(pattern="interaction",fileext=".sif")
write.table(sifMatrix, file = temp.file, sep = "\t",
row.names = FALSE, col.names = FALSE,
quote = FALSE)
PKN <- CellNOptR::readSIF(temp.file)
CNolist <- dummyCNolist("A", c("B","C","D"), maxStim = 1, maxInhibit = 2,
signals = c("A", "B","C","D"))
model <- CellNOptR::preprocessing(CNolist, PKN, maxInputsPerGate = 100)
expression <- matrix(rnorm(nrow(slot(CNolist, "cues"))*10), 10,
nrow(slot(CNolist, "cues")))
fc <- computeFc(CNolist, expression)

```

---

convertGraph	<i>Convert normal form</i>
--------------	----------------------------

---

**Description**

converts a disjunctive normal form into a conjunctive normal form and vice versa; input graph as disjunctive normal form like that: c("A+B=D", "C=D", "G+F=U", ...); output is the dual element also in disjunctive normal form;

**Usage**

```
convertGraph(g)
```

**Arguments**

g                      graph in normal form

**Value**

converted graph normal form

**Author(s)**

Martin PirkI

**Examples**

```
g <- "A+B=C"
g2 <- convertGraph(g)
```

---

dummyCNolist	<i>Create dummy CNolist</i>
--------------	-----------------------------

---

**Description**

creates a general CNolist object from meta information

**Usage**

```
dummyCNolist(
  stimuli = NULL,
  inhibitors = NULL,
  maxStim = 0,
  maxInhibit = 0,
  signals = NULL
)
```

**Arguments**

<code>stimuli</code>	Character vector of stimuli names.
<code>inhibitors</code>	Character vector of inhibitors.
<code>maxStim</code>	maximal number of stimulated genes for a single experiment
<code>maxInhibit</code>	maximal number of inhibited genes for a single experiment
<code>signals</code>	Optional character vector of signals. Signals are S-genes, which can directly regulate E-genes. If left NULL, all stimuli and inhibitors are defined as signals.

**Value**

CNolist object

**Author(s)**

Martin Pirkel

**Examples**

```
sifMatrix <- rbind(c("A", 1, "B"), c("A", 1, "C"), c("B", 1, "D"),
c("C", 1, "D"))
temp.file <- tempfile(pattern="interaction",fileext=".sif")
write.table(sifMatrix, file = temp.file, sep = "\t",
row.names = FALSE, col.names = FALSE,
quote = FALSE)
PKN <- CellNOptR::readSIF(temp.file)
CNolist <- dummyCNolist("A", c("B","C","D"), maxStim = 1, maxInhibit = 2,
signals = c("A", "B","C","D"))
```

---

epiNEM2Bg

---

*Switch between epiNEM and B-NEM*


---

**Description**

Convert epiNEM model into general Boolean graph. Only needed for comparing accuracy of inferred network for bnem and epiNEM.

**Usage**

```
epiNEM2Bg(t)
```

**Arguments**

<code>t</code>	full epiNEM model
----------------	-------------------

**Value**

differential effects pattern

**Author(s)**

Martin PirkI

**See Also**

CreateTopology

**Examples**

```
topology <- epiNEM::CreateTopology(3, 1, force = TRUE)
topology <- unlist(unique(topology), recursive = FALSE)
extTopology <- epiNEM::ExtendTopology(topology$model, 100)
b <- epiNEM2Bg(extTopology)
```

findResiduals

*Compute residuals***Description**

calculates residuals (data and optimized network do not match) and visualizes them

**Usage**

```
findResiduals(
  bString,
  CNolist,
  model,
  fc = NULL,
  expression = NULL,
  egenes = NULL,
  parameters = list(cutOffs = c(0, 1, 0), scoring = c(0.1, 0.2, 0.9)),
  method = "s",
  sizeFac = 10^-10,
  main = "residuals for decoupled vertices",
  sub = paste0("green residuals are added effects (left positive,",
    " right negative) and red residuals are deleted ", "effects"),
  cut = TRUE,
  parallel = NULL,
  verbose = TRUE,
  ...
)
```

**Arguments**

bString	Binary vector denoting the network given a model
CNolist	CNolist object (see package CellNOptR), if available.
model	Model object including the search space, if available. See CellNOptR::preprocessing.

<code>fc</code>	<code>m x l</code> matrix of foldchanges of gene expression values or equivalent input (normalized pvalues, logodds, ...) for <code>m</code> E-genes and <code>l</code> contrasts. If left <code>NULL</code> , the gene expression data is used to calculate naive foldchanges.
<code>expression</code>	Optional normalized <code>m x l</code> matrix of gene expression data for <code>m</code> E-genes and <code>l</code> experiments.
<code>egenes</code>	list object; each list entry is named after an S-gene and contains the names of egenes which are potential children
<code>parameters</code>	parameters for discrete case (not recommended); has to be a list with entries <code>cutOffs</code> and <code>scoring</code> : <code>cutOffs = c(a,b,c)</code> with <code>a</code> (cutoff for real zeros), <code>b</code> (cutoff for real effects), <code>c = -1</code> for normal scoring, <code>c</code> between 0 and 1 for keeping only relevant between -1 and 0 for keeping only a specific quantile of E-genes, and <code>c &gt; 1</code> for keeping the top <code>c</code> E-genes; <code>scoring = c(a,b,c)</code> with <code>a</code> (weight for real effects), <code>c</code> (weight for real zeros), <code>b</code> (multiplicator for effects/zeros between <code>a</code> and <code>c</code> );
<code>method</code>	Scoring method can be "cosine", a correlation, or a distance measure. See <code>?cor</code> and <code>?dist</code> for details.
<code>sizeFac</code>	Size factor penelizing the hyper-graph size.
<code>main</code>	Main title of the figure.
<code>sub</code>	Subtitle of the figure.
<code>cut</code>	If <code>TRUE</code> does not visualize experiments/S-genes which do not have any residuals.
<code>parallel</code>	Parallelize the search. An integer value specifies the number of threads on the local machine or a list object as in <code>list(c(1,2,3), c("machine1", "machine2", "machine3"))</code> specifies the threads distributed on different machines (local or others).
<code>verbose</code>	<code>TRUE</code> for verbose output
<code>...</code>	additional parameters for <code>epiNEM::HeatmapOP</code>

**Value**

numeric matrices indicating experiments and/or genes, where the network and the data disagree

**Author(s)**

Martin Pirkel

**Examples**

```
sifMatrix <- rbind(c("A", 1, "B"), c("A", 1, "C"), c("B", 1, "D"),
c("C", 1, "D"))
temp.file <- tempfile(pattern="interaction",fileext=".sif")
write.table(sifMatrix, file = temp.file, sep = "\t",
row.names = FALSE, col.names = FALSE,
quote = FALSE)
PKN <- CellNOptR::readSIF(temp.file)
CNolist <- dummyCNolist("A", c("B","C","D"), maxStim = 1, maxInhibit = 2,
signal = c("A", "B","C","D"))
model <- CellNOptR::preprocessing(CNolist, PKN, maxInputsPerGate = 100)
```

```

expression <- matrix(rnorm(nrow(slot(CNolist, "cues"))*10), 10,
nrow(slot(CNolist, "cues")))
fc <- computeFc(CNolist, expression)
initBstring <- rep(0, length(model$reacID))
res <- bnem(search = "greedy", CNolist = CNolist, fc = fc, model = model,
parallel = NULL, initBstring = initBstring, draw = FALSE, verbose = FALSE,
maxSteps = Inf)
rownames(fc) <- seq_len(nrow(fc))
## val <- validateGraph(CNolist = CNolist, fc = fc, model = model,
## bString = res$bString, Egenes = 10, Sgene = 4)
residuals <- findResiduals(res$bString, CNolist, model, fc = fc)

```

plot.bnem

*plot bnem object***Description**

plots the boolean network as disjunctive normal form

**Usage**

```

## S3 method for class 'bnem'
plot(x, ...)

```

**Arguments**

```

x                bnemsim object
...              further arguments; see function mnem::plotDnf

```

**Value**

plot of boolean network

**Author(s)**

Martin PirkI

**Examples**

```

sifMatrix <- rbind(c("A", 1, "B"), c("A", 1, "C"), c("B", 1, "D"),
c("C", 1, "D"))
temp.file <- tempfile(pattern="interaction",fileext=".sif")
write.table(sifMatrix, file = temp.file, sep = "\t",
row.names = FALSE, col.names = FALSE,
quote = FALSE)
PKN <- CellNOptR::readSIF(temp.file)
CNolist <- dummyCNolist("A", c("B","C","D"), maxStim = 1,
maxInhibit = 2, signals = c("A", "B","C","D"))
model <- CellNOptR::preprocessing(CNolist, PKN, maxInputsPerGate = 100)

```

```

expression <- matrix(rnorm(nrow(slot(CNolist, "cues"))*10), 10,
nrow(slot(CNolist, "cues")))
fc <- computeFc(CNolist, expression)
initBstring <- rep(0, length(model$reacID))
res <- bnem(search = "greedy", model = model, CNolist = CNolist,
fc = fc, pkn = PKN, stimuli = "A", inhibitors = c("B","C","D"),
parallel = NULL, initBstring = initBstring, draw = FALSE, verbose = FALSE,
maxSteps = Inf, seeds = 10)
plot(res)

```

---

plot.bnemBs

*Plot Bootstrap result*


---

## Description

Shows the result of a Bootstrap with either edge frequencies or confidence intervals

## Usage

```

## S3 method for class 'bnemBs'
plot(
  x,
  scale = 3,
  shift = 0.1,
  cut = 0.5,
  dec = 2,
  ci = 0,
  cip = 0.95,
  method = "exact",
  ...
)

```

## Arguments

x	bnemBs object
scale	numeric value for scaling the edgewidth
shift	numeric value for shifting the edgewidth
cut	shows only edges with a fraction larger than cut
dec	integer for function round
ci	if TRUE shows confidence intervals
cip	range for the confidence interval, e.g. 0.95
method	method to use for confidence interval computation (see function binom.confint from package binom)
...	additional parameters for the function mnem::plotDnf



**Value**

plot of the network from the bootstrap

**Author(s)**

Martin Pirkel

**Examples**

```
sifMatrix <- rbind(c("A", 1, "B"), c("A", 1, "C"), c("B", 1, "D"),
c("C", 1, "D"))
temp.file <- tempfile(pattern="interaction",fileext=".sif")
write.table(sifMatrix, file = temp.file, sep = "\t",
row.names = FALSE, col.names = FALSE,
quote = FALSE)
PKN <- CellNOptR::readSIF(temp.file)
CNolist <- dummyCNolist("A", c("B","C","D"), maxStim = 1,
maxInhibit = 2, signals = c("A", "B","C","D"))
model <- CellNOptR::preprocessing(CNolist, PKN, maxInputsPerGate = 100)
expression <- matrix(rnorm(nrow(slot(CNolist, "cues"))*10), 10,
nrow(slot(CNolist, "cues")))
fc <- computeFc(CNolist, expression)
initBstring <- rep(0, length(model$reacID))
res <- bnemBs(search = "greedy", model = model, CNolist = CNolist,
fc = fc, pkn = PKN, stimuli = "A", inhibitors = c("B","C","D"),
parallel = NULL, initBstring = initBstring, draw = FALSE, verbose = FALSE,
maxSteps = Inf)
```

---

plot.bnemsim

*plot simulation object*


---

**Description**

plots the boolean network from a simulation as disjunctive normal form

**Usage**

```
## S3 method for class 'bnemsim'
plot(x, ...)
```

**Arguments**

x                      bnemsim object  
...                      further arguments; see function mnem::plotDnf

**Value**

plot of boolean network

**Author(s)**

Martin PirkI

**Examples**

```
sim <- simBoolGtn()
plot(sim)
```

---

processDataBCR

*BCR perturbation reproduction*

---

**Description**

Produce the application data from the BCR paper of PirkI, et al., 2016, Bioinformatics. Raw data is available at <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE68761>

**Usage**

```
processDataBCR(path = "", combsign = FALSE)
```

**Arguments**

path	path to the CEL.gz/Cel files
combsign	if TRUE includes all covariates in ComBat analysis to estimate batch effects.

**Value**

list with the full foldchanges and epxression matrix, a reduced foldchange matrix and the design matrix for the computations

**Author(s)**

Martin PirkI

**Examples**

```
## Not run:
processDataBCR()

## End(Not run)
data(bcr)
```

---

randomDnf	<i>sample normal form</i>
-----------	---------------------------

---

**Description**

creates a random normal form or hyper-graph

**Usage**

```
randomDnf(  
  vertices = 10,  
  negation = TRUE,  
  max.edge.size = NULL,  
  max.edges = NULL,  
  dag = FALSE  
)
```

**Arguments**

vertices	number of vertices
negation	if TRUE, negations (NOT gates) are allowed
max.edge.size	maximal number of inputs per edge
max.edges	maximal number of hyper-edges
dag	if TRUE, graph will be acyclic

**Value**

random hyper-graph in normal form

**Author(s)**

Martin PirkI

**Examples**

```
g <- randomDnf(10)
```

---

reduceGraph	<i>Reduce graph</i>
-------------	---------------------

---

## Description

reduces the size of a graph, if possible, to an equivalent sub-graph

## Usage

```
reduceGraph(bString, model, CNolist)
```

## Arguments

bString	binary vector indicating the sub-graph given a model
model	Model object including the search space, if available. See CellNOptR::preprocessing.
CNolist	CNolist object (see package CellNOptR), if available.

## Value

equivalent sub-graph denoted by a bString

## Author(s)

Martin PirkI

## Examples

```
sifMatrix <- rbind(c("A", 1, "B"), c("A", 1, "C"), c("B", 1, "D"),
c("C", 1, "D"))
temp.file <- tempfile(pattern="interaction",fileext=".sif")
write.table(sifMatrix, file = temp.file, sep = "\t",
row.names = FALSE, col.names = FALSE,
quote = FALSE)
PKN <- CellNOptR::readSIF(temp.file)
CNolist <- dummyCNolist("A", c("B","C","D"), maxStim = 1, maxInhibit = 2,
signal = c("A", "B","C","D"))
model <- CellNOptR::preprocessing(CNolist, PKN, maxInputsPerGate = 100)
bString <- reduceGraph(rep(1, length(model$reacID)), model, CNolist)
```

---

scoreDnf	<i>score a boolean network</i>
----------	--------------------------------

---

## Description

computes the score of a boolean network given the model and data

## Usage

```
scoreDnf(
  bString,
  CN0list,
  fc,
  expression = NULL,
  model,
  method = "cosine",
  sizeFac = 10^-10,
  NAFac = 1,
  parameters = list(cutOffs = c(0, 1, 0), scoring = c(0.25, 0.5, 2)),
  NEmlist = NULL,
  relFit = FALSE,
  verbose = FALSE
)
```

## Arguments

bString	binary string denoting the boolean network
CN0list	CN0list object (see package CellNOptR), if available.
fc	m x l matrix of foldchanges of gene expression values or equivalent input (normalized pvalues, logodds, ...) for m E-genes and l contrasts. If left NULL, the gene expression data is used to calculate naive foldchanges.
expression	Optional normalized m x l matrix of gene expression data for m E-genes and l experiments.
model	Model object including the search space, if available. See CellNOptR::preprocessing.
method	Scoring method can be "cosine", a correlation, or a distance measure. See ?cor and ?dist for details.
sizeFac	Size factor penelizing the hyper-graph size.
NAFac	factor penelizing NAs in the data.
parameters	parameters for discrete case (not recommended); has to be a list with entries cutOffs and scoring: cutOffs = c(a,b,c) with a (cutoff for real zeros), b (cutoff for real effects), c = -1 for normal scoring, c between 0 and 1 for keeping only relevant between -1 and 0 for keeping only a specific quantile of E-genes, and c > 1 for keeping the top c E-genes; scoring = c(a,b,c) with a (weight for real effects), c (weight for real zeros), b (multiplicator for effects/zeros between a and c);

NEMlist	NEMlist object (optional)
relFit	if TRUE a relative fit for each E-gene is computed (not recommended)
verbose	TRUE for verbose output

**Value**

numeric value (score)

**Author(s)**

Martin Pirkl

**Examples**

```
sim <- simBoolGtn()
scoreDnf(sim$bString, sim$CNolist, sim$fc, model=sim$model)
```

---

simBoolGtn	<i>Sample random network and simulate data</i>
------------	--

---

**Description**

Draws a random prior network, samples a ground truth from the full boolean extension and generates data

**Usage**

```
simBoolGtn(
  Sgenes = 10,
  maxEdges = 25,
  stimGenes = 2,
  layer = 1,
  frac = 0.1,
  maxInDeg = 2,
  dag = TRUE,
  maxSize = 2,
  maxStim = 2,
  maxInhibit = 1,
  Egenes = 10,
  flip = 0.33,
  reps = 1,
  keepsif = FALSE,
  negation = 0.25,
  allstim = FALSE,
  and = 0.25,
  positive = TRUE,
  verbose = FALSE
)
```

**Arguments**

Sgenes	number of S-genes
maxEdges	number of maximum edges (upper limit) in the DAG
stimGenes	number of stimulated S-genes
layer	scaling factor for the sampling of next Sgene layer of the prior. high (5-10) mean more depth and low (0-2) means more breadth
frac	fraction of hyper-edges in the ground truth (GTN)
maxInDeg	maximum number of incoming hyper-edges
dag	if TRUE, graph will be acyclic
maxSize	maximum number of S-genes in a hyper-edge
maxStim	maximum of stimulated S-genes in an experiment (=data samples)
maxInhibit	maximum number of inhibited S-genes in an experiment (=data samples)
Egenes	number of E-genes per S-gene, e.g. 10 S-genes and 10 E-genes will return 100 E-genes overall
flip	fraction of inhibited E-genes
reps	number of replicates
keepsif	if TRUE does not delete sif file, which encodes the prior network
negation	sample probability for negative or NOT edges
allstim	full network in which all S-genes are also stimulated
and	probability for AND-gates in the GTN
positive	if TRUE, sets all stimulation edges to activation, else samples inhibitory edges by 'negation' probability
verbose	TRUE for verbose output

**Value**

list with the corresponding prior graph, ground truth network and data

**Author(s)**

Martin PirkI

**Examples**

```
sim <- simBoolGtn()
plot(sim)
```

---

simulateStatesRecursive

*Simulate states*


---

## Description

simulates the activation pattern (truth table) of a hyper-graph and annotated perturbation experiments

## Usage

```
simulateStatesRecursive(CNolist, model, bString, NEMlist = NULL)
```

## Arguments

CNolist	CNolist object (see package CellNOptR), if available.
model	Model object including the search space, if available. See CellNOptR::preprocessing.
bString	binary vector denoting the sub-graph given model
NEMlist	NEMlist object only for devel

## Value

return the truth tables for certain perturbation experiments as a numeric matrix

## Author(s)

Martin PirkI

## Examples

```
sifMatrix <- rbind(c("A", 1, "B"), c("A", 1, "C"), c("B", 1, "D"),
c("C", 1, "D"))
temp.file <- tempfile(pattern="interaction",fileext=".sif")
write.table(sifMatrix, file = temp.file, sep = "\t",
row.names = FALSE, col.names = FALSE,
quote = FALSE)
PKN <- CellNOptR::readSIF(temp.file)
CNolist <- dummyCNolist("A", c("B","C","D"), maxStim = 1, maxInhibit = 2,
signal = c("A", "B","C","D"))
model <- CellNOptR::preprocessing(CNolist, PKN, maxInputsPerGate = 100)
states <- simulateStatesRecursive(CNolist, model,
rep(1, length(model$reacID)))
```



---

transClose	<i>transitive closure</i>
------------	---------------------------

---

**Description**

calculates transitive closure of a hyper-graph

**Usage**

```
transClose(g, max.iter = NULL, verbose = FALSE)
```

**Arguments**

g	hyper-graph in normal form
max.iter	maximal iteration till convergence
verbose	TRUE for verbose output

**Value**

transitive closure in normal form

**Author(s)**

Martin PirkI

**Examples**

```
g <- c("A=B", "B=C")
gclose <- transClose(g)
```

---

transRed	<i>transitive reduction</i>
----------	-----------------------------

---

**Description**

calculates transitive reduction of a hyper-graph in normal form

**Usage**

```
transRed(g, max.iter = NULL, verbose = FALSE)
```

**Arguments**

g	hyper-graph in normal form
max.iter	maximal number of iterations till convergence
verbose	TRUE for verbose output

**Value**

transitive reduction of the hyper-graph in normal form

**Author(s)**

Martin PirkI

**Examples**

```
g <- c("A=B", "A=C", "B=C", "B=D", "!A=D")
gred <- transRed(g)
```

---

validateGraph

*validate graph*

---

**Description**

plotting the observed differential effects of an effect reporter and the expected differential effects of the regulating signalling gene

**Usage**

```
validateGraph(
  CN0list,
  fc = NULL,
  expression = NULL,
  model,
  bString,
  Egenes = 25,
  Sgene = 1,
  parameters = list(cutOffs = c(0, 1, 0), scoring = c(0.1, 0.2, 0.9)),
  plot = TRUE,
  disc = 0,
  affyIds = TRUE,
  relFit = FALSE,
  xrot = 25,
  Rowv = FALSE,
  Colv = FALSE,
  dendrogram = "none",
  soft = TRUE,
  colSideColors = NULL,
  affychip = "hgu133plus2",
  method = "s",
  ranks = FALSE,
  breaks = NULL,
  col = "RdYlGn",
  sizeFac = 10^-10,
```

```

    order = "rank",
    verbose = TRUE,
    ...
)

```

## Arguments

CNOlist	CNOlist object (see package CellNOptR), if available.
fc	m x l matrix of foldchanges of gene expression values or equivalent input (normalized pvalues, logodds, ...) for m E-genes and l contrasts. If left NULL, the gene expression data is used to calculate naive foldchanges.
expression	Optional normalized m x l matrix of gene expression data for m E-genes and l experiments.
model	Model object including the search space, if available. See CellNOptR::preprocessing.
bString	Binary string denoting the hyper-graph.
Egenes	Maximal number of visualized E-genes.
Sgene	Integer denoting the S-gene. See colnames(getSignals(CNOlist)[[1]]) to match integer with S-gene name.
parameters	parameters for discrete case (not recommended); has to be a list with entries cutOffs and scoring: cutOffs = c(a,b,c) with a (cutoff for real zeros), b (cutoff for real effects), c = -1 for normal scoring, c between 0 and 1 for keeping only relevant between -1 and 0 for keeping only a specific quantile of E-genes, and c > 1 for keeping the top c E-genes; scoring = c(a,b,c) with a (weight for real effects), c (weight for real zeros), b (multiplicator for effects/zeros between a and c);
plot	Plot the heatmap. If FALSE, only corresponding information is printed.
disc	Discretize the data.
affyIds	Experimental. Turn Affymetrix Ids into HGNC gene symbols.
relFit	if TRUE a relative fit for each E-gene is computed (not recommended)
xrot	See function epiNEM::HeatmapOP
Rowv	See function epiNEM::HeatmapOP
Colv	See function epiNEM::HeatmapOP
dendrogram	See function epiNEM::HeatmapOP
soft	if TRUE, assigns weights to the expected pattern
colSideColors	See function epiNEM::HeatmapOP
affychip	Define Affymetrix chip used to generate the data (optional and experimental).
method	Scoring method can be "cosine", a correlation, or a distance measure. See ?cor and ?dist for details.
ranks	if TRUE, turns data into ranks
breaks	See function epiNEM::HeatmapOP
col	See function epiNEM::HeatmapOP
sizeFac	Size factor penelizing the hyper-graph size.

order	Order by "rank", "name" or "none"
verbose	TRUE for verbose output
...	additional arguments for epiNEM::HeatmapOP

**Value**

lattice object with matrix information

**Author(s)**

Martin Pirkel

**Examples**

```
sifMatrix <- rbind(c("A", 1, "B"), c("A", 1, "C"), c("B", 1, "D"),
c("C", 1, "D"))
temp.file <- tempfile(pattern="interaction",fileext=".sif")
write.table(sifMatrix, file = temp.file, sep = "\t",
row.names = FALSE, col.names = FALSE,
quote = FALSE)
PKN <- CellNOptR::readSIF(temp.file)
CNolist <- dummyCNolist("A", c("B","C","D"), maxStim = 1, maxInhibit = 2,
signal = c("A", "B","C","D"))
model <- CellNOptR::preprocessing(CNolist, PKN, maxInputsPerGate = 100)
expression <- matrix(rnorm(nrow(slot(CNolist, "cues"))*10), 10,
nrow(slot(CNolist, "cues")))
fc <- computeFc(CNolist, expression)
initBstring <- rep(0, length(model$reacID))
res <- bnem(search = "greedy", CNolist = CNolist, fc = fc,
model = model, parallel = NULL, initBstring = initBstring, draw = FALSE,
verbose = FALSE, maxSteps = Inf)
rownames(fc) <- seq_len(nrow(fc))
val <- validateGraph(CNolist = CNolist, fc = fc, model = model,
bString = res$bString, Egenes = 10, Sgene = 4)
```

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