

# Package ‘mnem’

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**Type** Package

**Title** Mixture Nested Effects Models

**Version** 1.21.0

**Description** Mixture Nested Effects Models (mnem) is an extension of Nested Effects Models and allows for the analysis of single cell perturbation data provided by methods like Perturb-Seq (Dixit et al., 2016) or Crop-Seq (Datlinger et al., 2017). In those experiments each of many cells is perturbed by a knock-down of a specific gene, i.e. several cells are perturbed by a knock-down of gene A, several by a knock-down of gene B, ... and so forth. The observed read-out has to be multi-trait and in the case of the Perturb-/Crop-Seq gene are expression profiles for each cell. mnem uses a mixture model to simultaneously cluster the cell population into k clusters and infer k networks causally linking the perturbed genes for each cluster. The mixture components are inferred via an expectation maximization algorithm.

**Depends** R (>= 4.1)

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**biocViews** Pathways, SystemsBiology, NetworkInference, Network, RNASeq, PooledScreens, SingleCell, CRISPR, ATACSeq, DNaseq, GeneExpression

**RoxygenNote** 7.3.2

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**BugReports** <https://github.com/cbg-ethz/mnem/issues>

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**Author** Martin Pirkl [aut, cre]

**Maintainer** Martin Pirkl <martinpirkl@yahoo.de>

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---

app

*Processed scRNAseq from pooled CRISPR screens*

---

### Description

Example data: mnem results for the Dixit et al., 2016 and Datlinger et al., pooled CRISPR screens. For details see the vignette or function createApp().

### Usage

app

## References

Datlinger, P., Rendeiro, A., Schmidl, C., Krausgruber, T., Traxler, P., Klughammer, J., Schuster, L. C., Kuchler, A., Alpar, D., and Bock, C. (2017). Pooled crispr screening with single-cell transcriptome readout. *Nature Methods*, 14, 297-301.

Dixit, A., Parnas, O., Li, B., Chen, J., Fulco, C. P., Jerby-Arnon, L., Marjanovic, N. D., Dionne, D., Burks, T., Raychowdhury, R., Adamson, B., Norman, T. M., Lander, E. S., Weissman, J. S., Friedman, N., and Regev, A. (2016). Perturb-seq: Dissecting molecular circuits with scalable single-cell rna profiling of pooled genetic screens. *Cell*, 167(7), 1853-1866.e17.

## Examples

```
data(app)
```

---

bootstrap	<i>Bootstrap.</i>
-----------	-------------------

---

## Description

Run bootstrap simulations on the components ( $\phi$ ) of an object of class `mnem`.

## Usage

```
bootstrap(x, size = 1000, p = 1, logtype = 2, complete = FALSE, ...)
```

## Arguments

<code>x</code>	<code>mnem</code> object
<code>size</code>	size of the bootstrap simulations
<code>p</code>	percentage of samples (e.g. for 100 E-genes $p=0.5$ means sampling 50)
<code>logtype</code>	logarithm type of the data (e.g. 2 for log2 data or $\exp(1)$ for natural)
<code>complete</code>	if TRUE, complete data log likelihood is considered (for very large data sets, e.g. 1000 cells and 1000 E-genes)
<code>...</code>	additional parameters for the <code>mnem</code> function

## Value

returns bootstrap support for each edge in each component ( $\phi$ ); list of adjacency matrices

## Author(s)

Martin Pirkl

## Examples

```
sim <- simData(Sgenes = 3, Egenes = 2, Nems = 2, mw = c(0.4,0.6))
data <- (sim$data - 0.5)/0.5
data <- data + rnorm(length(data), 0, 1)
result <- mnem(data, k = 2, starts = 1)
boot <- bootstrap(result, size = 2)
```

clustNEM

*Cluster NEM.***Description**

This function clusters the data and performs standard nem on each cluster.

**Usage**

```
clustNEM(
  data,
  k = 2:10,
  cluster = NULL,
  starts = 1,
  logtype = 2,
  nem = TRUE,
  getprobspars = list(),
  getaffinitypars = list(),
  Rho = NULL,
  ...
)
```

**Arguments**

data	data of log ratios with cells in columns and features in rows
k	number of clusters to check
cluster	given clustering has to correspond to the columns of data
starts	number of random starts for the kmeans algorithm
logtype	logarithm type of the data
nem	if FALSE only clusters the data
getprobspars	list of parameters for the getProbs function
getaffinitypars	list of parameters for the getAffinity function
Rho	perturbation matrix with dimensions nxl with n S-genes and l samples; either as probabilities with the sum of probabilities for a sample less or equal to 1 or discrete with 1s and 0s
...	additional arguments for standard nem function

**Value**

family of nems; the first k list entries hold full information of the standard nem search

comp	list of all adjacency matrices phi
mw	vector of mixture weights
probs	fake cell probabilities (see mw: mixture weights)

**Author(s)**

Martin Pirkl

**Examples**

```
sim <- simData(Sgenes = 3, Egenes = 2, Nems = 2, mw = c(0.4,0.6))
data <- (sim$data - 0.5)/0.5
data <- data + rnorm(length(data), 0, 1)
resultst <- clustNEM(data, k = 2:3)
```

---

createApp

*Creating app data.*


---

**Description**

This function is for the reproduction of the application results in the vignette and publication. See the publication Pirkl & Beerenwinkel (2018) on how to download the data files: GSE92872\_CROPseq\_Jurkat\_TCR.digital\_expression.csv k562\_both\_filt.txt GSM2396861\_k562\_ccycle\_cbc\_gbc\_dict.csv GSM2396858\_k562\_tfs\_7\_cbc\_gbc\_dict.csv

**Usage**

```
createApp(
  sets = seq_len(3),
  m = NULL,
  n = NULL,
  o = NULL,
  maxk = 5,
  parallel = NULL,
  path = "",
  types = c("data", "lods", "mnem"),
  allcrop = FALSE,
  multi = FALSE,
  file = NULL,
  ...
)
```

**Arguments**

sets	numeric vector with the data sets: 1 (CROPseq), 2, 3 (both PERTURBseq); default is all three
m	number of Sgenes (for testing)
n	number of most variable E-genes (for testing)
o	number of samples per S-gene (for testing)
maxk	maximum number of component in mnem inference (default: 5)
parallel	number of threads for parallelisation
path	path to the data files path/file.csv: "path/"
types	types of data/analysis; "data" creates the gene expression matrix, "lods" includes the log odds, "mnem" additionally performs the mixture nem analysis; default c("data", "lods", "mnem")
allcrop	if TRUE, does not restrict and uses the full CROPseq dataset
multi	if TRUE, includes cells with more than one perturbed gene

file path and filename of the rda file with the raw data from the command "data <- createApp(..., types = "data")"

... additional parameters for the mixture nem function

**Value**

app data object

**Author(s)**

Martin Pirkl

**Examples**

```
## recreate the app data object (takes very long, i.e. days)
## Not run:
createApp()

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

---

fitacc

*Simulation accuracy.*

---

**Description**

Computes the accuracy of the fit between simulated and inferred mixture.

**Usage**

```
fitacc(x, y, strict = FALSE, unique = TRUE, type = "ham")
```

**Arguments**

x mnem object

y simulation object or another mnem object

strict if TRUE, accounts for over/underfitting, i.e. the number of components

unique if TRUE, phis of x and y are made unique each (FALSE if strict is TRUE)

type type of accuracy. "ham" for hamming, "sens" for sensitivity and "spec for Specificity"

**Value**

plot of EM convergence

**Author(s)**

Martin Pirkl

**Examples**

```

sim <- simData(Sgenes = 3, Egenes = 2, Nems = 2, mw = c(0.4,0.6))
data <- (sim$data - 0.5)/0.5
data <- data + rnorm(length(data), 0, 1)
result <- mnem(data, k = 2, starts = 1)
fitacc(result, sim)
fitacc(result, sim, type = "sens")
fitacc(result, sim, type = "spec")
fitacc(result, sim, strict = TRUE, type = "sens")
fitacc(result, sim, strict = TRUE, type = "spec")

```

fuzzyindex

*Calculate fuzzy ground truth.***Description**

Calculates responsibilities and mixture weights based on the ground truth and noisy data.

**Usage**

```
fuzzyindex(x, data, logtype = 2, complete = FALSE, marginal = FALSE, ...)
```

**Arguments**

x	mnem_sim object
data	noisy data matrix
logtype	logarithm type of the data
complete	if TRUE, complete data log likelihood is considered (for very large data sets, e.g. 1000 cells and 1000 E-genes)
marginal	logical to compute the marginal likelihood (TRUE)
...	additional parameters for the function getAffinity

**Value**

list with cell log odds mixture weights and log likelihood

**Author(s)**

Martin Pirkl

**Examples**

```

sim <- simData(Sgenes = 3, Egenes = 2, Nems = 2, mw = c(0.4,0.6))
data <- sim$data
data[which(sim$data == 1)] <- rnorm(sum(sim$data == 1), 1, 1)
data[which(sim$data == 0)] <- rnorm(sum(sim$data == 0), -1, 1)
fuzzy <- fuzzyindex(sim, data)

```

---

 getAffinity

*Calculate responsibilities.*


---

### Description

This function calculates the responsibilities of each component for all cells from the expected log distribution of the hidden data.

### Usage

```
getAffinity(
  x,
  affinity = 0,
  norm = TRUE,
  logtype = 2,
  mw = NULL,
  data = matrix(0, 2, ncol(x)),
  complete = FALSE
)
```

### Arguments

x	log odds for l cells and k components as a kxl matrix
affinity	0 for standard soft clustering, 1 for hard clustering during inference (not recommended)
norm	if TRUE normalises to probabilities (recommended)
logtype	logarithm type of the data (e.g. 2 for log2 data or exp(1) for natural)
mw	mixture weights of the components
data	data in log odds
complete	if TRUE, complete data log likelihood is considered (for very large data sets, e.g. 1000 cells and 1000 E-genes)

### Value

responsibilities as a kxl matrix (k components, l cells)

### Author(s)

Martin Pirkl

### Examples

```
sim <- simData(Sgenes = 3, Egenes = 2, Nems = 2, mw = c(0.4,0.6))
data <- (sim$data - 0.5)/0.5
data <- data + rnorm(length(data), 0, 1)
result <- mnem(data, k = 2, starts = 1)
resp <- getAffinity(result$probs, mw = result$mw, data = data)
```



---

getIC

*Calculate negative penalized log likelihood.*


---

### Description

This function calculates a negative penalized log likelihood given a object of class `mnem`. This penalized likelihood is based on the normal likelihood and penalizes complexity of the mixture components (i.e. the networks).

### Usage

```
getIC(
  x,
  man = FALSE,
  degree = 4,
  logtype = 2,
  pen = 2,
  useF = FALSE,
  Fnorm = FALSE
)
```

### Arguments

<code>x</code>	<code>mnem</code> object
<code>man</code>	logical. manual data penalty, e.g. <code>man=TRUE</code> and <code>pen=2</code> for an approximation of the Akaike Information Criterion
<code>degree</code>	different degree of penalty for complexity: positive entries of transitively reduced phis or $\phi^r$ ( <code>degree=0</code> ), $\phi^r$ and mixture components minus one $k-1$ (1), $\phi^r$ , $k-1$ and positive entries of thetas (2), positive entries of transitively closed phis or $\phi^t$ , $k-1$ (3), $\phi^t$ , theta, $k-1$ (4, default), all entries of phis, thetas and $k-1$ (5)
<code>logtype</code>	logarithm type of the data (e.g. 2 for <code>log2</code> data or <code>exp(1)</code> for natural)
<code>pen</code>	penalty weight for the data (e.g. <code>pen=2</code> for approximate Akaike Information Criterion)
<code>useF</code>	use F (see publication) as complexity instead of phi and theta
<code>Fnorm</code>	normalize complexity of F, i.e. if two components have the same entry in F, it is only counted once

### Value

penalized log likelihood

### Author(s)

Martin Pirkl

**Examples**

```
sim <- simData(Sgenes = 3, Egenes = 2, Nems = 2, mw = c(0.4,0.6))
data <- (sim$data - 0.5)/0.5
data <- data + rnorm(length(data), 0, 1)
pen <- numeric(3)
result <- list()
for (k in seq_len(2)) {
  result[[k]] <- mnem(data, k = k, starts = 1)
  pen[k] <- getIC(result[[k]])
}
print(pen)
```

---

hamSim

*Accuracy for twophis.*

---

**Description**

This function uses the hamming distance to calculate an accuracy for two networks ( $\phi$ ).

**Usage**

```
hamSim(a, b, diag = 1, symmetric = TRUE)
```

**Arguments**

a	adjacency matrix ( $\phi$ )
b	adjacency matrix ( $\phi$ )
diag	if 1 includes diagonal in distance, if 0 not
symmetric	comparing a to b is asymmetrical, if TRUE includes comparison b to a

**Value**

normalized hamming accuracy for a and b

**Author(s)**

Martin Pirkl

**Examples**

```
sim <- simData(Sgenes = 3, Egenes = 2, Nems = 2, mw = c(0.4,0.6))
similarity <- hamSim(sim$Nem[[1]], sim$Nem[[2]])
```

---

mnem	<i>Mixture NEMs - main function.</i>
------	--------------------------------------

---

## Description

This function simultaneously learns a mixture of causal networks and clusters of a cell population from single cell perturbation data (e.g. log odds of fold change) with a multi-trait readout. E.g. Pooled CRISPR scRNA-Seq data (Perturb-Seq. Dixit et al., 2016, Crop-Seq. Datlinger et al., 2017).

## Usage

```
mnem(  
  D,  
  inference = "em",  
  search = "greedy",  
  phi = NULL,  
  theta = NULL,  
  mw = NULL,  
  method = "llr",  
  marginal = FALSE,  
  parallel = NULL,  
  reduce = FALSE,  
  runs = 1,  
  starts = 3,  
  type = "networks",  
  complete = FALSE,  
  p = NULL,  
  k = NULL,  
  kmax = 10,  
  verbose = FALSE,  
  max_iter = 100,  
  parallel2 = NULL,  
  converged = -Inf,  
  redSpace = NULL,  
  affinity = 0,  
  evolution = FALSE,  
  lambda = 1,  
  subtopoX = NULL,  
  ratio = TRUE,  
  logtype = 2,  
  domean = TRUE,  
  modulesize = 5,  
  compress = FALSE,  
  increase = TRUE,  
  fpdf = c(0.1, 0.1),  
  Rho = NULL,  
  ksel = c("kmeans", "silhouette", "cor"),  
  nullcomp = FALSE,  
  tree = FALSE,  
  burnin = 10,  
)
```

```

    hastings = TRUE,
    nodeswitch = TRUE,
    postgaps = 10,
    penalized = FALSE,
    accept_range = 1,
    ...
)

```

### Arguments

D	data with cells indexing the columns and features (E-genes) indexing the rows
inference	inference method "em" for expectation maximization or "mcmc" for markov chain monte carlo sampling
search	search method for single network inference "greedy", "exhaustive" or "modules" (also possible: "small", which is greedy with only one edge change per M-step to make for a smooth convergence)
phi	a list of n lists of k networks for n starts of the EM and k components
theta	a list of n lists of k attachment vector for the E-genes for n starts of the EM and k components
mw	mixture weights; if NULL estimated or uniform
method	"llr" for log ratios or foldchanges as input (see ratio)
marginal	logical to compute the marginal likelihood (TRUE)
parallel	number of threads for parallelization of the number of em runs
reduce	logical - reduce search space for exhaustive search to unique networks
runs	number of runs for greedy search
starts	number of starts for the em or mcmc
type	initialize with responsibilities either by "random", "cluster" (each S-gene is clustered and the different S-gene clustered differently combined for several starts), "cluster2" (clustNEM is used to infer reasonable phis, which are then used as a start for one EM run), "cluster3" (global clustering as a start), or "networks" (initialize with random phis), inference='mcmc' only supports 'networks' and 'empty' for unconnected networks phi
complete	if TRUE, optimizes the expected complete log likelihood of the model, otherwise the log likelihood of the observed data
p	initial probabilities as a k (components) times l (cells) matrix
k	number of components
kmax	maximum number of components when k=NULL is inferred
verbose	verbose output
max_iter	maximum iterations (moves for inference='mcmc'. adjust parameter burnin)
parallel2	if parallel=NULL, number of threads for single component optimization
converged	absolute distance for convergence between new and old log likelihood; if set to -Inf, the EM stops if neither the phis nor thetas were changed in the most recent iteration
redSpace	space for "exhaustive" search
affinity	0 is default for soft clustering, 1 is for hard clustering
evolution	logical. If TRUE components are penalized for being different from each other.

lambda	smoothness value for the prior put on the components, if evolution set to TRUE
subtopoX	hard prior on theta as a vector with entry i equal to j, if E-gene i is attached to S-gene j
ratio	logical, if true data is log ratios, if false foldchanges
logtype	logarithm type of the data (e.g. 2 for log2 data or exp(1) for natural)
domean	average the data, when calculating a single NEM (speed improvement)
modulesize	max number of S-genes per module in module search
compress	compress networks after search (warning: penalized likelihood not interpretable)
increase	if set to FALSE, the algorithm will not stop if the likelihood decreases
fpfn	numeric vector of length two with false positive and false negative rates for discrete data
Rho	perturbation matrix with dimensions nxl with n S-genes and l samples; either as probabilities with the sum of probabilities for a sample less or equal to 1 or discrete with 1s and 0s
kse1	character vector of methods for the inference of k; can combine as the first two vlues "hc" (hierarchical clustering) or "kmeans" with "silhouette", "BIC" or "AIC"; the third value is either "cor" for correlation distance or any method accepted by the function 'dist'
nullcomp	if TRUE, adds a null component (k+1)
tree	if TRUE, restrict inference on trees (MCMC not included)
burnin	number of iterations to be discarded prior to analyzing the posterior distribution of the mcmc
hastings	if set to TRUE, the Hastings ratio is calculated
nodeswitch	if set to TRUE, node switching is allowed as a move, additional to the edge moves
postgaps	can be set to numeric. Determines after how many iterations the next Phi mixture is added to the Phi edge Frequency tracker in the mcmc
penalized	if set to TRUE, the penalized likelihood will be used for the mcmc. Per default this is FALSE, since no component learning is involved and sparcity is hence not enforced
accept_range	the random probability the acceptance probability is compared to (default: 1)
...	arguments to function nem

### Value

object of class mnem	
comp	list of the component with each component being a list of the causal network phi and the E-gene attachment theta
data	input data matrix
limits	list of results for all independent searches
ll	log likelihood of the best model
lls	log likelihood ascent of the best model search
mw	vector with mixture weights
probs	kxl matrix containing the cell log likelihoods of the model

**Author(s)**

Martin Pirkl

**Examples**

```
sim <- simData(Sgenes = 3, Egenes = 2, Nems = 2, mw = c(0.4,0.6))
data <- (sim$data - 0.5)/0.5
data <- data + rnorm(length(data), 0, 1)
result <- mnemh(data, k = 2, starts = 1)
```

---

mnemh

*Hierarchical mixture.*

---

**Description**

This function does a hierarchical mixture. That means it uses the approximate BIC to check, if there are more than one component. It recursively splits the data if there is evidence for  $k > 1$  components.

**Usage**

```
mnemh(data, k = 2, logtype = 2, getprobspars = list(), ...)
```

**Arguments**

data	data matrix either binary or log odds
k	number of maximal components for each hierarchy leaf
logtype	log type of the data
getprobspars	list of parameters for the getProbs function
...	additional parameters for the mnem function

**Value**

object of class mnem

**Author(s)**

Martin Pirkl

**Examples**

```
sim <- simData(Sgenes = 3, Egenes = 2, Nems = 2, mw = c(0.4,0.6))
data <- (sim$data - 0.5)/0.5
data <- data + rnorm(length(data), 0, 1)
result <- mnemh(data, starts = 1, k = 1)
```

mnemk

*Learn the number of components K and optimize the mixture.***Description**

High level function for learning the number of components  $k$ , if unknown.

**Usage**

```
mnemk(
  D,
  ks = seq_len(5),
  man = FALSE,
  degree = 4,
  logtype = 2,
  pen = 2,
  useF = FALSE,
  Fnorm = FALSE,
  ...
)
```

**Arguments**

D	data with cells indexing the columns and features (E-genes) indexing the rows
ks	vector of number of components $k$ to test
man	logical. manual data penalty, e.g. <code>man=TRUE</code> and <code>pen=2</code> for an approximation of the Akaike Information Criterion
degree	different degree of penalty for complexity: positive entries of transitively reduced phis or $\phi^r$ ( <code>degree=0</code> ), $\phi^r$ and mixture components minus one $k-1$ (1), $\phi^r$ , $k-1$ and positive entries of thetas (2), positive entries of transitively closed phis or $\phi^t$ , $k-1$ (3), $\phi^t$ , theta, $k-1$ (4, default), all entries of phis, thetas and $k-1$ (5)
logtype	logarithm type of the data (e.g. 2 for log2 data or <code>exp(1)</code> for natural)
pen	penalty weight for the data (e.g. <code>pen=2</code> for approximate Akaike Information Criterion)
useF	use F (see publication) as complexity instead of phi and theta
Fnorm	normalize complexity of F, i.e. if two components have the same entry in F, it is only counted once
...	additional parameters for the mnem main function

**Value**

list containing the result of the best  $k$  as an mnem object and the raw and penalized log likelihoods

**Author(s)**

Martin Pirkl

**Examples**

```

sim <- simData(Sgenes = 3, Egenes = 2, Nems = 2, mw = c(0.4,0.6))
data <- (sim$data - 0.5)/0.5
data <- data + rnorm(length(data), 0, 1)
result <- mnemk(data, ks = seq_len(2), starts = 1)

```

---

moreboxplot

*Boxplot with scatter and density options*


---

**Description**

Plots a boxplots plus x-axis randomised scatter and mirrored densities to visualise a distribution.

**Usage**

```

moreboxplot(
  x,
  box = TRUE,
  dens = TRUE,
  scatter = "no",
  polygon = TRUE,
  sd = 0.1,
  dcol = NULL,
  scol = NULL,
  dlty = 1,
  dlwd = 1,
  spch = 1,
  gcol = rgb(0, 0, 0, 0.5),
  glty = 2,
  glen = 2001,
  gmin = -100,
  gmax = 100,
  ...
)

```

**Arguments**

x	list, matrix or data.frame
box	if TRUE, draws boxes
dens	if TRUE, draws densities
scatter	if set to "random", draws x-axis randomised scatter points
polygon	if TRUE, fills the densities
sd	standard deviation of the scatter
dcol	color of the densities
scol	color of the scatter points
dlty	line type of the densities
dlwd	line width of the densities
spch	type of scatter points



gcol	color of the grid
glty	line type of the grid
glen	length of the grid
gmin	minimal point of the grid
gmax	maximal point of the grid
...	optional parameters for boxplot or plot

**Value**

transitively closed matrix or graphNEL

**Author(s)**

Martin Pirkl

**Examples**

```
D <- matrix(rnorm(100*3), 100, 3)
moreboxplot(D)
```

---

nem

*Implementation of the original NEM*

---

**Description**

Infers a signalling pathway from perturbation experiments.

**Usage**

```
nem(
  D,
  search = "greedy",
  start = NULL,
  method = "llr",
  marginal = FALSE,
  parallel = NULL,
  reduce = FALSE,
  weights = NULL,
  runs = 1,
  verbose = FALSE,
  redSpace = NULL,
  trans.close = TRUE,
  subtopo = NULL,
  prior = NULL,
  ratio = TRUE,
  domean = TRUE,
  modulesize = 5,
  fpdf = c(0.1, 0.1),
  Rho = NULL,
  logtype = 2,
```

```

    modified = FALSE,
    tree = FALSE,
    learnRates = FALSE,
    stepSize = 0.01,
    ...
)

```

### Arguments

D	data matrix with observed genes as rows and knock-down experiments as columns
search	either "greedy", "modules" or "exhaustive" (not recommended for more than five S-genes)
start	either NULL ("null") or a specific network to start the greedy
method	"llr" for log odds or p-values densities or "disc" for binary data
marginal	logical to compute the marginal likelihood (TRUE)
parallel	NULL for no parallel optimization or an integer for the number of threads
reduce	reduce search space (TRUE) for exhaustive search
weights	a numeric vector of weights for the columns of D
runs	the number of runs for the greedy search
verbose	for verbose output (TRUE)
redSpace	reduced search space for exhaustive search; see result of exhaustive search with reduce = TRUE
trans.close	if TRUE uses the transitive closure of adj
subtopo	optional matrix with the subtopology theta as adjacency matrix
prior	a prior network matrix for adj
ratio	if FALSE uses alternative distance for the model score
domean	if TRUE summarizes duplicate columns
modulesize	the max number of S-genes included in one module for search = "modules"
fpfn	numeric vector of length two with false positive and false negative rates
Rho	optional perturbation matrix
logtype	log base of the log odds
modified	if TRUE, assumes a preprocessed data matrix
tree	if TRUE forces tree; does not allow converging edges
learnRates	if TRUE learns rates for false positives/negatives
stepSize	numerical step size for learning rates
...	optional parameters for future search methods

### Value

transitively closed matrix or graphNEL

### Author(s)

Martin Pirkl

**Examples**

```
D <- matrix(rnorm(100*3), 100, 3)
colnames(D) <- 1:3
rownames(D) <- 1:100
adj <- diag(3)
colnames(adj) <- rownames(adj) <- 1:3
scoreAdj(D, adj)
```

---

plot.bootmnem                      *Plot bootstrap mnem result.*

---

**Description**

Plot bootstrap mnem result.

**Usage**

```
## S3 method for class 'bootmnem'
plot(x, reduce = TRUE, ...)
```

**Arguments**

x	bootmnem object
reduce	if TRUE transitively reduces the graphs
...	additional parameters for the plotting function plotDNF

**Value**

visualization of bootstrap mnem result with Rgraphviz

**Author(s)**

Martin Pirkl

**Examples**

```
sim <- simData(Sgenes = 3, Egenes = 2, Nems = 2, mw = c(0.4,0.6))
data <- (sim$data - 0.5)/0.5
data <- data + rnorm(length(data), 0, 1)
result <- mnem(data, k = 2, starts = 1)
boot <- bootstrap(result, size = 2)
plot(boot)
```

---

plot.mnem

*Plot mnem result.*


---

### Description

Plot mnem result.

### Usage

```
## S3 method for class 'mnem'
plot(
  x,
  oma = c(3, 1, 1, 3),
  main = "M&NEM",
  anno = TRUE,
  cexAnno = 1,
  scale = NULL,
  global = TRUE,
  egenes = TRUE,
  sep = FALSE,
  tsne = FALSE,
  affinity = 0,
  logtype = 2,
  cells = TRUE,
  pch = ".",
  legend = FALSE,
  showdata = FALSE,
  bestCell = TRUE,
  showprobs = FALSE,
  shownull = TRUE,
  ratio = TRUE,
  method = "llr",
  marginal = FALSE,
  showweights = TRUE,
  ...
)
```

### Arguments

x	mnem object
oma	outer margin
main	main text
anno	annotate cells by their perturbed gene
cexAnno	text size of the cell annotations
scale	scale cells to show relative and not absolute distances
global	if TRUE clusters all cells, if FALSE clusters cells within a component
egenes	show egene attachments, i.e. number of E-genes assigned to each S-gene
sep	separate clusters and not put them on top of each other for better visualization

tsne	if TRUE use tsne instead of pca
affinity	use hard clustering if TRUE
logtype	logarithm type of the data (e.g. 2 for log2 data or exp(1) for natural)
cells	show cell attachments, .i.e how many cells are assigned to each S-gene
pch	cell symbol
legend	show legend
showdata	show data if TRUE
bestCell	show probability of best fitting cell for each S-gene
showprobs	if TRUE, shows responsibilities for all cells and components
shownull	if TRUE, shows the null node
ratio	use log ratios (TRUE) or foldchanges (FALSE)
method	"llr" for ratios
marginal	logical to compute the marginal likelihood (TRUE)
showweights	if TRUE, shows mixture weights for all components
...	additional parameters

**Value**

visualization of mnem result with Rgraphviz

**Author(s)**

Martin Pirkl

**Examples**

```
sim <- simData(Sgenes = 3, Egenes = 2, Nems = 2, mw = c(0.4,0.6))
data <- (sim$data - 0.5)/0.5
data <- data + rnorm(length(data), 0, 1)
result <- mnem(data, k = 2, starts = 1)
plot(result)
```

---

plot.mnem\_mcmc

*Plot mnem\_mcmc result.*

---

**Description**

Plot mnem\_mcmc result.

**Usage**

```
## S3 method for class 'mnem_mcmc'
plot(x, starts = NULL, burnin = 0, ...)
```

**Arguments**

x	mnem_mcmc object
starts	restarts of mcmc as used in mnem function
burnin	number of iteration to start from
...	parameters for function ggplot2

**Value**

visualization of mcmc result with Rgraphviz

**Author(s)**

Viktoria Brunner

**Examples**

```
sim <- simData(Sgenes = 3, Egenes = 2, Nems = 2, mw = c(0.4,0.6))
data <- (sim$data - 0.5)/0.5
data <- data + rnorm(length(data), 0, 1)
result <- mnem(data, k = 2, starts = 1)
plot(result)
```

---

plot.mnem\_sim

*Plot simulated mixture.*

---

**Description**

Plot simulated mixture.

**Usage**

```
## S3 method for class 'mnem_sim'
plot(x, data = NULL, logtype = 2, fuzzypars = list(), ...)
```

**Arguments**

x	mnem_sim object
data	noisy data matrix (optional)
logtype	logarithm type of the data
fuzzypars	list of parameters for the function fuzzyindex
...	additional parameters for the plotting function plotDNF

**Value**

visualization of simulated mixture with Rgraphviz

**Author(s)**

Martin Pirkl

**Examples**

```
sim <- simData(Sgenes = 3, Egenes = 2, Nems = 2, mw = c(0.4,0.6))
plot(sim)
```

---

plotConvergence	<i>Plot convergence of EM</i>
-----------------	-------------------------------

---

**Description**

Generic function plotting convergence diagnostics for different methods.

**Usage**

```
plotConvergence(x, ...)
```

**Arguments**

x	object with convergence statistics
...	additional parameters for the specific object type

**Value**

plot of EM convergence

**Author(s)**

Martin Pirkl

**Examples**

```
sim <- simData(Sgenes = 3, Egenes = 2, Nems = 2, mw = c(0.4,0.6))
data <- (sim$data - 0.5)/0.5
data <- data + rnorm(length(data), 0, 1)
result <- mnem(data, k = 2, starts = 1)
par(mfrow=c(2,2))
plotConvergence(result)
```

---

plotConvergence.mnem	<i>Plot convergence of EM</i>
----------------------	-------------------------------

---

**Description**

This function plots the convergence of the different EM iterations (four figures, e.g. `par(mfrow=(2,2))`).

**Usage**

```
## S3 method for class 'mnem'
plotConvergence(x, col = NULL, type = "b", convergence = 0.1, ...)
```

**Arguments**

x	mnem object
col	vector of colors for the iterations
type	see ?plot.default
convergence	difference of when two log likelihoods are considered equal; see also convergence for the function mnem()
...	additional parameters for the plots/lines functions

**Value**

plot of EM convergence

**Author(s)**

Martin Pirkl

**Examples**

```
sim <- simData(Sgenes = 3, Egenes = 2, Nems = 2, mw = c(0.4,0.6))
data <- (sim$data - 0.5)/0.5
data <- data + rnorm(length(data), 0, 1)
result <- mnem(data, k = 2, starts = 1)
par(mfrow=c(2,2))
plotConvergence(result)
```

---

plotDnf

*Plot disjunctive normal form.*

---

**Description**

This function visualizes a graph encoded as a disjunctive normal form. See the graphviz documentation for possible input arguments, like edgehead/tail: <https://graphviz.org/docs/attr-types/arrowType/>

**Usage**

```
plotDnf(
  dnf = NULL,
  freq = NULL,
  stimuli = c(),
  signals = c(),
  inhibitors = c(),
  connected = TRUE,
  CNlist = NULL,
  cex = NULL,
  fontsize = NULL,
  labelsize = NULL,
  type = 2,
  lwd = 1,
  edgelwd = 1,
  legend = 0,
```



```

x = 0,
y = 0,
xjust = 0,
yjust = 0,
width = 1,
height = 1,
layout = "dot",
main = "",
sub = "",
cex.main = 1.5,
cex.sub = 1,
col.sub = "grey",
fontcolor = NULL,
nodestates = NULL,
simulate = NULL,
edgecol = NULL,
labels = NULL,
labelcol = "blue",
nodelabel = NULL,
nodecol = NULL,
bordercol = NULL,
nodeshape = NULL,
verbose = FALSE,
edgestyle = NULL,
nodeheight = NULL,
nodewidth = NULL,
edgewidth = NULL,
lty = NULL,
hierarchy = NULL,
showall = FALSE,
edgehead = NULL,
edgelabel = NULL,
edgetail = NULL,
bool = TRUE,
draw = TRUE,
...
)

```

### Arguments

dnf	Hyper-graph in disjunctive normal form, e.g. $c("A=B", "A=C+D", "E=!B")$ with the child on the left and the parents on the right of the equation with $"A=C+D"$ for $A = C \text{ AND } D$ . Alternatively, dnf can be an adjacency matrix, which is converted on the fly to a disjunctive normal form.
freq	Frequency of hyper-edges which are placed on the edges.
stimuli	Highlights vertices which can be stimulated.
signals	Highlights vertices which regulate E-genes.
inhibitors	Highlights vertices which can be inhibited.
connected	If TRUE, only includes vertices which are connected to other vertices.
CNOlist	CNOlist object. Optional instead of stimuli, inhibitors or signals. See package CellNOptR.

<code>cex</code>	Global font size.
<code>fontsize</code>	Vertice label size.
<code>labelsize</code>	Edge label size.
<code>type</code>	Different plot types. 2 for Rgraphviz and 1 for graph.
<code>lwd</code>	Line width of nodeborder.
<code>edgelwd</code>	Global edgeline width.
<code>legend</code>	0 shows no legend. 1 shows legend as a graph. 2 shows legend in a standard box.
<code>x</code>	x coordinate of box legend.
<code>y</code>	y coordinate of box legend.
<code>xjust</code>	Justification of legend box left, right or center (-1,1,0).
<code>yjust</code>	Justification of legend box top, bottom or middle (-1,1,0).
<code>width</code>	Vertice width.
<code>height</code>	Vertice height.
<code>layout</code>	Graph layout. See <code>graphvizCapabilities()\$layoutTypes</code> .
<code>main</code>	Main title.
<code>sub</code>	Subtitle.
<code>cex.main</code>	Main title font size.
<code>cex.sub</code>	Subtitle font size.
<code>col.sub</code>	Font color of subtitle.
<code>fontcolor</code>	Global font color.
<code>nodestates</code>	Binary state of each vertice.
<code>simulate</code>	Simulate stimulation and inhibition of a list of vertices. E.g. <code>simulate = list(stimuli = c("A", "B"), inhibitors = c("C", "D"))</code> .
<code>edgecol</code>	Vector with colors for every edge of the graph (not hyper-graph). E.g. an AND gate consists of three distinct edges.
<code>labels</code>	Vector with labels for the edges.
<code>labelcol</code>	Vector with label colors for the edges.
<code>nodelabel</code>	List of vertices with labels as input. E.g. <code>labels = list(A="test", B="label for B")</code> .
<code>nodecol</code>	List of vertices with colors as input.
<code>bordercol</code>	List of vertices with colors as input.
<code>nodeshape</code>	List of vertices with shapes (diamond, box, square,...).
<code>verbose</code>	Verbose output.
<code>edgestyle</code>	set the edge style like dashed, can be numerical
<code>nodeheight</code>	List of vertices with height as input.
<code>nodewidth</code>	List of vertices with width as input.
<code>edgewidth</code>	Vector with edge widths for individual edges.
<code>lty</code>	Vector with edge styles (line, dotted,...).
<code>hierarchy</code>	List with the hierarchy of the vertices. E.g. <code>list(top = c("A", "B"), bottom = c("C", "D"))</code> .

showall	See "connected" above.
edgehead	Vector with edge heads.
edgelabel	Vector with edge labels.
edgetail	Vector with edge tails.
bool	If TRUE, only shows normal graph and no AND gates.
draw	Do not plot the graph and only output the graphNEL object.
...	additional arguments

**Value**

Rgraphviz object

**Author(s)**

Martin Pirkl

**Examples**

```
g <- c("!A+B+C=G", "C=G", "!D=G")
plotDnf(g)
```

---

scoreAdj

*Network score*

---

**Description**

Computes the fit (score of a network) of the data given a network matrix

**Usage**

```
scoreAdj(
  D,
  adj,
  method = "llr",
  marginal = FALSE,
  logtype = 2,
  weights = NULL,
  trans.close = TRUE,
  subtopo = NULL,
  prior = NULL,
  ratio = TRUE,
  fpdf = c(0.1, 0.1),
  Rho = NULL,
  dotopo = FALSE,
  P = NULL,
  oldadj = NULL,
  modified = TRUE
)
```

**Arguments**

D	data matrix; use modified = FALSE
adj	adjacency matrix of the network phi
method	either llr if D consists of log odds or disc, if D is binary
marginal	logical to compute the marginal likelihood (TRUE)
logtype	log base of the log odds
weights	a numeric vector of weights for the columns of D
trans.close	if TRUE uses the transitive closure of adj
subtopo	optional matrix with the subtopology theta as adjacency matrix
prior	a prior network matrix for adj
ratio	if FALSE uses alternative distance for the model score
fpfn	numeric vector of length two with false positive and false negative rates
Rho	optional perturbation matrix
dotopo	if TRUE computes and returns the subtopology theta (optional)
P	previous score matrix (only used internally)
oldadj	previous adjacency matrix (only used internally)
modified	if TRUE, assumes a preprocessed data matrix

**Value**

transitively closed matrix or graphNEL

**Author(s)**

Martin Pirkl

**Examples**

```
D <- matrix(rnorm(100*3), 100, 3)
colnames(D) <- 1:3
rownames(D) <- 1:100
adj <- diag(3)
colnames(adj) <- rownames(adj) <- 1:3
scoreAdj(D, adj)
```

---

simData

*Simulate data.*

---

**Description**

This function simulates single cell data from a random mixture of networks.

**Usage**

```

simData(
  Sgenes = 5,
  Egenes = 1,
  Nems = 2,
  reps = NULL,
  mw = NULL,
  evolution = FALSE,
  nCells = 1000,
  uninform = 0,
  unitheta = FALSE,
  edgeprob = c(0, 1),
  multi = FALSE,
  subsample = 1,
  scalefree = FALSE,
  badCells = 0,
  exactProb = TRUE,
  tree = FALSE,
  ...
)

```

**Arguments**

Sgenes	number of Sgenes
Egenes	number of Egenes
Nems	number of components
reps	number of replicates, if set (not realistic for cells)
mw	mixture weights (has to be vector of length Nems)
evolution	evolving and not purely random network, if set to TRUE
nCells	number of cells
uninform	number of uninformative Egenes
unitheta	uniform theta, if TRUE
edgeprob	edge probability, value between 0 and 1 for sparse or dense networks or a range c(l,u) with lower and upper bound
multi	a vector with the percentages of cell with multiple perturbations, e.g. c(0.2,0.1,0) for 20 no quadruple knock-downs
subsample	range to subsample data. 1 means the full simulated data is used
scalefree	if TRUE, graph is scale free
badCells	number of cells, which are just noise and not connected to the ground truth network
exactProb	logical; if TRUE generates random network with exact fraction of edges provided by edgeprob
tree	if TRUE, restricts dag to a tree
...	additional parameters for the scale free network sampler (see 'nem' package)

**Value**

simulation object with meta information and data

Nem	list of adjacency matrixes generatign the data
theta	E-gene attachaments
data	data matrix
index	index for which Nem generated which cell (data column)
mw	vector of input mixture weights

**Author(s)**

Martin Pirkl

**Examples**

```
sim <- simData(Sgenes = 3, Egenes = 2, Nems = 2, mw = c(0.4,0.6))
```

---

transitive.closure      *Transitive closure of a directed acyclic graph (dag)*

---

**Description**

Computes the transitive closure of a dag or only of a deletion/addition of an edge

**Usage**

```
transitive.closure(g, u = NULL, v = NULL)
```

**Arguments**

g	graph as matrix or graphNEL object
u	index of the parent of an edge (optional)
v	index of the child of an edge (optional)

**Value**

transitively closed matrix or graphNEL

**Author(s)**

Martin Pirkl

**Examples**

```
g <- matrix(c(0,0,0,1,0,0,0,1,0), 3)
transitive.closure(g)
```

---

transitive.reduction *Transitive reduction*

---

**Description**

Computes the transitive reduction of an adjacency matrix or graphNEL object. Originally imported from the package 'nem'.

**Usage**

```
transitive.reduction(g)
```

**Arguments**

*g* adjacency matrix or graphNEL object

**Value**

transitively reduced adjacency matrix

**Author(s)**

Holger Froehlich

**References**

R. Sedgewick, Algorithms, Pearson, 2002.

**Examples**

```
g <- matrix(c(0,0,0,1,0,0,0,1,0), 3)
rownames(g) <- colnames(g) <- seq_len(3)
g.tr <- transitive.reduction(g)
```

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