Package ‘lpNet’
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Title   Linear Programming Model for Network Inference
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Depends lpSolve, nem
Description lpNet aims at inferring biological networks, in particular signaling and gene networks.
For that it takes perturbation data, either steady-state or time-series,
as input and generates an LP model which allows the inference of signaling networks.
For parameter identification either leave-one-out cross-validation or
stratified n-fold cross-validation can be used.
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calcActivation

Description

Calculate the activation matrix assuming that the signaling is deterministically propagated along the network. For a given network and perturbation experiment the theoretical states of the genes are computed. So, if a gene has been silenced in an experiment, then the state of this gene is assumed to be inactive, otherwise if its inflow (coming from parent nodes) is activating, it is active. Cycles within a network are not resolved, therefore this function can be used only for networks without cycles. This function is also used to generate the network states for time-series data (by generateTimeSeriesNetStates), in which case flag_gen_data is set to true, and the activation matrix is calculated without taking the edges sign into account.
Usage

calcActivation(T_nw, b, n, K, flag_gen_data = FALSE)

Arguments

T_nw  Adjacency matrix: the network which is used to compute the activities and in-activities.

b  Vector of 0/1 values describing the experiments (entry is 0 if gene is inactivated in the respective experiment and 1 otherwise). The measurements of the genes of each experiment are appended as a long vector.

n  Integer: number of genes.

K  Integer: number of perturbation experiments.

flag_gen_data  Logical: if set to TRUE the edges sign will not be taken into account. It should be TRUE if the function is used to generate the network states for time-series data.

Value

Matrix of 0/1 values; rows corresponding to genes, columns to experiments. If an entry is 1, it means that the corresponding gene is active in the corresponding experiment and inactive otherwise.

Examples

n <- 5 # number of genes
K <- 7 # number of perturbations experiments

# perturbation vector, entry is 0 if gene is inactivated and 1 otherwise
b <- c(0,1,1,1,1, # perturbation exp1: gene 1 perturbed, gene 2-5 unperturbed
1,0,1,1,1, # perturbation exp2: gene 2 perturbed, gene 1,3,4,5 unperturbed
1,1,0,1,1, # perturbation exp3....
1,1,1,0,1,
1,1,1,1,0,
1,0,0,1,1,
1,1,1,1,1)

# example network
T_nw <- matrix(c(0,1,1,0,0,
0,0,0,-1,0,
0,0,0,1,0,
0,0,0,0,1,
0,0,0,0,0), nrow=n,ncol=n,byrow=TRUE)

# compute theoretical activation of genes from example network with given perturbations
act_mat <- calcActivation(T_nw, b, n, K)

calcPrediction  Calculate Predicted Observation.
calcPrediction

Description

Calculate the predicted observation of a perturbation experiment. If observations of an experiment are missing this function can be used to determine for a given network the predicted outcome. The missing measurement is predicted from two normal distributions, one for observations coming from active and one coming from inactive genes. The state of the gene is predicted based on the states of its parents.

Usage

calcPredictionLOOCV(obs, delta, b, n, K, adja, baseline, rem_gene, rem_k, rem_t=NULL, active_mu, active_sd, inactive_mu, inactive_sd, mu_type, flag_time_series=FALSE)
calcPredictionKfoldCV(obs, delta, b, n, K, adja, baseline, rem_entries=NULL, rem_entries_vec=NULL, active_mu, active_sd, inactive_mu, inactive_sd, mu_type, flag_time_series=FALSE)

Arguments

obs Numeric matrix/array: the observation matrix/array. It can have up to 3 dimensions, where dimension 1 are the network nodes, dimension 2 are the perturbation experiments, and dimension 3 are the time points (if considered).
delta Numeric vector defining the thresholds for each gene to determine its observation to be active or inactive.
b Binary vector representing the perturbation experiments (entry is 0 if gene is inactive in the respective experiment and 1 otherwise).
n Number of genes in the observation matrix.
K Number of perturbation experiments.
adja Numeric matrix: the adjacency matrix of the given network.
baseline Vector containing the inferred baseline vectors of each gene.
rem_gene Integer: the index of the gene that is missing.
rem_k Integer: the index of the perturbation experiment that is missing.
rem_t Integer: the index of the time point that is missing.
rem_entries Numeric matrix: each row represents an entry that was removed from the observation matrix, while the 3 columns represent the gene, perturbation experiment and time point, respectively.
rem_entries_vec Numeric vector: contains the entries that were removed in an "absolute form", i.e., if entry (2,1,2) was removed, it will appear in this vector as simply 5.
active_mu Numeric: the average value assumed for observations coming from active nodes. The parameter active_mu and active_sd are used for predicting the observations of the normal distribution of activate genes. This parameter can be either a numeric, a vector, a matrix, or a 3D array, depending on the specified mu_type.
active_sd Numeric: the variation assumed for observations coming from active nodes. The parameter active_mu and active_sd are used for predicting the observations of the normal distribution of activate genes. This parameter can be either a numeric, a vector, a matrix, or a 3D array, depending on the specified mu_type.
inactive_mu Numeric: the average value assumed for observations coming from inactive nodes. The parameter inactive_mu and inactive_sd are used for predicting the observations of the normal distribution of inactivate genes. This parameter can be either a numeric, a vector, a matrix, or a 3D array, depending on the specified mu_type.

inactive_sd Numeric: the variation assumed for observations coming from inactive nodes. The parameter inactive_mu and inactive_sd are used for predicting the observations of the normal distribution of inactivate genes. This parameter can be either a numeric, a vector, a matrix, or a 3D array, depending on the specified mu_type.

mu_type Character: can have the following values and meanings:
- "simple" - the value of active_mu/sd and inactive_mu/sd is independent of the gene/perturbation experiment/time point;
- "perGene" - the value of active_mu/sd and inactive_mu/sd depends on the gene;
- perGeneExp" - the value of active_mu/sd and inactive_mu/sd depends on the gene and perturbation experiment;
- perGeneTime" - the value of active_mu/sd and inactive_mu/sd depends on the gene and time point;
- "perGeneExpTime" - the value of active_mu/sd and inactive_mu/sd depends on the gene, perturbation experiment, and time point;

flag_time_series Logical: specifies whether steady-state (FALSE) or time series data (TRUE) is used.

See Also
loocv, kfoldCV

Examples
n <- 3 # number of genes
K <- 4 # number of experiments
T_ <- 4 # number of time points

# perturbation vector, entry is 0 if gene is inactivated and 1 otherwise
b <- c(0,1,1, # perturbation exp1: gene 1 perturbed, gene 2,3 unperturbed
      1,0,1, # perturbation exp2: gene 2 perturbed, gene 1,3 unperturbed
      1,1,0, # perturbation exp3....
      1,1,1)

# adjacency matrix
adja <- matrix(c(0,1,0,
                 0,0,1,
                 0,0,0), nrow=n, ncol=n, byrow=TRUE)

# define node baseline values
baseline <- c(0.75, 0, 0)

# define delta value
delta <- rep(0.75, n)

# define the parameters for the observation generated from the normal distributions
mu_type <- "single"
active_mu <- 0.9
inactive_mu <- 0.5
active_sd <- inactive_sd <- 0.01

#### kfoldCV

# generate random observation matrix
obs <- array(rnorm(n*K*T_), c(n,K,T_))

# define the observation to be removed, whose values will be predicted
obs[2,4,2] <- NA
obs[3,4,3] <- NA

rem_entries <- which(is.na(obs), arr.ind=TRUE)
rem_entries_vec <- which(is.na(obs))

# compute the predicted observation matrix for the "kfoldCV"
calcPredictionKfoldCV(obs=obs, delta=delta, b=b, n=n, K=K, adja=adja, baseline=baseline,
                       rem_entries=rem_entries, rem_entries_vec=rem_entries_vec,
                       active_mu=active_mu, active_sd=active_sd, inactive_mu=inactive_mu,
                       inactive_sd=inactive_sd, mu_type=mu_type, flag_time_series=TRUE)

#### LOOCV

# generate random observation matrix
obs <- matrix(rnorm(n*K), nrow=n, ncol=K)

# define the observation to be removed
rem_k <- 3
rem_gene <- 2
obs[rem_gene, rem_k] <- NA

# compute the predicted value
calcPredictionLOOCV(obs=obs, delta=delta,b=b, n=n ,K=K, adja=adja, baseline=baseline,
                     rem_gene=rem_gene, rem_k=rem_k, active_mu=active_mu, active_sd=active_sd,
                     inactive_mu=inactive_mu, inactive_sd=inactive_sd, mu_type=mu_type)

---

calcRangeLambda  
Compute Range Of Penalty Parameter Lambda.

**Description**

The penalty parameter lambda can range from zero to infinity and it controls the introduction of slack variables in the network inference lp model. To limit the introduction of slack variables we restrict lambda to be not larger than lambdaMax (=the number of slack variables times the variance of all measurements given). This function computes the range from zero to lambdaMax with a given stepsize that increases exponentially.

**Usage**

calcRangeLambda(obs, delta, delta_type, flag_time_series=FALSE)
**Arguments**

- **obs** Numeric matrix/array: the observation matrix/array. It can have up to 3 dimensions, where dimension 1 are the network nodes, dimension 2 are the perturbation experiments, and dimension 3 are the time points (if considered).

- **delta** Numeric: defines the thresholds for each gene to determine its observation to be active or inactive. This parameter can be either a numeric vector, a matrix, or a 3D array, depending on the specified delta_type.

- **delta_type** Character: can have the following values and meanings:
  - "perGene" - the value of delta depends on the gene;
  - "perGeneExp" - the value of delta depends on the gene and perturbation experiment;
  - "perGeneTime" - the value of delta depends on the gene and time point;
  - "perGeneExpTime" - the value of delta depends on the gene, perturbation experiment, and time point;

- **flag_time_series** Logical: specifies whether steady-state (FALSE) or time series data (TRUE) is used.

**Value**

Numeric vector of possible values for lambda.

**Examples**

```r
# generate random observation matrix with 5 experiments and 5 genes
obs <- matrix(rnorm(5*5, 1, 0.1), nrow=5, ncol=5)

# define delta to be 1 for each gene
delta <- rep(1, 5)
delta_type <- "perGene"

lambda_values <- calcRangeLambda(obs, delta, delta_type)
```

---

**Description**

Performs a stratified k-fold cross-validation or a Leave-One-Out cross-validation.

**Usage**

```r
loocv(kfold=NULL, times, obs, delta, lambda, b, n, K, T_=NULL, annot, annot_node, active_mu, active_sd, inactive_mu, inactive_sd, mu_type, delta_type, prior=NULL, sourceNode=NULL, sinkNode=NULL, allint=FALSE, allpos=FALSE, flag_time_series=FALSE)
```

```r
kfoldCV(kfold, times, obs, delta, lambda, b, n, K, T_=NULL, annot, annot_node, active_mu, active_sd, inactive_mu, inactive_sd, mu_type, delta_type, prior=NULL, sourceNode=NULL, sinkNode=NULL, allint=FALSE, allpos=FALSE, flag_time_series=FALSE)
```
Arguments

kfold
Integer value of the number "k" in the k-fold cross-validation.

times
Integer: the number of times the cross-validation shall be performed.

obs
Numeric matrix/array: the measured observation matrix/array. It can have up to
3 dimensions, where dimension 1 are the network nodes, dimension 2 are the
perturbation experiments, and dimension 3 are the time points (if considered).

delta
Numeric vector, matrix, or array defining the thresholds to determine an obser-
vation active or inactive.

lambda
Numeric value defining the penalty parameter lambda. It can range from zero to
infinity and it controls the introduction of slack variables in the network infer-
ence lp model.

n
Integer: number of genes.

b
Vector of 0/1 values describing the experiments (entry is 0 if gene is inactivated
in the respective experiment and 1 otherwise). The measurements of the genes of
each experiment are appended as a long vector.

K
Integer: number of perturbation experiments.

T_
Integer: number of time points in time-series data.

annot
Vector of character strings: the annotation of the edges as returned by "get-
EdgeAnnot".

annot_node
Vector of character strings: the annotation of the nodes.

active_mu
Numeric: the average value assumed for observations coming from activated
nodes. The parameter active_mu and active_sd are used for predicting the obser-
vations of the normal distribution of activate genes. This parameter can be
either a numeric, a vector, a matrix, or a 3D array, depending on the specified
mu_type.

active_sd
Numeric: the variation assumed for observations coming from activated nodes.
The parameter active_mu and active_sd are used for predicting the observations
of the normal distribution of activate genes. This parameter can be either a
numeric, a vector, a matrix, or a 3D array, depending on the specified mu_type.

inactive_mu
Numeric: the average value assumed for observations coming from inactivated
nodes. The parameter inactive_mu and inactive_sd are used for predicting the obser-
vations of the normal distribution of inactivate genes. This parameter can be
either a numeric, a vector, a matrix, or a 3D array, depending on the specified
mu_type.

inactive_sd
Numeric: the variation assumed for observations coming from inactivated nodes.
The parameter inactive_mu and inactive_sd are used for predicting the observa-
tions of the normal distribution of inactivate genes. This parameter can be either
a numeric, a vector, a matrix, or a 3D array, depending on the specified mu_type.

mu_type
Character: can have the following values and meanings:

• "simple" - the value of active_mu/sd and inactive_mu/sd is independent of
  the gene/perturbation experiment/time point;
• "perGene" - the value of active_mu/sd and inactive_mu/sd depends on the
gene;
• perGeneExp" - the value of active_mu/sd and inactive_mu/sd depends on
the gene and perturbation experiment;
• perGeneTime" - the value of active_mu/sd and inactive_mu/sd depends on
the gene and time point;
- "perGeneExpTime" - the value of active_mu/sd and inactive_mu/sd depends on the gene, perturbation experiment, and time point;

**delta_type**

Character: can have the following values and meanings:

- "perGene" - the value of delta depends on the gene;
- "perGeneExp" - the value of delta depends on the gene and perturbation experiment;
- "perGeneTime" - the value of delta depends on the gene and time point;
- "perGeneExpTime" - the value of delta depends on the gene, perturbation experiment, and time point;

**prior**

Prior knowledge, given as a list of constraints. Each constraint consists of a vector with four entries describing the prior knowledge of one edge. For example the edge between node 1 and 2, called w+_1_2, is defined to be bigger than 1 with constraint c("w+_1_2",1,">",2). The first entry specifies the annotation of the edge (see function "getEdgeAnnot") and the second defines the coefficient of the objective function (see parameter "objective.in" in the "lp" function of the package "lpSolve"). Furthermore, the third, respectively the fourth elements give the direction, respectively the right-hand side of the constraint (see the parameters "const.dir", respectively "const.rhs" in the "lp" function of the package "lpSolve").

**sourceNode**

Integer vector: indices of the known source nodes.

**sinkNode**

Integer vector: indices of the known sink nodes.

**allint**

Logical: should all variables be integer? Corresponds to an Integer Linear Program (see "lp" function in package "lpSolve"). Default: FALSE.

**allpos**

Logical: should all variables be positive? Corresponds to learning only activating edges. Default: FALSE.

**flag_time_series**

Logical: specifies whether steady-state (FALSE) or time series data (TRUE) is used.

**Value**

A list of

**MSE**

The mean squared error (MSE) of predicted and observed measurements of the corresponding cross-validation step.

**edges_all**

The learned edge weights for each cross-validation step.

**baseline_all**

The learned baseline weights for each cross-validation step.

**Examples**

```r
n <- 3 # number of genes
K <- 4 # number of experiments
T_ <- 4 # number of time points

annot_node <- seq(1, n)
annot <- getEdgeAnnot(n)

# generate random observation matrix
obs <- array(rnorm(n*K*T_), c(n,K,T_))

baseline <- c(0.75, 0, 0)
```
# define delta
delta <- apply(obs, 1, mean, na.rm=TRUE)

# perturbation vector, entry is 0 if gene is inactivated and 1 otherwise
b <- c(0,1,1, # perturbation exp1: gene 1 perturbed, gene 2,3 unperturbed
      1,0,1, # perturbation exp2: gene 2 perturbed, gene 1,3 unperturbed
      1,1,0, # perturbation exp3....
      1,1,1)

T_nw <- matrix(c(0,1,0,
                 0,0,1,
                 0,0,0), nrow=n, ncol=n, byrow=TRUE)
colnames(T_nw) <- rownames(T_nw) <- annot_node

## calculate observation matrix with given parameters for the
# Gaussian distributions for activation and deactivation
active_mu <- 0.95
inactive_mu <- 0.56
active_sd <- inactive_sd <- 0.1
times <- kfold <- 10  # can be increased i.e. to 1000 to produce stable results
mu_type <- "single"
delta_type <- "perGene"

lambda <- 1/10

### LOOCV
loocv(kfold=NULL, times=times, obs=obs, delta=delta, lambda=lambda, b=b, n=n, K=K, T_=T_, annot=annot,
      annot_node=annot_node, active_mu=active_mu, active_sd=active_sd, inactive_mu=inactive_mu,
      inactive_sd=inactive_sd, mu_type=mu_type, delta_type=delta_type, prior=NULL, sourceNode=NULL,
      sinkNode=NULL, allint=FALSE, allpos=FALSE, flag_time_series=FALSE)

### K-fold CV
kfoldCV(kfold=kfold, times=times, obs=obs, delta=delta, lambda=lambda, b=b, n=n, K=K, T_=T_, annot=annot,
        annot_node=annot_node, active_mu=active_mu, active_sd=active_sd, inactive_mu=inactive_mu,
        inactive_sd=inactive_sd, mu_type=mu_type, delta_type=delta_type, prior=NULL, sourceNode=NULL,
        sinkNode=NULL, allint=FALSE, allpos=FALSE, flag_time_series=FALSE)

---

**doILP**

**Do The Network Inference With The Linear Programming Approach.**

---

**Description**

This function converts observation data into a linear programming problem.

**Usage**

```r
doILP(obs, delta, lambda, b, n, K, T_=NULL, annot, delta_type, prior=NULL, sourceNode=NULL, sinkNode=NULL, all.int=FALSE, all.pos=FALSE, flag_time_series=FALSE)
```
doILP

Arguments

obs Numeric matrix/array: the given observation matrix/array. It can have up to 3 dimensions, where dimension 1 are the network nodes, dimension 2 are the perturbation experiments, and dimension 3 are the time points (if considered).

delta Numeric: defining the thresholds for each gene to determine its observation to be active or inactive. This parameter can be either a numeric vector, a matrix, or a 3D array, depending on the specified delta_type.

lambda Numeric value defining the penalty parameter lambda. It can range from zero to infinity and it controls the introduction of slack variables in the network inference lp model.

b Vector of 0/1 values describing the experiments (entry is 0 if gene is inactivated in the respective experiment and 1 otherwise). The measurements of the genes of each experiment are appended as a long vector.

n Integer: number of genes.

K Integer: number of perturbation experiments.

T Integer: number of time points.

annot Vector of character strings: the annotation of the edges as returned by "getEdgeAnnot".

delta_type Character: can have the following values and meanings: - "perGene" - the value of delta depends on the gene; - "perGeneExp" - the value of delta depends on the gene and perturbation experiment; - "perGeneTime" - the value of delta depends on the gene and time point; - "perGeneExpTime" - the value of delta depends on the gene, perturbation experiment, and time point;

prior Prior knowledge, given as a list of constraints. Each constraint consists of a vector with four entries describing the prior knowledge of one edge. For example the edge between node 1 and 2, called w+_1_2, is defined to be bigger than 1 with constraint c("w+_1_2","","","2"). The first entry specifies the annotation of the edge (see function "getEdgeAnnot") and the second defines the coefficient of the objective function (see parameter "objective.in" in the "lp" function of the package "lpSolve"). Furthermore, the third, respectively the fourth elements give the direction, respectively the right-hand side of the constraint (see the parameters "const.dir", respectively "const.rhs" in the "lp" function of the package "lpSolve").

sourceNode Integer vector: indices of the known source nodes.

sinkNode Integer vector: indices of the known sink nodes.

all.int Logical: should all variables be integer? Corresponds to an Integer Linear Program (see "lp" function in package "lpSolve"). Default: FALSE.

all.pos Logical: should all variables be positive? Corresponds to learning only activating edges. Default: FALSE.

flag_time_series Logical: specifies whether steady-state (FALSE) or time series data (TRUE) is used.

Value

An lp object. See "lp.object" in package "lpSolve" for details.
Examples

n <- 3  # number of genes
K <- 4  # number of experiments
T_ <- 4  # number of time points

# generate random observation matrix
obs <- array(rnorm(n*K*T_), c(n,K,T_))

baseline <- c(0.75, 0, 0)

delta <- rep(0.75, n)

# perturbation vector, entry is 0 if gene is inactivated and 1 otherwise
b <- c(0,1,1, # perturbation exp1: gene 1 perturbed, gene 2,3 unperturbed
      1,0,1, # perturbation exp2: gene 2 perturbed, gene 1,3 unperturbed
      1,1,0, # perturbation exp3....
      1,1,1)

delta_type <- "perGene"
lambda <- 1/10
annot <- getEdgeAnnot(n)

res <- doILP(obs, delta, lambda, b, n, K, T_, annot, delta_type, prior=NULL,
           sourceNode=NULL, sinkNode=NULL, all.int=FALSE, all.pos=FALSE, flag_time_series=TRUE)

---

generateTimeSeriesNetStates

Generate Time Series Network States

Description

The function returns all gene states for each network state in time-series data. The signalling propa-
gates downstream one edge per time-point. The stopping criteria is when all edges have been active
at least once, so that infinite loops are avoided. The number of time points for the data can be de-
defined by the user or not, if not the number of time points will be the same as the number of different
network states. If the number of time points is defined by the user, network states will be either
repeated or removed, so that there are as many network states as time points.

Usage

generateTimeSeriesNetStates(nw_und, b, n, K, T_user=NULL)

Arguments

nw_und  Numeric matrix: the adjacency matrix representing the underlying network.
b       Vector of 0/1 values describing the experiments (entry is 0 if gene is inactivated
       in the respetive experiment and 1 otherwise). The measurements of the genes of
       each experiment are appended as a long vector.
n       Integer: number of genes.
K       Integer: number of perturbation experiments.
T_user  Integer defining the number of time points in the network.
**getAdja**

**Value**

List containing an array with all nodes states and the number of time points.

**Examples**

```r
n <- 3  # number of genes
K <- 4  # number of experiments

# perturbation vector, entry is 0 if gene is inactivated and 1 otherwise
b <- c(0,1,1, # perturbation exp1: gene 1 perturbed, gene 2,3 unperturbed
       1,0,1, # perturbation exp2: gene 2 perturbed, gene 1,3 unperturbed
       1,1,0, # perturbation exp3....
       1,1,1)

# adjacency matrix
nw_und <- matrix(c(0,1,0,
                   0,0,1,
                   0,0,0), nrow=n, ncol=n, byrow=TRUE)
generateTimeSeriesNetStates(nw_und,b, n, K, T_user=5)
```

---

**getAdja**

*Get Adjacency Matrix.*

**Description**

The function returns the adjacency matrix of the network computed with the "doILP" function.

**Usage**

```r
getAdja(res, n, annot=NULL)
```

**Arguments**

- **res**
  - Result returned by the "doILP" function.

- **n**
  - Integer: the number of nodes of the inferred network.

- **annot**
  - Vector of character strings: the annotation of the edges as returned by "get-EdgeAnnot".

**Value**

Numeric matrix: the adjacency matrix of the network.

**See Also**

- **doILP**
getBaseline

Examples

n <- 3 # number of genes
K <- 4 # number of experiments
T_ <- 4 # number of time points

# generate random observation matrix
obs <- array(rnorm(n*K*T_), c(n,K,T_))

baseline <- c(0.75, 0, 0)

delta <- rep(0.75, n)

# perturbation vector, entry is 0 if gene is inactivated and 1 otherwise
b <- c(0,1,1, # perturbation exp1: gene 1 perturbed, gene 2,3 unperturbed
      1,0,1, # perturbation exp2: gene 2 perturbed, gene 1,3 unperturbed
      1,1,0, # perturbation exp3....
      1,1,1)

delta_type <- "perGene"
lambda <- 1/10
annot <- getEdgeAnnot(n)

#infer the network
res <- doILP(obs, delta, lambda, b, n, K, T_, annot, delta_type, prior=NULL,
           sourceNode=NULL, sinkNode=NULL, all.int=FALSE, all.pos=FALSE, flag_time_series=TRUE)

# make the adjacency matrix
adja <- getAdja(res, n)

getBaseline

Get Baseline Vector.

Description

The function returns a vector with the baseline values of each node in the network computed with the "doILP" function.

Usage

getBaseline(res, n, allpos=FALSE)

Arguments

res Result returned by the "doILP" or "doILP_timeSeries" function.
n Integer: the number of nodes of the inferred network.
allpos Logical: should all variables be positive? Corresponds to learning only activating edges. Default: FALSE.

Value

Numeric matrix: the adjacency matrix of the network.
getEdgeAnnot

Get the annotation of the edges.

Description

The function returns the annotation of the edges needed for the LP. Positive edges are annotated with "w+" and negative with "w-". The given nodes are just enumerated from 1 to n and the edge between node i and j is given by "w+_i_j" for the positive, respectively by "w-_i_j" for the negative edges. The annotation "w_i_^_0" defines the baseline activity of gene i.

Usage

getEdgeAnnot(n, allpos)

Arguments

n Integer: number of genes.

allpos Logical: should all edges be positive? Corresponds to learning only activating edges. Default: FALSE.

Examples

n <- 3 # number of genes
K <- 4 # number of experiments
T_ <- 4 # number of time points

# generate random observation matrix
obs <- array(rnorm(n*K*T_), c(n,K,T_))

baseline <- c(0.75, 0, 0)

delta <- rep(0.75, n)

# perturbation vector, entry is 0 if gene is inactivated and 1 otherwise
b <- c(0,1,1, # perturbation exp1: gene 1 perturbed, gene 2,3 unperturbed
      1,0,1, # perturbation exp2: gene 2 perturbed, gene 1,3 unperturbed
      1,1,0, # perturbation exp3....
      1,1,1)

delta_type <- "perGene"
lambda <- 1/10
annot <- getEdgeAnnot(n)

# infer the network
res <- doILP(obs, delta, lambda, b, n, K, T_, annot, delta_type, prior=NULL, sourceNode=NULL,
             sinkNode=NULL, all.int=FALSE, all.pos=FALSE, flag_time_series=TRUE)

# make the adjacency matrix
adja <- getBaseline(res, n)
getObsMat

Description

The function generates the observation matrix where active/inactive observations are generated from a normal distribution with the average and variation as given in the parameters. This matrix can either be generated from the activation matrix calculated with calcActivation or from the network states calculated with generateTimeSeriesNetStates.

Usage

getObsMat(act_mat=NULL, net_states=NULL, active_mu, active_sd, inactive_mu, inactive_sd, mu_type)

Arguments

act_mat Matrix of 0/1 values called the activation matrix. Rows correspond to genes, columns to experiments. If an entry is 1, it means that the corresponding gene is active in the corresponding experiment and inactive otherwise.

net_states Array of 0/1 values called the network states. Rows correspond to genes, columns to experiments, and the third dimension corresponds to time points. If an entry is 1, it means that the corresponding gene is active in the corresponding experiment and inactive otherwise.

active_mu Numeric: the average value assumed for observations coming from activated nodes. The parameter active_mu and active_sd are used for predicting the observations of the normal distribution of activate genes. This parameter can be either a numeric, a vector, a matrix, or a 3D array, depending on the specified mu_type.

active_sd Numeric: the variation assumed for observations coming from activated nodes. The parameter active_mu and active_sd are used for predicting the observations of the normal distribution of activate genes. This parameter can be either a numeric, a vector, a matrix, or a 3D array, depending on the specified mu_type.

inactive_mu Numeric: the average value assumed for observations coming from inactivated nodes. The parameter inactive_mu and inactive_sd are used for predicting the observations of the normal distribution of inactivate genes. This parameter can be either a numeric, a vector, a matrix, or a 3D array, depending on the specified mu_type.

inactive_sd Numeric: the variation assumed for observations coming from inactivated nodes. The parameter inactive_mu and inactive_sd are used for predicting the observations of the normal distribution of inactivate genes. This parameter can be either a numeric, a vector, a matrix, or a 3D array, depending on the specified mu_type.

mu_type Character: can have the following values and meanings:

- "simple" - the value of active_mu/sd and inactive_mu/sd is independent of the gene/perturbation experiment/time point;
getObsMat

- "perGene" - the value of active_mu/sd and inactive_mu/sd depends on the gene;
- perGeneExp" - the value of active_mu/sd and inactive_mu/sd depends on the gene and perturbation experiment;
- perGeneTime" - the value of active_mu/sd and inactive_mu/sd depends on the gene and time point;
- "perGeneExpTime" - the value of active_mu/sd and inactive_mu/sd depends on the gene, perturbation experiment, and time point;

Value

Numeric matrix/array: the observation matrix/array. It can have up to 3 dimensions, where dimension 1 are the network nodes, dimension 2 are the perturbation experiments, and dimension 3 are the time points (if considered).

See Also

calcActivation

Examples

n <- 5 # number of genes
K <- 7 # number of knockdowns

# perturbation vector, entry is 0 if gene is inactivated and 1 otherwise
b <- c(0,1,1,1,1, # perturbation exp1: gene 1 perturbed, gene 2-5 unperturbed
       1,0,1,1,1, # perturbation exp2: gene 2 perturbed, gene 1,3,4,5 unperturbed
       1,1,0,1,1, # perturbation exp3....
       1,1,1,0,1,
       1,1,1,1,0,
       1,0,0,1,1,
       1,1,1,1,1)

T_nw <- matrix(c(0,1,1,0,0,
                 0,0,0,-1,0,
                 0,0,0,1,0,
                 0,0,0,0,1,
                 0,0,0,0,0), nrow=n, ncol=n, byrow=TRUE)

act_mat <- calcActivation(T_nw, b, n, K)

# define the parameters for the observation generated from the normal distribution
active_mu <- 0.9
inactive_mu <- 0.5
active_sd <- inactive_sd <- 0.1
mu_type <- "single"

# compute the observations matrix
getObsMat(act_mat=act_mat, active_mu=active_mu, active_sd=active_sd, inactive_mu=inactive_mu, inactive_sd=inactive_sd)
getSampleAdja

Get The Sample Adjacency.

Description
The function computes the adjacency of the edges computed in each step of the "loocv" or the "kfoldCV" function. If the variance of each edge shall be taken into account use "getSampleAdjaMAD", otherwise "getSampleAdja".

Usage
getSampleAdjaMAD(edges_all, n, annot_node, method = median, method2 = mad, septype = "->")
getSampleAdja(edges_all, n, annot_node, method = median, septype = "->")

Arguments
edges_all The inferred edges using the "loocv" or the "kfoldCV" function.
n Integer: the number of nodes.
annot_node Vector of character strings: the annotation of the nodes.
method Character string: the method used to summarize the edges of the individual steps. Default: "median".
method2 Character string: the method used for the computation of the variation of the edges of the individual steps. Default: "mad".
septype Character string: the type of separation of two nodes in the annot string vector. Default: "->".

Value
Numeric matrix: the adjacency matrix.

See Also
loocv, kFoldCV

Examples
# compute random edge weights
edges_all <- matrix(rnorm(5*6), nrow=5, ncol=6)

# annotation of the edges as returned by "loocv" and kfoldCV
colnames(edges_all) <- c("1->2", "1->3", "2->1", "2->3", "3->1", "3->2")

# annotation of the nodes
annot_node <- c(1,2,3)
getSampleAdjaMAD(edges_all, n=3, annot_node, method = "median", method2 = "mad", septype = "->")

getSampleAdja(edges_all, n=3, annot_node, method = "median", septype = "->")
summarizeRepl

### Summarize Replicate Measurements

**Description**

The function returns the summarized replicate measurements.

**Usage**

```r
summarizeRepl(data, type=median)
```

**Arguments**

- `data`: The data matrix.
- `type`: The summarization type which shall be used. Default: median.

**Value**

Numeric matrix: the summarized data.

**Examples**

```r
data("SahinRNAi2008")
## process data
dataStim <- dat.normalized[dat.normalized[,17] == 1, -17]
# summarize replicates
dataSt <- t(summarizeRepl(dataStim, type=mean))
```
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