# Package ‘netbenchmark’

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**Type**  Package  
**Title**  Benchmarking of several gene network inference methods  
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**Description**  This package implements a benchmarking of several gene network inference algorithms from gene expression data.  
**License**  CC BY-NC-SA 4.0  
**URL**  https://imatge.upc.edu/netbenchmark/  
**Imports**  Rcpp (>= 0.11.0), minet, randomForest, c3net, PCIT, GeneNet, tools, pracma, Matrix, corpcor, fdrtool  
**LinkingTo**  Rcpp  
**Depends**  grndata (>= 0.99.3)  
**Suggests**  RUnit, BiocGenerics, knitr, graph  
**biocViews**  Microarray, GraphAndNetwork, Network, NetworkInference, GeneExpression  
**VignetteBuilder**  knitr  
**NeedsCompilation**  yes

## R topics documented:

- netbenchmark-package  
- aracne.wrap  
- c3net.wrap  
- clr.wrap  
- comp.metr  
- datasource.subsample  
- evaluate  
- experiments.bench  
- GeneNet.wrap  

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netbenchmark-package

Benchmarking of several inference networks methods

Description

For a given list of network inference algorithms, netbenchmark performs a benchmark between them. It makes use of five different big gene datasources, it relies on a random subsampling of each one of the datasource and noise addition in order to generate the datasets. This package is licensed under a Creative Commons Attribution-NonCommercial-ShareAlike 4.0 International.

Author(s)

Pau Bellot, Catharina Olsen, Patrick E Meyer, with contributions from Alexandre Irrthum

Maintainer: Pau Bellot <pau.bellot@upc.edu>

References


Examples

```r
## Not run:
AUPR20.list<-netbenchmark(datasources.names=c("syntren300", "rogers1000"),datasets.num=7)
AUPR20.300exp.list<-netbenchmark(methods=c("aracne.wrap","mrnet.wrap","GeneNet.wrap"),
datasources.names=c("syntren300","rogers1000"),
experiments=300,global.noise=10,noiseType="lognormal")
AUPR20.n30.list<-netbenchmark(methods=c("all.fast","mrnet.wrap","Genie3.wrap"),
eval="AUROC",local.noise=30)

## End(Not run)
```
Description

Default wrapper function for the aracne network inference algorithm

Usage

aracne.wrap(data)

Arguments

data

Numeric matrix with the microarray dataset to infer the network. Columns contain variables and rows contain samples.

Details

The motivation of the Algorithm for the Reconstruction of Accurate Cellular Networks (ARACNE) is that many similar measures between variables may be the result of indirect effects. In order to delete the indirect effect the algorithm relies on the “Data Processing Inequality”, this process removes the weakest link in every triplet of connected variables.

Value

aracne.wrapper returns a matrix which is the weighted adjacency matrix of the network inferred by aracne algorithm. The wrapper uses the “spearman” correlation (can be used with continuous data) to estimate the entropy - see build.mim

References


See Also

netbenchmark, evaluate, aracne

Examples

# Data
data <- grndata::getData(datasource.name = "toy",FALSE)
# Inference
net <- aracne.wrap(data)
Description

Default wrapper function for the C3net network inference algorithm

Usage

\texttt{c3net.wrap(data)}

Arguments

- \texttt{data} Numeric matrix with the microarray dataset to infer the network. Columns contain variables and rows contain samples.

Details

The Conservative Causal Core NETwork (C3NET) consists of two main steps. The first step is the elimination of non-significant edges, and the second step selects for each gene the edge among the remaining ones with maximum mutual information value. C3NET does not aim at inferring the entire network underlying gene regulation but mainly tries to recover the core structure.

Value

\texttt{c3net.wrap} returns a matrix which is the weighted adjacency matrix of the network inferred by \texttt{c3net} algorithm. The Mutual Information threshold is set to 0 - see \texttt{c3net}.

References


See Also

\texttt{netbenchmark}, \texttt{evaluate}, \texttt{c3net}

Examples

```
# Data
data <- grndata::getData(datasource.name = "toy", FALSE)
# Inference
net <- c3net.wrap(data)
```
**Description**

Default wrapper function for the CLR network inference algorithm

**Usage**

```r
clr.wrap(data)
```

**Arguments**

- `data` Numeric matrix with the microarray dataset to infer the network. Columns contain variables and rows contain samples.

**Details**

The Context Likelihood or Relatedness network (CLR) method derives a score that is associated to the empirical distribution of the mutual information values, in practice the score between gene \( X_i \) and gene \( X_j \) is defined as follows:

\[
z_{ij} = \sqrt{z_i^2 + z_j^2},
\]

where:

\[
z_i = \max \left( 0, \frac{I(X_i; X_j) - \mu_i}{\sigma_i} \right)
\]

\( \mu_i \) and \( \sigma_i \) are respectively the mean and standard deviation of the empirical distribution of the mutual information between both genes.

**Value**

`clr.wrap` returns a matrix which is the weighted adjacency matrix of the network inferred by CLR algorithm. The wrapper uses the "spearman" correlation (can be used with continuous data) to estimate the entropy - see `build.mim`.

**References**


**See Also**

`netbenchmark`, `evaluate`, `clr`

**Examples**

```r
# Data
data <- grndata::getData(datasource.name = "toy", FALSE)
# Inference
net <- clr.wrap(data)
```
**Compute metrics**

**Description**

A group of functions to plot precision-recall and ROC curves and to compute f-scores from the matrix returned by the `evaluate` function.

**Usage**

```r
fscore(table, beta=1)
auroc(table,k=-1)
aupr(table,k=-1)
pr.plot(table, device=-1,...)
roc.plot(table, device=-1,...)
```

**Arguments**

- `table` This is the matrix returned by the `evaluate` function where columns contain the confusion matrix TP,FP,TN,FN values. - see `evaluate`.
- `beta` Numeric used as the weight of the recall in the f-score formula - see details. The default value of this argument is -1, meaning precision as important as recall.
- `k` Numeric used as the index to compute the area under the curve until that point - see details. The default value of this argument is -1, meaning that the whole area under the curve is computed.
- `device` The device to be used. This parameter allows the user to plot precision-recall and receiver operating characteristic curves for various inference algorithms on the same plotting window - see examples.
- `...` Arguments passed to `plot`.

**Details**

A confusion matrix contains FP,TP,FN,FP values.

- "true positive rate" \( tpr = \frac{TP}{TN+TP} \)
- "false positive rate" \( fpr = \frac{FP}{FN+FP} \)
- "precision" \( p = \frac{TP}{FP+TP} \)
- "recall" \( r = \frac{TP}{TP+FN} \)
- "f-beta-score" \( F\beta = (1+\beta) \frac{pr}{r+\beta p} \) with \( 0 \lt \beta \lt 1 \)

**Value**

The function `roc.plot` (pr.plot) plots the ROC-curve (PR-curve) and returns the device associated with the plotting window.

The function `auroc` (aupr) computes the area under the ROC-curve (PR-curve) using the trapezoidal approximation until point `k`.

The function `fscore` returns f-scores according to the confusion matrices contained in the 'table' argument - see details.
See Also

evaluate, plot

Examples

```r
# Inference
Net <- cor(syntren300.data)
# Validation
tbl <- evaluate(Net,syntren300.net)
# Plot PR-Curves
max(fscore(tbl))
dev <- pr.plot(tbl, col="green", type="l")
aupr(tbl)
idx <- which.max(fscore(tbl))
```

datasource.subsample  Subsampling datasource procedure

Description

datasource.subsample picks randomly the specified amount of samples from the original datasource and also adds noise to the subsampled dataset if it is specified.

Usage

```r
datasource.subsample(datasource,experiments=NA,datasets.num=5,
local.noise=20,global.noise=0,noiseType="normal",
samplevar=TRUE, seed = NULL)
```

Arguments

data.frame where columns contain variables and rows contain experiments.

- **experiments**: Integer specifying the number of experiments that for performing the subsampling of datasources (default: NA).
- **datasets.num**: Integer specifying the number of datasets to be generated for each of the selected original datasources (default: 5).
- **local.noise**: Integer specifying the desired percentage of local noise to be added at each of the subsampled datasets (default: 20).
- **global.noise**: Integer specifying the desired percentage of global noise to be added at each of the subsampled datasets (default: 0).
- **noiseType**: Character specifying the type of the noise to be added: "normal" (default: "normal").
- **samplevar**: Logical specifying if the datasets should have variability in the number of experiments between them (default: TRUE).
- **seed**: A single value, interpreted as an integer to specify seeds, useful for creating simulations that can be reproduced (default: NULL) - see `set.seed`.
Details

If the argument experiments is NA, the value experiments will be calculated automatically in order to have datasets.num smaller datasets that does not have the same experiment twice inside each dataset. Each of the subsampled datasets experiments would have a number of experiments around experiments ±20% that would be chosen randomly among the original the original number of experiments without replacement.

If the argument experiments is a number, the number of datasets.num is calculated automatically. If the number of specified experiments is greater or equal than the original number of experiments, then only a replicate will be generated and the subsampled dataset would have the same dimensions as the original one but the experiments will be unsorted randomly.

Two different types of noises could be added, that are specified with the argument noiseType:

- "local": the variance of the noise is different for each variable and it is the percentage specified of the variance of each variable (±20%).
- "Globlal": the variance of the noise is the same for the whole datasource, it is the percentage specified of the mean variance of all the variables (±20%).

Value

datasource.subsample returns a list with datasets.num elements, each one of objects contains a data.frame of the subsampled dataset with the amount of Gaussian noise specified that would contain the same number of variables.

See Also

netbenchmark

Examples

# Subsample
data.list.1 <- datasource.subsample(syntren300.data)
data.list.2 <- datasource.subsample(syntren300.data, local.noise=10)
# Inference
inf.net.1 <- cor(data.list.1[[1]])
inf.net.2 <- cor(data.list.2[[4]])

evaluate (Inference Evaluation)

Description

evaluate compares the inferred network to the true underlying network for several threshold values and appends the resulting confusion matrices to the returned object.

Usage

evaluate(inf.net, true.net, sym=TRUE, extend=0)
Arguments

- **inf.net**: An adjacency matrix representing the inferred network.
- **true.net**: An adjacency matrix representing the true underlying network.
- **sym**: Logical, make a symmetric evaluation (default = TRUE).
- **extend**: Integer, specifying the desired number of links to extend in the network (default = 0)

Details

The first edgelist network `inet` is compared to the true underlying network, `tnet`, in order to compute the metrics of the performance. If `extend` is specified, extend links that network `inet` has set to 0 are added to the inferred network randomly at the end of the edgelist.

Value

evaluate returns a matrix with four columns representing TP, FP, TN, FN. These values are computed for each of the predicted links that should be sorted. Thus, each row of the returned object contains the confusion matrix as a function of the cutoff in the edgelist.

See Also

- netbenchmark

Examples

```r
# Inference
inf.net <- cor(syntren300.data)
# Evaluate
table <- evaluate(inf.net, syntren300.net)
table.nosym <- evaluate(inf.net, syntren300.net, sym=FALSE)
```

Description

For a given vector of character of the names of wrapper functions that compute a network inference methods, experiments.bench performs a number of experiments sensitivity test. It makes use of five different big gene datasets subsampling them to generate different datasets.num of the network with different number of experiments.

Usage

```r
experiments.bench(methods = "all.fast", datasources.names = "all", experiments = c(20, 50, 150), eval = "AUPR", no.topedges = 20, datasets.num = 3, local.noise = 20, global.noise = 0, noiseType = "normal", sym = TRUE, seed = NULL, verbose= TRUE)
```
Arguments

methods A vector of characters containing the names of network inference algorithms wrappers to be compared (default: "all.fast").

datasources.names A vector of characters containing the names of network datasets to be included in the benchmark (default: "all").

experiments A vector to set the number of experiments to test the methods (default=c(20,50,150)).

eval The name of the evaluation metric among the following ones: "no.truepos", "AUROC" or "AUPR" (default: "AUPR") - see evaluate.

no.topedges Float specifying the percentage number of links to be considered in the evaluation (default: 20).

datasets.num Number of repetitions in the noise evaluation, for each method and each dataset and each noise intensity (default: 3).

local.noise Integer specifying the desired percentage of local noise to be added at each of the subsampled datasets (default: 20) - see datasource.subsample.

global.noise Integer specifying the desired percentage of global noise to be added at each of the subsampled datasets (default: 20) - see datasource.subsample.

noiseType Character specifying the type of the noise to be added: "normal" or "lognormal" (default: "normal") - see datasource.subsample.

sym Logical specifying if the evaluation is symmetric (default: TRUE) - see evaluate.

seed A single value, interpreted as an integer to specify seeds, useful for creating simulations that can be reproduced (default: NULL) - see set.seed.

verbose Logical specifying if the code should provide a log about what the function is doing (default: TRUE).

Details

The argument methods accepts "all.fast" and "all" (case insensitive) as a parameters:

• "all.fast" performs network inference with "aracne", "c3net", "clr", "GeneNet", "mutual ranking", "mrnet", "pcit"

• "all" performs network inference with "aracne", "c3net", "clr", "GeneNet", "Genie3", "mutual ranking", "mrnet", "mrnetb", "pcit"

It evaluates the first no.topedges % of the possible links inferred by each algorithm at each dataset.

Two different types of noises are added independently:

• "Local": the standard deviation of the noise is different for each variable. local.noise specifies the percentage for each variable (±20%).

• "Global": the standard deviation of the noise is the same for the whole dataset. global.noise specifies the percentage of the mean standard deviation of all the variables (±20%).

The distribution of noise is set with noiseType, it is possible to choose between "normal" (rnorm) and "lognormal" (rlnorm). The argument noiseType can be a single character, this specifies the same distribution for both "Local" and "Global" noise, it also can be a vector of characters with two elements, the former specifies the distribution of "Local" noise and the later the distribution of "Global" noise.
Value

experiments.bench returns a list with three elements:

1. A data.frame which is the result table containing the number of true positives as an evaluation measure. It evaluates each algorithm specified at methods at each one of the specified datasources.names with different noise intensities.
2. A data.frame which is the corresponding pvalue table of the corresponding statistical test for each one of the datasets.num between the best algorithm and the others.
3. The seed of the random number generators that allows the replication of the results.

Author(s)
Pau Bellot and Patrick Meyer

See Also

netbenchmark, noise.bench

Examples

results <- experiments.bench(datasources.names="toy", datasets.num=2, methods="all.fast", experiments=c(20,40))

Description

Default wrapper function for the GeneNet network inference algorithm

Usage

GeneNet.wrap(data)

Arguments

data Numeric matrix with the microarray dataset to infer the network. Columns contain variables and rows contain samples.

Details

GeneNEt uses an heuristic for learning statistically a causal network. It relies on a conversion of a network inferred through correlation into a partial correlation graph. Then, a partial ordering of the nodes is assigned by means of a multiple testing of the log-ratio of standardized partial variances. This allows identifying a directed acyclic causal network as a sub-graph of the partial correlation network.

Value

GeneNet.wrap The function returns a matrix which is the weighted adjacency matrix of the network inferred by GeneNet algorithm. The shrinkage method used to estimate the partial correlation matrix is "static". - see ggm.estimate.pcor. The probability threshold is set to 0.8. - see ggm.estimate.pcor.
References


See Also

netbenchmark, evaluate, GeneNet-package

Examples

```r
# Data
data <- grndata::getData(datasource.name = "toy", FALSE)
# Inference
net <- GeneNet.wrap(data)
```

Description

Default wrapper function for the Genie3 network inference algorithm

Usage

```r
Genie3.wrap(data)
```

Arguments

data Numeric matrix with the microarray dataset to infer the network. Columns contain variables and rows contain samples.

Details

GEne Network Inference with Ensemble of trees (Genie3) algorithm uses the Random Forests feature selection technique to solve a regression problem for each of the genes in the network. In each of the regression problems, the expression pattern of the target gene should be predicted from the expression patterns of all transcription factors. The importance of each transcription factor in the prediction of the target gene is taken as an indication of an apparent regulatory link. Then these candidate regulatory links are aggregated over all genes to generate a ranking for the whole network.

Value

Genie3.wrap returns a matrix which is the weighted adjacency matrix of the network inferred by Genie3 algorithm. 500 trees are used in ensemble for each target gene.
References


See Also

netbenchmark, evaluate

Examples

```r
# Data
data <- grndata::getData(datasource.name = "toy",FALSE)
# Inference
net <- Genie3.wrap(data)
```

Description

Default function for the MRNET network inference algorithm

Usage

```r
mrnet.wrap(data)
```

Arguments

data Numeric matrix with the microarray dataset to infer the network. Columns contain variables and rows contain samples.

Details

The MRNET approach consists in repeating a MRMR feature selection procedure for each variable of the dataset. The MRMR method starts by selecting the variable $X_i$ having the highest mutual information with the target $Y$. In the following steps, given a set $S$ of selected variables, the criterion updates $S$ by choosing the variable $X_k$ that maximizes $I(X_k;Y) - \frac{1}{|S|} \sum_{X_i \in S} I(X_k;X_i)$

The weight of each pair $X_i, X_j$ will be the maximum score between the one computed when $X_i$ is the target and the one computed when $X_j$ is the target.

Value

mrnet.wrap returns a matrix which is the weighted adjacency matrix of the network inferred by MRNET algorithm. The wrapper uses the "spearman" correlation (can be used with continuous data) to estimate the entropy - see build.mim.
mrnetb.wrap

References


See Also

netbenchmark, evaluate, mrnet

Examples

```r
# Data
data <- grndata::getData(datasource.name = "toy",FALSE)
# Inference
net <- mrnet.wrap(data)
```

Description

Default wrapper function for the MRNETB network inference algorithm

Usage

`mrnetb.wrap(data)`

Arguments

data Numeric matrix with the microarray dataset to infer the network. Columns contain variables and rows contain samples.

Details

`mrnetb` takes the mutual information matrix as input in order to infer the network using the maximum relevance/minimum redundancy criterion combined with a backward elimination and a sequential replacement - see references. This method is a variant of mrnet.

Value

`mrnetb.wrap` returns a matrix which is the weighted adjacency matrix of the network inferred by `mrnetb` algorithm. The wrapper uses the "spearman" correlation (can be used with continuous data) to estimate the entropy - see `build.mim`. 
mutrank.wrap

References


See Also

netbenchmark, evaluate, mrnet

Examples

```r
# Data
data <- grndata::getData(datasource.name = "toy", FALSE)
# Inference
net <- mrnetb.wrap(data)
```

---

mutrank.wrap  

*Mutual Rank wrapper function*

Description

A wrapper function for mutual rank.

Usage

```r
mutrank.wrap(data)
```

Arguments

data  

Numeric matrix with the microarray dataset to infer the network. Columns contain variables and rows contain samples.

Value

mutrank.wrap returns a matrix which is the weighted adjacency matrix of the network inferred by Mutual Rank algorithm.

References


Examples

```r
# Data
data <- grndata::getData(datasource.name = "toy", FALSE)
# Inference
net <- mutrank.wrap(data)
```
Description

For a given vector of character of the names of wrapper functions that compute a network inference methods, netbenchmark performs a benchmark between them. It makes use of four different big gene datasources, it relies on a random subsampling without repetition of each one of the datasets and noise addition in order to generate the source data.

Usage

 netbenchmark(methods="all.fast",datasources.names="all",experiments=150, eval="AUPR",no.topedges=20,datasets.num=5,local.noise=20, global.noise=0,noiseType="normal",sym=TRUE,plot=FALSE,seed=NULL, verbose=TRUE)

Arguments

methods A vector of characters containing the names of network inference algorithms wrappers to be compared (default: "all.fast").

datasources.names A vector of characters containing the names of network datasources to be included in the benchmark (default: "all").

experiments Integer specifying the number of experiments to generate the subsampled datasets (default: 150) - see datasource.subsample.

eval The name of the evaluation metric among the following ones: "no.truepos", "AUROC" or "AUPR" (default : "AUPR") - see evaluate.

no.topedges Float specifying the percentage number of links to be considered in the evaluation (default: 20).

datasets.num Integer specifying the number of datasets.num to be generated for each of the selected original datasources (default: 5).

local.noise Integer specifying the desired percentage of local noise to be added at each of the subsampled datasets (default: 20) - see datasource.subsample.

global.noise Integer specifying the desired percentage of global noise to be added at each of the subsampled datasets (default: 20) - see datasource.subsample.

noiseType Character specifying the type of the noise to be added: "normal" or "lognormal" (default: "normal") - see datasource.subsample.

sym Logical specifying if the evaluation is symmetric (default: TRUE) - see evaluate.

plot (default: FALSE)

return.nets (default: FALSE)

seed A single value, interpreted as an integer to specify seeds, useful for creating simulations that can be reproduced (default: NULL) - see set.seed.

verbose Logical specifying if the code should provide a log about what the function is doing (default: TRUE).
Details

The argument methods accepts "all.fast" and "all" (case insensitive) as a parameters:

- "all.fast" performs network inference with "aracne", "c3net", "clr", "GeneNet", "mutual ranking", "mrnet", "pcit" (and registered methods with RegisterWrapper.)
- "all" performs network inference with "aracne", "c3net", "clr", "GeneNet", "Genie3", "mutual ranking", "mrnet", "mrnetb", "pcit" (and registered methods with RegisterWrapper.)

The argument datasources.names accepts "all" or a selection of the following datasources Availabledata:

- "rogers1000"
- "syntren300"
- "syntren1000"
- "gnw1565"
- "gnw2000"

All the measures only evaluates the first no.topedges % of the possible links inferred by each algorithm at each dataset. The statistical used is the Wilcoxon Rank Sum Test (wilcox.test). This test compares the number of true positives of any method with number of trials specified with the best method at each replicate.

Value

netbenchmark returns a list with six elements.

1. A data.frame which is the result table of the selected measure.
2. A data.frame which is the corresponding pvalue table of the corresponding statistical test for each one of the datasets.num between the best algorithm and the others.
3. A data.frame that sumarizes the first data.frame presenting the mean and standard deviation of the measures of each algorithm per datasource.
4. A data.frame which contains the CPU Time Used (in seconds) by the algorithm to infer the network.
5. A list containing the mean precision recall curves of the different algorithms for each data-source.
6. The seed of the random number generators that allows the replication of the results.

Each of these data.frame will have the same number of columns as methods provided by the user and an additional one for a random method, and the number of rows will depend on the number of datasets.num and datasources.name specified by the user.

Author(s)

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See Also
datasource.subsample, evaluate, comp.metr
Examples

top20.aupr <- netbenchmark(methods = "all", datasources.names = "Toy", 
local.noise = 20, global.noise = 10, 
noiseType = c("normal", "lognormal"),
datasets.num = 2, experiments = 40)

## Not run:
# Other possible studies

top20.fast.list <- netbenchmark()
top20.list <- netbenchmark(methods = "all", eval = "no.truepos")
top50.auroc.list <- netbenchmark(datasets.num = 8, eval = "AUROC", 
no.topedges = 50, global.noise = 10)
top9.list <- netbenchmark(datasets.num = 8, no.topedges = 9, local.noise = 15,
noiseType = "lognormal")

# To export the tables to LaTeX
# library(xtable)
# xtable(top20.fast.list[[1]])

## End(Not run)

netbenchmark.data

Benchmarking of several network inference algorithms for your own data

Description

Benchmarking of several network inference algorithms for your own data

Usage

netbenchmark.data(methods = "all.fast", data = NULL, true.net = NULL, 
eval = "AUPR", no.topedges = 20, sym = TRUE, plot = FALSE, 
verbose = TRUE)

Arguments

methods A vector of characters containing the names of network inference algorithms
wrappers to be compared (default: "all.fast").
data data.frame containing the data. Each row should contain a microarray experiment and each column a gene (default: NULL).
true.net matrix containing underlying network in the form of adjacency matrix (default: NULL).
eval The name of the evaluation metric among the following ones: "no.truepos", "AUROC" or "AUPR" (default: "AUPR").
no.topedges Float specifying the percentage number of links to be considered in the evaluation (default: 20)
sym Logical specifying if the evaluation is symmetric (default: TRUE) - see evaluate
plot (default: FALSE)
verbose Logical specifying if the code should provide a log about what the function is doing (default: TRUE).
Details

The argument methods accepts "all.fast" and "all" (case insensitive) as a parameters:

- "all.fast" performs network inference with "aracne", "c3net", "clr", "GeneNet", "mutual ranking", "mrnet", "pcit" (and registered methods with RegisterWrapper.)
- "all" performs network inference with "aracne", "c3net", "clr", "GeneNet", "Genie3", "mutual ranking", "mrnet", "mrnetb", "pcit" (and registered methods with RegisterWrapper.)

All the measures only evaluates the first no.topedges % of the possible links inferred by each algorithm at each dataset.

Value

netbenchmark.data returns a list with three elements.

1. A data.frame which is the result table of the selected measure.
2. A data.frame which contains the CPU Time Used (in seconds) by the algorithm to infer the network.
3. A list containing the mean precision recall curves of the different algorithms for each datasource.

Each of these data.frame will have the same number of columns as methods provided by the user and an additional one for a random method.

Author(s)

Pau Bellot, Catharina Olsen and Patrick E Meyer Maintainer: Pau Bellot <pau.bellot@upc.edu>

See Also

netbenchmark, evaluate, comp.metr

Examples

```r
Data <- grndata::getData(datasource.name="toy")
top20.aupr <- netbenchmark.data(methods="all", data = Data[[1]],
                        true.net = Data[[2]])
```

Description

For a given vector of character of the names of wrapper functions that compute a network inference methods, noise.bench performs a noise sensitivity test. It makes use of different big gene datasets adding Gaussian noise with different intensity to evaluate the performance of the methods.

Usage

```r
noise.bench(methods = "all.fast", datasources.names = "all",
            eval = "AUPR", no.topedges = 20, experiments=150,
            datasets.num = 3, local.noise = seq(0, 100, len = 3),
            global.noise = 0, noiseType = "normal", sym = TRUE,
            seed = NULL, verbose = TRUE)
```
Arguments

methods A vector of characters containing the names of network inference algorithms wrappers to be compared (default: "all.fast").
datasources.names A vector of characters containing the names of network datasets to be included in the benchmark (default: "all").
eval The name of the evaluation metric among the following ones: "no.truepos", "AUROC" or "AUPR" (default: "AUPR") - see evaluate.
experiments Integer specifying the number of experiments to generate the subsampled datasets (default: 150) - see datasource.subsample.
datasets.num Number of repetitions in the noise evaluation, for each method and each dataset and each noise intensity (default: 5).
no.topedges Float specifying the percentage number of links to be considered in the evaluation (default: 20).
local.noise Vector specifying the desired percentage of local noise to be added at each of the subsampled datasets (default: seq(0, 100, len = 3)).
global.noise Vector specifying the desired percentage of global noise to be added at each of the subsampled datasets (default: 0).
noiseType Character specifying the type of the noise to be added: "normal" (default: "normal").
sym Logical specifying if the evaluation is symmetric (default: TRUE) - see evaluate.
seed A single value, interpreted as an integer to specify seeds, useful for creating simulations that can be reproduced (default: NULL) - see set.seed.
verbose Logical specifying if the code should provide a log about what the function is doing (default: TRUE).

Details

The argument methods accepts "all.fast" and "all" (case insensitive) as a parameters:

- "all.fast" performs network inference with "aracne", "c3net", "clr", "GeneNet", "mutual ranking", "mrnetb", "pcit"
- "all" performs network inference with "aracne", "c3net", "clr", "GeneNet", "Genie3", "mutual ranking", "mrnet", "mrnetb", "pcit"

It evaluates the first no.topedges % of the possible links inferred by each algorithm at each dataset.

Value

noise.bench returns a list with three elements:

1. A data.frame which is the result table containing the number of true positives as an evaluation measure. It evaluates each algorithm specified at methods at each one of the specified datasources.names with the local.noise and global.noise specified. For each combination the algorithms are evaluated datasets.num times and their results are averaged.

2. A data.frame which is the corresponding pvalue table of the corresponding statistical test for each one of the datasets.num between the best algorithm and the others.

3. The seed of the random number generators that allows the replication of the results.
**ntb_globals**

**Author(s)**

Pau Bellot and Patrick Meyer

**See Also**

*netbenchmark, experiments.bench*

**Examples**

```r
results <- noise.bench(datasources.names="toy",
                       datasets.num=2,methods="all.fast",experiments=NULL)
```

---

**ntb_globals**  
*Available wrappers in the package of the fast methods*

**Description**

Environment containing a character vector containing the names of the wrappers in the package of the registered methods.

**Usage**

```r
ntb_globals
```

**Format**

Character vector containing the names of the registered wrapper methods.

**Examples**

```r
print(ntb_globals$Fast)
print(ntb_globals$All)
```

---

**pcit.wrap**  
*pcit wrapper function*

**Description**

Default wrapper function for the pcit network inference algorithm

**Usage**

```r
pcit.wrap(data)
```

**Arguments**

| data       | Numeric matrix with the microarray dataset to infer the network. Columns contain variables and rows contain samples. |
Details

The Partial Correlation coefficient with Information Theory (PCIT) algorithm, combines the concept of partial correlation coefficient with information theory to identify significant gene-to-gene associations.

For every trio of genes in $X_i$, $X_j$ and $X_l$, the three first-order partial correlation coefficients are computed. These coefficients indicate the strength of the linear relationship between $X_i$ and $X_j$ that is uncorrelated with $X_l$, being therefore a measure of conditional independence. Then, the average ratio of partial to direct correlation is computed in order to obtain the tolerance level to be used as the local threshold for eliminating non-significant associations.

Value

pcit.wrap returns a matrix which is the weighted adjacency matrix of the network inferred by pcit algorithm.

References


See Also

netbenchmark, evaluate, pcit

Examples

```r
# Data
data <- grndata::getData(datasource.name = "toy", FALSE)
# Inference
net <- pcit.wrap(data)
```

Description

rate compares the inferred network to the true underlying network for all the sorted predictions provided and appends the resulting confusion matrices to the returned object.

Usage

rate(PredEdgeList, GSEdgeList, ngenes, sym)

Arguments

- **PredEdgeList**: The inferred network in the form of a EdgeList.
- **GSEdgeList**: The true underlying in the form of a EdgeList.
- **ngenes**: Integer denoting the number of total genes in the network.
- **sym**: Logical specifying if the evaluation is symmetric (default: TRUE) - see evaluate.
**Value**

A matrix of numerics with the contingency table for each link in PredEdgeList.

**Author(s)**

Pau Bellot

**See Also**

netbenchmark, evaluate, comp.metr

**Examples**

```r
# Data
net <- matrix(0, 10, 10)
net[sample(1:100, 20)] <- 1
# Simulated Inference
inf <- net + matrix(rnorm(100, sd=0.5), 10, 10)
table <- evaluate(inf, net)
```

---

**RegisterWrapper**  
*Wrapper (un)registration routine*

**Description**

These function allows the registration and unregistration of a wrapper function to the all.fast or all methods of netbenchmark. After registering it wrapper.name function will belong to all.fast or all methods during the R session. Unregistering the wrapper.name function will remove it from all.fast or all methods during the R session.

**Usage**

```r
RegisterWrapper(wrapper.name=NULL, all.fast=TRUE)
UnregisterWrapper(wrapper.name=NULL, all.fast=TRUE)
```

**Arguments**

- `wrapper.name`: The character (vector) of wrapper names (default: NULL).
- `all.fast`: Logical indicating if the wrapper.name should be added to all.fast or all methods (default: TRUE).

**Value**

Displays a message if the registration could be performed or not.

**Author(s)**

Pau Bellot, Catharina Olsen and Patrick E Meyer  
Maintainer: Pau Bellot <pau.bellot@upc.edu>

**See Also**

netbenchmark
Examples

```r
# Define a wrapper function
SpearmanCor <- function(data){
  cor(data, method="spearman")
}
## Not run:
# Register it to all.fast methods
RegisterWrapper("SpearmanCor")
# Register it to all methods
RegisterWrapper("SpearmanCor", all.fast=FALSE)
# Unregister it from all.fast methods
UnregisterWrapper("SpearmanCor")
# Unregister it from all methods
UnregisterWrapper("SpearmanCor", all.fast=FALSE)
## End(Not run)
```

---

### zsc

#### Z-score c++ function

**Description**

Z-score c++ function

**Usage**

```r
zsc(x)
```

**Arguments**

- `x` Numeric matrix with the microarray dataset to infer the network. Columns contain variables and rows contain samples.

**Value**

A matrix of numerics with the inferred adjacency matrix.

**References**


**See Also**

`netbenchmark`

**Examples**

```r
# Data
data <- runif(100)
dim(data) <- c(10,10)
# Inference
net <- zsc(data)
```
zscore.wrap

Zscore wrapper function.

Usage

zscore.wrap(data)

Arguments

data Numeric matrix with the microarray dataset to infer the network. Columns contain variables and rows contain samples.

Details

Zscore is a method that assumes interventional data, more concretely knockout experiments that leads to a change in other genes. The assumption is that the knocked-out gene \( i \) in the experiment \( k \) affects more strongly to the genes that it regulates than the others, the effect of the gene \( i \) over the gene \( j \) is captured with the Zscore \( z_{ij} \):

\[
z_{ij} = \left| \frac{x_{jk} - \mu_j}{\sigma_j} \right|
\]

\( \mu_j \) and \( \sigma_j \) are respectively the mean and standard deviation of the empirical distribution of the gene \( j \).

Value

zscore.wrap returns a matrix which is the weighted adjacency matrix of the network inferred by Zscore algorithm.

References


Examples

# Data
data <- grndata::getData(datasource.name = "toy",FALSE)
# Inference
net <- zscore.wrap(data)
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