

Package ‘netresponse’

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Type Package

Title Functional Network Analysis

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Description Algorithms for functional network analysis. Includes an implementation of a variational Dirichlet process Gaussian mixture model for nonparametric mixture modeling.

License GPL (>=2)

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Imports ggplot2, graph, igraph, parallel, plyr, qvalue, RColorBrewer

Suggests knitr

URL <https://github.com/antagomir/netresponse>

BugReports <https://github.com/antagomir/netresponse/issues>

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| | |
|---------------------|--|
| netresponse-package | <i>NetResponse: Global modeling of transcriptional responses in interaction networks</i> |
|---------------------|--|

Description

Global modeling of transcriptional responses in interaction networks.

| | |
|-----------|---------------------------------------|
| Package: | netresponse |
| Type: | Package |
| Version: | See sessionInfo() or DESCRIPTION file |
| Date: | 2011-02-03 |
| License: | GNU GPL >=2 |
| LazyLoad: | yes |

Author(s)

Leo Lahti, Olli-Pekka Huovilainen, Antonio Gusmao and Juuso Parkkinen. Maintainer: Leo Lahti <leo.lahti@iki.fi>

References

Leo Lahti et al.: Global modeling of transcriptional responses in interaction networks. *Bioinformatics* (2010). See citation('netresponse') for details.

Examples

```
## Not run:
# Define parameters for toy data
Ns <- 200 # number of samples (conditions)
Nf <- 10  # number of features (nodes)
feature.names <- paste('feat', seq(Nf), sep='')
sample.names <- paste('sample', seq(Ns), sep='')
# random seed
set.seed( 123 )
# Random network
netw <- pmax(array(sign(rnorm(Nf^2))), dim = c(Nf, Nf)), 0)
# in pathway analysis nodes correspond to genes
rownames(netw) <- colnames(netw) <- feature.names
# Random responses of the nodes across conditions
D <- array(rnorm(Ns*Nf), dim = c(Ns,Nf), dimnames = list(sample.names, feature.names))
D[1:100, 4:6] <- t(sapply(1:(Ns/2),function(x){rnorm(3, mean = 1:3)}))
D[101:Ns, 4:6] <- t(sapply(1:(Ns/2),function(x){rnorm(3, mean = 7:9)}))
# Calculate the model
#model <- detect.responses(D, netw)
## Subnets (each is a list of nodes)
#get.subnets( model )

## End(Not run)
```

add.ellipse

Add ellipse to an existing plot

Description

Calculates and plots ellipse corresponding to specified confidence interval in 2-dimensional plot

Usage

```
add.ellipse(
  centroid,
  covmat,
  confidence = 0.95,
  npoints = 100,
  col = "black",
  ...
)
```

Arguments

| | |
|------------|---|
| centroid | Vector with two elements defining the ellipse centroid. |
| covmat | Covariance matrix for the investigated data. Only diagonal covariances supported. |
| confidence | Confidence level determining the ellipse borders based on the covariance matrix. |
| npoints | Number of plotting points. |
| col | Color. |
| ... | Other arguments to be passed. |

Value

Used for plotting side effects.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

bic.mixture

BIC mixture

Description

Latent class analysis based on (infinite) Gaussian mixture model. If the input is data matrix, a multivariate model is fitted; if the input is a vector, a univariate model is fitted

Usage

```
bic.mixture(x, max.modes, bic.threshold = 0, min.modes = 1, ...)
```

Arguments

| | |
|---------------|--|
| x | samples x features matrix for multivariate analysis, or a vector for univariate analysis |
| max.modes | Maximum number of modes to be checked for mixture model selection |
| bic.threshold | BIC threshold which needs to be exceeded before a new mode is added to the mixture. |
| min.modes | minimum number of modes |
| ... | Further optional arguments to be passed |

Value

Fitted latent class model (parameters and free energy)

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

bic.mixture.multivariate

Multivariate BIC mixture

Description

Latent class analysis based on (infinite) Gaussian mixture model. If the input (dat) is data matrix, a multivariate model is fitted.

Usage

```
bic.mixture.multivariate(x, max.modes, bic.threshold = 0, min.modes = 1, ...)
```

Arguments

| | |
|---------------|---|
| x | matrix (for multivariate analysis) |
| max.modes | Maximum number of modes to be checked for mixture model selection |
| bic.threshold | BIC threshold which needs to be exceeded before a new mode is added to the mixture. |
| min.modes | Minimum number of modes to be checked for mixture model selection |
| ... | Further optional arguments to be passed |

Value

Fitted latent class model (parameters and free energy)

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

`bic.mixture.univariate`*Univariate BIC mixture*

Description

Latent class analysis based on (infinite) Gaussian mixture model. If the input (`dat`) is data matrix, a multivariate model is fitted. If the input is a vector or a 1-dimensional matrix, a univariate model is fitted.

Usage

```
bic.mixture.univariate(x, max.modes, bic.threshold = 0, min.modes = 1, ...)
```

Arguments

| | |
|----------------------------|---|
| <code>x</code> | <code>dat</code> vector (for univariate analysis) or a matrix (for multivariate analysis) |
| <code>max.modes</code> | Maximum number of modes to be checked for mixture model selection |
| <code>bic.threshold</code> | BIC threshold which needs to be exceeded before a new mode is added to the mixture. |
| <code>min.modes</code> | minimum number of modes |
| <code>...</code> | Further optional arguments to be passed |

Value

Fitted latent class model (parameters and free energy)

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See `citation('netresponse')`

`bic.select.best.mode` *Select best mode with BIC*

Description

Select optimal number of mixture components by adding components until the increase in objective function is below threshold.

Usage

```
bic.select.best.mode(x, max.modes = 1, bic.threshold = 1, min.modes = 1)
```

Arguments

| | |
|----------------------------|---|
| <code>x</code> | dat vector (for univariate analysis) or a matrix (for multivariate analysis) |
| <code>max.modes</code> | Maximum number of modes to be checked for mixture model selection |
| <code>bic.threshold</code> | BIC threshold which needs to be exceeded before a new mode is added to the mixture. |
| <code>min.modes</code> | Optional. Minimum number of modes. |

Value

Fitted latent class model (parameters and free energy)

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

`centerData` *Center data matrix.*

Description

Center data matrix to 0 for each variable by removing the means.

Usage

```
centerData(X, rm.na = TRUE, meanvalue = NULL)
```


Arguments

X The data set: samples x features. Each feature will be centered.
rm.na Ignore NAs.
meanvalue Can be used to set a desired center value. The default is 0.

Value

Centered data matrix.

Note

Note that the model assumes samples x features matrix, and centers each feature.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

Examples

```
centerData(matrix(rnorm(100), 10, 10))
```

check.matrix *check.matrix*

Description

Mostly for internal purposes. Check input matrix format.

Usage

```
check.matrix(datamatrix)
```

Arguments

datamatrix See detect.responses

Value

The datamatrix, possibly added with necessary formatting for the netresponse algorithm.

Author(s)

Leo Lahti, Olli-Pekka Huovilainen and Antonio Gusmao. Maintainer: Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

See Also

detect.responses

Examples

```
# datamatrix <- check.matrix(datamatrix)
```

| | |
|---------------|----------------------|
| check.network | <i>check.network</i> |
|---------------|----------------------|

Description

Internal use to check input network and format detect.responses.

Usage

```
check.network(network, datamatrix, verbose = FALSE)
```

Arguments

| | |
|------------|--|
| network | Input network, see detect.responses |
| datamatrix | Input datamatrix, see detect.responses |
| verbose | Print intermediate messages |

Value

| | |
|-----------|---|
| formatted | Formatted network (self-links removed) |
| original | Original network (possible in another representation format) |
| delta | Cost function changes corresponding to the 'formatted' network. |
| nodes | Nodes corresponding to the 'formatted' network. |

Author(s)

Maintainer: Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

See Also

detect.responses

Examples

```
# check.network(network, datamatrix, verbose = FALSE)
```

```
continuous.responses  Continuous responses
```

Description

Quantify association between modes and continuous variable

Usage

```
continuous.responses(  
  annotation.vector,  
  model,  
  method = "t-test",  
  min.size = 2,  
  data = NULL  
)
```

Arguments

| | |
|-------------------|---|
| annotation.vector | annotation vector with discrete factor levels, and named by the samples |
| model | NetResponse model object |
| method | method for enrichment calculation |
| min.size | minimum sample size for a response |
| data | data matrix (samples x features) |

Value

List with each element corresponding to one variable and listing the responses according to association strength

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

Examples

```
res <- continuous.responses(annotation.vector = NULL, model = NULL)
```

detect.responses *detect.responses*

Description

Main function of the NetResponse algorithm. Detect condition-specific network responses, given network and a set of measurements of node activity in a set of conditions. Returns a set of subnetworks and their estimated context-specific responses.

Usage

```
detect.responses(
  datamatrix,
  network = NULL,
  initial.responses = 1,
  max.responses = 10,
  max.subnet.size = 10,
  verbose = TRUE,
  prior.alpha = 1,
  prior.alphaKsi = 0.01,
  prior.betaKsi = 0.01,
  update.hyperparams = 0,
  implicit.noise = 0,
  vdp.threshold = 1e-05,
  merging.threshold = 0,
  ite = Inf,
  information.criterion = "BIC",
  speedup = TRUE,
  speedup.max.edges = 10,
  positive.edges = FALSE,
  mc.cores = 1,
  mixture.method = "vdp",
  bic.threshold = 0,
  pca.basis = FALSE,
  ...
)
```

Arguments

| | |
|------------|---|
| datamatrix | Matrix of samples x features. For example, gene expression matrix with conditions on the rows, and genes on the columns. The matrix contains same features than the 'network' object, characterizing the network states across the different samples. |
| network | Binary network describing undirected pairwise interactions between features of 'datamatrix'. The following formats are supported: binary matrix, graphNEL, igraph, graphAM, Matrix, dgCMatrix, dgeMatrix |

| | |
|---|--|
| <code>initial.responses</code> | Initial number of components for each subnetwork model. Used to initialize calculations. |
| <code>max.responses</code> | Maximum number of responses for each subnetwork. Can be used to limit the potential number of network states. |
| <code>max.subnet.size</code> | Numeric. Maximum allowed subnetwork size. |
| <code>verbose</code> | Logical. Verbose parameter. |
| <code>prior.alpha, prior.alphaKsi, prior.betaKsi</code> | Prior parameters for Gaussian mixture model that is calculated for each subnetwork (normal-inverse-Gamma prior). <code>alpha</code> tunes the mean; <code>alphaKsi</code> and <code>betaKsi</code> are the shape and scale parameters of the inverse Gamma function, respectively. |
| <code>update.hyperparams</code> | Logical. Indicate whether to update hyperparameters during modeling. |
| <code>implicit.noise</code> | Implicit noise parameter. Add implicit noise to vdp mixture model. Can help to avoid overfitting to local optima, if this appears to be a problem. |
| <code>vdp.threshold</code> | Minimal free energy improvement after which the variational Gaussian mixture algorithm is deemed converged. |
| <code>merging.threshold</code> | Minimal cost value improvement required for merging two subnetworks. |
| <code>ite</code> | Defines maximum number of iterations on posterior update (<code>updatePosterior</code>). Increasing this can potentially lead to more accurate results, but computation may take longer. |
| <code>information.criterion</code> | Information criterion for model selection. Default is BIC (Bayesian Information Criterion); other options include AIC and AICc. |
| <code>speedup</code> | Takes advantage of approximations to PCA, mutual information etc in various places to speed up calculations. Particularly useful with large and densely connected networks and/or large sample size. |
| <code>speedup.max.edges</code> | Used if <code>speedup = TRUE</code> . Applies prefiltering of edges for calculating new joint models between subnetwork pairs when potential cost changes (<code>delta</code>) are updated for a newly merged subnetwork and its neighborghs. Empirical mutual information between each such subnetwork pair is calculated based on their first principal components, and joint models will be calculated only for the top candidates up to the number specified by <code>speedup.max.edges</code> . It is expected that the subnetwork pair that will benefit most from joint modeling will be among the top mutual infomation candidates. This way it is possible to avoid calculating exhaustive many models on the network hubs. |
| <code>positive.edges</code> | Consider only the edges with positive association. Currently measured with Spearman correlation. |
| <code>mc.cores</code> | Number of cores to be used in parallelization. See <code>help(mclapply)</code> for details. |
| <code>mixture.method</code> | Specify the approach to use in mixture modeling. Options. <code>vdp</code> (nonparametric Variational Dirichlet process mixture model); <code>bic</code> (based on Gaussian mixture modeling with EM, using BIC to select the optimal number of components) |

`bic.threshold` BIC threshold which needs to be exceeded before a new mode is added to the mixture with `mixture.method = "bic"`

`pca.basis` Transform data first onto PCA basis to try to avoid problems with non-diagonal covariances.

`...` Further optional arguments to be passed.

Value

NetResponseModel object.

Author(s)

Maintainer: Leo Lahti <leo.lahti@iki.fi>

References

See citation("netresponse").

Examples

```
## Not run:
#data(toydata)      # Load toy data set
#D <- toydata$emat # Response matrix (for example, gene expression)
#netw <- toydata$netw # Network

# Run NetReponse algorithm
# model <- detect.responses(D, netw, verbose = FALSE)

## End(Not run)
```

dna

Dna damage data set (PPI and expression)

Description

A combined yeast data set with protein-protein interactions and gene expression (dna damage). Gene expression profiles are transformed into links by computing a Pearson correlation for all pairs of genes and treating all correlations above 0.85 as additional links. Number of genes: 1823, number of interactions: 12382, number of gene expression observations: 52, number of total links with PPI and expression links: 15547.

Usage

`data(dna)`

Format

List of following objects:

ppi PPI data matrix

exp gene expression profiles data matrix

gids Vector of gene ids corresponding to indices used in data matrices

obs Gene expression observation details

combined.links pooled matrix of PPI and expression links

Source

PPI data pooled from yeast data sets of [1] and [2]. Dna damage expression set of [3].

References

Ulitsky, I. and Shamir, R. *Identification of functional modules using network topology and high-throughput data*. BMC Systems Biology 2007, 1:8.

Nariai, N., Kolaczyk, E. D. and Kasif, S. *Probabilistic Protein Function Prediction from Heterogeneous Genome-Wide Data*. PLoS ONE 2007, 2(3):e337.

Gasch, A., Huang, M., Metzner, S., Botstein, D. and Elledge, S. *Genomic expression responses to DNA-damaging agents and the regulatory role of the yeast ATR homolog Mex1p*. Molecular Biology of the Cell 2001, 12:2987-3003.

Examples

```
data(dna)
```

```
enrichment.list.factor
```

```
enrichment.list.factor
```

Description

Orders the responses by association strength (enrichment score) to a given sample set. For instance, if the samples correspond to a particular experimental factor, this function can be used to prioritize the responses according to their association strength to this factor.

Usage

```
enrichment.list.factor(models, level.samples, method, verbose = FALSE)
```

Arguments

| | |
|----------------------------|--|
| <code>models</code> | List of models. Each model should have a sample-cluster assignment matrix <code>qofz</code> . |
| <code>level.samples</code> | Measure enrichment of this sample (set) across the observed responses. |
| <code>method</code> | 'hypergeometric' measures enrichment of factor levels in this response; 'precision' measures response purity for each factor level; 'dependency' measures logarithm of the joint density between response and factor level vs. their marginal densities: $\log(P(r,s)/(P(r)P(s)))$ |
| <code>verbose</code> | Follow progress by intermediate messages. |

Value

A data frame which gives a data frame of responses ordered by enrichment score for the investigated sample. The model, response id and enrichment score are shown. The method field indicates the enrichment calculation method. The sample field lists the samples et for which the enrichments were calculated. The info field lists additional information on enrichment statistics.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See `citation('netresponse')` for citation details.

Examples

#

```
enrichment.list.factor.minimal
      enrichment.list.factor
```

Description

Orders the responses by association strength (enrichment score) to a given sample set. For instance, if the samples correspond to a particular experimental factor, this function can be used to prioritize the responses according to their association strength to this factor.

Usage

```
enrichment.list.factor.minimal(
  groupings,
  method,
  verbose = FALSE,
  annotation.vector,
  level
)
```


Arguments

| | |
|-------------------|--|
| groupings | List of groupings. Each model should have a sample-cluster assignment matrix qofz. |
| method | 'hypergeometric' measures enrichment of factor levels in this response; 'precision' measures response purity for each factor level; 'dependency' measures logarithm of the joint density between response and factor level vs. their marginal densities: $\log(P(r,s)/(P(r)P(s)))$ |
| verbose | Follow progress by intermediate messages. |
| annotation.vector | annotation vector |
| level | level |

Value

A data frame which gives a data frame of responses ordered by enrichment score for the investigated sample. The model, response id and enrichment score are shown. The method field indicates the enrichment calculation method. The sample field lists the samples et for which the enrichments were calculated. The info field lists additional information on enrichment statistics.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse') for citation details.

Examples

```
res <- enrichment.list.factor.minimal(groupings = NULL,
  method = NULL,
  annotation.vector = NULL,
  level = NULL)
```

factor.responses *Factor responses*

Description

List responses for each level of the given factor

Usage

```
factor.responses(  
  annotation.vector,  
  groupings,  
  method = "hypergeometric",  
  min.size = 2,  
  data = NULL  
)
```

Arguments

| | |
|-------------------|---|
| annotation.vector | annotation vector with discrete factor levels, and named by the samples |
| groupings | List of groupings. Each model should have a sample-cluster assignment matrix qofz, or a vector of cluster indices named by the samples. |
| method | method for enrichment calculation |
| min.size | minimum sample size for a response |
| data | data (samples x features; or a vector in univariate case) |

Value

List with each element corresponding to one factor level and listing the responses according to association strength

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

Examples

```
res <- factor.responses(annotation.vector = NULL, groupings = NULL)
```

```
factor.responses.minimal
```

Factor responses (minimal)

Description

List responses for each level of the given factor

Usage

```
factor.responses.minimal(  
  annotation.vector,  
  groupings,  
  method = "hypergeometric",  
  min.size = 2,  
  data = NULL  
)
```

Arguments

| | |
|-------------------|---|
| annotation.vector | annotation vector with discrete factor levels, and named by the samples |
| groupings | List of groupings. Each model should have a sample-cluster assignment matrix qofz, or a vector of cluster indices named by the samples. |
| method | method for enrichment calculation |
| min.size | minimum sample size for a response |
| data | data (samples x features; or a vector in univariate case) |

Value

List with each element corresponding to one factor level and listing the responses according to association strength

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

Examples

```
res <- factor.responses.minimal(annotation.vector = NULL, groupings = NULL)
```

filter.netw

filter.netw

Description

Mostly for internal use. Prefilter edges if speedups required.

Usage

```
filter.netw(network, delta, datamatrix, params)
```

Arguments

| | |
|------------|--|
| network | network |
| delta | associated cost function value changes for each node merge |
| datamatrix | datamatrix |
| params | parameters |

Details

Include only edges with the highest mutual information, calculated based on the first principal components.

Value

Filtered network

Author(s)

Leo Lahti, Olli-Pekka Huovilainen and Antonio Gusmao. Maintainer: Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

| | |
|----------------|-----------------------|
| filter.network | <i>filter.network</i> |
|----------------|-----------------------|

Description

Include to the network only the edges with the highest mutual information, calculated based on the first principal components.

Usage

```
filter.network(network, delta, datamatrix, params)
```

Arguments

| | |
|------------|--|
| network | network |
| delta | associated cost function value changes for each node merge |
| datamatrix | datamatrix |
| params | parameters |

Value

Filtered network

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

Examples

```
#
```

```
find.similar.features Find similar features with a given subnetwork.
```

Description

Given subnetwork, orders the remaining features (genes) in the input data based on similarity with the subnetwork. Allows the identification of similar features that are not directly connected in the input network.

Usage

```
find.similar.features(model, subnet.id, datamatrix = NULL, verbose =  
FALSE, information.criterion = NULL)
```

Arguments

| | |
|-----------------------|---|
| model | NetResponseModel object. |
| subnet.id | Investigated subnetwork. |
| datamatrix | Optional. Can be used to compare subnetwork similarity with new data which was not used for learning the subnetworks. |
| verbose | Logical indicating whether progress of the algorithm should be indicated on the screen. |
| information.criterion | Information criterion for model selection. By default uses the same than in the 'model' object. |

Details

The same similarity measure is used as when agglomerating the subnetworks: the features are ordered by delta (change) in the cost function, assuming that the feature would be merged in the subnetwork. The smaller the change, the more similar the feature is (change would minimize the new cost function value). Negative values of delta mean that the cost function would be improved by merging the new feature in the subnetwork, indicating features having coordinated response.

Value

A data frame with elements `feature.names` (e.g. gene IDs) and `delta`, which indicates similarity level. See details for details. The smaller, the more similar. The data frame is ordered such that the features are listed by decreasing similarity.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See `citation('netresponse')` for reference details.

Examples

```
data(toydata)
model <- toydata$model
subnet.id <- 'Subnet-1'
# g <- find.similar.features(model, subnet.id)
# List features that are similar to this subnetwork (delta < 0)
# (ordered by decreasing similarity)
# subset(g, delta < 0)
```

generate.toydata *generate.toydata*

Description

Generate toy data.

Usage

```
D <- generate.toydata()
```

Arguments

| | |
|-------------------------|--|
| <code>Dim</code> | Dimensionality of data |
| <code>Nc</code> | Number of modes |
| <code>Ns</code> | Number of data points |
| <code>sd0</code> | Component spread |
| <code>rgam.shape</code> | Shape parameter for Gamma distribution |
| <code>rgam.scale</code> | Scale parameter for Gamma distribution |

Value

Simulated data matrix (samples x features)

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

Examples

```
D <- generate.toydata()
```

get.dat,NetResponseModel-method
Get subnetwork data

Description

Get subnetwork data

Usage

```
## S4 method for signature 'NetResponseModel'  
get.dat(model, subnet.id, sample = NULL)
```

Arguments

| | |
|-----------|---|
| model | Result from NetResponse (detect.responses function). |
| subnet.id | Subnet identifier. A natural number which specifies one of the subnetworks within the 'model' object. |
| sample | Define the retrieved samples |

Value

Subnet data matrix

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

Examples

```
## Load a pre-calculated netresponse model obtained with  
# model <- detect.responses(toydata$emat, toydata$netw, verbose = FALSE)  
# data( toydata ); get.dat(toydata$model)
```

| | |
|----------------------|----------------|
| <code>get.mis</code> | <i>get.mis</i> |
|----------------------|----------------|

Description

Estimate mutual information for node pairs based on the first principal components.

Usage

```
get.mis(datamatrix, network, delta, network.nodes, G, params)
```

Arguments

| | |
|----------------------------|----------------------------|
| <code>datamatrix</code> | <code>datamatrix</code> |
| <code>network</code> | <code>network</code> |
| <code>delta</code> | <code>delta</code> |
| <code>network.nodes</code> | <code>network.nodes</code> |
| <code>G</code> | <code>G</code> |
| <code>params</code> | <code>params</code> |

Value

mutual information matrix

Author(s)

Maintainer: Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

| | |
|-----------------------------------|-----------------------------|
| <code>get.model.parameters</code> | <i>get.model.parameters</i> |
|-----------------------------------|-----------------------------|

Description

Retrieve the mixture model parameters of the NetResponse algorithm for a given subnetwork.

Usage

```
get.model.parameters(model, subnet.id = NULL)
```


Arguments

| | |
|-----------|---|
| model | Result from NetResponse (detect.responses function). |
| subnet.id | Subnet identifier. A natural number which specifies one of the subnetworks within the 'model' object. |

Details

Only the non-empty components are returned. Note: the original data matrix needs to be provided for function call separately.

Value

A list with the following elements:

| | |
|-------|--|
| mu | Centroids for the mixture components. Components x nodes. |
| sd | Standard deviations for the mixture components. A vector over the nodes for each component, implying the diagonal covariance matrix of the model (i.e. $\text{diag}(\text{std}^2)$). Components x nodes |
| w | Vector of component weights. |
| nodes | List of nodes in the subnetwork. |
| K | Number of mixture components. |

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

Leo Lahti et al.: Global modeling of transcriptional responses in interaction networks. *Bioinformatics* (2010). See citation('netresponse') for details.

Examples

```
# Load toy data
data( toydata )          # Load toy data set
D     <- toydata$emat    # Response matrix (for example, gene expression)
model <- toydata$model   # Pre-calculated model

# Get model parameters for a given subnet
# (Gaussian mixture: mean, covariance diagonal, mixture proportions)
get.model.parameters(model, subnet.id = 1)
```

`get.subnets,NetResponseModel-method`
get.subnets

Description

List the detected subnetworks (each is a list of nodes in the corresponding subnetwork).

Usage

```
## S4 method for signature 'NetResponseModel'  
get.subnets(  
  model,  
  get.names = TRUE,  
  min.size = 2,  
  max.size = Inf,  
  min.responses = 2  
)
```

Arguments

| | |
|---------------------------------|---|
| <code>model</code> | Output from the <code>detect.responses</code> function. An object of <code>NetResponseModel</code> class. |
| <code>get.names</code> | Logical. Indicate whether to return subnetwork nodes using node names (TRUE) or node indices (FALSE). |
| <code>min.size, max.size</code> | Numeric. Filter out subnetworks whose size is not within the limits specified here. |
| <code>min.responses</code> | Numeric. Filter out subnetworks with less responses (mixture components) than specified here. |

Value

A list of subnetworks.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

Leo Lahti et al.: Global modeling of transcriptional responses in interaction networks. *Bioinformatics* (2010). See `citation('netresponse')` for details.

Examples

```
## Load a pre-calculated netresponse model obtained with
# model <- detect.responses(toydata$emat, toydata$netw, verbose = FALSE)
# data( toydata ); get.subnets(toydata$model)
```

getqofz, NetResponseModel-method

Sample-to-response matrix of probabilities P(rls).

Description

Retrieve P(rls) from NetResponseModel model.

Usage

```
getqofz(model, subnet.id, log = FALSE)
```

Arguments

| | |
|-----------|------------------------------|
| model | NetResponseModel object. |
| subnet.id | Subnetwork to investigate. |
| log | Output in log probabilities. |

Details

Calculates probability density for each response on a given sample based on the estimated Gaussian mixture model.

Value

Samples x responses matrix. Each entry is a probability P(rls).

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse').

Examples

```
# qofz <- getqofz(model, subnet.id, log = FALSE)
```

`independent.models` *independent.models*

Description

Mainly for internal use. Provide independent models for each node.

Usage

```
independent.models(datamatrix, params)
```

Arguments

| | |
|-------------------------|-------------------------|
| <code>datamatrix</code> | <code>datamatrix</code> |
| <code>params</code> | <code>parameters</code> |

Value

| | |
|--------------------|-----------------------------|
| <code>nodes</code> | Model for each node |
| <code>C</code> | Costs for individual models |

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

Examples

```
res <- independent.models(datamatrix = NULL, params = NULL)
```

`list.responses.continuous.multi`

Investigate association of a continuous variable and the modes

Description

Investigate association of a continuous variable and the modes given a list of groupings

Usage

```
list.responses.continuous.multi(  
  annotation.df,  
  groupings,  
  method = "t-test",  
  pth = Inf,  
  verbose = TRUE,  
  rounding = NULL  
)
```

Arguments

| | |
|---------------|--|
| annotation.df | annotation data.frame with discrete factor levels, rows named by the samples |
| groupings | Sample mode information. Each element corresponds to one grouping; each grouping lists samples for the modes within that grouping. |
| method | method for quantifying the association |
| pth | p-value threshold applied to adjusted p-values |
| verbose | verbose |
| rounding | rounding digits |

Value

Table listing all associations between the factor levels and responses

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

Examples

```
res <- list.responses.continuous.multi(annotation.df = NULL, groupings = NULL)
```

```
list.responses.continuous.single
```

Investigate association of a continuous variable and the modes

Description

Investigate association of a continuous variable and the modes.

Usage

```
list.responses.continuous.single(  
  annotation.df,  
  groupings,  
  method = "t-test",  
  pth = Inf,  
  verbose = TRUE,  
  rounding = NULL,  
  adjust.p = TRUE  
)
```

Arguments

| | |
|----------------------------|--|
| <code>annotation.df</code> | annotation data.frame with discrete factor levels, rows named by the samples |
| <code>groupings</code> | Sample mode information. Each element corresponds to one of the modes and lists the samples assignment matrix <code>qofz</code> . Alternatively, a vector of mode indices named by the samples can be given. |
| <code>method</code> | method for quantifying the association |
| <code>pth</code> | p-value threshold (for adjusted p-values) |
| <code>verbose</code> | verbose |
| <code>rounding</code> | rounding digits |
| <code>adjust.p</code> | Adjust p-values (this will add <code>p.adj</code> column and remove <code>pvalue</code> column in the output table) |

Value

Table listing all associations between the factor levels and responses

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See `citation('netresponse')`

Examples

```
res <- list.responses.continuous.single(annotation.df = NULL, groupings = NULL)
```

list.responses.factor *List significant responses*

Description

List significantly associated responses for all factors and levels in the given annotation matrix

Usage

```
list.responses.factor(  
  annotation.df,  
  models,  
  method = "hypergeometric",  
  min.size = 2,  
  qth = Inf,  
  verbose = TRUE,  
  data = NULL,  
  rounding = NULL  
)
```

Arguments

| | |
|---------------|--|
| annotation.df | annotation data.frame with discrete factor levels, rows named by the samples |
| models | List of models. Each model should have a sample-cluster assignment matrix qofz, or a vector of cluster indices named by the samples. |
| method | method for enrichment calculation |
| min.size | minimum sample size for a response |
| qth | q-value threshold |
| verbose | verbose |
| data | data (samples x features; or a vector in univariate case) |
| rounding | rounding digits |

Value

Table listing all associations between the factor levels and responses

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

```
list.responses.factor.minimal
```

List factor responses (minimal)

Description

List significantly associated responses for all factors and levels in the given annotation matrix

Usage

```
list.responses.factor.minimal(  
  annotation.df,  
  groupings,  
  method = "hypergeometric",  
  min.size = 2,  
  pth = Inf,  
  verbose = TRUE,  
  data = NULL,  
  rounding = NULL  
)
```

Arguments

| | |
|----------------------------|---|
| <code>annotation.df</code> | annotation data.frame with discrete factor levels, rows named by the samples |
| <code>groupings</code> | List of groupings. Each model should have a sample-cluster assignment matrix <code>qofz</code> , or a vector of cluster indices named by the samples. |
| <code>method</code> | method for enrichment calculation |
| <code>min.size</code> | minimum sample size for a response |
| <code>pth</code> | p-value threshold; applied to adjusted p-value |
| <code>verbose</code> | verbose |
| <code>data</code> | data (samples x features; or a vector in univariate case) |
| <code>rounding</code> | rounding digits |

Value

A list with two elements: Table listing all associations between the factor levels and responses; multiple p-value adjustment method

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

`list.significant.responses`*Listing significant responses*

Description

List responses with significant associations to a given sample group.

Usage

```
list.significant.responses(model, sample, qth = 1, method = "hypergeometric")
```

Arguments

| | |
|---------------------|--|
| <code>model</code> | NetResponseModel object. |
| <code>sample</code> | User-specified samples group for which the enrichments are calculated. For instance, an annotation category. |
| <code>qth</code> | q-value threshold for enrichments |
| <code>method</code> | Enrichment method. |

Value

Statistics of the significantly associated responses.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

See Also

`response.enrichment`

Examples

```
#
```

| | |
|-------------------|--|
| listify.groupings | <i>Convert grouping info into a list; each element corresponds to a group and lists samples in that group.</i> |
|-------------------|--|

Description

Convert grouping info into a list; each element corresponds to a group and lists samples in that group.

Usage

```
listify.groupings(groupings, verbose = FALSE)
```

Arguments

| | |
|-----------|--|
| groupings | a list, a vector, or a samplesxmodes assignment matrix |
| verbose | verbose |

Value

Group list

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

Examples

```
res <- listify.groupings(groupings = NULL)
```

| | |
|---------------|----------------------|
| mixture.model | <i>Mixture model</i> |
|---------------|----------------------|

Description

Fit Gaussian mixture model

Usage

```

mixture.model(
  x,
  mixture.method = "vdp",
  max.responses = 10,
  implicit.noise = 0,
  prior.alpha = 1,
  prior.alphaKsi = 0.01,
  prior.betaKsi = 0.01,
  vdp.threshold = 1e-05,
  initial.responses = 1,
  ite = Inf,
  speedup = TRUE,
  bic.threshold = 0,
  pca.basis = FALSE,
  min.responses = 1,
  ...
)

```

Arguments

| | |
|---|--|
| <code>x</code> | data matrix (samples x features, for multivariate analysis) or a vector (for univariate analysis) |
| <code>mixture.method</code> | Specify the approach to use in mixture modeling. Options: <code>vdp</code> (nonparametric Variational Dirichlet process mixture model); <code>bic</code> (based on Gaussian mixture modeling with EM, using BIC to select the optimal number of components) |
| <code>max.responses</code> | Maximum number of responses for each subnetwork. Can be used to limit the potential number of network states. |
| <code>implicit.noise</code> | Implicit noise parameter. Add implicit noise to <code>vdp</code> mixture model. Can help to avoid overfitting to local optima, if this appears to be a problem. |
| <code>prior.alpha</code> , <code>prior.alphaKsi</code> , <code>prior.betaKsi</code> | Prior parameters for Gaussian mixture model that is calculated for each subnetwork (normal-inverse-Gamma prior). <code>alpha</code> tunes the mean; <code>alphaKsi</code> and <code>betaKsi</code> are the shape and scale parameters of the inverse Gamma function, respectively. |
| <code>vdp.threshold</code> | Minimal free energy improvement after which the variational Gaussian mixture algorithm is deemed converged. |
| <code>initial.responses</code> | Initial number of components for each subnetwork model. Used to initialize calculations. |
| <code>ite</code> | Maximum number of iterations on posterior update (<code>updatePosterior</code>). Increasing this can potentially lead to more accurate results, but computation may take longer. |
| <code>speedup</code> | Takes advantage of approximations to PCA, mutual information etc in various places to speed up calculations. Particularly useful with large and densely connected networks and/or large sample size. |

bic.threshold BIC threshold which needs to be exceeded before a new mode is added to the mixture with `mixture.method = "bic"`
pca.basis `pca.basis`
min.responses minimum number of responses
... Further optional arguments to be passed.

Value

List with two elements: `model`: fitted mixture model (parameters and free energy); `model.params`: model parameters

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See citation("netresponse")

Examples

```
res <- mixture.model(NULL)
```

`model.stats`

model.stats

Description

Subnetwork statistics: size and number of distinct responses for each subnet.

Usage

```
model.stats(models)
```

Arguments

`models` NetResponse object or list of models

Value

A 'subnetworks x properties' data frame containing the following elements.

`subnet.size`: Vector of subnetwork sizes.

`subnet.responses`:

Vector giving the number of responses in each subnetwork.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

Leo Lahti et al.: Global modeling of transcriptional responses in interaction networks. *Bioinformatics* (2010). See `citation('netresponse')` for reference details.

Examples

```
# Load a pre-calculated netresponse model obtained with
# model <- detect.responses(toydata$emat, toydata$netw, verbose = FALSE)
data(toydata)
# Calculate summary statistics for the model
stat <- model.stats(toydata$model)
```

NetResponseModel-class

Class 'NetResponseModel'

Description

A NetResponse model.

Objects from the Class

Returned by `detect.responses` function.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

Examples

```
showClass('NetResponseModel')
```

`order.responses`

order.responses

Description

Orders the responses by association strength (enrichment score) to a given sample set. For instance, if the samples correspond to a particular experimental factor, this function can be used to prioritize the responses according to their association strength to this factor.

Usage

```
order.responses(
  models,
  sample,
  method = "hypergeometric",
  min.size = 2,
  max.size = Inf,
  min.responses = 2,
  subnet.ids = NULL,
  verbose = FALSE,
  data = NULL
)
```

Arguments

| | |
|-----------------------------------|--|
| models | List of models. Each model should have a sample-cluster assignment matrix qofz. |
| sample | Measure enrichment of this sample (set) across the observed responses. |
| method | 'hypergeometric' measures enrichment of factor levels in this response; 'precision' measures response purity for each factor level; 'dependency' measures logarithm of the joint density between response and factor level vs. their marginal densities: $\log(P(r,s)/(P(r)P(s)))$ |
| min.size, max.size, min.responses | Optional parameters to filter the results based on subnet size and number of responses. |
| subnet.ids | Specify subnets for which the responses shall be ordered. By default, use all subnets. |
| verbose | Follow progress by intermediate messages. |
| data | data (samples x features; or a vector in univariate case) |

Value

A data frame with elements 'ordered.responses' which gives a data frame of responses ordered by enrichment score for the investigated sample. The subnetwork, response id and enrichment score are shown. The method field indicates the enrichment calculation method. The sample field lists the samples et for which the enrichments were calculated. The info field lists additional information on enrichment statistics.

Note

Tools for analyzing end results of the model.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse') for citation details.

Examples

```
res <- order.responses(models = NULL, sample = NULL)
# - for given sample/s (factor level),
#   order responses (across all subnets) by association strength
#   (enrichment score); overrepresentation
# order.responses(model, sample, method = 'hypergeometric')
```

osmo

Osmoshock data set (PPI and expression)

Description

A combined yeast data set with protein-protein interactions and gene expression (osmotick shock response). Gene expression profiles are transformed into links by computing a Pearson correlation for all pairs of genes and treating all correlations above 0.85 as additional links. Number of genes: 1711, number of interactions: 10250, number of gene expression observations: 133, number of total links with PPI and expression links: 14256.

Usage

```
data(osmo)
```

Format

List of following objects:

ppi PPI data matrix

exp gene expression profiles data matrix

gids Vector of gene ids corresponding to indices used in data matrices

obs Gene expression observation details

combined.links pooled matrix of PPI and expression links

Source

PPI data pooled from yeast data sets of [1] and [2]. Dna damage expression set of [3].

References

Ulitsky, I. and Shamir, R. *Identification of functional modules using network topology and high-throughput data*. BMC Systems Biology 2007, 1:8.

Nariai, N., Kolaczyk, E. D. and Kasif, S. *Probabilistic Protein Function Prediction from Heterogeneous Genome-Wide Data*. PLoS ONE 2007, 2(3):e337.

O'Rourke, S. and Herskowitz, I. *Unique and redundant roles for Hog MAPK pathway components as revealed by whole-genome expression analysis*. Molecular Biology of the Cell 2004, 15:532-42.

Examples

```
data(osmo)
```

P.r.s

*Description: Probabiity of mode given a sample (a data vector)
Mainly for internal use; documentation will be provided later. Tools
for calculating densities with Gaussian mixture models.*

Description

Arguments: @param dat features x samples data matrix for mixture modeling @param pars Gaussian mixture model parameters (diagonal covariances); list with elements mu (mean vectors), sd (covariance diagonals), w (weights). The mu and sd are component x features matrices, w is vector giving weight for each component. @param log Logical. Return densities in log domain. @param scaling Try to avoid floating errors. To be improved later.

Usage

```
P.r.s(dat, pars, log = TRUE, scaling = 0)
```

Details

Returns: @return Probability density

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See citation("netresponse")

P.rS

*Description: Probabiity of mode given multiple samples (ie. data matrix)
Mainly for internal use; documentation will be provided later.
Tools for calculating densities with Gaussian mixture models.*

Description

Arguments: @param dat features x samples data matrix for mixture modeling @param pars Gaussian mixture model parameters (diagonal covariances); list with elements mu (mean vectors), sd (covariance diagonals), w (weights). The mu and sd are component x features matrices, w is vector giving weight for each component. @param log Logical. Return densities in log domain.

Usage

```
P.rs(dat, pars, log = TRUE)
```

Details

Returns: @return Probability density

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See citation("netresponse")

| | |
|------------|--|
| P.rs.joint | <i>Description: Joint probability density for mode and sample group Mainly for internal use; documentation will be provided later. Tools for calculating densities with Gaussian mixture models.</i> |
|------------|--|

Description

Arguments: @param dat features x samples data matrix for mixture modeling @param pars Gaussian mixture model parameters (diagonal covariances); list with elements mu (mean vectors), sd (covariance diagonals), w (weights). The mu and sd are component x features matrices, w is vector giving weight for each component. @param log Logical. Return densities in log domain.

Usage

```
P.rs.joint(dat, pars, log = TRUE)
```

Details

Returns: @return Probability density

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See citation("netresponse")

`P.rs.joint.individual` *Description: Joint probability density for mode and sample Mainly for internal use; documentation will be provided later. Tools for calculating densities with Gaussian mixture models.*

Description

Arguments: @param dat features x samples data matrix for mixture modeling @param pars Gaussian mixture model parameters (diagonal covariances); list with elements mu (mean vectors), sd (covariance diagonals), w (weights). The mu and sd are component x features matrices, w is vector giving weight for each component. @param log Logical. Return densities in log domain.

Usage

```
P.rs.joint.individual(dat, pars, log = TRUE)
```

Details

Returns: @return Probability density

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See citation("netresponse")

`P.S` *Description: Probability density for sample Mainly for internal use; documentation will be provided later. Tools for calculating densities with Gaussian mixture models.*

Description

Arguments: @param dat features x samples data matrix for mixture modeling @param pars Gaussian mixture model parameters (diagonal covariances); list with elements mu (mean vectors), sd (covariance diagonals), w (weights). The mu and sd are component x features matrices, w is vector giving weight for each component. @param log Logical. Return densities in log domain.

Usage

```
P.S(dat, pars, log = TRUE)
```

Details

Returns: @return Probability density

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See citation("netresponse")

| | |
|----------------|--|
| P.s.individual | <i>Description: Probability density for individual sample Mainly for internal use; documentation will be provided later. Tools for calculating densities with Gaussian mixture models.</i> |
|----------------|--|

Description

Arguments: @param dat features x samples data matrix for mixture modeling @param pars Gaussian mixture model parameters (diagonal covariances); list with elements mu (mean vectors), sd (covariance diagonals), w (weights). The mu and sd are component x features matrices, w is vector giving weight for each component. @param log Logical. Return densities in log domain.

Usage

```
P.s.individual(dat, pars, log = TRUE)
```

Details

Returns: @return Probability density

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See citation("netresponse")

P.s.r

Description: Probability density for sample given mode Mainly for internal use; documentation will be provided later. Tools for calculating densities with Gaussian mixture models.

Description

Arguments: @param dat features x samples data matrix for mixture modeling @param pars Gaussian mixture model parameters (diagonal covariances); list with elements mu (mean vectors), sd (covariance diagonals), w (weights). The mu and sd are component x features matrices, w is vector giving weight for each component. @param log Logical. Return densities in log domain.

Usage

```
P.s.r(dat, pars, log = TRUE)
```

Details

Returns: @return Probability density

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See citation("netresponse")

P.Sr

Description: Probability density for sample group given mode Mainly for internal use; documentation will be provided later. Tools for calculating densities with Gaussian mixture models.

Description

Arguments: @param dat features x samples data matrix for mixture modeling @param pars Gaussian mixture model parameters (diagonal covariances); list with elements mu (mean vectors), sd (covariance diagonals), w (weights). The mu and sd are component x features matrices, w is vector giving weight for each component. @param log Logical. Return densities in log domain.

Usage

```
P.Sr(dat, pars, log = TRUE)
```

Details

Returns: @return Probability density

Author(s)

Contact: Leo Lahti <leo.lahti@iki.fi>

References

See citation("netresponse")

`pick.model.pairs` *Pick model pairs*

Description

Mainly for internal use. Calculate joint model for each node pair

Usage

```
pick.model.pairs(network, network.nodes, node.models, datamatrix, params)
```

Arguments

| | |
|----------------------------|---------------|
| <code>network</code> | network |
| <code>network.nodes</code> | network.nodes |
| <code>node.models</code> | node.models |
| <code>datamatrix</code> | datamatrix |
| <code>params</code> | parameters |

Value

| | |
|--------------------------|---|
| <code>model.pairs</code> | joint models for each node pair |
| <code>delta</code> | corresponding delta value for the cost function |

Author(s)

Maintainer: Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

Examples

```
#
```

`pick.model.parameters` *pick.model.parameters*

Description

Pick model parameters

Usage

```
pick.model.parameters(m, nodes)
```

Arguments

| | |
|--------------------|--------------------------------|
| <code>m</code> | vdp.mixt output |
| <code>nodes</code> | node names for naming purposes |

Value

Model parameters

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

Examples

```
pick.model.parameters(m = NULL, nodes = NULL)
```

PlotMixture

Plot mixtures

Description

Plot mixtures.

Usage

```
PlotMixture(  
  x,  
  qofz,  
  binwidth = 0.05,  
  xlab.text = NULL,  
  ylab.text = NULL,  
  title.text = NULL  
)
```

Arguments

| | |
|------------|---|
| x | data vector |
| qofz | Mode assignment probabilities for each sample. Samples x modes. |
| binwidth | binwidth for histogram |
| xlab.text | xlab.text |
| ylab.text | ylab.text |
| title.text | title.text |

Value

Used for its side-effects

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse') for citation details.

Examples

```
# PlotMixture(x, qofz)
```

PlotMixtureBivariate *PlotMixtureBivariate*

Description

Visualize data, centroids and response confidence intervals for a given Gaussian mixture model in two-dimensional (bivariate) case. Optionally, color the samples according to annotations labels.

Usage

```
PlotMixtureBivariate(  
  x,  
  means,  
  sds,  
  ws,  
  labels = NULL,  
  confidence = 0.95,  
  main = "",  
  ...  
)
```

Arguments

| | |
|------------|--|
| x | data matrix (samples x features) |
| means | mode centroids (modes x features) |
| sds | mode standard deviations, assuming diagonal covariance matrices (modes x features, each row giving the sqrt of covariance diagonal for the corresponding mode) |
| ws | weight for each mode |
| labels | Optional: sample class labels to be indicated in colors. |
| confidence | Confidence interval for the responses based on the covariances of each response. If NULL, no plotting. |
| main | title text |
| ... | Further arguments for plot function. |

Value

Used for its side-effects.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse') for citation details.

Examples

```
#plotMixture(dat, means, sds, ws)
```

PlotMixtureMultivariate

PlotMixtureMultivariate

Description

Visualize data, centroids and response confidence intervals for a given Gaussian mixture model with PCA. Optionally, color the samples according to annotations labels.

Usage

```
PlotMixtureMultivariate(
  x,
  means,
  sds,
  ws,
  labels = NULL,
  title = NULL,
  modes = NULL,
  pca = FALSE,
  qofz = NULL,
  ...
)
```

Arguments

| | |
|---------------------|--|
| <code>x</code> | data matrix (samples x features) |
| <code>means</code> | mode centroids (modes x features) |
| <code>sds</code> | mode standard deviations, assuming diagonal covariance matrices (modes x features, each row giving the sqrt of covariance diagonal for the corresponding mode) |
| <code>ws</code> | weight for each mode |
| <code>labels</code> | Optional: sample class labels to be indicated in colors. |
| <code>title</code> | title |
| <code>modes</code> | Optional: provide sample modes for visualization already in the input |
| <code>pca</code> | The data is projected on PCA plane by default (<code>pca = TRUE</code>). By setting this off (<code>pca = FALSE</code>) it is possible to visualize two-dimensional data in the original domain. |
| <code>qofz</code> | Sample-response probabilistic assignments matrix (samples x responses) |
| <code>...</code> | Further arguments for plot function. |

Value

Used for its side-effects.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See `citation('netresponse')` for citation details.

Examples

```
#plotMixture(dat, means, sds, ws)
```

PlotMixtureUnivariate *Plot univariate mixtures*

Description

Visualize data, centroids and stds for a given univariate Gaussian mixture model with PCA.

Usage

```
PlotMixtureUnivariate(  
  x,  
  means = NULL,  
  sds = NULL,  
  ws = NULL,  
  title.text = NULL,  
  xlab.text = NULL,  
  ylab.text = NULL,  
  binwidth = 0.05,  
  qofz = NULL,  
  density.color = "darkgray",  
  cluster.assignments = NULL,  
  ...  
)
```

Arguments

| | |
|---------------------|---|
| x | data vector |
| means | mode centroids |
| sds | mode standard deviations |
| ws | weight for each mode |
| title.text | Plot title |
| xlab.text | xlab.text |
| ylab.text | ylab.text |
| binwidth | binwidth for histogram |
| qofz | Mode assignment probabilities for each sample. Samples x modes. |
| density.color | Color for density lines |
| cluster.assignments | Vector of cluster indices, indicating cluster for each data point |
| ... | Further arguments for plot function. |

Value

Used for its side-effects

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse') for citation details.

Examples

```
# plotMixtureUnivariate(dat, means, sds, ws)
```

plotPCA

plotPCA

Description

Visualize data, centroids and response confidence intervals for a given subnetwork with PCA. Optionally, color the samples according to annotations labels.

Usage

```
plotPCA(x, subnet.id, labels = NULL, confidence = 0.95, npoints = NULL, ...)
```

Arguments

| | |
|------------|--|
| x | NetResponseModel object. Output from the detect.responses function. |
| subnet.id | Subnetwork id. Either character as 'Subnetwork-2' or numeric as 2, which is then converted to character. |
| labels | Optional: sample class labels to be indicated in colors. |
| confidence | Confidence interval for the responses based on the covariances of each response. If NULL, no plotting. |
| npoints | Argument to the ellipse function |
| ... | Further arguments for plot function. |

Value

Used for its side-effects.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse') for citation details.

Examples

```
#plotPCA(x, subnet.id)
```

| | |
|-------------------|--|
| plot_associations | <i>Association strength between category labels and responses.</i> |
|-------------------|--|

Description

Plot association strength between user-defined category labels and responses in a selected subnetwork. Associations are shown in terms $-\log_{10}(p)$ enrichment values for the annotation categories for the responses within the specified subnetwork. No correction for multiple testing.

Usage

```
plot_associations(
  x,
  subnet.id,
  labels,
  method = "hypergeometric",
  mode = "group.by.classes",
  ...
)
```

Arguments

| | |
|-----------|---|
| x | NetResponseModel object |
| subnet.id | Subnetwork. |
| labels | Factor. Labels for the data samples. Name by samples, or provide in the same order as in the original data. |
| method | Method to calculate association strength. |
| mode | group.by.responses or group.by.classes: indicate barplot grouping type. |
| ... | Other arguments to be passed for plot_ |

Value

Used for side effect (plotting).

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse').

See Also

plot_responses

Examples

```
#
```

| | |
|-----------|----------------------------|
| plot_data | <i>Plot observed data.</i> |
|-----------|----------------------------|

Description

Plotting tool for measurement data. Produces boxplot for each feature in each annotation category for the selected subnetwork.

Usage

```
plot_data(x, subnet.id, labels, ...)
```

Arguments

| | |
|-----------|--------------------------------------|
| x | NetResponseModel object. |
| subnet.id | Specify the subnetwork. |
| labels | Annotation categories. |
| ... | Further arguments for plot function. |

Value

ggplot2 plot object

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

See Also

plot_responses

Examples

```
#
```

plot_expression *plot_expression*

Description

Plot expression matrix in color scale. For one-channel data; plot expression of each gene relative to its mean expression level over all samples. Blue indicates decreased expression and red indicates increased expression. Brightness of the color indicates magnitude of the change. Black denotes no change.

Usage

```
plot_expression(x, maintext, ...)
```

Arguments

| | |
|----------|---------------------------|
| x | samples x features matrix |
| maintext | main title |
| ... | optional arguments |

Value

Used for its side effects.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse').

See Also

[plot_scale](#)

Examples

```
#plot_expression(x)
```

| | |
|-------------|--|
| plot_matrix | <i>Visualize a matrix with one or two-way color scale.</i> |
|-------------|--|

Description

Fast investigation of matrix objects; standard visualization choices are made automatically; fast and easy-to-use but does not necessarily provide optimal visualization.

Usage

```
plot_matrix(
  mat,
  type = "tway",
  midpoint = 0,
  palette = NULL,
  colors = NULL,
  col.breaks = NULL,
  interval = 0.1,
  plot_axes = "both",
  row.tick = 1,
  col.tick = 1,
  cex.xlab = 0.9,
  cex.ylab = 0.9,
  xlab = NULL,
  ylab = NULL,
  limit.trunc = 0,
  mar = c(5, 4, 4, 2),
  ...
)
```

Arguments

| | |
|------------|--|
| mat | matrix |
| type | String. Specifies visualization type. Options: 'oneway' (color scale ranges from white to dark red; the color can be changed if needed); 'tway' (color scale ranges from dark blue through white to dark red; colors can be changed if needed) |
| midpoint | middle point for the color plot: smaller values are shown with blue, larger are shown with red in type = 'tway' |
| palette | Optional. Color palette. |
| colors | Optional. Colors. |
| col.breaks | breakpoints for the color palette |
| interval | interval for palette color switches |
| plot_axes | String. Indicates whether to plot x-axis ('x'), y-axis ('y'), or both ('both'). |
| row.tick | interval for plotting row axis texts |

| | |
|-------------|---|
| col.tick | interval for plotting column axis texts |
| cex.xlab | use this to specify distinct font size for the x axis |
| cex.ylab | use this to specify distinct font size for the y axis |
| xlab | optional x axis labels |
| ylab | optional y axis labels |
| limit.trunc | color scale limit breakpoint |
| mar | image margins |
| ... | optional parameters to be passed to function 'image', see help(image) for further details |

Value

A list with the color palette (colors), color breakpoints (breaks), and palette function (palette.function)

Author(s)

Leo Lahti <microbiome-admin@googlegroups.com>

References

See citation('microbiome')

Examples

```
mat <- rbind(c(1,2,3,4,5), c(1, 3, 1), c(4,2,2))
plot_matrix(mat, 'tway', midpoint = 3)
```

| | |
|---------------|----------------------|
| plot_response | <i>plot_response</i> |
|---------------|----------------------|

Description

Plot a specific transcriptional response for a given subnetwork. TRUE, colors = TRUE, plot_type = 'twopi', ...)

Usage

```
plot_response(
  x,
  mynet,
  mybreaks,
  mypalette,
  plot_names = TRUE,
  colors = TRUE,
  plot_type = "twopi",
  ...
)
```


Arguments

| | |
|------------|--|
| x | A numerical vector, or NULL. |
| mynet | Binary matrix specifying the interactions between nodes. |
| mybreaks | Specify breakpoints for color plot_ |
| mypalette | Specify palette for color plot_ |
| plot_names | Plot node names (TRUE) or indices (FALSE). |
| colors | Plot colors. Logical. |
| plot_type | Network plot mode. For instance, 'neato' or 'twopi'. |
| ... | Further arguments for plot function. |

Value

Used for its side-effects.

Author(s)

Leo Lahti, Olli-Pekka Huovilainen and Antonio Gusmao. Maintainer: Leo Lahti <leo.lahti@iki.fi>

References

L. Lahti et al.: Global modeling of transcriptional responses in interaction networks. Submitted.

Examples

```
#tmp <- plot_response(model, mynet,
# \tmaintext = paste('Subnetwork', subnet.id))
```

| | |
|----------------|-----------------------|
| plot_responses | <i>plot_responses</i> |
|----------------|-----------------------|

Description

Plot the detected transcriptional responses for a given subnetwork. plot_mode = 'network', xaxis = TRUE, yaxis = TRUE, plot_type = 'twopi', mar = c(5, 4, 4, 2), horiz = TRUE, datamatrix = NULL, scale = FALSE, ...)

Usage

```
plot_responses(
  x,
  subnet.id,
  nc = 3,
  plot_names = TRUE,
  plot_mode = "network",
  xaxis = TRUE,
```

```

    yaxis = TRUE,
    plot_type = "twopi",
    mar = c(5, 4, 4, 2),
    horiz = TRUE,
    datamatrix = NULL,
    scale = FALSE,
    ...
)

```

Arguments

| | |
|--------------|--|
| x | Result from NetResponse (detect.responses function). |
| subnet.id | Subnet id. |
| nc | Number of columns for an array of images. |
| plot_names | Plot node names (TRUE) or indices (FALSE). |
| plot_mode | network: plot responses as a subnetwork graph; matrix, heatmap: plot subnetwork expression matrix. For both, expression of each gene is shown relative to the mean expression level of the gene; boxplot_data: feature-wise boxplots for hard sample-to-response assignments; response.barplot: estimated response centroids as barplot including 95 confidence intervals for the means; pca: PCA projection with estimated centroids and 95 two-dimensional case the original coordinates are used. |
| xaxis, yaxis | Logical. Plot row/column names. |
| plot_type | Network plot mode. For instance, 'neato' or 'twopi'. |
| mar | Figure margins. |
| horiz | Logical. Horizontal barplot_ |
| datamatrix | datamatrix |
| scale | scale the phylotypes to unit length (only implemented for plot_mode = 'matrix') |
| ... | Further arguments for plot function. |

Value

Used for its side-effects.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

See Also

[plot_scale](#)

Examples

```
#
#res <- detect.responses(D, netw)
#vis <- plot_responses(res, subnet.id)
```

plot_scale

plot_scale

Description

Plot the color scale used in visualization.

Usage

```
plot_scale(
  x,
  y,
  m = NULL,
  cex.axis = 1.5,
  label.step = 2,
  interval = 0.1,
  two.sided = TRUE,
  label.start = NULL,
  Nlab = 3,
  ...
)
```

Arguments

| | |
|-------------|---|
| x | Breakpoints for the plot_ |
| y | Color palette. |
| m | Breakpoints' upper limit. |
| cex.axis | Axis scale. |
| label.step | Density of the labels. |
| interval | Interval. |
| two.sided | Plot two-sided (TRUE) or one-sided (FALSE) visualization. |
| label.start | Label starting point. |
| Nlab | Number of labels to plot_ |
| ... | Further arguments for plot function. |

Value

Used for its side-effects.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

Examples

```
#
#res <- detect.responses(D, netw, verbose = FALSE)
#vis <- plot_responses(res, subnet.idx)
#plot_scale(vis$breaks, vis$palette)
```

plot_subnet

plot_subnet

Description

Plot the given subnetwork.

Usage

```
plot_subnet(x, subnet.id, network, plot_names = TRUE, ...)
```

Arguments

| | |
|------------|--|
| x | Result from NetResponse (detect.responses function). |
| subnet.id | Subnet id. |
| network | Original network used in the modelling. |
| plot_names | Plot node names (TRUE) or indices (FALSE). |
| ... | Further arguments for plot function. |

Value

Used for its side-effects. Returns a matrix that describes the investigated subnetwork.

Author(s)

Leo Lahti, Olli-Pekka Huovilainen and Antonio Gusmao. Maintainer: Leo Lahti <leo.lahti@iki.fi>

References

L. Lahti et al.: Global modeling of transcriptional responses in interaction networks. Submitted.

Examples

```
#  
# res <- detect.responses(D, netw, verbose = FALSE)  
# net <- plot_subnet(res, subnet.idx = 1)
```

| | |
|----------|------------------------------|
| read.sif | <i>Reading network files</i> |
|----------|------------------------------|

Description

Function to read network files.

Usage

```
read.sif(sif.file, format = 'graphNEL', directed = FALSE, header =  
TRUE, sep = '\t', ...)
```

Arguments

| | |
|----------|--|
| sif.file | Name of network file in SIF format. |
| format | Output format: igraph or graphNEL |
| directed | Logical. Directed/undirected graph. Not used in the current model. |
| header | Logical. Indicate whether the SIF file has header or not. |
| sep | Field separator. |
| ... | Further optional arguments to be passed for file reading. |

Details

Read in SIF network file, return R graph object in igraph or graphNEL format.

Value

R graph object in igraph or graphNEL format.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

Examples

```
#net <- read.sif('network.sif')
```

```
remove.negative.edges  remove.negative.edges
```

Description

Remove edges where the connected nodes correlate negatively

Usage

```
remove.negative.edges(network, delta, datamatrix)
```

Arguments

| | |
|------------|--|
| network | network |
| delta | associated cost function value changes for each node merge |
| datamatrix | datamatrix |

Value

Filtered network

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

Examples

```
#
```

```
response.enrichment  Enrichment for a specified sample group in the given response.
```

Description

Calculate enrichment values for a specified sample group in the given response.

Usage

```
response.enrichment(  
  total.samples,  
  response.samples,  
  annotated.samples,  
  method = "hypergeometric"  
)
```

Arguments

total.samples All samples in the data
response.samples
Samples in the investigated subset
annotated.samples
Samples at the investigated annotation level for enrichment calculation
method Enrichment method.

Value

List with enrichment statistics, depending on enrichment method.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

See Also

order.responses

Examples

```
#enr <- response.enrichment(subnet.id, models, sample, response, method)
```

response2sample *response2sample*

Description

List the most strongly associated response of a given subnetwork for each sample.

Usage

```
response2sample(  
  model,  
  subnet.id = NULL,  
  component.list = TRUE,  
  verbose = FALSE,  
  data = NULL  
)
```

Arguments

| | |
|----------------|--|
| model | A NetResponseModel object or list. |
| subnet.id | Subnet id. A natural number which specifies one of the subnetworks within the 'model' object. |
| component.list | List samples separately for each mixture component (TRUE). Else list the most strongly associated component for each sample (FALSE). |
| verbose | Follow progress by intermediate messages. |
| data | Data (features x samples; or a vector for univariate case) to predict response for given data points (currently implemented only for mixture.model output) |

Return:

Value

A list. Each element corresponds to one subnetwork response, and contains a list of samples that are associated with the response (samples for which this response has the highest probability $P(\text{response} | \text{sample})$).

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

Leo Lahti et al.: Global modeling of transcriptional responses in interaction networks. *Bioinformatics* (2010). See citation('netresponse') for citation details.

Examples

```
# Load example data
data( toydata )           # Load toy data set
D   <- toydata$emat      # Response matrix (for example, gene expression)
model <- toydata$model    # Pre-calculated model

# Find the samples for each response (for a given subnetwork)
response2sample(model, subnet.id = 1)
```

| | |
|-----------------|------------------------|
| sample2response | <i>sample2response</i> |
|-----------------|------------------------|

Description

Probabilistic sample-response assignments for given subnet.

Usage

```
sample2response(model, subnet.id, mode = 'soft')
```


Arguments

| | |
|-----------|---|
| model | Result from NetResponse (detect.responses function). |
| subnet.id | Subnet identifier. A natural number which specifies one of the subnetworks within the 'model' object. |
| mode | soft: gives samples x responses probabilistic assignment matrix; hard: gives the most likely response for each sample |

Value

A matrix of probabilities. Sample-response assignments for given subnet, listing the probability of each response, given a sample.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

Leo Lahti et al.: Global modeling of transcriptional responses in interaction networks. *Bioinformatics* (2010). See citation('netresponse') for citation details.

Examples

```
data( toydata )      # Load toy data set
D   <- toydata$emat  # Response matrix (for example, gene expression)
netw <- toydata$netw # Network

# Detect network responses
#model <- detect.responses(D, netw, verbose = FALSE)

# Assign samples to responses (soft, probabilistic assignments sum to 1)
#response.probabilities <- sample2response(model, subnet.id = 'Subnet-1')
```

set.breaks

Set breaks

Description

Set breakpoints for two-way color palette.

Usage

```
set.breaks(mat, interval = 0.1)
```

Arguments

| | |
|----------|-------------------------------|
| mat | Matrix to visualize. |
| interval | Density of color breakpoints. |

Value

A vector listing the color breakpoints.

Author(s)

Leo Lahti, Olli-Pekka Huovilainen and Antonio Gusmao. Maintainer: Leo Lahti <leo.lahti@iki.fi>

References

L. Lahti et al.: Global modeling of transcriptional responses in interaction networks. Submitted.

Examples

```
set.breaks(array(rnorm(100), dim = c(10, 10)), interval = .1)
```

split.qofz

split.qofz

Description

Split q of z.

Main function of the NetResponse algorithm. Detect condition-specific network responses, given network and a set of measurements of node activity in a set of conditions. Returns a set of subnetworks and their estimated context-specific responses.

Usage

```
## S3 method for class 'qofz'
split(qOFz, c, new.c, dat, speedup = TRUE, min.size = 4)
```

Arguments

| | |
|----------|----------|
| qOFz | qOFz |
| c | c |
| new.c | new.c |
| dat | dat |
| speedup | speedup |
| min.size | min.size |

Details

INPUT: data, qOFz, hp_posterior, hp_prior, opts OUTPUT: list(new.qOFz, new.c); * new.qOFz: posterior over labels including the split clusters. * new.c: index of the newly created cluster. DESCRIPTION: Implements the VDP algorithm step 3a.

Value

object Component must have at least min.size samples to be splitted.'

| | |
|---------|----------------|
| toydata | <i>toydata</i> |
|---------|----------------|

Description

Toy data for NetResponse examples.

Usage

```
data(toydata)
```

Format

Toy data: a list with three elements:

`emat`: Data matrix (samples x features). This contains the same features that are provided in the network (`toydata$netw`). The matrix characterizes measurements of network states across different conditions.

`netw`: Binary matrix that describes pairwise interactions between features. This defines an undirected network over the features. A link between two nodes is denoted by 1.

`model`: A pre-calculated model. Object of `NetResponseModel` class, resulting from applying the `netresponse` algorithm on the `toydata` with `model <- detect.responses(D, netw)`.

References

Leo Lahti et al.: Global modeling of transcriptional responses in interaction networks. *Bioinformatics* (2010).

Examples

```
data(toydata)
D <- toydata$emat # Response matrix (samples x features)
netw <- toydata$netw # Network between the features
model <- toydata$model # Pre-calculated NetResponseModel obtained with
# model <- detect.responses(D, netw)
```

| | |
|--------------------------------|--------------------------|
| <code>update.model.pair</code> | <i>update.model.pair</i> |
|--------------------------------|--------------------------|

Description

Mainly for internal use. Calculate joint model for given node pair and update delta accordingly.

Usage

```
update.model.pair(datamatrix, delta, network, edge, network.nodes, G,
  params, model.nodes, model.pairs)
```

Arguments

| | |
|---------------|---------------|
| datamatrix | datamatrix |
| delta | delta |
| network | network |
| edge | edge |
| network.nodes | network.nodes |
| G | G |
| params | params |
| model.nodes | model.nodes |
| model.pairs | model.pairs |

Return:

Value

| | |
|-------------|-------------|
| model.pairs | model.pairs |
| delta | delta |

Author(s)

Leo Lahti, Olli-Pekka Huovilainen and Antonio Gusmao. Maintainer: Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

Examples

```
#
```

vdp.mixt

vdp.mixt

Description

Accelerated variational Dirichlet process Gaussian mixture.

Usage

```
vdp.mixt(
  dat,
  prior.alpha = 1,
  prior.alphaKsi = 0.01,
  prior.betaKsi = 0.01,
  do.sort = TRUE,
  threshold = 1e-05,
  initial.K = 1,
  ite = Inf,
  implicit.noise = 0,
  c.max = 10,
  speedup = TRUE,
  min.size = 5
)
```

Arguments

| | |
|---|---|
| <code>dat</code> | Data matrix (samples x features). |
| <code>prior.alpha</code> , <code>prior.alphaKsi</code> , <code>prior.betaKsi</code> | Prior parameters for Gaussian mixture model (normal-inverse-Gamma prior). <code>alpha</code> tunes the mean; <code>alphaKsi</code> and <code>betaKsi</code> are the shape and scale parameters of the inverse Gamma function, respectively. |
| <code>do.sort</code> | When true, <code>qOFz</code> will be sorted in decreasing fashion by component size, based on <code>colSums(qOFz)</code> . The <code>qOFz</code> matrix describes the sample-component assignments in the mixture model. |
| <code>threshold</code> | Defines the minimal free energy improvement that stops the algorithm: used to define convergence limit. |
| <code>initial.K</code> | Initial number of mixture components. |
| <code>ite</code> | Defines maximum number of iterations on posterior update (<code>updatePosterior</code>). Increasing this can potentially lead to more accurate results, but computation may take longer. |
| <code>implicit.noise</code> | Adds implicit noise; used by <code>vdp.mk.log.lambda.so</code> and <code>vdp.mk.hp.posterior.so</code> . By adding noise (positive values), one can avoid overfitting to local optima in some cases, if this happens to be a problem. |
| <code>c.max</code> | Maximum number of candidates to consider in <code>find.best.splitting</code> . During mixture model calculations new mixture components can be created until this upper limit has been reached. Defines the level of truncation for a truncated stick-breaking process. |
| <code>speedup</code> | When learning the number of components, each component is splitted based on its first PCA component. To speed up, approximate by using only subset of data to calculate PCA. |
| <code>min.size</code> | Minimum size for a component required for potential splitting during mixture estimation. |

Details

Implementation of the Accelerated variational Dirichlet process Gaussian mixture model algorithm by Kenichi Kurihara et al., 2007.

ALGORITHM SUMMARY This code implements Gaussian mixture models with diagonal covariance matrices. The following greedy iterative approach is taken in order to obtain the number of mixture models and their corresponding parameters:

1. Start from one cluster, $T = 1$.
2. Select a number of candidate clusters according to their values of $'Nc' = \sum_{n=1}^N q_{z_n}(z_n = c)$ (larger is better).
3. For each of the candidate clusters, c :
 - 3a. Split c into two clusters, c_1 and c_2 , through the bisector of its principal component. Initialise the responsibilities $q_{z_n}(z_n = c_1)$ and $q_{z_n}(z_n = c_2)$.
 - 3b. Update only the parameters of c_1 and c_2 using the observations that belonged to c , and determine the new value for the free energy, $FT+1$.
 - 3c. Reassign cluster labels so that cluster 1 corresponds to the largest cluster, cluster 2 to the second largest, and so on.
4. Select the split that lead to the maximal reduction of free energy, $FT+1$.
5. Update the posterior using the newly split data.
6. If $FT - FT+1 < \epsilon$ then halt, else set $T := T + 1$ and go to step 2.

The loop is implemented in the function `greedy(...)`

Value

| | |
|---------------------------|--|
| <code>prior</code> | Prior parameters of the vdp-gm model (<code>qofz</code> : priors on observation lables; <code>Mu</code> : centroids; <code>S2</code> : variance). |
| <code>posterior</code> | Posterior estimates for the model parameters and statistics. |
| <code>weights</code> | Mixture proportions, or weights, for the Gaussian mixture components. |
| <code>centroids</code> | Centroids of the mixture components. |
| <code>sds</code> | Standard deviations for the mixture model components (posterior modes of the covariance diagonals square root). Calculated as $\sqrt{\text{invgam.scale}/(\text{invgam.shape} + 1)}$. |
| <code>qOfz</code> | Sample-to-cluster assignments (soft probabilistic associations). |
| <code>Nc</code> | Component sizes |
| <code>invgam.shape</code> | Shape parameter (α) of the inverse Gamma distribution |
| <code>invgam.scale</code> | Scale parameter (β) of the inverse Gamma distribution |
| <code>Nparams</code> | Number of model parameters |
| <code>K</code> | Number of components in the mixture model |
| <code>opts</code> | Model parameters that were used. |
| <code>free.energy</code> | Free energy of the model. |

Note

This implementation is based on the Variational Dirichlet Process Gaussian Mixture Model implementation, Copyright (C) 2007 Kenichi Kurihara (all rights reserved) and the Agglomerative Independent Variable Group Analysis package (in Matlab): Copyright (C) 2001-2007 Esa Alhoniemi, Antti Honkela, Krista Lagus, Jeremias Seppa, Harri Valpola, and Paul Wagner.

Author(s)

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References

Kenichi Kurihara, Max Welling and Nikos Vlassis: Accelerated Variational Dirichlet Process Mixtures. In B. Schölkopf and J. Platt and T. Hoffman (eds.), Advances in Neural Information Processing Systems 19, 761–768. MIT Press, Cambridge, MA 2007.

Examples

```
set.seed(123)

# Generate toy data with two Gaussian components
dat <- rbind(array(rnorm(400), dim = c(200,2)) + 5,
            array(rnorm(400), dim = c(200,2)))

# Infinite Gaussian mixture model with
# Variational Dirichlet Process approximation
mixt <- vdp.mixt( dat )

# Centroids of the detected Gaussian components
mixt$posterior$centroids

# Hard mixture component assignments for the samples
apply(mixt$posterior$qOfz, 1, which.max)
```

vectorize.groupings *Convert grouping info into a vector; each element corresponds to a group and lists samples in that group.*

Description

Convert grouping info into a vector; each element corresponds to a group and lists samples in that group.

Usage

```
vectorize.groupings(groupings, verbose = FALSE)
```

Arguments

| | |
|-----------|--|
| groupings | a list, a vector, or a samplesxmodes assignment matrix |
| verbose | verbose |

Value

Indicator vector

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

Examples

#

```
write.netresponse.results
```

Write NetResponse results summary into a file.

Description

Experimental version.

Usage

```
write.netresponse.results(x, subnet.ids = NULL, filename)
```

Arguments

| | |
|------------|--|
| x | NetResponseModel |
| subnet.ids | List of subnet ids to consider. By default, all subnets. |
| filename | Output file name. |

Value

Used for side effects.

Author(s)

Leo Lahti <leo.lahti@iki.fi>

References

See citation('netresponse')

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