Package 'EGAD'

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Type Package

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Description The package implements a series of highly efficient tools to calculate functional properties of networks based on guilt by association methods.

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`assortativity` *Calculating network assortativity*

Description

The function calculates the assortativity of a network, that measures the preference of interactions between similar nodes. As in most literature, 'similarity' is here defined in terms of node degrees.

Usage

```
assortativity(network)
```

Arguments

`network`	matrix indicating network structure (symmetric)

Value

Numeric value

Examples

```
network <- matrix( sample(c(0,1),36, replace=TRUE), nrow=6,byrow=TRUE)
assort_value <- assortativity(network)
```

`attr.human` *Human GENCODE annotations (v22)*

Description

A dataset containing identifiers for gene transcripts

Format

A data frame with 60483 rows and 10 variables:

chr chromosome

start chromosomal start position, in base pairs

end chromosomal end position, in base pairs

strand chromosomal strand, + or -

un unknown

ensemblID ENSEMBL identifier

type type of transcript

stat status of transcript

name HUGO identifier

entrezID Entrez identifier

@source ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_22/

---

attr.mouse *Mouse GENCODE annotations (M7)*

Description

A dataset containing identifiers for gene transcripts

Format

A data frame with 46517 rows and 10 variables:

chr chromosome

start chromosomal start position, in base pairs

end chromosomal end position, in base pairs

strand chromosomal strand, + or -

un unknown

ensemblID ENSEMBL identifier

type type of transcript

stat status of transcript

name HUGO identifier

entrezID Entrez identifier

@source ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M7/

auc_multifunc *Calculating AUC for functional groups from ranked lists*

Description

The function calculates the AUC for a functional group analytically using an optimal ranked list of genes that indicates association between genes and groups.

Usage

```
auc_multifunc(annotations, optimallist)
```

Arguments

annotations	binary matrix indicating which list elements are in which functional groups.
optimallist	Ranked list (multifunctionality analysis, see calculate_multifunc).

Value

aucs array of aucs for each group in annotations

Examples

```
annotations <- c(rep(0,10))
annotations[c(1,3,5)] <- 1
optimallist <- 10:1
aurocs_mf <- auc_multifunc(annotations, optimallist)
```

auprc *Area under the precision recall curve*

Description

The function calculates the area under the precision-recall curve

Usage

```
auprc(scores, labels)
```

Arguments

scores	numeric array
labels	binary array

Value

auprc Numeric value

Examples

```
labels <- c(rep(0,10))
labels[c(1,3,5)] <- 1
scores <- 10:1
auprc <- auprc(scores, labels)
```

---

auroc_analytic *Area under the receiver operating characteristic curve*

Description

The function calculates the area under the receiver operating characteristic (ROC) curve analytically

Usage

```
auroc_analytic(ranks, labels)
```

Arguments

ranks	numeric array
labels	binary array

Value

auroc Numeric value

Examples

```
labels <- c(rep(0,10))
labels[c(1,3,5)] <- 1
scores <- 10:1
auroc <- auroc_analytic(scores, labels)
```

---

biogrid *BIOGRID v3.4.126*

Description

A data frame containing protein-protein interactions

Format

A data frame with 211506 rows and 2 variables:

entrezID_A List of Entrez identifiers, interactor A

entrezID_B List of Entrez identifiers, interactor B

@source http://thebiogrid.org/

build_binary_network *Builds a binary network*

Description

The function creates a gene-by-gene matrix with binary entries indicating interaction (1) or no interaction (0) between the genes.

Usage

```
build_binary_network(data, list)
```

Arguments

data	2-column matrix, each row a pair indicating a relationship or interaction
list	string array of genes/labels/ids

Value

net matrix binary characterizing interactions

Examples

```
data <- cbind(edgeA=c('gene1','gene2'),edgeB=c('gene3','gene3'))
list <- c('gene1','gene2','gene3')
network <- build_binary_network(data,list)
```

build_coexp_expressionSet *Builds a coexpression network from an expressionSet*

Description

The function generates a dense coexpression network from expression data stored in the expressionSet data type. Correlation coefficicents are used as to weight the edges of the nodes (genes). Calls build_coexp_network.

Usage

```
build_coexp_expressionSet(
  exprsSet,
  gene.list,
  method = "spearman",
  flag = "rank"
)
```

Arguments

exprsSet	data class ExpressionSet
gene.list	array of gene labels
method	correlation method to use, default Spearman's rho
flag	string to indicate if the network should be ranked

Value

net Matrix symmetric

Examples

```
exprs <- matrix( rnorm(1000), ncol=10,byrow=TRUE)
gene.list <- paste('gene',1:100, sep='')
sample.list <- paste('sample',1:10, sep='')
rownames(exprs) <- gene.list
colnames(exprs) <- sample.list
network <- build_coexp_expressionSet(exprs, gene.list, method='pearson')
```

---

build_coexp_GEOID *Builds a coexpression network given a GEO ID*

Description

The function generates a dense coexpression network from expression data stored in GEO. The expression data is downloaded from GEO. Correlation coefficicents are used as to weight the edges of the nodes (genes). Calls get_expression_matrix_from_GEO and build_coexp_network.

Usage

```
build_coexp_GEOID(gseid, gene.list, method = "spearman", flag = "rank")
```

Arguments

gseid	string GEO ID of expression experiment
gene.list	array of gene labels
method	correlation method to use, default Spearman's rho
flag	string to indicate if the network should be ranked

Value

net Matrix symmetric

build_coexp_network *Builds a coexpression network from an expressionSet*

Description

The function generates a dense coexpression network from expression data stored as a matrix, with the genes as row labels, and samples as column labels. Correlation coefficicents are used as to weight the edges of the nodes (genes). Calls `cor`.

Usage

```
build_coexp_network(exprs, gene.list, method = "spearman", flag = "rank")
```

Arguments

`exprs`	matrix of expression data
`gene.list`	array of gene labels
`method`	correlation method to use, default Spearman's rho
`flag`	string to indicate if the network should be ranked

Value

net Matrix symmetric

Examples

```
exprs <- matrix( rnorm(1000), ncol=10,byrow=TRUE)
gene.list <- paste('gene',1:100, sep='')
sample.list <- paste('sample',1:10, sep='')
rownames(exprs) <- gene.list
colnames(exprs) <- sample.list
network <- build_coexp_network(exprs, gene.list)
```

build_semantic_similarity_network *Builds a semantic similarity network*

Description

The function builds a semantic similarity network given a data and labels

Usage

```
build_semantic_similarity_network(genes.labels, genes)
```

Arguments

`genes.labels`	matrix with rows as genes and columns as a function/label
`genes`	array of gene IDs

Value

net Numeric value

Examples

```
genes.labels <- matrix( sample(c(0,1), 100, replace=TRUE),ncol=10,nrow=10)
rownames(genes.labels) <- 1:10
genes <- 1:10
net <- build_semantic_similarity_network(genes.labels, genes)
```

`build_weighted_network`

Builds a weighted network

Description

The function creates a gene-by-gene matrix with binary entries indicating interaction (1) or no interaction (0) between the genes.

Usage

```
build_weighted_network(data, list)
```

Arguments

`data`	3-column matrix, each row a pair indicating a relationship or interaction, and the last column the weight
`list`	string array of genes/labels/ids

Value

net matrix characterizing interactions

Examples

```
data <- cbind(edgeA=c('gene1','gene2'),edgeB=c('gene3','gene3'), weight=c(0.5, 0.9))
list <- c('gene1','gene2','gene3')
network <- build_weighted_network(data,list)
```

calculate_multifunc *Performing multifunctionality analysis*

Description

The function performs multifunctionality analysis ([1]) for a set of annotated genes and creates a rank based optimallist. For annotations use an ontology that is large enough to serve as a prior (e.g. GO, Phenocarta).

Usage

```
calculate_multifunc(genes.labels)
```

Arguments

genes.labels	Annotation matrix

Value

gene.mfs Returns matrix with evaluation of gene function prediction by given labels:

Examples

```
genes.labels <- matrix( sample(c(0,1), 100, replace=TRUE),ncol=10,nrow=10)
rownames(genes.labels) = paste('gene', 1:10, sep='')
colnames(genes.labels) = paste('label', 1:10, sep='')
mf <- calculate_multifunc(genes.labels)
```

conv_smoother *Plot smoothed curve*

Description

The function plots a smoothed curve using the convolve function.

Usage

```
conv_smoother(X, Y, window, raw = FALSE, output = FALSE, ...)
```

Arguments

X	numeric array
Y	numeric array
window	numeric value indicating size of window to use
raw	boolean
output	boolean
...	other input into the plot function

Value

smoothed X,Y and std Y matrix

Examples

```
x <- 1:1000
y <- rnorm(1000)
conv <- conv_smoother(x,y,10)
```

`example_annotations` *Example of annotations*

Description

This dataset includes

`example_binary_network` *Example of binary network*

Description

This dataset includes

Format

Matrices and vectors

`example_coexpression` *Example of binary network*

Description

This dataset includes

Format

Matrices and vectors

example_neighbor_voting *Example of binary network*

Description

This dataset includes

Format

entrezID chromosomal start position, in base pairs

name HUGO gene identifier

species species

disease disease

extend_network *Builds an extended network from a binary network*

Description

The function extends a binary network by using the inverse of the path length between nodes as a weighted edge

Usage

```
extend_network(net, max = 6)
```

Arguments

net	matrix binary and symmetric
max	numeric maximum number of jumps

Value

ext_net matrix dense and symmetric

Examples

```
net <- matrix( sample(c(0,1),36, replace=TRUE), nrow=6,byrow=TRUE)
ext_net <- extend_network(net)
```

filter_network *Filter on matrix*

Description

The function filters out the rows or columns of a matrix such that the size of the group is exclusively between given min and max values

Usage

```
filter_network(network, flag = 1, min = 0, max = 1, ids = NA)
```

Arguments

network	numeric matrix
flag	numeric 1 for row filtering, 2 for column filtering
min	numeric value
max	numeric value
ids	array to filter on

Value

network numeric matrix

Examples

```
net <- matrix( rnorm(10000), nrow=100)
filt_net <- filter_network(net,1,10,100)
```

filter_network_cols *Filter on columns*

Description

The function filters out the columns of a matrix such that the size of the group is exclusively between given min and max values

Usage

```
filter_network_cols(network, min = 0, max = 1, ids = NA)
```

Arguments

network	numeric matrix
min	numeric value
max	numeric value
ids	array

Value

network numeric matrix

Examples

```
genes.labels <- matrix( sample( c(0,1), 10000, replace=TRUE), nrow=100)
rownames(genes.labels) = paste('gene', 1:100, sep='')
colnames(genes.labels) = paste('function', 1:100, sep='')
genes.labels <- filter_network_cols(genes.labels,50,200)

genes.labels <- matrix( sample( c(0,1), 10000, replace=TRUE), nrow=100)
rownames(genes.labels) = paste('gene', 1:100, sep='')
colnames(genes.labels) = paste('function', 1:100, sep='')
genes.labels <- filter_network_cols(genes.labels,ids = paste('function', 1:20, sep=''))
```

---

filter_network_rows *Filter on rows*

Description

The function filters out the rows of a matrix such that the size of the group is exclusively between given min and max values

Usage

```
filter_network_rows(network, min = 0, max = 1, ids = NA)
```

Arguments

network	numeric matrix
min	numeric value
max	numeric value
ids	array to filter on

Value

network numeric matrix

Examples

```
genes.labels <- matrix( sample( c(0,1), 10000, replace=TRUE), nrow=100)
rownames(genes.labels) = paste('gene', 1:100, sep='')
colnames(genes.labels) = paste('function', 1:100, sep='')
genes.labels <- filter_network_rows(genes.labels,50,200)

genes.labels <- matrix( sample( c(0,1), 10000, replace=TRUE), nrow=100)
rownames(genes.labels) = paste('gene', 1:100, sep='')
colnames(genes.labels) = paste('function', 1:100, sep='')
genes.labels <- filter_network_rows(genes.labels,ids = paste('gene', 1:20, sep=''))
```

filter_orthologs *Filter on orthologs*

Description

The function filters away the labels for the genes that are not in the orthologs list

Usage

```
filter_orthologs(annotations, genelist, orthologs)
```

Arguments

annotations	binary matrix
genelist	array of gene ids
orthologs	array to filter on

Value

annotations_filtered binary matrix

Examples

```
genes.labels <- matrix( sample( c(0,1), 1000, replace=TRUE), nrow=100)
rownames(genes.labels) = paste('gene', 1:100, sep='')
colnames(genes.labels) = paste('function', 1:10, sep='')
gene.list <- paste('gene', 1:100, sep='')
orthologs <- paste('gene', (1:50)*2, sep='')
genes.labels.filt <- filter_orthologs(genes.labels, gene.list, orthologs)
```

fmeasure *Fmeasure of precision-recall*

Description

The function calculates fmeasure for a given beta of a precision-recall curve

Usage

```
fmeasure(recall, precis, beta = 1)
```

Arguments

recall	numeric array
precis	numeric array
beta	numeric value, default is 1

Value

fmeasure Numeric value

Examples

```
labels <- c(rep(0,10))
labels[c(1,3,5)] <- 1
scores <- 10:1
prc <- get_prc(scores, labels)
fm <- fmeasure(prc[,1], prc[,2])
```

---

genes *Genes from BIOGRID v3.4.126*

Description

An array containing identifiers for genes in biogrid

Format

Array

genes List of Entrez identifiers

@source http://thebiogrid.org/

---

get_auc *Calculates the area under a curve*

Description

The function calculates the area under the curve defined by x and y

Usage

```
get_auc(x, y)
```

Arguments

x	numeric array
y	numeric array

Value

auc numeric value

Examples

```
x <- 1:100
y <- 1:100
auc <- get_auc(x,y)
```

get_biogrid *Downloading and filtering BIOGRID*

Description

The function downloads the specifed version of biogrid for a particular taxon

Usage

```
get_biogrid(species = "9606", version = "3.5.181", interactions = "physical")
```

Arguments

species	numeric taxon of species
version	string of biogrid version
interactions	string stating either physical or genetic interactions

Value

biogrid data.frame with interactions

get_counts *Get counts*

Description

The function formats the count distribution from the histogram function

Usage

```
get_counts(hist)
```

Arguments

hist	histogram

Value

x,y

Examples

```
x <- runif(1000)
counts <- get_counts( hist(x, plot=FALSE))
```

get_density *Get density*

Description

The function formats the density distribution from the histogram function

Usage

```
get_density(hist)
```

Arguments

hist	histogram

Value

array

Examples

```
x <- runif(1000)
density <- get_density( hist(x, plot=FALSE))
```

get_expression_data_gemma *Obtain expression matrix from the GEMMA database*

Description

The function downloads and parses the expression matrix from the GEMMA database, specified by the GEO ID

Usage

```
get_expression_data_gemma(gseid, filtered = "true")
```

Arguments

gseid	GEO ID of the expression experiment
filtered	flag to indicate whether or not the data is QC

Value

list of genes and the expression matrix

`get_expression_matrix_from_GEO` *Obtain expression matrix from GEO database*

Description

The function downloads and parses the expression matrix from the GEO file specified by the GEO ID

Usage

```
get_expression_matrix_from_GEO(gseid)
```

Arguments

`gseid`	GEO ID of the expression experiment

Value

list of genes and the expression matrix

`get_phenocarta` *Downloading and filtering Phenocarta*

Description

The function downloads the latest version of phenocarta

Usage

```
get_phenocarta(species = "human", type = "all")
```

Arguments

`species`	string
`type`	string

Value

data data.frame with phenocarta data

get_prc *Build precision-recall curve*

Description

The function calculates the recall and precision

Usage

```
get_prc(ranks, labels)
```

Arguments

ranks	numeric array
labels	binary array

Value

recall,precision numeric arrays

Examples

```
labels <- c(rep(0,10))
labels[c(1,3,5)] <- 1
scores <- 10:1
ranks <- rank(scores)
prc <- get_prc(ranks, labels)
```

get_roc *Build receiver operating characteristic curve*

Description

The function calculates the FPR and TRPR for the receiver operating characteristic (ROC)

Usage

```
get_roc(ranks, labels)
```

Arguments

ranks	numeric array
labels	binary array

Value

FPR,TPR numeric arrays

Examples

```
labels <- c(rep(0,10))
labels[c(1,3,5)] <- 1
scores <- 10:1
ranks <- rank(scores)
roc <- get_roc(ranks, labels)
```

GO.human *GO - human*

Description

A dataset of the gene GO associations

Format

A data frame with 2511938 rows and 4 variables:

name gene symbol

entrezID entrez identifier

GO gene ontology term ID

evidence evidence code

@source http://geneontology.org/

GO.mouse *GO - mouse*

Description

A dataset of the gene GO associations

Format

A data frame with 2086086 rows and 4 variables:

name gene symbol

entrezID entrez identifier

GO gene ontology term ID

evidence evidence code

@source http://geneontology.org/

GO.voc *Gene ontology vocabulary*

Description

A dataset of the gene ontology vocabulary

Format

A data frame with 42266 rows and 3 variables:

GOID GO identifier

term GO description

domain GO domain

@source http://geneontology.org/

make_annotations *Creating gene annotations*

Description

The function annotates a list of genes according to a given ontology. It creates a binary matrix associating genes (rows) with labels (columns).

Usage

```
make_annotations(data, listA, listB)
```

Arguments

data	2-column matrix, each row a pair indicating a relationship or interaction
listA	string array of genes
listB	string array of labels/functions

Value

net matrix binary

Examples

```
gene.list <- paste('gene', 1:100, sep='')
labels.list <- paste('labels', 1:10, sep='')
data <- matrix(0,nrow=100, ncol=2)
data[,1] <- sample(gene.list, 100, replace=TRUE)
data[,2] <- sample(labels.list, 100, replace=TRUE)
net <- make_annotations(data, gene.list, labels.list)
```

make_genelist *Creating list of all genes in the data set.*

Description

The function extracts the list of all genes in the data set

Usage

```
make_genelist(gene_data_interacting)
```

Arguments

gene_data_interacting	2-column matrix, each row a pair indicating a relationship or interaction

Value

list array of data labels

Examples

```
gene.list <- paste('gene', 1:100, sep='')
data <- matrix(0,nrow=100, ncol=2)
data[,1] <- sample(gene.list, 50, replace=TRUE)
data[,2] <- sample(gene.list, 50, replace=TRUE)
genes <- make_genelist(data)
```

make_gene_network *Creating gene-by-gene network*

Description

The function creates a gene-by-gene matrix with binary entries indicating interaction (1) or no interaction (0) between the genes.

Usage

```
make_gene_network(data, list)
```

Arguments

data	2-column matrix, each row a pair indicating a relationship or interaction
list	string array of genes

Value

net matrix binary characterizing interactions

Examples

```
gene.list <- paste('gene', 1:100, sep='')
data <- matrix(0,nrow=100, ncol=2)
data[,1] <- sample(gene.list, 100)
data[,2] <- sample(gene.list, 100)
net <- make_gene_network(data, gene.list)
```

`make_transparent` *Make a color transparent (Taken from an answer on StackOverflow by Nick Sabbe)*

Description

Make a color transparent (Taken from an answer on StackOverflow by Nick Sabbe)

Usage

```
make_transparent(color, alpha = 100)
```

Arguments

`color`	color number, string or hexidecimal code
`alpha`	numeric transparency

Value

someColor rgb

`neighbor_voting` *Evaluating Gene Function Prediction*

Description

The function performs gene function prediction based on 'guilt by association' using cross validation ([1]). Performance and significance are evaluated by calculating the AUROC or AUPRC of each functional group.

Usage

```
neighbor_voting(
  genes.labels,
  network,
  nFold = 3,
  output = "AUROC",
  FLAG_DRAW = FALSE
)
```

Arguments

genes.labels	numeric array
network	numeric array symmetric, gene-by-gene matrix
nFold	numeric value, default is 3
output	string, default is AUROC
FLAG_DRAW	binary flag to draw roc plot

Value

scores numeric matrix with a row for each gene label and columns auc: the average area under the ROC or PR curve for the neighbor voting predictor across cross validation replicates avg_node_degree: the average node degree degree_null_auc: the area the ROC or PR curve for the node degree predictor

Examples

```
genes.labels <- matrix( sample( c(0,1), 1000, replace=TRUE), nrow=100)
rownames(genes.labels) = paste('gene', 1:100, sep='')
colnames(genes.labels) = paste('function', 1:10, sep='')
net <- cor( matrix( rnorm(10000), ncol=100), method='spearman')
rownames(net) <- paste('gene', 1:100, sep='')
colnames(net) <- paste('gene', 1:100, sep='')

aurocs <- neighbor_voting(genes.labels, net, output = 'AUROC')

avgprcs <- neighbor_voting(genes.labels, net, output = 'PR')
```

---

node_degree *Calculate node degree*

Description

The function calculates the node degree of a network

Usage

```
node_degree(net)
```

Arguments

net	numeric matrix

Value

node_degree numeric array

Examples

```
net <- cor( matrix(rnorm(1000), ncol=10))
n <- 10
net <- matrix(rank(net, na.last = 'keep', ties.method = 'average'), nrow = n, ncol = n)
net <- net/max(net, na.rm=TRUE)
nd <- node_degree(net)
```

---

ortho *Gene orthologs*

Description

A list containing identifiers for the subsets of gene orthologs

Format

List orthologs for 5 species

dros List of Entrez identifiers, Drosophila

celeg List of Entrez identifiers, C. elegans

yeast List of Entrez identifiers, Yeast

mouse List of Entrez identifiers, Mouse

zf List of Entrez identifiers, Zebrafish

@source http://useast.ensembl.org/index.html/

---

pheno *Phenocarta*

Description

A dataset of gene disease associations

Format

A data frame with 142272 rows and 4 variables:

entrezID chromosomal start position, in base pairs

name HUGO gene identifier

species species

disease disease

@source http://www.chibi.ubc.ca/Gemma/phenotypes.html

plot_densities *Plot densities*

Description

The function plots multiple density curves and compares their modes

Usage

```
plot_densities(
  hists,
  id,
  col = c("lightgrey"),
  xlab = "",
  ylab = "Density",
  mode = "hist"
)
```

Arguments

hists	list of histogram objects or density objects
id	string
col	color for shading
xlab	string x-axis label
ylab	string y-axis label
mode	flag indicating histogram or density

Value

null

Examples

```
aurocsA <- density((runif(1000)+runif(1000)+runif(1000)+runif(1000))/4)
aurocsB <- density((runif(1000)+runif(1000)+runif(1000))/3)
aurocsC <- density(runif(1000))
hists <- list(aurocsA, aurocsB, aurocsC)
temp <- plot_densities(hists,'', mode='density')
```

plot_density_compare *Plot density comparisons*

Description

The function plots two density curves and compares their modes

Usage

```
plot_density_compare(
  aucA,
  aucB,
  col = "lightgrey",
  xlab = "AUROC (neighbor voting)",
  ylab = "Density",
  mode = TRUE
)
```

Arguments

aucA	numeric array of aurocs
aucB	numeric array of aurocs
col	color of lines
xlab	string label
ylab	string label
mode	boolean to plot mode or mean

Value

null

Examples

```
aurocsA <- (runif(1000)+runif(1000)+runif(1000)+runif(1000))/4
aurocsB <- runif(1000)
plot_density_compare(aurocsA, aurocsB)
```

plot_distribution *Plot distribution histogram*

Description

The function plots a the distribution of AUROCs

Usage

```
plot_distribution(
  auc,
  b = 20,
  col = "lightgrey",
  xlab = "",
  ylab = "Density",
  xlim = c(0.4, 1),
  ylim = c(0, 5),
  med = TRUE,
  avg = TRUE,
  density = TRUE,
  bars = FALSE
)
```

Arguments

auc	numeric aucs
b	array of breaks
col	color of line
xlab	string label
ylab	string label
xlim	range of values for xaxis
ylim	range of values for yaxis
med	boolean to plot median auc
avg	boolean to plot average auc
density	boolean
bars	boolena for barplot

Value

auc list and quartiles

Examples

```
aurocs <- (runif(1000)+runif(1000)+runif(1000)+runif(1000))/4
d <- plot_distribution(aurocs)
```

---

plot_network_heatmap *Plot network heatmap*

Description

The function draws a heatmap to visualize a network

Usage

```
plot_network_heatmap(net, colrs)
```

Arguments

net	a numeric matrix of edge weights
colrs	a range of colors to plot the network

Value

null

Examples

```
network <- cor(matrix( rnorm(10000), nrow=100))
plot_network_heatmap(network)
```

---

plot_prc *Plot precision recall curve*

Description

The function calculates the precision and recall and plots the curve

Usage

```
plot_prc(scores, labels)
```

Arguments

scores	numeric array
labels	binary array

Value

prc numeric arrays

Examples

```
labels <- c(rep(0,10))
labels[c(1,3,5)] <- 1
scores <- 10:1
roc <- plot_prc(scores, labels)
```

plot_roc *Plot receiver operating characteristic curve*

Description

The function calculates the FPR and TRPR for the receiver operating characteristic (ROC) and plots the curve

Usage

```
plot_roc(scores, labels)
```

Arguments

scores	numeric array
labels	binary array

Value

FPR,TPR numeric arrays

Examples

```
labels <- c(rep(0,10))
labels[c(1,3,5)] <- 1
scores <- 10:1
roc <- plot_roc(scores, labels)
```

plot_roc_overlay *Plot ROC overlay*

Description

The function plots a density overlay of ROCs given the scores and labels

Usage

```
plot_roc_overlay(scores.mat, labels.mat, nbins = 100)
```

Arguments

scores.mat	numeric array
labels.mat	numeric array
nbins	numeric value

Value

list of Z(matrix) and roc_sum (average ROC curve)

Examples

```
genes.labels <- matrix( c(rep(1, 1000), rep(0,9000)), nrow=1000, byrow=TRUE)
rownames(genes.labels) = paste('gene', 1:1000, sep='')
colnames(genes.labels) = paste('function', 1:10, sep='')

scores <- matrix( rnorm(10000), nrow=1000)
scores <- apply(scores, 2, rank)
rownames(scores) = paste('gene', 1:1000, sep='')
colnames(scores) = paste('function', 1:10, sep='')

z <- plot_roc_overlay(scores, genes.labels)
```

`plot_value_compare` *Plot value comparisons*

Description

The function plots a scatter

Usage

```
plot_value_compare(
  aucA,
  aucB,
  xlab = "AUROC",
  ylab = "AUROC",
  xlim = c(0, 1),
  ylim = c(0, 1)
)
```

Arguments

`aucA`	numeric array of aucs
`aucB`	numeric array of aucs
`xlab`	string label
`ylab`	string label
`xlim`	range of values for xaxis
`ylim`	range of values for yaxis

Value

null

predictions *Performing Gene Function Prediction*

Description

The function performs gene function prediction on the whole data set using the 'guilt by association'-principle ([1]).

Usage

```
predictions(genes.labels, network)
```

Arguments

genes.labels	numeric array
network	numeric array symmetric, gene-by-gene matrix

Value

scores numeric matrix

Examples

```
genes.labels <- matrix( sample( c(0,1), 1000, replace=TRUE), nrow=100)
rownames(genes.labels) = paste('gene', 1:100, sep='')
colnames(genes.labels) = paste('function', 1:10, sep='')
net <- cor( matrix( rnorm(10000), ncol=100), method='spearman')
rownames(net) <- paste('gene', 1:100, sep='')
colnames(net) <- paste('gene', 1:100, sep='')

preds <- predictions(genes.labels, net)
```

repmat *Rep function for matrices*

Description

The function generates a matrix by binding the columns and rows

Usage

```
repmat(X, m, n)
```

Arguments

X	numeric matrix
m	numeric value, repeat rows m times
n	numeric value, repeat columns n times

Value

list of genes and the expression matrix

Examples

```
genes.labels <- matrix( sample( c(0,1), 1000, replace=TRUE), nrow=100)
expand <- repmat( genes.labels, 1,2)
```

---

run_GBA *Performing 'Guilt by Association' Analysis*

Description

The function runs and evaluates gene function prediction based on the 'guilt by association'-principle using neighbor voting (neighbor_voting) [1]. As a measure of performance and significance of results, AUCs of all evaluated functional groups are calculated.

Usage

```
run_GBA(network, labels, min = 20, max = 1000, nfold = 3)
```

Arguments

network	numeric array symmetric, gene-by-gene matrix
labels	numeric array
min	numeric value to limit gene function size
max	numeric value to limit gene function size
nfold	numeric value, default is 3

Value

list roc.sub, genes, auroc

Examples

```
genes.labels <- matrix( sample( c(0,1), 1000, replace=TRUE), nrow=100)
rownames(genes.labels) = paste('gene', 1:100, sep='')
colnames(genes.labels) = paste('function', 1:10, sep='')
net <- cor( matrix( rnorm(10000), ncol=100), method='spearman')
rownames(net) <- paste('gene', 1:100, sep='')
colnames(net) <- paste('gene', 1:100, sep='')

gba <- run_GBA(net, genes.labels, min=10)
```

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