

# Package ‘EGAD’

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**Type** Package

**Title** Extending guilt by association by degree

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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.

**License** GPL-2

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---

<i>assortativity</i>	<i>Calculating network assortativity</i>
----------------------	--

---

### 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)
```

---

<i>attr.human</i>	<i>Human GENCODE annotations (v22)</i>
-------------------	--

---

### 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/](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/](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M7/)

---

auc_multifunc	<i>Calculating AUC for functional groups from ranked lists</i>
---------------	--

---

**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 <a href="#">calculate_multifunc</a> ).

**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	<i>Area under the precision recall curve</i>
-------	--

---

**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	<i>Area under the receiver operating characteristic curve</i>
----------------	---

---

**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	<i>BIOGRID v3.4.126</i>
---------	-------------------------

---

**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 coefficients 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	<i>Builds a coexpression network given a GEO ID</i>
-------------------	---

---

**Description**

The function generates a dense coexpression network from expression data stored in GEO. The expression data is downloaded from GEO. Correlation coefficients 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 coefficients 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

<code>exprs</code>	matrix of expression data
<code>gene.list</code>	array of gene labels
<code>method</code>	correlation method to use, default Spearman's rho
<code>flag</code>	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

<code>genes.labels</code>	matrix with rows as genes and columns as a function/label
<code>genes</code>	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	<i>Performing multifunctionality analysis</i>
---------------------	---

---

**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	<i>Plot smoothed curve</i>
---------------	----------------------------

---

**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	<i>Filter on matrix</i>
----------------	-------------------------

---

**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	<i>Filter on columns</i>
---------------------	--------------------------

---

**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 specified version of biogrid for a particular taxon

**Usage**

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

**Arguments**

<code>species</code>	numeric taxon of species
<code>version</code>	string of biogrid version
<code>interactions</code>	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**

<code>hist</code>	histogram
-------------------	-----------

**Value**

x,y

**Examples**

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

---

get_density	<i>Get density</i>
-------------	--------------------

---

**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	<i>Obtain expression matrix from the GEMMA database</i>
---------------------------	---

---

**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	<i>Gene ontology vocabulary</i>
--------	---------------------------------

---

**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_annotatations	<i>Creating gene annotations</i>
--------------------	----------------------------------

---

**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_annotatations(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_annotatations(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	<i>Make a color transparent (Taken from an answer on StackOverflow by Nick Sabbe)</i>
------------------	---

---

**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 hexadecimal code
alpha	numeric transparency

**Value**

someColor rgb

---

neighbor_voting	<i>Evaluating Gene Function Prediction</i>
-----------------	--

---

**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	<i>Plot densities</i>
----------------	-----------------------

---

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

### Value

null

### Examples

```
auropsA <- (runif(1000)+runif(1000)+runif(1000)+runif(1000))/4  
auropsB <- runif(1000)  
plot_density_compare(auropsA, auropsB)
```

---

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	boolean 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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