

# Package ‘EGAD’

July 27, 2025

**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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## Contents

|                                             |    |
|---------------------------------------------|----|
| assortativity . . . . .                     | 3  |
| attr.human . . . . .                        | 4  |
| attr.mouse . . . . .                        | 4  |
| auc_multifunc . . . . .                     | 5  |
| auprc . . . . .                             | 6  |
| auroc_analytic . . . . .                    | 6  |
| biogrid . . . . .                           | 7  |
| build_binary_network . . . . .              | 7  |
| build_coexp_expressionSet . . . . .         | 8  |
| build_coexp_GEOID . . . . .                 | 9  |
| build_coexp_network . . . . .               | 9  |
| build_semantic_similarity_network . . . . . | 10 |
| build_weighted_network . . . . .            | 11 |
| calculate_multifunc . . . . .               | 11 |
| conv_smoother . . . . .                     | 12 |
| example_annotations . . . . .               | 13 |
| example_binary_network . . . . .            | 13 |
| example_coexpression . . . . .              | 13 |
| example_neighbor_voting . . . . .           | 13 |
| extend_network . . . . .                    | 14 |
| filter_network . . . . .                    | 14 |
| filter_network_cols . . . . .               | 15 |
| filter_network_rows . . . . .               | 16 |
| filter_orthologs . . . . .                  | 17 |
| fmeasure . . . . .                          | 17 |
| genes . . . . .                             | 18 |
| get_auc . . . . .                           | 18 |
| get_biogrid . . . . .                       | 19 |
| get_counts . . . . .                        | 19 |
| get_density . . . . .                       | 20 |
| get_expression_data_gemma . . . . .         | 20 |
| get_expression_matrix_from_GEO . . . . .    | 21 |
| get_phenocarta . . . . .                    | 21 |
| get_prc . . . . .                           | 22 |
| get_roc . . . . .                           | 22 |
| GO.human . . . . .                          | 23 |
| GO.mouse . . . . .                          | 23 |
| GO.voc . . . . .                            | 24 |
| make_annotations . . . . .                  | 24 |
| make_genelist . . . . .                     | 25 |
| make_gene_network . . . . .                 | 25 |
| make_transparent . . . . .                  | 26 |
| neighbor_voting . . . . .                   | 26 |
| node_degree . . . . .                       | 27 |
| ortho . . . . .                             | 28 |
| pheno . . . . .                             | 29 |

assortativity

3

plot\_densities . . . . .

29

plot\_density\_compare . . . . .

30

plot\_distribution . . . . .

31

plot\_network\_heatmap . . . . .

32

plot\_prc . . . . .

33

plot\_roc . . . . .

33

plot\_roc\_overlay . . . . .

34

plot\_value\_compare . . . . .

35

predictions . . . . .

35

repmat . . . . .

36

run\_GBA . . . . .

37

Index

38

---

|               |                                          |
|---------------|------------------------------------------|
| assortativity | <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)
```

---

|            |                                        |
|------------|----------------------------------------|
| attr.human | <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 | <i>Mouse GENCODE annotations (M7)</i> |
|------------|---------------------------------------|

---

### 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

*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 | <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

*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 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 | <i>Builds a coexpression network from an expressionSet</i> |
|---------------------|------------------------------------------------------------|

---

### 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

|           |                                                    |
|-----------|----------------------------------------------------|
| 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**

|                   |                                                                                                           |
|-------------------|-----------------------------------------------------------------------------------------------------------|
| <code>data</code> | 3-column matrix, each row a pair indicating a relationship or interaction, and the last column the weight |
| <code>list</code> | 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**

|                           |                   |
|---------------------------|-------------------|
| <code>genes.labels</code> | 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 | <i>Example of annotations</i> |
|---------------------|-------------------------------|

---

**Description**

This dataset includes

---

|                        |                                  |
|------------------------|----------------------------------|
| example_binary_network | <i>Example of binary network</i> |
|------------------------|----------------------------------|

---

**Description**

This dataset includes

**Format**

Matrices and vectors

---

|                      |                                  |
|----------------------|----------------------------------|
| example_coexpression | <i>Example of binary network</i> |
|----------------------|----------------------------------|

---

**Description**

This dataset includes

**Format**

Matrices and vectors

---

|                         |                                  |
|-------------------------|----------------------------------|
| example_neighbor_voting | <i>Example of binary network</i> |
|-------------------------|----------------------------------|

---

**Description**

This dataset includes

**Format**

**entrezID** chromosomal start position, in base pairs  
**name** HUGO gene identifier  
**species** species  
**disease** disease

---

|                |                                                         |
|----------------|---------------------------------------------------------|
| extend_network | <i>Builds an extended network from a binary network</i> |
|----------------|---------------------------------------------------------|

---

### 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 | <i>Filter on rows</i> |
|---------------------|-----------------------|

---

## 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 | <i>Filter on orthologs</i> |
|------------------|----------------------------|

---

**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 | <i>Fmeasure of precision-recall</i> |
|----------|-------------------------------------|

---

**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 | <i>Genes from BIOGRID v3.4.126</i> |
|-------|------------------------------------|

---

**Description**

An array containing identifiers for genes in biogrid

**Format**

Array

**genes** List of Entrez identifiers

@source <http://thebiogrid.org/>

---

|         |                                          |
|---------|------------------------------------------|
| get_auc | <i>Calculates the area under a curve</i> |
|---------|------------------------------------------|

---

**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**

|              |                                                        |
|--------------|--------------------------------------------------------|
| 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 | <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 | <i>Build precision-recall curve</i> |
|---------|-------------------------------------|

---

**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 | <i>Build receiver operating characteristic curve</i> |
|---------|------------------------------------------------------|

---

**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_annotations | <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_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 | <i>Creating list of all genes in the data set.</i> |
|---------------|----------------------------------------------------|

---

**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 | <i>Creating gene-by-gene network</i> |
|-------------------|--------------------------------------|

---

**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 | <i>Phenocarta</i> |
|-------|-------------------|

---

**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 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 | <i>Plot distribution histogram</i> |
|-------------------|------------------------------------|

---

**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 | <i>Plot network heatmap</i> |
|----------------------|-----------------------------|

---

**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 | <i>Plot precision recall curve</i> |
|----------|------------------------------------|

---

**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 | <i>Plot receiver operating characteristic curve</i> |
|----------|-----------------------------------------------------|

---

**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 | <i>Plot ROC overlay</i> |
|------------------|-------------------------|

---

**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 | <i>Plot value comparisons</i> |
|--------------------|-------------------------------|

---

**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 | <i>Performing Gene Function Prediction</i> |
|-------------|--------------------------------------------|

---

**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**

|                      |                                              |
|----------------------|----------------------------------------------|
| <code>network</code> | numeric array symmetric, gene-by-gene matrix |
| <code>labels</code>  | numeric array                                |
| <code>min</code>     | numeric value to limit gene function size    |
| <code>max</code>     | numeric value to limit gene function size    |
| <code>nfold</code>   | 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)
```

# Index

- \* **AUC**
  - auc\_multifunc, 5
- \* **AUROC**
  - plot\_distribution, 31
- \* **ExpressionSet**
  - build\_coexp\_expressionSet, 8
  - build\_coexp\_network, 9
- \* **FPR**
  - get\_roc, 22
  - plot\_roc, 33
- \* **GEMMA**
  - get\_expression\_data\_gemma, 20
- \* **GEO**
  - build\_coexp\_GEOID, 9
  - get\_expression\_data\_gemma, 20
  - get\_expression\_matrix\_from\_GEO, 21
- \* **GSE**
  - build\_coexp\_GEOID, 9
  - get\_expression\_data\_gemma, 20
  - get\_expression\_matrix\_from\_GEO, 21
- \* **PRC**
  - plot\_prc, 33
- \* **ROC**
  - auroc\_analytic, 6
  - get\_roc, 22
  - plot\_distribution, 31
  - plot\_roc, 33
  - plot\_roc\_overlay, 34
- \* **TPR**
  - get\_roc, 22
  - plot\_roc, 33
- \* **analytic**
  - auroc\_analytic, 6
- \* **annotations**
  - filter\_orthologs, 17
  - make\_annotations, 24
- \* **area**
  - auprc, 6
  - auroc\_analytic, 6
- get\_auc, 18
- \* **association**
  - neighbor\_voting, 26
  - predictions, 35
  - run\_GBA, 37
- \* **assortativity**
  - assortativity, 3
- \* **a**
  - get\_auc, 18
- \* **biogrid**
  - get\_biogrid, 19
- \* **by**
  - neighbor\_voting, 26
  - predictions, 35
  - run\_GBA, 37
- \* **characteristic**
  - auroc\_analytic, 6
  - get\_roc, 22
  - plot\_roc, 33
- \* **coexpression**
  - build\_coexp\_expressionSet, 8
  - build\_coexp\_GEOID, 9
  - build\_coexp\_network, 9
- \* **cross**
  - neighbor\_voting, 26
  - run\_GBA, 37
- \* **curve**
  - get\_auc, 18
- \* **degree**
  - node\_degree, 27
- \* **dense**
  - build\_coexp\_expressionSet, 8
  - build\_coexp\_GEOID, 9
  - build\_coexp\_network, 9
- \* **density**
  - plot\_densities, 29
- \* **distribution**
  - plot\_distribution, 31
- \* **download**

- get\_biogrid, 19
- get\_phenocarta, 21
- \* **evaluation**
  - calculate\_multifunc, 11
  - neighbor\_voting, 26
  - run\_GBA, 37
- \* **evaluation**
  - auc\_multifunc, 5
- \* **experiment**
  - get\_expression\_data\_gemma, 20
  - get\_expression\_matrix\_from\_GEO, 21
- \* **expressionSet**
  - build\_coexp\_expressionSet, 8
  - build\_coexp\_network, 9
- \* **expression**
  - get\_expression\_data\_gemma, 20
  - get\_expression\_matrix\_from\_GEO, 21
- \* **extended**
  - extend\_network, 14
- \* **extract**
  - make\_genelist, 25
- \* **filter**
  - filter\_network, 14
  - filter\_network\_cols, 15
  - filter\_network\_rows, 16
  - filter\_orthologs, 17
- \* **fmeasure**
  - fmeasure, 17
- \* **function**
  - calculate\_multifunc, 11
  - make\_annotations, 24
  - neighbor\_voting, 26
  - predictions, 35
  - run\_GBA, 37
- \* **gene-by-gene**
  - build\_binary\_network, 7
  - build\_weighted\_network, 11
  - make\_gene\_network, 25
- \* **gene**
  - calculate\_multifunc, 11
  - make\_annotations, 24
  - make\_genelist, 25
  - neighbor\_voting, 26
  - predictions, 35
  - run\_GBA, 37
- \* **guilt**
  - neighbor\_voting, 26
  - predictions, 35
- run\_GBA, 37
- \* **heatmap**
  - plot\_network\_heatmap, 32
- \* **histogram**
  - get\_counts, 19
  - get\_density, 20
- \* **igraph**
  - extend\_network, 14
- \* **image**
  - plot\_network\_heatmap, 32
- \* **interaction**
  - build\_binary\_network, 7
  - build\_weighted\_network, 11
  - make\_gene\_network, 25
- \* **jaccard**
  - build\_semantic\_similarity\_network, 10
- \* **labels**
  - make\_annotations, 24
- \* **length**
  - extend\_network, 14
- \* **list**
  - make\_genelist, 25
- \* **matrix**
  - repmat, 36
- \* **mean**
  - get\_auc, 18
- \* **metric**
  - auprc, 6
  - auroc\_analytic, 6
  - get\_roc, 22
  - node\_degree, 27
  - plot\_prc, 33
  - plot\_roc, 33
- \* **multifunctionality**
  - auc\_multifunc, 5
- \* **neighbor**
  - neighbor\_voting, 26
  - predictions, 35
  - run\_GBA, 37
- \* **network**
  - assortativity, 3
  - build\_binary\_network, 7
  - build\_coexp\_expressionSet, 8
  - build\_coexp\_GEOID, 9
  - build\_coexp\_network, 9
  - build\_semantic\_similarity\_network, 10

- build\_weighted\_network, 11
  - extend\_network, 14
  - filter\_network, 14
  - filter\_network\_cols, 15
  - filter\_network\_rows, 16
  - make\_gene\_network, 25
  - node\_degree, 27
  - plot\_network\_heatmap, 32
- \* **node**
  - node\_degree, 27
- \* **ontology**
  - calculate\_multifunc, 11
  - make\_annotations, 24
- \* **operating**
  - auroc\_analytic, 6
  - get\_roc, 22
  - plot\_roc, 33
- \* **orthologs**
  - filter\_orthologs, 17
- \* **overlay**
  - plot\_roc\_overlay, 34
- \* **path**
  - extend\_network, 14
- \* **phenocarta**
  - get\_phenocarta, 21
- \* **plot**
  - conv\_smoother, 12
  - get\_density, 20
  - plot\_densities, 29
  - plot\_density\_compare, 30
  - plot\_distribution, 31
  - plot\_network\_heatmap, 32
  - plot\_prc, 33
  - plot\_roc\_overlay, 34
  - plot\_value\_compare, 35
- \* **precision-recall**
  - auprc, 6
  - fmeasure, 17
- \* **precision**
  - get\_prc, 22
  - plot\_prc, 33
- \* **precision-recall**
  - get\_prc, 22
- \* **prediction**
  - calculate\_multifunc, 11
  - neighbor\_voting, 26
  - predictions, 35
  - run\_GBA, 37
- \* **properties**
  - assortativity, 3
- \* **recall**
  - get\_prc, 22
  - plot\_prc, 33
- \* **receiver**
  - auroc\_analytic, 6
  - get\_roc, 22
  - plot\_roc, 33
- \* **repeat**
  - repmat, 36
- \* **repmat**
  - repmat, 36
- \* **rolling**
  - get\_auc, 18
- \* **rows**
  - filter\_network, 14
  - filter\_network\_cols, 15
  - filter\_network\_rows, 16
- \* **semantic**
  - build\_semantic\_similarity\_network, 10
- \* **shortest**
  - extend\_network, 14
- \* **similarity**
  - build\_semantic\_similarity\_network, 10
- \* **smooth**
  - conv\_smoother, 12
- \* **topology**
  - assortativity, 3
  - node\_degree, 27
- \* **to**
  - make\_annotations, 24
- \* **under**
  - get\_auc, 18
- \* **validation**
  - neighbor\_voting, 26
  - run\_GBA, 37
- \* **voting**
  - neighbor\_voting, 26
  - predictions, 35
  - run\_GBA, 37
- assortativity, 3
- attr.human, 4
- attr.mouse, 4
- auc\_multifunc, 5
- auprc, 6

auroc\_analytic, 6

biogrid, 7

build\_binary\_network, 7

build\_coexp\_expressionSet, 8

build\_coexp\_GEOID, 9

build\_coexp\_network, 8, 9, 9

build\_semantic\_similarity\_network, 10

build\_weighted\_network, 11

calculate\_multifunc, 5, 11

conv\_smoother, 12

convolve, 12

cor, 9

example\_annotations, 13

example\_binary\_network, 13

example\_coexpression, 13

example\_neighbor\_voting, 13

extend\_network, 14

filter\_network, 14

filter\_network\_cols, 15

filter\_network\_rows, 16

filter\_orthologs, 17

fmeasure, 17

genes, 18

get\_auc, 18

get\_biogrid, 19

get\_counts, 19

get\_density, 20

get\_expression\_data\_gemma, 20

get\_expression\_matrix\_from\_GEO, 9, 21

get\_phenocarta, 21

get\_prc, 22

get\_roc, 22

GO.human, 23

GO.mouse, 23

GO.voc, 24

make\_annotations, 24

make\_gene\_network, 25

make\_genelist, 25

make\_transparent, 26

neighbor\_voting, 26, 37

node\_degree, 27

ortho, 28

pheno, 29

plot\_densities, 29

plot\_density\_compare, 30

plot\_distribution, 31

plot\_network\_heatmap, 32

plot\_prc, 33

plot\_roc, 33

plot\_roc\_overlay, 34

plot\_value\_compare, 35

predictions, 35

repmat, 36

run\_GBA, 37