

# Package ‘RITAN’

November 21, 2025

**Type** Package

**Title** Rapid Integration of Term Annotation and Network resources

**Version** 1.35.0

**Description** Tools for comprehensive gene set enrichment and extraction of multi-resource high confidence subnetworks. RITAN facilitates bioinformatic tasks for enabling network biology research.

**LazyData** TRUE

**Depends** R (>= 4.0),

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'interconnectivity\_functions.R'

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**License** file LICENSE

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**Author** Michael Zimmermann [aut, cre]

**Maintainer** Michael Zimmermann <mtzimmermann@mcw.edu>

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|          |                 |
|----------|-----------------|
| as.graph | <i>as.graph</i> |
|----------|-----------------|

---

Description

wrapper to convert a data.frame from RITAN an igraph graph object

Usage

as.graph(mat, p1 = 1, p2 = 3, ...)

Arguments

- |     |                                              |
|-----|----------------------------------------------|
| mat | matrix or data frame describing a network    |
| p1  | [1] column of first interactor               |
| p2  | [3] column of second interactor              |
| ... | further options passed on to igraph::graph() |

**Value**

igraph object

**Examples**

```
## Not run:  
G <- as.graph(network_list$PID)  
  
## End(Not run)
```

---

|                     |                            |
|---------------------|----------------------------|
| check_any_net_input | <i>check_any_net_input</i> |
|---------------------|----------------------------|

---

**Description**

A Quality Control function. This function applies check\_net\_input() to all available resources (default).

**Usage**

```
check_any_net_input(set, resources = names(network_list))
```

**Arguments**

|           |                                                      |
|-----------|------------------------------------------------------|
| set       | An input list of genes to check against references.  |
| resources | The collection of network resources to check within. |

**Value**

Logical vector indicating if the genes in "set" are within ANY of the resources.

**Examples**

```
#' ## Check if genes in myGeneSet are annotated by any resource in "network_list" (default).  
library(RITANData)  
myGeneSet <- c('BRCA1', 'RAD51C', 'VAV1', 'HRAS', 'ABCC1', 'CYP1B1', 'CYP3A5')  
yorn <- check_any_net_input( myGeneSet )  
print(yorn)
```

---

|                 |                        |
|-----------------|------------------------|
| check_net_input | <i>check_net_input</i> |
|-----------------|------------------------|

---

## Description

A Quality Control function. This function will compare an input list of genes to a network reference and report if each member of the input is present in the resource.

## Usage

```
check_net_input(
  set,
  ref,
  check4similar = FALSE,
  entity1name = "p1",
  entity2name = "p1"
)
```

## Arguments

|               |                                                                                                                                                                                                                                                                                                              |
|---------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| set           | An input list of genes to check against a reference.                                                                                                                                                                                                                                                         |
| ref           | A reference of network data. See readSIF().                                                                                                                                                                                                                                                                  |
| check4similar | Logical flag. If TRUE, a case-insensitive grep will be used for name matching. For genes in families with many related members (e.g. ABC*, FAM*, etc.), this will not be ideal. We intend this option as a QC screening method to identify if case, punctuation, etc is causing fewer than expected matches. |
| entity1name   | The column name in "ref" of the first entity. Default = "p1."                                                                                                                                                                                                                                                |
| entity2name   | The column name in "ref" of the second entity. Default = "p2."                                                                                                                                                                                                                                               |

## Value

Character vector of "yes/no" indicating "within-ref/not"

## Examples

```
## Return a "yes/no" vector indicating if each gene in myGeneSet is annotated with any term in GO
## If no match, this function can attempt to suggest closest matches (check4similar = TRUE)
library(RITANdata)
myGeneSet <- c('BRCA1', 'RAD51C', 'VAV1', 'HRAS', 'ABCC1', 'CYP1B1', 'CYP3A5')
yorn <- check_net_input( myGeneSet, network_list[["CCSB"]] )
print(yorn)

yorn <- check_net_input( myGeneSet, network_list[["PID"]] )
print(yorn)

## See check_any_net_input() for efficiently checking across all resources.
```

---

|                |                                                                                                           |
|----------------|-----------------------------------------------------------------------------------------------------------|
| cov_undirected | <i>cov_undirected</i> function to show the un-directed coverabe between two nodes lists from two networks |
|----------------|-----------------------------------------------------------------------------------------------------------|

---

### Description

cov\_undirected function to show the un-directed coverabe between two nodes lists from two networks

### Usage

```
cov_undirected(this_nodes1, this_nodes2, this_net1, this_net2)
```

### Arguments

|             |                                  |
|-------------|----------------------------------|
| this_nodes1 | list of nodes for first network  |
| this_nodes2 | list of nodes for second network |
| this_net1   | the first network                |
| this_net2   | the second network               |

---

|                    |                           |
|--------------------|---------------------------|
| enrichment_symbols | <i>enrichment_symbols</i> |
|--------------------|---------------------------|

---

### Description

This function is called by term\_enrichment() and term\_enrichment\_by\_subset(). The user may call it directly, but we suggest using term\_enrichment(). The function uses the resources currently loaded into the active\_genesets vector. See load\_geneset\_symbols().

### Usage

```
enrichment_symbols(geneset, term = NULL, all_symbols = NA, ...)
```

### Arguments

|             |                                                                                                                                                                                                                                                            |
|-------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| geneset     | vector of gene symbols to be evaluated                                                                                                                                                                                                                     |
| term        | a list containing specific gene set term(s) and their corresponding gene symbols contained in one of the annotation resources, default is all gene set terms in the GO, ReactomePathways, KEGG_filtered_canonical_pathways, and MSigDB_Hallmarks libraries |
| all_symbols | gene symbols to be evaluated, identified by gene symbol name. Default is all protein coding genes. This parameter should be manipulated to include only the gene symbols that pertain to the user's analysis.                                              |
| ...         | additional arguments are not used                                                                                                                                                                                                                          |

## Details

Outputs a data frame containing the gene set name, a hypergeometric-test p value, the number of genes from the input gene list that occur in the gene set, the number of genes in the gene set, the gene symbols for the genes in the input gene list, and the q value.

## Value

results matrix of input gene list compared to active gene sets. Q value is calculated using entire group of active gene sets.

## Examples

```
require(RITANData)
myGeneSet <- c('BRCA1', 'RAD51C', 'VAV1', 'HRAS', 'ABCC1', 'CYP1B1', 'CYP3A5')

## Not run:
## We suggest using term_enrichment() instead. E.g.:
e <- term_enrichment(myGeneSet, 'GO')

## End(Not run)

## But, you may use enrichment_symbols() directly for an individual term:
load_geneset_symbols('GO')
e <- enrichment_symbols(myGeneSet, 'DNA_repair', all_symbols = cached_coding_genes)
print(e)

## Not run:
## Gene set enrichment using intersection of gene symbols
## provided in geneset parameter and all protein coding genes.
enrichment_symbols(geneset = vac1.day0vs31.de.genes)

## choose which terms to evaluate
t <- active_genesets[1:5]

## Test enrichment of that set of terms
enrichment_symbols(geneset = vac1.day0vs31.de.genes, term = t)

## End(Not run)
```

---

geneset\_overlap

*geneset\_overlap*

---

## Description

Return assymmetric matrix of the fraction of genes shared between sets. E.G. The fraction of the first set that is "covered" by or "overlaps" the second set.

## Usage

```
geneset_overlap(s1, s2 = s1, s.size = unlist(lapply(s1, length)))
```

**Arguments**

|        |                                                                                                  |
|--------|--------------------------------------------------------------------------------------------------|
| s1     | The first geneset                                                                                |
| s2     | the second geneset                                                                               |
| s.size | Denominator used in each comparison. The default is to determint the lengths of elements in "s1" |

**Value**

results matrix of input gene list compared to active gene sets. Q value is calculated using entire group of active gene sets.

**Examples**

```
require(RITANData)
r <- geneset_overlap( geneset_list$MSigDB_Hallmarks, geneset_list$NetPath_Gene_regulation )
heatmap(r, col = rev(gray(seq(0,1,length.out = 15)))) )
summary(c(r))
```

---

|                    |                                                                    |
|--------------------|--------------------------------------------------------------------|
| icon_single_within | <i>icon_single_within</i> interconnectivity score within a network |
|--------------------|--------------------------------------------------------------------|

---

**Description**

icon\_single\_within interconnectivity score within a network

**Usage**

```
icon_single_within(nodes = NULL, net = NULL, s = 10, verbose = TRUE)
```

**Arguments**

|         |                                                  |
|---------|--------------------------------------------------|
| nodes   | the node labels to use                           |
| net     | the network to use                               |
| s       | [10] the number of repeated random draws to make |
| verbose | [TRUE] if more verbose output should be shown    |

---

|           |                  |
|-----------|------------------|
| icon_test | <i>icon_test</i> |
|-----------|------------------|

---

## Description

"icon" is an abbreviation for the "interconnectivity" of a network or graph.

## Usage

```
icon_test(nodes1 = NULL, nodes2 = NULL, s = 100, verbose = TRUE, ...)
```

## Arguments

|         |                                                                   |
|---------|-------------------------------------------------------------------|
| nodes1  | [NULL] the first network. See network_overlap().                  |
| nodes2  | [NULL] the second network. See network_overlap().                 |
| s       | [100] the number of random permutations to make.                  |
| verbose | [TRUE] Extent of text shown in the console.                       |
| ...     | Additional argumetns are passed on to the specific test performed |

## Details

This function handles different inputs and directs them to the appropriate "icon" testing method. Depending on the values given to "nodes1" and "nodes2," a different specific test is performed.

Note that the specific functions called make use of the "param" attribute of each input. These parameters are populated by network\_overlap() so that the permutation reflects the exact procedure that was done to generate "nodes1" and/or "nodes2."

## Value

metrics and significance of the network overlap

## Examples

```
## Not run:
icon_test( nodes1=n, s=10)

## End(Not run)
```

---

```
load_all_protein_coding_symbols
      load_all_protein_coding_symbols
```

---

### Description

The character array returned is, by default, all human protein coding gene symbols. This variable defines the "universe of possible genes" for use in enrichment. Users should load a different "universe" or filter this one down to the most appropriate setting for their current study. For example, if running RNA-Seq, genes are in the universe if they are detected in any sample.

### Usage

```
load_all_protein_coding_symbols()
```

### Value

A unique list of gene symbols for protein coding genes according to EnsDb.Hsapiens.v86

---

```
load_geneset_symbols  load_geneset_symbols
```

---

### Description

For most applications, this function is used internally by term\_enrichment(). Users may call this function directly in some cases to force FDR adjustment to be across multiple resources. See Vignette for more details.

### Usage

```
load_geneset_symbols(gmt = NA, gmt_dir = "", verbose = TRUE)
```

### Arguments

|         |                                                                                                                                           |
|---------|-------------------------------------------------------------------------------------------------------------------------------------------|
| gmt     | Either 1) name of pre-loaded resource (i.e. names(geneset_list)) or 2) gmt file containing annotation resources for enrichment annotation |
| gmt_dir | location of gmt file named in gmt parameter                                                                                               |
| verbose | print results to screen                                                                                                                   |

**Details**

`load_geneset_symbols` allows the user to specify an annotation resource (e.g. Gene Ontology terms) to use in enrichment analysis. The expectation is that the annotation resource contains of at least one set of genes in the form of a list. The RITAN package comes with 15 pre-loaded annotation resources. The default active annotation resources are GO, ReactomePathways, KEGG\_filtered\_canonical\_pathways, and MSigDB\_Hallmarks.

The result of calling this function is to set the variable "active\_genesets" which will be used by further functions.

**Value**

R list object named `active_genesets`

**Examples**

```
## Load generic GO-slim terms
require(RITANdata)
load_geneset_symbols("GO_slim_generic")
print(length(active_genesets))
print(head(active_genesets[[1]]))

## Not run:
## load the default set of resources into "active_genesets"
load_geneset_symbols()

## Use only the Reactome Pathways annotation resource.
load_geneset_symbols(gmt="ReactomePathways")

## Suppresses output message describing the annotation resource and size.
load_geneset_symbols(gmt="ReactomePathways", verbose=FALSE)

## To list the available resources within RITAN:
print(names(geneset_list))

## You can also load your own data
load_geneset_symbols(gmt="myFile.gmt")

## End(Not run)
```

---

network\_overlap

network\_overlap

---

**Description**

network\_overlap

**Usage**

```
network_overlap(
  gene_list = NA,
  resources = c("PID", "TF", "dPPI", "CCSB", "STRING"),
  minStringScore = 700,
  minHumanNetScore = 0.4,
  minScore = 0,
  verbose = TRUE,
  dedup = TRUE,
  directed_net = FALSE,
  include_neighbors = FALSE,
  STRING_cache_directory = NA,
  STRING_species = 9606,
  STRING_version = "10"
)
```

**Arguments**

|                        |                                                                                                                                                                                                                                                          |
|------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| gene_list              | A list of genes to use. The function will identify edges across resources for or among these genes; identify the induced subnetwork around the gene_list.                                                                                                |
| resources              | Name of network resource(s) to use.                                                                                                                                                                                                                      |
| minStringScore         | If STRING is among the resources, only edges of at least the indicated score will be included.                                                                                                                                                           |
| minHumanNetScore       | If HumanNet is among the resources, only edges of at least the indicated score will be included.                                                                                                                                                         |
| minScore               | Same as above, but used for any other networks where "score" is provided                                                                                                                                                                                 |
| verbose                | If TRUE (default), the function will update the user on what it is doing and how many edges are identified for each resource.                                                                                                                            |
| dedup                  | If TRUE (Default = TRUE), remove edges reported by multiple resources. The edge type will be a semi-colon delimited list of the resources that had reported the interaction.                                                                             |
| directed_net           | Logical indicating if the network resources should be interpreted as directed.                                                                                                                                                                           |
| include_neighbors      | Logical to include 1st neighbors of "gene_list" (genes not in gene_list, but directly connected to them) in the induced subnetwork.                                                                                                                      |
| STRING_cache_directory | A directory where STRING data files are cached to speed up subsequent queries; no need to re-download. If NA (the default), caches STRING data in your Rpackages directory. If "", uses a temporary directory that is cleared when the R-session closes. |
| STRING_species         | Species taxon ID (number) to use in searching STRING data. (Default = 9606)                                                                                                                                                                              |
| STRING_version         | Version of the STRING database (Default = "10")                                                                                                                                                                                                          |

**Value**

Data table describing the induced subnetwork for "gene\_list" across the requested resources.

**Examples**

```
## Get interactions among a list of genes from the PID: Pathway Interaction Database
require(RITANdata)
myGeneSet <- c('BRCA1', 'RAD51C', 'VAV1', 'HRAS', 'ABCC1', 'CYP1B1', 'CYP3A5')
sif <- network_overlap( myGeneSet, resources = 'PID')
print(sif)

## Not run:
## Get the PPI network induced by genes within myGeneSet
## Use 4 separate resources, but trim STRING to only include more confident interactions
sif <- network_overlap( myGeneSet, c('dPPI', 'PID', 'CCSB', 'STRING'), minStringScore = 500 )

## End(Not run)
```

---

```
plot.term_enrichment  plot.term_enrichment
```

---

**Description**

```
plot.term_enrichment
```

**Usage**

```
## S3 method for class 'term_enrichment'
plot(x = NA, min_q = 0.05, max_terms = 25, extend_mar = c(0, 10, 0, 0), ...)
```

**Arguments**

|            |                                                                                                                                                            |
|------------|------------------------------------------------------------------------------------------------------------------------------------------------------------|
| x          | data frame returned by term_enrichment                                                                                                                     |
| min_q      | Only q-values more significant than this threshold will be plotted. Default = 0.05.                                                                        |
| max_terms  | Up to max_terms will be plotted. Default = 25.                                                                                                             |
| extend_mar | Term names can be long. We attempt to keep them readable by extending the left-hand-side margins automatically. Default = c(0,10,0,0) added to par()\$mar. |
| ...        | Additional arguments are passed on to plot()                                                                                                               |

**Value**

```
silent return from plot
```

**Examples**

```
require(RITANdata)
e <- term_enrichment(vac1.day0vs31.de.genes, resources = 'GO_slim_generic')
plot(e, min_q = .1)
```

---

```
plot.term_enrichment_by_subset
      plot.term_enrichment_by_subset
```

---

## Description

plot.term\_enrichment\_by\_subset

## Usage

```
## S3 method for class 'term_enrichment_by_subset'
plot(
  x,
  show_values = TRUE,
  annotation_matrix = NA,
  low = "white",
  high = "#2166AC",
  return_ggplot_object = FALSE,
  label_size_x = 16,
  label_angle_x = -30,
  label_size_y = 9,
  wrap_y_labels = 20,
  grid_line_color = "white",
  mid = 0,
  cap = NA,
  annotation_palates = c("Reds", "Greens", "Purples", "Greys", "BuPu", "RdPu", "BrBG",
    "PiYG", "Spectral"),
  annotation_legend_x = -0.3,
  trim_resource_names = TRUE,
  ...
)
```

## Arguments

|                      |                                                                                       |
|----------------------|---------------------------------------------------------------------------------------|
| x                    | data frame returned by term_enrichment_by_subset                                      |
| show_values          | True or False, plot values on the heatmap                                             |
| annotation_matrix    | a matrix() of group-level characteristics - same number of columns as "m"             |
| low                  | color for low end of range                                                            |
| high                 | color for high end of range                                                           |
| return_ggplot_object | logical flag (default FALSE) that if TRUE, the ggplot object for the plot is returned |
| label_size_x         | size of text for x label. Default label_size_x=16                                     |
| label_angle_x        | angle for text for x label. Default is -30 degrees                                    |

label\_size\_y    size of text for y label. Default label\_size\_y=9  
 wrap\_y\_labels   Number of characters to wrap row labels  
 grid\_line\_color    color o grid lines between cells. Default is white.  
 mid    sets lower threshold for color scale  
 cap    Clip numeric values to this maximum threshold  
 annotation\_palates    Color palates (RColorBrewer) used for each row of the annotation matrix  
 annotation\_legend\_x    offset for placing the legend  
 trim\_resource\_names    [TRUE] remove any text in rownames preceeding a period characte. This convention is usually used in RITAN to prepend the resource name to the term name, which may not be needed in plotting.  
 ...    further areguments are not used at this time. If the user wants to modify the plot, use return\_ggplot\_object = TRUE.

### Value

silent return, unless return\_ggplot\_object==TRUE. Then, the ggplot object for the plot is returned.

### Examples

```

## Create list of gene sets to evaluate.
## This example is from a vaccine study where we pre-generated differentially expressed genes.
## This object will be passed to the groups parameter.
require(RITANdata)
vac1.de.genes <- list(vac1.day0vs31.de.genes, vac1.day0vs56.de.genes)
names(vac1.de.genes) <- c("Day0vs31", "Day0vs56")
print(str(vac1.de.genes))

## Not run:
## Run term_enrichment_by_subset on the two results.
## This function usually takes a few seconds to a minute to run.
m <- term_enrichment_by_subset(groups = vac1.de.genes, q_value_threshold = .9)
summary(m)
plot( m, label_size_y = 4, show_values = FALSE )

## End(Not run)

```

---

readGMT

---

readGMT

---

### Description

Created for simplification of reading .gmt files into RITAN.

**Usage**

```
readGMT(f = NA)
```

**Arguments**

**f** GMT file name. Please provide a full path if the file is not in the current working directory.

**Value**

A list() where the name of each entry is the term (first column of GMT file) and the value is a chr array of genes associated with the term.

**Examples**

```
# Make an example list() to show the GMT format
set <- list( term1=c('gene_name1','gene_name2'),
             term2=c('gene_name3','gene_name4','gene_name5') )
## Not run:
# Write a GMT file for "set"
writeGMT( set, 'my_file.gmt' )

# Reading GMT files
geneset <- readGMT( 'my_file.gmt' )

# Additional GMT files are available from multiple sources.
# We recommend:
# http://software.broadinstitute.org/gsea/msigdb/

## End(Not run)
```

---

readSIF

*readSIF*


---

**Description**

This function reads a data table into R; the data table describes network interactions. It is named for the Simple Interaction Format (SIF), but can read any data table if the users identifies which columns contain the pertinent data (see below).

**Usage**

```
readSIF(
  file = NA,
  header = FALSE,
  sep = "\t",
  as.is = TRUE,
```

```

    p1 = 1,
    p2 = 2,
    et = 3,
    score = NA,
    ...
  )

```

### Arguments

|        |                                                                                                                                                          |
|--------|----------------------------------------------------------------------------------------------------------------------------------------------------------|
| file   | location of file                                                                                                                                         |
| header | indicator of presense of header on file                                                                                                                  |
| sep    | file delimiter - used by read.table()                                                                                                                    |
| as.is  | logical (default TRUE)                                                                                                                                   |
| p1     | Column number for the 1st entity. Default = 1.                                                                                                           |
| p2     | Column number for the 2nd entity. Default = 2.                                                                                                           |
| et     | Column number for the edge type. Default = 3. Optionally, it may be a string label to be used as the edge type for all interactions from the input file. |
| score  | Column number for edge scores or weights. Default = NA (no score read).                                                                                  |
| ...    | Other options to read.table().                                                                                                                           |

### Details

The SIF file format is a 3-column format, with an optional 4th column: <entity-1><tab><edge-type><tab><entity-2><tab><score>

Entities may be genes, proteins, metabolites, etc. The edge type typically conveys the type of relationship that exists between the two entities, such as physical interaction, phosphorylation, or activation.

### Value

Returns a data.frame with 3 (or 4) columns of data.

### Examples

```

# Make a simple example to show the SIF file format
s <- matrix(c('gene1','gene2','PPI',
              'gene1','gene3','Chip-Seq',
              'gene4','gene5','PPI'), ncol=3, byrow=TRUE)

## Not run:
# Read a SIF file
write.table( s, "myFile.sif", sep='\t', col.names=FALSE, row.names=FALSE )
sif <- readSIF("myFile.sif")

## End(Not run)

```

---

|                 |                                                                                                                |
|-----------------|----------------------------------------------------------------------------------------------------------------|
| resource_reduce | <i>resource_reduce Merge terms across resources to reduce the number of redundant and semi-redundant terms</i> |
|-----------------|----------------------------------------------------------------------------------------------------------------|

---

**Description**

resource\_reduce Merge terms across resources to reduce the number of redundant and semi-redundant terms

**Usage**

```
resource_reduce(genesets = NULL, min_overlap = 0.8, verbose = TRUE)
```

**Arguments**

|             |                                                                        |
|-------------|------------------------------------------------------------------------|
| genesets    | the input genesets to consider. May be from one or multiple resources. |
| min_overlap | terms that share at least this fraction of genes will be merged        |
| verbose     | if TRUE, print status and summary output                               |

**Value**

the list of terms, after merging to reduce redundnat and semi-redundant terms

**Examples**

```
require(RITANdata)
r <- resource_reduce( geneset_list$DisGeNet )
```

---

|                           |                                  |
|---------------------------|----------------------------------|
| show_active_genesets_hist | <i>show_active_genesets_hist</i> |
|---------------------------|----------------------------------|

---

**Description**

function to plot distribution of size of active\_genesets object

**Usage**

```
show_active_genesets_hist(nbins = 50, ...)
```

**Arguments**

|       |                                           |
|-------|-------------------------------------------|
| nbins | Number of bins to include in histogram    |
| ...   | further argumants are passed on to plot() |

**Value**

NULL. The plot is shown.

**Examples**

```
require(RITANdata)
load_geneset_symbols('GO_slim_generic')
show_active_genesets_hist()

## Not run:
## Show the distribution of geneset sizes for the default set of geneset resources
load_geneset_symbols()
show_active_genesets_hist()

## Show the distribution of geneset sizes for a specific resource
load_geneset_symbols(gmt="ReactomePathways")
show_active_genesets_hist()

## End(Not run)
```

---

```
summary.term_enrichment
```

```
summary.term_enrichment
```

---

**Description**

summary.term\_enrichment

**Usage**

```
## S3 method for class 'term_enrichment'
summary(object, ...)
```

**Arguments**

|        |                                           |
|--------|-------------------------------------------|
| object | data frame returned by term_enrichment()  |
| ...    | Further arguments are passed on to head() |

**Value**

the data.frame of top enrichment results

**Examples**

```
require(RITANdata)
e <- term_enrichment( vac1.day0vs31.de.genes, "MSigDB_Hallmarks" )
summary(e, n=3)
```

---

```
summary.term_enrichment_by_subset
      summary.term_enrichment_by_subset
```

---

## Description

summary.term\_enrichment\_by\_subset

## Usage

```
## S3 method for class 'term_enrichment_by_subset'
summary(object, verbose = TRUE, ...)
```

## Arguments

|         |                                                            |
|---------|------------------------------------------------------------|
| object  | data frame returned by term_enrichment_by_subset()         |
| verbose | if TRUE (default), print a header describing the data type |
| ...     | Further arguments are passed on to head()                  |

## Value

the data.frame of top enrichment results

## Examples

```
require(RITANdata)
vac1.de.genes <- list(vac1.day0vs31.de.genes, vac1.day0vs56.de.genes)
names(vac1.de.genes) <- c("Day0vs31", "Day0vs56")
e <- term_enrichment_by_subset(vac1.de.genes, "MSigDB_Hallmarks", q_value_threshold = 0.1 )
summary(e)
```

---

|                 |                        |
|-----------------|------------------------|
| term_enrichment | <i>term_enrichment</i> |
|-----------------|------------------------|

---

## Description

term\_enrichment evaluates the input gene list for enrichment within each of the annotation resources. This differs from the enrichment\_symbols function which evaluates the gene list for enrichment against all of the annotation resources grouped together.

**Usage**

```
term_enrichment(
  geneset,
  resources = resources.default,
  report_resources_separately = FALSE,
  verbose = TRUE,
  all_symbols = NA,
  filter_to_intersection = FALSE,
  ...
)
```

**Arguments**

|                                          |                                                                                                                                                                  |
|------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>geneset</code>                     | vector of gene symbols to be evaluated                                                                                                                           |
| <code>resources</code>                   | list containing the reference gene sets to test for enrichment                                                                                                   |
| <code>report_resources_separately</code> | logical (default FALSE) flag to report enrichments separately for each requested resource, or to combine them and produce FDR adjustment across the combined set |
| <code>verbose</code>                     | print the top results for each annotation resource                                                                                                               |
| <code>all_symbols</code>                 | the background/global set of gene symbols (study dependent; we provide all protein coding genes as a default)                                                    |
| <code>filter_to_intersection</code>      | [FALSE] should the background and foreground genesets be subsetted to one another?                                                                               |
| <code>...</code>                         | further arguments are passed on to <code>enrichment_symbols()</code>                                                                                             |

**Value**

results matrix of input gene list compared to active gene sets. Q value is calculated within each of the active gene sets.

**Examples**

```
## Check if there is enrichment for any "Hallmark" functions within a input set of genes
require(RITANData)
myGeneSet <- c('BRCA1', 'RAD51C', 'VAV1', 'HRAS', 'ABCC1', 'CYP1B1', 'CYP3A5')
e <- term_enrichment(myGeneSet, "MSigDB_Hallmarks")
print( e[1:2, -6] )

## Not run:
term_enrichment(geneset = vac1.day0vs31.de.genes)
term_enrichment(geneset = vac1.day0vs31.de.genes, resources = "MSigDB_Hallmarks")
vac1.day0vs31.enrichment <- term_enrichment(geneset = vac1.day0vs31.de.genes, verbose = FALSE)

## End(Not run)
```

---

```
term_enrichment_by_subset
      term_enrichment_by_subset
```

---

## Description

Run enrichment simultaneously across a group of prioritized gene lists. For example, in a time course dataset, one may have a different list of genes that are differentially expressed at each time point. This function facilitates rapid evaluation of term enrichment across time point comparisons. Alternatively, one may have a different list of differentially expressed genes by drug treatment, environmental condition, ect.

## Usage

```
term_enrichment_by_subset(
  groups = NA,
  resources = resources.default,
  q_value_threshold = 0.01,
  verbose = TRUE,
  display_type = "q",
  phred = TRUE,
  ...
)
```

## Arguments

|                                |                                                                                                                                                                 |
|--------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>groups</code>            | A list() of genes for enrichment. Each entry in the list() is an input set of genes. Enrichment is performed for each of these entries.                         |
| <code>resources</code>         | character vector for which resources to use in enrichment                                                                                                       |
| <code>q_value_threshold</code> | minimum q-value (FDR adjusted p-value) in any group for the term to be included in results                                                                      |
| <code>verbose</code>           | print additional status updates on what the function is doing                                                                                                   |
| <code>display_type</code>      | Flag for which data type will be returned. One of "q" (default) for q-values, "p" for unadjusted p-values, or "n" for the number of genes overlapping the term. |
| <code>phred</code>             | Logical flag (default TRUE) to return the -log10 of p/q values                                                                                                  |
| <code>...</code>               | Further arguments are passed on to <code>enrichment_symbols()</code>                                                                                            |

## Value

Returns a term-by-study matrix of enrichment values (value determined by "display\_type")

## Examples

```
## Create list of gene sets to evaluate.
## This example is from a vaccine study where we pre-generated differentially expressed genes.
## This object will be passed to the groups parameter.
require(RITANdata)
vac1.de.genes <- list(vac1.day0vs31.de.genes, vac1.day0vs56.de.genes)
names(vac1.de.genes) <- c("Day0vs31", "Day0vs56")
print(str(vac1.de.genes))

## Not run:
## Run term_enrichment_by_subset on the two results.
## This function usually takes a few seconds to a minute to run.
m <- term_enrichment_by_subset(groups = vac1.de.genes, q_value_threshold = .9)
summary(m)
plot( m, label_size_y = 4, show_values = FALSE )

## End(Not run)
```

---

vac1.day0vs31.de.genes

*This dataset is included as an example in the package:*

---

## Description

This dataset is included as an example in the package:

## Usage

```
vac1.day0vs31.de.genes
```

## Format

An object of class character of length 669.

## Value

differentially expressed genes at 31 days post-vaccination with vaccine1

## References

<https://www.ncbi.nlm.nih.gov/pubmed/26755593>

**Examples**

```
## Not run:  
#data("vac1.day0vs31.de.genes")  
te <- term_enrichment(geneset = vac1.day0vs31.de.genes)  
  
## End(Not run)
```

---

```
vac1.day0vs56.de.genes
```

*This dataset is included as an example in the package:*

---

**Description**

This dataset is included as an example in the package:

**Usage**

```
vac1.day0vs56.de.genes
```

**Format**

An object of class character of length 471.

**Value**

differentially expressed genes at 56 days post-vaccination with vaccine1

**References**

<https://www.ncbi.nlm.nih.gov/pubmed/26755593>

**Examples**

```
## Not run:  
#data("vac1.day0vs56.de.genes")  
te <- term_enrichment(geneset = vac1.day0vs56.de.genes)  
  
## End(Not run)
```

---

`vac2.day0vs31.de.genes`

*This dataset is included as an example in the package:*

---

**Description**

This dataset is included as an example in the package:

**Usage**

```
vac2.day0vs31.de.genes
```

**Format**

An object of class character of length 522.

**Value**

differentially expressed genes at 31 days post-vaccination with vaccine2

**References**

<https://www.ncbi.nlm.nih.gov/pubmed/26755593>

**Examples**

```
## Not run:  
#data("vac2.day0vs31.de.genes")  
te <- term_enrichment(geneset = vac2.day0vs31.de.genes)  
  
## End(Not run)
```

---

`vac2.day0vs56.de.genes`

*This dataset is included as an example in the package:*

---

**Description**

This dataset is included as an example in the package:

**Usage**

```
vac2.day0vs56.de.genes
```

**Format**

An object of class character of length 660.

**Value**

differentially expressed genes at 56 days post-vaccination with vaccine2

**References**

<https://www.ncbi.nlm.nih.gov/pubmed/26755593>

**Examples**

```
## Not run:
#data("vac2.day0vs56.de.genes")
te <- term_enrichment(geneset = vac2.day0vs56.de.genes)

## End(Not run)
```

---

writeGMT

*writeGMT*


---

**Description**

Created for future use and simplification of writing .gmt files from the package.

**Usage**

```
writeGMT(s, file = NA, link = rep("", length(s)))
```

**Arguments**

|      |                                                                                                                        |
|------|------------------------------------------------------------------------------------------------------------------------|
| s    | list of gene sets in current R session. Each entry will become a row in the GMT file.                                  |
| file | file name to write to                                                                                                  |
| link | default is "". This is the second column of a GMT file and is usually a hyperlink or note about the origin of the term |

**Value**

Nothing is returned. A file is written.

### Examples

```
# Make an example list() to show the GMT format
set <- list( term1=c('gene_name1','gene_name2'),
             term2=c('gene_name3','gene_name4','gene_name5') )

## Not run:
# Write a GMT file for "set"
writeGMT( set, 'my_file.gmt')

## End(Not run)
```

---

|                    |                           |
|--------------------|---------------------------|
| write_simple_table | <i>write_simple_table</i> |
|--------------------|---------------------------|

---

### Description

This is a simple wrapper around "write.table" that writes a tab-delimited table with column names, no quoting, and no row names.

### Usage

```
write_simple_table(d = NULL, f = NULL, ...)
```

### Arguments

|     |                                          |
|-----|------------------------------------------|
| d   | R data object                            |
| f   | file path                                |
| ... | further options passed on to write.table |

### Value

invisible (nothing is returned)

### Examples

```
## Not run:
simple wrapper around write.table for writing a tab-delimited, no row names, tab-separated file

## End(Not run)
```

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