

# Package ‘RITAN’

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**Type** Package

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

**Version** 1.19.0

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**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

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**Imports** graphics, stats, utils, grid, gridExtra, reshape2, gplots, ggplot2, plotrix, RColorBrewer, STRINGdb, MCL, linkcomm, dynamicTreeCut, gsubfn, hash, png, sqldf, igraph, BgeeDB, knitr, RITANdata

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'interconnectivity\_functions.R'

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---

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

**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    *check\_any\_net\_input*

---

**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, punctuaiton, 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 <- enrichment_symbols(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')
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      *icon\_single\_within 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(file = "ftp://ftp.ebi.ac.uk/pub/databases/genenames/new/tsv/locus_g
col_name = "symbol")
```

### Arguments

file	file name of a table containing gene symbols
col_name	column name within "file" that contains symbols

### Value

A unique list of gene symbols from the current protein coding set at the EBI

---

```
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", "TFe", "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

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

## 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, ...)
```

## 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 of 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
...	further arguments 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' )

# GMT files are available from multiple sources including 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 redundant and semi-redundant terms



**Examples**

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

---

```
show_active_genesets_hist
      show_active_genesets_hist
```

---

**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 arguments 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**

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

**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.day0v31.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**

groups	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.
resources	character vector for which resources to use in enrichment
q_value_threshold	minimum q-value (FDR adjusted p-value) in any group for the term to be included in results
verbose	print additional status updates on what the function is doing
display_type	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.
phred	Logical flag (default TRUE) to return the -log10 of p/q values
...	Further arguments are passed on to enrichment_symbols()

**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 vaccine 1

**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      *write\_simple\_table*

---

**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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