

Package ‘hypeR’

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Description An R Package for Geneset Enrichment Workflows.

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clean_genesets	<i>Clean labels of genesets</i>
----------------	---------------------------------

Description

Clean labels of genesets

Usage

```
clean_genesets(x)
```

Arguments

x A vector of labels

Examples

```
HALLMARK <- msigdb_download("Homo sapiens", "H", "")
names(HALLMARK) <- clean_genesets(names(HALLMARK))
head(names(HALLMARK))
```

enrichr_available *Get enrichr available genesets*

Description

Get enrichr available genesets

Usage

```
enrichr_available(
  db = c("Enrichr", "YeastEnrichr", "FlyEnrichr", "WormEnrichr", "FishEnrichr")
)
```

Arguments

db A species

Value

A dataframe of available genesets

Examples

```
enrichr_available()
```

enrichr_download *Download data from enrichr in the form of a named list*

Description

Download data from enrichr in the form of a named list

Usage

```
enrichr_download(  
  genesets,  
  db = c("Enrichr", "YeastEnrichr", "FlyEnrichr", "WormEnrichr", "FishEnrichr")  
)
```

Arguments

genesets A name corresponding to available genesets
db A species

Value

A list of genesets

Examples

```
ATLAS <- enrichr_download("Human_Gene_Atlas")
```

enrichr_gsets *Download data from enrichr in the form of a gsets object*

Description

Download data from enrichr in the form of a gsets object

Usage

```
enrichr_gsets(  
  genesets,  
  db = c("Enrichr", "YeastEnrichr", "FlyEnrichr", "WormEnrichr", "FishEnrichr"),  
  clean = FALSE  
)
```

Arguments

genesets	A name corresponding to available genesets
db	A species
clean	Use true to clean labels of genesets

Value

A gsets object

Examples

```
ATLAS <- enrichr_gsets("Human_Gene_Atlas")
```

genesets_Server *Shiny server module for geneset selection*

Description

Shiny server module for geneset selection

Usage

```
genesets_Server(id, clean = FALSE)
```

Arguments

id	A unique namespace identifier matching to interface
clean	Use true to clean geneset names

Value

Shiny server code

genesets_UI	<i>Shiny interface module for geneset selection</i>
-------------	---

Description

Shiny interface module for geneset selection

Usage

```
genesets_UI(id)
```

Arguments

id	A unique namespace identifier
----	-------------------------------

Value

Shiny ui elements

ggempty	<i>An empty ggplot</i>
---------	------------------------

Description

An empty ggplot

Usage

```
ggempty()
```

Value

A ggplot object

ggeplot *Enrichment plot implemented in ggplot*

Description

Enrichment plot implemented in ggplot

Usage

```
ggeplot(n, positions, x_axis, y_axis, title = "")
```

Arguments

n	The length of a ranked list
positions	A vector of positions in the ranked list
x_axis	The x-axis of a running enrichment score
y_axis	The y-axis of a running enrichment score
title	Plot title

Value

A ggplot object

ggvenn *Venn diagram implemented in ggplot*

Description

Venn diagram implemented in ggplot

Usage

```
ggvenn(a, b, ga, gb, title = "")
```

Arguments

a	A vector for group a
b	A vector for group b
ga	A string label for group a
gb	A string label for group b
title	Plot title

Value

A ggplot object

`gsets`

A genesets object

Description

A genesets object

A genesets object

See Also

`rgsets`

Public fields

`genesets` A named list of genesets

`name` A character vector describing source of genesets

`version` A character vector describing versioning

Methods

Public methods:

- [gsets\\$new\(\)](#)
- [gsets\\$print\(\)](#)
- [gsets\\$list\(\)](#)
- [gsets\\$info\(\)](#)
- [gsets\\$reduce\(\)](#)
- [gsets\\$clone\(\)](#)

Method `new()`: Create a gsets object

Usage:

```
gsets$new(  
  genesets,  
  name = "Custom",  
  version = "",  
  clean = FALSE,  
  quiet = FALSE  
)
```

Arguments:

`genesets` A named list of genesets

`name` A character vector describing source of genesets

`version` A character vector describing versioning

`clean` Use true to clean labels of genesets

`quiet` Use true to silence warnings

Returns: A new gsets object

Method print(): Print genesets information

Usage:

```
gsets$print()
```

Returns: NULL

Method list(): Return genesets as a list

Usage:

```
gsets$list()
```

Returns: A list of genesets

Method info(): Returns versioning information

Usage:

```
gsets$info()
```

Returns: A character vector with name and version

Method reduce(): Reduces genesets to a background distribution of symbols

Usage:

```
gsets$reduce(background)
```

Arguments:

background A character vector of symbols

Returns: A gsets object

Method clone(): The objects of this class are cloneable with this method.

Usage:

```
gsets$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

Examples

```
genesets <- list("GSET1" = c("GENE1", "GENE2", "GENE3"),
               "GSET2" = c("GENE4", "GENE5", "GENE6"),
               "GSET3" = c("GENE7", "GENE8", "GENE9"))

gsets_obj <- gsets$new(genesets, name="example", version="v1.0")
print(gsets_obj)
```

hyp *A hyp object*

Description

A hyp object

A hyp object

See Also

multihyp

Public fields

data A dataframe returned by hypeR()

plots A list of plots returned by hypeR()

args A list of arguments passed to hypeR()

info Exported information for reproducibility

Methods**Public methods:**

- [hyp\\$new\(\)](#)
- [hyp\\$print\(\)](#)
- [hyp\\$as.data.frame\(\)](#)
- [hyp\\$clone\(\)](#)

Method new(): Create a hyp object

Usage:

```
hyp$new(data, plots = NULL, args = NULL, info = NULL)
```

Arguments:

data A dataframe returned by hypeR()

plots A list of plots returned by hypeR()

args A list of arguments passed to hypeR()

info Exported information for reproducibility

Returns: A new hyp object

Method print(): Print hyp object

Usage:

```
hyp$print()
```

Returns: NULL

Method as.data.frame(): Extract dataframe from hyp object

Usage:

```
hyp$as.data.frame()
```

Returns: NULL

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
hyp$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
data <- data.frame(replicate(5, sample(0:1, 10, rep=TRUE)))
args <- list("arg_1"=1, "arg_2"=2, "arg_3"=3)
hyp_obj <- hyp$new(data, args=args)
```

hypeR

Calculate enrichment of one or more signatures

Description

Calculate enrichment of one or more signatures

Usage

```
hypeR(
  signature,
  genesets,
  test = c("hypergeometric", "kstest"),
  background = 23467,
  power = 1,
  absolute = FALSE,
  pval = 1,
  fdr = 1,
  plotting = FALSE,
  quiet = TRUE
)
```

Arguments

<code>signature</code>	A vector of symbols
<code>genesets</code>	A gsets/rgsets object or a named list of genesets
<code>test</code>	Choose an enrichment type e.g. <code>c("hypergeometric", "kstest")</code>
<code>background</code>	Size or character vector of background population genes

power	Exponent for weights (kstest only)
absolute	Takes max-min score rather than the max deviation from null (kstest only)
pval	Filter results to be less than pval cutoff
fdr	Filter results to be less than fdr cutoff
plotting	Use true to generate plots for each geneset test (may slow performance)
quiet	Use true to suppress logs and warnings

Value

A hyp object

Examples

```
genesets <- msigdb_gsets("Homo sapiens", "C2", "CP:KEGG")
signature <- c("IDH3B", "DLST", "PCK2", "CS", "PDHB", "PCK1", "PDHA1", "LOC642502",
              "PDHA2", "LOC283398", "FH", "SDHD", "OGDH", "SDHB", "IDH3A", "SDHC",
              "IDH2", "IDH1", "OGDHL", "PC", "SDHA", "SUCLG1", "SUCLA2", "SUCLG2")
hyp_obj <- hyper(signature, genesets, background=2522)
```

hyperdb_available *Check available data to download from hyperdb*

Description

Check available data to download from hyperdb

Usage

```
hyperdb_available()
```

Examples

```
hyperdb_available()
```

hyperdb_gsets	<i>Download data from hyperdb</i>
---------------	-----------------------------------

Description

Download data from hyperdb

Usage

```
hyperdb_gsets(source, gsets)
```

Arguments

source	A source identifier
gsets	A genesets identifier

Value

A list

Examples

```
KEGG <- hyperdb_gsets("KEGG", "KEGG_v92.0.rds")
```

hyperdb_rgsets	<i>Download data from hyperdb in the form of a rgsets object</i>
----------------	--

Description

Download data from hyperdb in the form of a rgsets object

Usage

```
hyperdb_rgsets(rgsets, version)
```

Arguments

rgsets	A name corresponding to an available relational genesets object
version	A version number

Value

An rgsets object

Examples

```
REACTOME <- hyperdb_rgsets("REACTOME", "70.0")
```

hyp_dots

Visualize hyp/multihyp objects as a dots plot

Description

Visualize hyp/multihyp objects as a dots plot

Usage

```
hyp_dots(  
  hyp_obj,  
  top = 20,  
  abrv = 50,  
  sizes = TRUE,  
  pval = 1,  
  fdr = 1,  
  val = c("fdr", "pval"),  
  title = "",  
  merge = FALSE  
)
```

Arguments

hyp_obj	A hyp or multihyp object
top	Limit number of genesets shown
abrv	Abbreviation length of geneset labels
sizes	Size dots by geneset sizes
pval	Filter results to be less than pval cutoff
fdr	Filter results to be less than fdr cutoff
val	Choose significance value for plot e.g. c("fdr", "pval")
title	Plot title
merge	Use true to merge a multihyp object into one plot

Value

A ggplot object

Examples

```
genesets <- msigdb_gsets("Homo sapiens", "C2", "CP:KEGG")

signature <- c("IDH3B", "DLST", "PCK2", "CS", "PDHB", "PCK1", "PDHA1", "LOC642502",
              "PDHA2", "LOC283398", "FH", "SDHD", "OGDH", "SDHB", "IDH3A", "SDHC",
              "IDH2", "IDH1", "OGDHL", "PC", "SDHA", "SUCLG1", "SUCLA2", "SUCLG2")

hyp_obj <- hypeR(signature, genesets, background=2522)

hyp_dots(hyp_obj, val="fdr")
```

hyp_emap

*Visualize hyp/multihyp objects as an enrichment map***Description**

Visualize hyp/multihyp objects as an enrichment map

Usage

```
hyp_emap(
  hyp_obj,
  similarity_metric = c("jaccard_similarity", "overlap_similarity"),
  similarity_cutoff = 0.2,
  pval = 1,
  fdr = 1,
  val = c("fdr", "pval"),
  top = NULL,
  title = ""
)
```

Arguments

hyp_obj	A hyp or multihyp object
similarity_metric	Metric to calculate geneset similarity
similarity_cutoff	Geneset similarity cutoff
pval	Filter results to be less than pval cutoff
fdr	Filter results to be less than fdr cutoff
val	Choose significance value shown above nodes e.g. c("fdr", "pval")
top	Limit number of pathways shown
title	Plot title

Value

A visNetwork object

Examples

```
genesets <- msigdb_gsets("Homo sapiens", "C2", "CP:KEGG")

signature <- c("IDH3B", "DLST", "PCK2", "CS", "PDHB", "PCK1", "PDHA1", "LOC642502",
              "PDHA2", "LOC283398", "FH", "SDHD", "OGDH", "SDHB", "IDH3A", "SDHC",
              "IDH2", "IDH1", "OGDHL", "PC", "SDHA", "SUCLG1", "SUCLA2", "SUCLG2")

hyp_obj <- hyper(signature, genesets, background=2522)

hyp_emap(hyp_obj, top=30, val="fdr")
```

hyp_hmap

Visualize hyp/multihyp objects as a hierarchy map

Description

Visualize hyp/multihyp objects as a hierarchy map

Usage

```
hyp_hmap(
  hyp_obj,
  pval = 1,
  fdr = 1,
  val = c("fdr", "pval"),
  top = NULL,
  title = ""
)
```

Arguments

hyp_obj	A hyp or multihyp object
pval	Filter results to be less than pval cutoff
fdr	Filter results to be less than fdr cutoff
val	Choose significance value displayed when hovering nodes e.g. c("fdr", "pval")
top	Limit number of pathways shown
title	Plot title

Value

A visNetwork object

Examples

```
genesets <- hyperdb_rgsets("REACTOME", "70.0")

signature <- c("IDH3B", "DLST", "PCK2", "CS", "PDHB", "PCK1", "PDHA1", "LOC642502",
              "PDHA2", "LOC283398", "FH", "SDHD", "OGDH", "SDHB", "IDH3A", "SDHC",
              "IDH2", "IDH1", "OGDHL", "PC", "SDHA", "SUCLG1", "SUCLA2", "SUCLG2")

hyp_obj <- hypeR(signature, genesets, background=2522)

hyp_hmap(hyp_obj, top=60)
```

hyp_show

*Convert a hyp object to a reactable table***Description**

Convert a hyp object to a reactable table

Usage

```
hyp_show(hyp_obj, simple = FALSE)
```

Arguments

hyp_obj	A hyp object
simple	Use true to only include essential columns

Value

A reactable table

Examples

```
genesets <- msigdb_gsets("Homo sapiens", "C2", "CP:KEGG")

signature <- c("IDH3B", "DLST", "PCK2", "CS", "PDHB", "PCK1", "PDHA1", "LOC642502",
              "PDHA2", "LOC283398", "FH", "SDHD", "OGDH", "SDHB", "IDH3A", "SDHC",
              "IDH2", "IDH1", "OGDHL", "PC", "SDHA", "SUCLG1", "SUCLA2", "SUCLG2")

hyp_obj <- hypeR(signature, genesets, background=2522)

hyp_show(hyp_obj)
```

hyp_to_excel	<i>Export hyp/multihyp object to excel</i>
--------------	--

Description

Export hyp/multihyp object to excel

Usage

```
hyp_to_excel(hyp_obj, file_path, cols = NULL, versioning = TRUE)
```

Arguments

hyp_obj	A hyp or multihyp object
file_path	A file path
cols	Dataframe columns to include
versioning	Add sheet with versioning information

Examples

```
genesets <- msigdb_gsets("Homo sapiens", "C2", "CP:KEGG")

signature <- c("IDH3B", "DLST", "PCK2", "CS", "PDHB", "PCK1", "PDHA1", "LOC642502",
              "PDHA2", "LOC283398", "FH", "SDHD", "OGDH", "SDHB", "IDH3A", "SDHC",
              "IDH2", "IDH1", "OGDHL", "PC", "SDHA", "SUCLG1", "SUCLA2", "SUCLG2")

hyp_obj <- hyper(signature, genesets, background=2522)

hyp_to_excel(hyp_obj, file_path="pathways.xlsx")
```

hyp_to_rmd	<i>Export hyp object to rmarkdown</i>
------------	---------------------------------------

Description

Export hyp object to rmarkdown

Usage

```

hyp_to_rmd(
  hyp_obj,
  file_path,
  title = "Workflow Report",
  subtitle = "",
  author = "",
  header = "Results",
  versioning = TRUE,
  show_dots = TRUE,
  show_emaps = TRUE,
  show_hmaps = FALSE,
  show_tables = TRUE,
  hyp_dots_args = list(top = 15, val = "fdr"),
  hyp_emap_args = list(top = 25, val = "fdr", similarity_metric = "jaccard_similarity",
    similarity_cutoff = 0.2),
  hyp_hmap_args = list(top = 25, val = "fdr"),
  custom_rmd_config = NULL,
  custom_pre_content = NULL,
  custom_post_content = NULL,
  session_info = FALSE
)

```

Arguments

hyp_obj	A hyp object, multihyp object, or list of multihyp objects
file_path	A file path
title	Title of markdown report
subtitle	Subtitle of markdown report
author	Authors of markdown report
header	Header name of tabset section
versioning	Add versioning information
show_dots	Option to show dots plots in tabs
show_emaps	Option to show enrichment maps in tabs
show_hmaps	Option to show hierarchy maps in tabs
show_tables	Option to show table in tabs
hyp_dots_args	A list of keyword arguments passed to hyp_dots
hyp_emap_args	A list of keyword arguments passed to hyp_emap
hyp_hmap_args	A list of keyword arguments passed to hyp_hmap
custom_rmd_config	Replace configuration section of markdown report
custom_pre_content	Insert custom content before tabset section

custom_post_content Insert custom content after tabset section

session_info Use true to include session info

hyp_to_table *Export hyp/multihyp object to table*

Description

Export hyp/multihyp object to table

Usage

```
hyp_to_table(hyp_obj, file_path, sep = "\t", cols = NULL, versioning = TRUE)
```

Arguments

hyp_obj A hyp or multihyp object

file_path A file path for hyp objects and directory for multihyp objects

sep The field separator string

cols Dataframe columns to include

versioning Add header with versioning information

Examples

```
genesets <- msigdb_gsets("Homo sapiens", "C2", "CP:KEGG")

signature <- c("IDH3B", "DLST", "PCK2", "CS", "PDHB", "PCK1", "PDHA1", "LOC642502",
               "PDHA2", "LOC283398", "FH", "SDHD", "OGDH", "SDHB", "IDH3A", "SDHC",
               "IDH2", "IDH1", "OGDHL", "PC", "SDHA", "SUCLG1", "SUCLA2", "SUCLG2")

hyp_obj <- hypeR(signature, genesets, background=2522)

hyp_to_table(hyp_obj, file_path="pathways.txt")
```

limma	<i>Differential Expression</i>
-------	--------------------------------

Description

A differential expression table

Usage

```
limma
```

Format

A data frame

msigdb_available	<i>Get msigdb available genesets</i>
------------------	--------------------------------------

Description

Get msigdb available genesets

Usage

```
msigdb_available(species = "Homo sapiens")
```

Arguments

species	A species to determine gene symbols (refer to <code>?msigdb::msigdb</code> for available species)
---------	---

Value

A dataframe of available genesets

Examples

```
msigdb_available("Homo sapiens")
```

`msigdb_download` *Download data from msigdb in the form of a named list*

Description

Download data from msigdb in the form of a named list

Usage

```
msigdb_download(species, category, subcategory = "")
```

Arguments

<code>species</code>	A species to determine gene symbols (refer to <code>?msigdb::msigdb</code> for available species)
<code>category</code>	Geneset category (refer to <code>?msigdb::msigdb</code> for available categories)
<code>subcategory</code>	Geneset subcategory (refer to <code>?msigdb::msigdb</code> for available subcategories)

Value

A list of genesets

Examples

```
HALLMARK <- msigdb_download("Homo sapiens", "H", "")
```

`msigdb_gsets` *Download data from msigdb in the form of a gsets object*

Description

Download data from msigdb in the form of a gsets object

Usage

```
msigdb_gsets(species, category, subcategory = "", clean = FALSE)
```

Arguments

<code>species</code>	A species to determine gene symbols (refer to <code>?msigdb::msigdb</code> for available species)
<code>category</code>	Geneset category (refer to <code>?msigdb::msigdb</code> for available categories)
<code>subcategory</code>	Geneset subcategory (refer to <code>?msigdb::msigdb</code> for available subcategories)
<code>clean</code>	Use true to clean labels of genesets

Value

A gsets object

Examples

```
HALLMARK <- msigdb_gsets("Homo sapiens", "H", "")
```

msigdb_info	<i>Print msigdb gsets information</i>
-------------	---------------------------------------

Description

Print msigdb gsets information

Usage

```
msigdb_info()
```

Examples

```
msigdb_info()
```

msigdb_species	<i>Get msigdb available species</i>
----------------	-------------------------------------

Description

Get msigdb available species

Usage

```
msigdb_species()
```

Value

A character vector of species

Examples

```
msigdb_species()
```

msigdb_version *Get msigdb package version number*

Description

Get msigdb package version number

Usage

```
msigdb_version()
```

Value

Version number

Examples

```
msigdb_version()
```

multihyp *A multihyp object*

Description

A multihyp object

A multihyp object

See Also

hyp

Public fields

data A list of hyp objects

Methods**Public methods:**

- [multihyp\\$new\(\)](#)
- [multihyp\\$print\(\)](#)
- [multihyp\\$as.list\(\)](#)
- [multihyp\\$clone\(\)](#)

Method `new()`: Create a multihyp object

Usage:

```
multihyp$new(data)
```

Arguments:

data A list of hyp objects

Returns: A new multihyp object

Method print(): Print multihyp object

Usage:

```
multihyp$print()
```

Returns: NULL

Method as.list(): Print multihyp object

Usage:

```
multihyp$as.list()
```

Returns: A list of hyp objects as dataframes

Method clone(): The objects of this class are cloneable with this method.

Usage:

```
multihyp$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

Examples

```
data <- data.frame(replicate(5, sample(0:1, 10, rep=TRUE)))
args <- list("arg_1"=1, "arg_2"=2, "arg_3"=3)
hyp_obj <- hyp$new(data, args=args)
data <- list("hyp_1"=hyp_obj, "hyp_2"=hyp_obj, "hyp_3"=hyp_obj)
multihyp_obj <- multihyp$new(data)
```

 rctbl_build

Reactable builder for hyp or mhyp objects

Description

Reactable builder for hyp or mhyp objects

Usage

```
rctbl_build(obj, ...)
```

Arguments

obj	A hyp or multihyp object
...	Arguments passed to table generators

Examples

```
genesets <- msigdb_gsets("Homo sapiens", "C2", "CP:KEGG")$genesets[1:5]

experiment <- list("S1"=c("IDH3B", "DLST", "PCK2", "CS", "PDHB", "PCK1", "PDHA1", "LOC642502"),
                  "S2"=c("PDHA2", "LOC283398", "FH", "SDHD", "OGDH", "SDHB", "IDH3A", "SDHC"))

mhyp_obj <- hypeR(experiment, genesets, background=2522)

rctbl_build(mhyp_obj)
```

rctbl_hyp	<i>Reactable table for hyp objects</i>
-----------	--

Description

Reactable table for hyp objects

Usage

```
rctbl_hyp(
  hyp,
  type = c("inner", "outer"),
  show_emaps = FALSE,
  show_hmaps = FALSE,
  hyp_emap_args = list(top = 25, val = "fdr"),
  hyp_hmap_args = list(top = 25, val = "fdr")
)
```

Arguments

hyp	A hyp object
type	Use style class for outer or inner tables
show_emaps	Option to show enrichment maps in tabs
show_hmaps	Option to show hierarchy maps in tabs
hyp_emap_args	A list of keyword arguments passed to hyp_emap
hyp_hmap_args	A list of keyword arguments passed to hyp_hmap

Examples

```
genesets <- msigdb_gsets("Homo sapiens", "C2", "CP:KEGG")$genesets[1:5]

signature <- c("IDH3B", "DLST", "PCK2", "CS", "PDHB", "PCK1", "PDHA1", "LOC642502",
              "PDHA2", "LOC283398", "FH", "SDHD", "OGDH", "SDHB", "IDH3A", "SDHC",
              "IDH2", "IDH1", "OGDHL", "PC", "SDHA", "SUCLG1", "SUCLA2", "SUCLG2")

hyp_obj <- hypeR(signature, genesets, background=2522)
```

```
rctbl_hyp(hyp_obj)
```

rctbl_mhyp

Reactable table for multihyp objects

Description

Reactable table for multihyp objects

Usage

```
rctbl_mhyp(  
  mhyp,  
  show_emaps = FALSE,  
  show_hmaps = FALSE,  
  hyp_emap_args = list(top = 25, val = "fdr"),  
  hyp_hmap_args = list(top = 25, val = "fdr")  
)
```

Arguments

mhyp	A multihyp object
show_emaps	Option to show enrichment maps in tabs
show_hmaps	Option to show hierarchy maps in tabs
hyp_emap_args	A list of keyword arguments passed to hyp_emap
hyp_hmap_args	A list of keyword arguments passed to hyp_hmap

Examples

```
genesets <- msigdb_gsets("Homo sapiens", "C2", "CP:KEGG")$genesets[1:5]  
  
experiment <- list("S1"=c("IDH3B", "DLST", "PCK2", "CS", "PDHB", "PCK1", "PDHA1", "LOC642502"),  
                  "S2"=c("PDHA2", "LOC283398", "FH", "SDHD", "OGDH", "SDHB", "IDH3A", "SDHC"))  
  
mhyp_obj <- hyper(experiment, genesets, background=2522)  
  
rctbl_mhyp(mhyp_obj)
```

rgsets *A relational genesets object*

Description

A relational genesets object

A relational genesets object

See Also

gsets

Public fields

genesets A list of genesets where list names refers to geneset labels and values are geneset members represented as a vector

nodes A data frame of labeled nodes

edges A data frame of directed edges

name A character vector describing source of genesets

version A character vector describing versioning

Methods

Public methods:

- [rgsets\\$new\(\)](#)
- [rgsets\\$print\(\)](#)
- [rgsets\\$info\(\)](#)
- [rgsets\\$reduce\(\)](#)
- [rgsets\\$subset\(\)](#)
- [rgsets\\$clone\(\)](#)

Method `new()`: Create a rgsets object

Usage:

```
rgsets$new(  
  genesets,  
  nodes,  
  edges,  
  name = "Custom",  
  version = "",  
  quiet = FALSE  
)
```

Arguments:

genesets A list of genesets where list names refers to geneset labels and values are geneset members represented as a vector

nodes A data frame of labeled nodes
edges A data frame of directed edges
name A character vector describing source of genesets
version A character vector describing versioning
quiet Use true to silence warnings
Returns: A new rgsets object

Method print(): Print relational genesets information

Usage:
rgsets\$print()
Returns: NULL

Method info(): Returns versioning information

Usage:
rgsets\$info()
Returns: A character vector with name and version

Method reduce(): Reduces genesets to a background distribution of symbols

Usage:
rgsets\$reduce(background)
Arguments:
background A character vector of symbols
Returns: A rgsets object

Method subset(): Subsets genesets on a character vector of labels

Usage:
rgsets\$subset(labels)
Arguments:
labels A character vector of genesets
Returns: A rgsets object

Method clone(): The objects of this class are cloneable with this method.

Usage:
rgsets\$clone(deep = FALSE)
Arguments:
deep Whether to make a deep clone.

Examples

```
testdat <- readRDS(file.path(system.file("extdata", package="hypeR"), "testdat.rds"))
rgsets <- rgsets$new(genesets=testdat$genesets, nodes=testdat$nodes, edges=testdat$edges,
                    name="Example", version="v1.0")
```

wgcna

Co-expression Modules

Description

A list of co-expression modules

Usage

wgcna

Format

A nested list of character vectors

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