Package ‘hypeR’

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Description An R Package for Geneset Enrichment Workflows.

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Contents

`.check_overlap` *Check overlap of signature across genesets*

Description

Check overlap of signature across genesets

Usage

```
.check_overlap(signature, genesets, threshold = 0.05)
```

Arguments

`signature`	A vector of symbols
`genesets`	A list of genesets
`threshold`	Minimum percent overlap

Value

Percent overlap

`.dots_multi_plot` *Plot top enriched genesets across multiple signatures*

Description

Plot top enriched genesets across multiple signatures

Usage

```
.dots_multi_plot(
  multihyp_data,
  top = 20,
  abrv = 50,
  size_by = c("genesets", "significance", "none"),
  pval_cutoff = 1,
  fdr_cutoff = 1,
  val = c("fdr", "pval"),
  title = ""
)
```

Arguments

`multihyp_data`	A list of hyp objects
`top`	Limit number of genesets shown
`abrv`	Abbreviation length of genesetlabels
`size_by`	Size dots by e.g. c("genesets", "significance", "none")
`pval_cutoff`	Filter results to be less than pval cutoff
`fdr_cutoff`	Filter results to be less than fdr cutoff
`val`	Choose significance value e.g. c("fdr", "pval")
`title`	Plot title

Value

A ggplot object

`.dots_plot` *Plot top enriched genesets*

Description

Plot top enriched genesets

Usage

```
.dots_plot(
  hyp_df,
  top = 20,
  abrv = 50,
  size_by = c("genesets", "significance", "none"),
  pval_cutoff = 1,
  fdr_cutoff = 1,
  val = c("fdr", "pval"),
  title = ""
)
```

Arguments

`hyp_df`	A dataframe from a hyp object
`top`	Limit number of genesets shown
`abrv`	Abbreviation length of genesetlabels
`size_by`	Size dots by e.g. c("genesets", "significance", "none")
`pval_cutoff`	Filter results to be less than pval cutoff
`fdr_cutoff`	Filter results to be less than fdr cutoff
`val`	Choose significance value e.g. c("fdr", "pval")
`title`	Plot title

Value

A ggplot object

`.enrichment_map` *Plot enrichment map*

Description

Plot enrichment map

Usage

```
.enrichment_map(
  hyp_df,
  genesets,
  similarity_metric = c("jaccard_similarity", "overlap_similarity"),
  similarity_cutoff = 0.2,
  pval_cutoff = 1,
  fdr_cutoff = 1,
  val = c("fdr", "pval"),
  top = NULL,
  title = ""
)
```

Arguments

`hyp_df`	A dataframe from a hyp object
`genesets`	A list of genesets
`similarity_metric`	Metric to calculate geneset similarity
`similarity_cutoff`	Geneset similarity cutoff
`pval_cutoff`	Filter results to be less than pval cutoff
`fdr_cutoff`	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

`.find_members` *Find geneset members*

Description

Find geneset members

Usage

```
.find_members(id, genesets, nodes, edges)
```

Arguments

`id`	A vector of ids
`genesets`	A list of genesets (see `rgsets`)
`nodes`	A data frame of labeled nodes (see `rgsets`)
`edges`	A data frame of directed edges (see `rgsets`)

Value

A vector of ids

`.format_str` *Format a string using placeholders*

Description

Format a string using placeholders

Usage

```
.format_str(string, ...)
```

Arguments

`string`	A an unformatted string with placeholders
`...`	Variables to format placeholders with

Value

A formatted string

Examples

```
## Not run:
format_str("Format with {1} and {2}", "x", "y")

## End(Not run)
```

`.github_rds` *Load an rds file directly from github*

Description

Load an rds file directly from github

Usage

```
.github_rds(url)
```

Arguments

`url`	A url

Value

A list

`.hexa` *Adjust alpha of a hex string*

Description

Adjust alpha of a hex string

Usage

```
.hexa(hex, percent = 1)
```

Arguments

`hex`	A 6-character hex string (e.g. #000000)
`percent`	Alpha level from 0-1

Value

A hex string

`.hiearchy_map` *Plot hiearchy map*

Description

Plot hiearchy map

Usage

```
.hiearchy_map(
  hyp_df,
  rgsets_obj,
  pval_cutoff = 1,
  fdr_cutoff = 1,
  val = c("fdr", "pval"),
  top = NULL,
  title = "",
  graph = FALSE
)
```

Arguments

`hyp_df`	A dataframe from a hyp object
`rgsets_obj`	A relatonal geneset from a hyp object
`pval_cutoff`	Filter results to be less than pval cutoff
`fdr_cutoff`	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
`graph`	Return an igraph object instead

Value

A visNetwork object

`.hyperdb_url` *Get base url for hyperdb*

Description

Get base url for hyperdb

Usage

```
.hyperdb_url(api = FALSE)
```

Value

A base url

`.hyper_enrichment` *Overrepresentation test via hyper-geometric distribution*

Description

Overrepresentation test via hyper-geometric distribution

Usage

```
.hyper_enrichment(
  signature,
  genesets,
  background = length(unique(unlist(genesets))),
  plotting = TRUE
)
```

Arguments

`signature`	A vector of symbols
`genesets`	A list of genesets
`background`	Size of background population genes
`plotting`	Use true to generate plots

Value

A list of data and plots

`.jaccard_similarity` *Calculate jaccard similarity of two sets*

Description

Calculate jaccard similarity of two sets

Usage

```
.jaccard_similarity(a, b)
```

Arguments

`a`	A vector
`b`	A vector

Value

A numerical value

`.kstest` *One-sided Kolmogorov–Smirnov test*

Description

One-sided Kolmogorov–Smirnov test

Usage

```
.kstest(
  n.x,
  y,
  weights = NULL,
  weights.pwr = 1,
  absolute = FALSE,
  plotting = FALSE,
  plot.title = ""
)
```

Arguments

`n.x`	The length of a ranked list
`y`	A vector of positions in the ranked list
`weights`	Weights for weighted score (Subramanian et al.)
`weights.pwr`	Exponent for weights (Subramanian et al.)
`absolute`	Takes max-min score rather than the max deviation from null
`plotting`	Use true to generate plot
`plot.title`	Plot title

Value

A list of data and plots

`.ks_enrichment` *Enrichment test via one-sided Kolmogorov–Smirnov test*

Description

Enrichment test via one-sided Kolmogorov–Smirnov test

Usage

```
.ks_enrichment(
  signature,
  genesets,
  weights = NULL,
  weights.pwr = 1,
  absolute = FALSE,
  plotting = TRUE
)
```

Arguments

`signature`	A vector of ranked symbols
`genesets`	A list of genesets
`weights`	Weights for weighted score (Subramanian et al.)
`weights.pwr`	Exponent for weights (Subramanian et al.)
`absolute`	Takes max-min score rather than the max deviation from null
`plotting`	Use true to generate plot

Value

A list of data and plots

`.overlap_similarity` *Calculate overlap similarity of two sets*

Description

Calculate overlap similarity of two sets

Usage

```
.overlap_similarity(a, b)
```

Arguments

`a`	A vector
`b`	A vector

Value

A numerical value

`.reverselog_trans` *Custom reverse log transformation of continous ggplot axes*

Description

Custom reverse log transformation of continous ggplot axes

Usage

```
.reverselog_trans(base = exp(1))
```

Arguments

`base`	Logarithm base

`.string_args` *Convert an arguments list to string format*

Description

Convert an arguments list to string format

Usage

```
.string_args(args)
```

Arguments

`args`	A list of keyword arguments

Value

A string of keyword arguments

Examples

```
## Not run:
string_args(list(x=15, y="fdr", z=TRUE))

## End(Not run)
```

`clean_genesets` *Clean labels of genesets*

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_connect` *Connect to the enrichr web application*

Description

Connect to the enrichr web application

Usage

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

Arguments

`endpoint`	The url endpoint to connect to
`db`	A species

Value

A web response

`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")
```

`enrichr_urls` *Get url base for species-specific enrichr libraries*

Description

Get url base for species-specific enrichr libraries

Usage

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

Arguments

`db`	A species

Value

A url

`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` *Shiny interface module for geneset selection*

Description

Shiny interface module for geneset selection

Usage

```
genesets_UI(id)
```

Arguments

`id`	A unique namespace identifier

Value

Shiny ui elements

`ggempty` *An empty ggplot*

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 obect

Usage:

```
hyp$print()
```

Returns: NULL

Method `as.data.frame()`**:** Extract dataframe from hyp obect

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

`signature`	A vector of symbols
`genesets`	A gsets/rgsets object or a named list of genesets
`test`	Choose an enrichment type e.g. c("hypergeometric", "kstest")
`background`	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` *Download data from hyperdb*

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` *Download data from hyperdb in the form of a rgsets object*

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,
  size_by = c("genesets", "significance", "none"),
  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
`size_by`	Size dots by e.g. c("genesets", "significance", "none")
`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 hiearchy map*

Description

Visualize hyp/multihyp objects as a hiearchy map

Usage

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

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
`graph`	Return an igraph object instead

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` *Export hyp/multihyp object to excel*

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_graph` *Convert a hyp object to an igraph object*

Description

Convert a hyp object to an igraph object

Usage

```
hyp_to_graph(hyp_obj)
```

Arguments

`hyp_obj`	A hyp object

Value

An igraph 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)

ig <- hyp_to_graph(hyp_obj)
```

`hyp_to_rmd` *Export hyp object to rmarkdown*

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 hiearchy 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` *Differential Expression*

Description

A differential expression table

Usage

```
limma
```

Format

A data frame

`msigdb_available` *Get msigdbr available genesets*

Description

Get msigdbr available genesets

Usage

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

Arguments

`species`	A species to determine gene symbols (refer to ?msigdbr::msigdbr for avilable species)

Value

A dataframe of available genesets

Examples

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

`msigdb_check_species` *Check if species is available*

Description

Check if species is available

Usage

```
msigdb_check_species(species = "")
```

Arguments

`species`	A species

Examples

```
## Not run:
msigdb_check_species("Homo sapiens")

## End(Not run)
```

`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

`species`	A species to determine gene symbols (refer to ?msigdbr::msigdbr for avilable species)
`category`	Geneset category (refer to ?msigdbr::msigdbr for avilable categories)
`subcategory`	Geneset subcategory (refer to ?msigdbr::msigdbr for avilable 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

`species`	A species to determine gene symbols (refer to ?msigdbr::msigdbr for avilable species)
`category`	Geneset category (refer to ?msigdbr::msigdbr for avilable categories)
`subcategory`	Geneset subcategory (refer to ?msigdbr::msigdbr for avilable subcategories)
`clean`	Use true to clean labels of genesets

Value

A gsets object

Examples

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

`msigdb_info` *Print msigdb gsets information*

Description

Print msigdb gsets information

Usage

```
msigdb_info()
```

Examples

```
msigdb_info()
```

`msigdb_species` *Get msigdbr available species*

Description

Get msigdbr available species

Usage

```
msigdb_species()
```

Value

A character vector of species

Examples

```
msigdb_species()
```

`msigdb_version` *Get msigdbr package version number*

Description

Get msigdbr 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 obect

Usage:

```
multihyp$print()
```

Returns: NULL

Method `as.list()`**:** Print multihyp obect

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)
```

`pvector` *A push/pop capable vector*

Description

A push/pop capable vector

A push/pop capable vector

Public fields

`values` A vector of values

Methods

Public methods:

- `pvector$new()`
- `pvector$print()`
- `pvector$length()`
- `pvector$pop()`
- `pvector$push()`
- `pvector$clone()`

Method `new()`**:** Create a pvector

Usage:

`pvector$new(values = c())`

Arguments:

`values` A vector of values

Returns: A new pvector

Method `print()`**:** Print pvector

Usage:

`pvector$print()`

Returns: NULL

Method `length()`**:** Get length of pvector

Usage:

`pvector$length()`

Returns: An integer

Method `pop()`**:** Pop vector

Usage:

```
pvector$pop()
```

Returns: Popped value

Method `push()`**:** Push values

Usage:

```
pvector$push(pushed.values)
```

Arguments:

`pushed.values` A vector of values

Returns: NULL

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

Usage:

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

Arguments:

`deep` Whether to make a deep clone.

`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` *Reactable table for hyp objects*

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 hiearchy 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 hiearchy 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.

`wgcna` *Co-expression Modules*

Description

A list of co-expression modules

Usage

```
wgcna
```

Format

A nested list of character vectors

Index