

# Package ‘hypeR’

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**Title** An R Package For Geneset Enrichment Workflows

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**Description** An R Package for Geneset Enrichment Workflows.

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---

<code>.check_overlap</code>	<i>Check overlap of signature across genesets</i>
-----------------------------	---

---

## Description

Check overlap of signature across genesets

## Usage

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

## Arguments

<code>signature</code>	A vector of symbols
<code>genesets</code>	A list of genesets
<code>threshold</code>	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

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

<code>hyp_df</code>	A dataframe from a hyp object
<code>genesets</code>	A list of genesets
<code>similarity_metric</code>	Metric to calculate geneset similarity
<code>similarity_cutoff</code>	Geneset similarity cutoff
<code>pval_cutoff</code>	Filter results to be less than pval cutoff
<code>fdr_cutoff</code>	Filter results to be less than fdr cutoff
<code>val</code>	Choose significance value shown above nodes e.g. c("fdr", "pval")
<code>top</code>	Limit number of pathways shown
<code>title</code>	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)
```

---

<code>.github_rds</code>	<i>Load an rds file directly from github</i>
--------------------------	--

---

**Description**

Load an rds file directly from github

**Usage**

```
.github_rds(url)
```

**Arguments**

<code>url</code>	A url
------------------	-------

**Value**

A list

---

<code>.hexa</code>	<i>Adjust alpha of a hex string</i>
--------------------	-------------------------------------

---

**Description**

Adjust alpha of a hex string

**Usage**

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

**Arguments**

<code>hex</code>	A 6-character hex string (e.g. #000000)
<code>percent</code>	Alpha level from 0-1

**Value**

A hex string



---

.hierarchy\_map      *Plot hierarchy map*

---

### Description

Plot hierarchy map

### Usage

```
.hierarchy_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 relational 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

---

<code>.hyperdb_url</code>	<i>Get base url for hyperdb</i>
---------------------------	---------------------------------

---

**Description**

Get base url for hyperdb

**Usage**

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

**Value**

A base url

---

<code>.hyper_enrichment</code>	<i>Overrepresentation test via hyper-geometric distribution</i>
--------------------------------	---

---

**Description**

Overrepresentation test via hyper-geometric distribution

**Usage**

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

**Arguments**

<code>signature</code>	A vector of symbols
<code>genesets</code>	A list of genesets
<code>background</code>	Size of background population genes
<code>plotting</code>	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**

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

**Value**

A list of data and plots

---

<code>.ks_enrichment</code>	<i>Enrichment test via one-sided Kolmogorov–Smirnov test</i>
-----------------------------	--

---

**Description**

Enrichment test via one-sided Kolmogorov–Smirnov test

**Usage**

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

**Arguments**

<code>signature</code>	A vector of ranked symbols
<code>genesets</code>	A list of genesets
<code>weights</code>	Weights for weighted score (Subramanian et al.)
<code>weights.pwr</code>	Exponent for weights (Subramanian et al.)
<code>absolute</code>	Takes max-min score rather than the max deviation from null
<code>plotting</code>	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**

<code>a</code>	A vector
<code>b</code>	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**

<code>base</code>	Logarithm base
-------------------	----------------

---

<code>.string_args</code>	<i>Convert an arguments list to string format</i>
---------------------------	---

---

**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)
```

---

<code>clean_genesets</code>	<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\_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	<i>Get url base for species-specific enrichr libraries</i>
--------------	--

---

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

---

**Description**

An empty ggplot

**Usage**

```
ggempty()
```

**Value**

A ggplot object

---

ggeplot	<i>Enrichment plot implemented in ggplot</i>
---------	--

---

**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**

<code>a</code>	A vector for group a
<code>b</code>	A vector for group b
<code>ga</code>	A string label for group a
<code>gb</code>	A string label for group b
<code>title</code>	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
<code>power</code>	Exponent for weights (kstest only)
<code>absolute</code>	Takes max-min score rather than the max deviation from null (kstest only)
<code>pval</code>	Filter results to be less than pval cutoff
<code>fdr</code>	Filter results to be less than fdr cutoff
<code>plotting</code>	Use true to generate plots for each geneset test (may slow performance)
<code>quiet</code>	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_rgsets("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	<i>Visualize hyp/multihyp objects as a dots plot</i>
----------	--

---

**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
abbrv	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 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 = "",
  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	<i>Convert a hyp object to an igraph object</i>
--------------	---

---

**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	<i>Export hyp object to markdown</i>
------------	--------------------------------------

---

**Description**

Export hyp object to markdown

**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 ?msigdb::msigdb for available 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 ?msigdb::msigdb for available species)  
category           Geneset category (refer to ?msigdb::msigdb for available categories)  
subcategory        Geneset subcategory (refer to ?msigdb::msigdb for available subcategories)

**Value**

A list of genesets

**Examples**

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

---

msigdb_gsets	<i>Download data from msigdb in the form of a gsets object</i>
--------------	--

---

**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 ?msigdb::msigdb for available species)
category	Geneset category (refer to ?msigdb::msigdb for available categories)
subcategory	Geneset subcategory (refer to ?msigdb::msigdb for available subcategories)
clean	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	<i>Get msigdb package version number</i>
----------------	--

---

**Description**

Get msigdb package version number

**Usage**

```
msigdb_version()
```

**Value**

Version number

**Examples**

```
msigdb_version()
```

---

multihyp	<i>A multihyp object</i>
----------	--------------------------

---

**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)
```

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	<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	<i>Reactable table for multihyp objects</i>
------------	---

---

### 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	<i>A relational genesets object</i>
--------	-------------------------------------

---

### 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

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