

Package ‘hypeR’

October 16, 2019

Title Hyper Enrichment

Version 1.0.0

Author Anthony Federico <anfed@bu.edu>,
Stefano Monti <smonti@bu.edu>

Maintainer Anthony Federico <anfed@bu.edu>

Description Geneset enrichment analysis based on hyper-geometric test.

Depends R (>= 3.6.0)

License GPL-3 + file LICENSE

URL <https://github.com/montilab/hypeR>

Encoding UTF-8

RoxygenNote 6.1.1

Imports plotly, DT, magrittr, dplyr, openxlsx, msigdb,

Suggests devtools, testthat, knitr, httr

biocViews GeneSetEnrichment, Annotation, Pathways

VignetteBuilder knitr

BugReports <https://github.com/montilab/hypeR/issues>

git_url <https://git.bioconductor.org/packages/hypeR>

git_branch RELEASE_3_9

git_last_commit 84cf083

git_last_commit_date 2019-05-02

Date/Publication 2019-10-15

R topics documented:

.hyper_enrichment	2
.VERBOSE	2
db_get	3
db_info	3
download_gsets	4
download_msigdb	4
ex_get	5
hypeR	5
hyp_plot	6

hyp_show	7
hyp_to_excel	7
hyp_to_table	8

Index 10

.hyper_enrichment	<i>Carry out set enrichment test based on hyper-geometric distribution</i>
-------------------	--

Description

Carry out set enrichment test based on hyper-geometric distribution

Usage

```
.hyper_enrichment(drawn, categories,
  ntotal = length(unique(unlist(categories))), min.drawsize = 4,
  mht = TRUE, verbose = FALSE)
```

Arguments

drawn	One or more sets of 'drawn' items (e.g., genes). Basically, a list of signatures.
categories	list of gene sets (e.g., MSigDB c2)
ntotal	background population, i.e., the total no. of items from which items are supposed to have been drawn
min.drawsize	min no. of drawn items that must be among categories' items
mht	correct for multiple hypothesis testing across multiple 'draws'
verbose	Use false to suppress logs

Value

a data.frame with rows indexed by the signature(s) tested

.VERBOSE	<i>Function wrapper to control verbosity</i>
----------	--

Description

Function wrapper to control verbosity

Usage

```
.VERBOSE(v, ...)
```

Arguments

v	A bool
...	What to print

Value

None

db_get	<i>Fetch downloaded gene sets from msigdb</i>
--------	---

Description

Fetch downloaded gene sets from msigdb

Usage

```
db_get(msigdb_info, symbol = c("C1", "C2.CGP", "C2.CP", "C2.CP.BIOCARTA",  
"C2.CP.KEGG", "C2.CP.REACTOME", "C3.MIR", "C3.TFT", "C4.CGN", "C4.CM",  
"C5.BP", "C5.CC", "C5.MF", "C6", "C7", "H"))
```

Arguments

msigdb_info A list containing the gene set directory and version number of gene sets
symbol A symbol corresponding to a msigdb gene set

Value

A list of gene sets

Examples

```
msigdb_info <- download_msigdb()  
REACTOME <- db_get(msigdb_info, "C2.CP.REACTOME")
```

db_info	<i>Print available gene sets</i>
---------	----------------------------------

Description

Print available gene sets

Usage

```
db_info()
```

Value

A table of values

Examples

```
db_info()
```

download_gsets *Fetch a gene sets from msigdb*

Description

Fetch a gene sets from msigdb

Usage

```
download_gsets(species = "Homo sapiens", category, subcategory)
```

Arguments

species	A species to determine gene symbols (refer to ?msigdb::msigdb for available species)
category	Gene set category (refer to ?msigdb::msigdb for available categories)
subcategory	Gene set subcategory (refer to ?msigdb::msigdb for available subcategories)

Value

A list of gene sets

Examples

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

download_msigdb *Download all gene sets from msigdb for a given species*

Description

Download all gene sets from msigdb for a given species

Usage

```
download_msigdb(species = "Homo sapiens", output_dir = NULL)
```

Arguments

species	A species to determine gene symbols (refer to ?msigdb::msigdb for available species)
output_dir	A directory path where gene sets are downloaded instead of to the package location

Value

A list containing the output directory and version number of gene sets

Examples

```
msigdb_info <- download_msigdb()
```

ex_get	<i>Fetch example gene sets</i>
--------	--------------------------------

Description

Fetch example gene sets

Usage

```
ex_get(symbol = c("C2.CP.REACTOME", "C2.CP.BIOCARTA", "C2.CP.KEGG"))
```

Arguments

symbol A symbol corresponding to an example gene set

Value

A list of gene sets

Examples

```
REACTOME <- ex_get("C2.CP.REACTOME")
```

hyperR	<i>Perform hyper enrichment</i>
--------	---------------------------------

Description

Perform hyper enrichment

Usage

```
hyperR(symbols, gsets, bg = 23467, min.drawsize = 4, pval.cutoff = 1,
       fdr.cutoff = 1, verbose = FALSE)
```

Arguments

symbols A character vector of gene symbols

gsets A list of gene sets

bg Size or character vector of background population genes

min.drawsize Min number of drawn items that must be among categories items

pval.cutoff Filter results to be less than pval cutoff

fdr.cutoff Filter results to be less than fdr cutoff

verbose Use false to suppress logs

Value

A hyper dataframe

Examples

```
# Grab a list of curated gene sets
REACTOME <- ex_get("C2.CP.REACTOME")

# Genes involved in tricarboxylic acid cycle
symbols <- 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")

# Perform hyper enrichment
hyp <- hyper(symbols, REACTOME, bg=2522, fdr=0.05)
```

hyp_plot

Visualize top enriched pathways

Description

Visualize top enriched pathways

Usage

```
hyp_plot(df, top = 10, val = c("fdr", "pval"))
```

Arguments

df	A hyper dataframe
top	Limit number of pathways shown
val	Choose significance value e.g. c("pval", "fdr")

Value

A plotly object

Examples

```
# Grab a list of curated gene sets
REACTOME <- ex_get("C2.CP.REACTOME")

# Genes involved in tricarboxylic acid cycle
symbols <- 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")

# Perform hyper enrichment
hyp <- hyper(symbols, REACTOME, bg=2522, fdr=0.05)

# Visualize
hyp_plot(hyp, top=3, val="fdr")
```

hyp_show	<i>Convert hyper dataframe to an interactive datatable</i>
----------	--

Description

Convert hyper dataframe to an interactive datatable

Usage

```
hyp_show(df, simple = TRUE, stylish = FALSE)
```

Arguments

df	A hyper dataframe
simple	Use true to only include essential dataframe columns
stylish	Use true to add a bootstrap styling theme to datatable

Value

A datatable object

Examples

```
# Grab a list of curated gene sets
REACTOME <- ex_get("C2.CP.REACTOME")

# Genes involved in tricarboxylic acid cycle
symbols <- 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")

# Perform hyper enrichment
hyp <- hypeR(symbols, REACTOME, bg=2522, fdr=0.05)

# Export
hyp_show(hyp)
```

hyp_to_excel	<i>Export hyper dataframe to excel</i>
--------------	--

Description

Export hyper dataframe to excel

Usage

```
hyp_to_excel(df, file.path, cols = seq_len(ncol(df)))
```

Arguments

df	A hyper dataframe
file.path	Output file path
cols	Dataframe columns to include

Value

None

Examples

```
# Grab a list of curated gene sets
REACTOME <- ex_get("C2.CP.REACTOME")

# Genes involved in tricarboxylic acid cycle
symbols <- 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")

# Perform hyper enrichment
hyp <- hyper(symbols, REACTOME, bg=2522, fdr=0.05)

# Export
hyp_to_excel(hyp, file.path="pathways.xlsx")
```

hyp_to_table	<i>Export hyper dataframe to table</i>
--------------	--

Description

Export hyper dataframe to table

Usage

```
hyp_to_table(df, file.path, sep = "\t", cols = seq_len(ncol(df)))
```

Arguments

df	A hyper dataframe
file.path	Output file path
sep	The field separator string
cols	Dataframe columns to include

Value

None

Examples

```
# Grab a list of curated gene sets
REACTOME <- ex_get("C2.CP.REACTOME")

# Genes involved in tricarboxylic acid cycle
symbols <- 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")

# Perform hyper enrichment
hyp <- hypeR(symbols, REACTOME, bg=2522, fdr=0.05)

# Export
hyp_to_table(hyp, file.path="pathways.txt")
```

Index

.VERBOSE, [2](#)
.hyper_enrichment, [2](#)

db_get, [3](#)
db_info, [3](#)
download_gsets, [4](#)
download_msigdb, [4](#)

ex_get, [5](#)

hyp_plot, [6](#)
hyp_show, [7](#)
hyp_to_excel, [7](#)
hyp_to_table, [8](#)
hypeR, [5](#)