

Package: enrichR (via r-universe)

February 2, 2025

Title Provides an R Interface to 'Enrichr'

Version 3.4

Description Provides an R interface to all 'Enrichr' databases.

'Enrichr' is a web-based tool for analysing gene sets and returns any enrichment of common annotated biological features.

Quoting from their website 'Enrichment analysis is a computational method for inferring knowledge about an input gene set by comparing it to annotated gene sets representing prior biological knowledge.' See

<<https://maayanlab.cloud/Enrichr/>> for further details.

Depends R (>= 3.5.0)

License GPL (>=2)

Encoding UTF-8

LazyData true

Imports httr, curl, rjson, ggplot2, WriteXLS

RoxygenNote 7.3.2

Suggests knitr, rmarkdown

VignetteBuilder knitr

Config/pak/sysreqs libssl-dev perl

Repository <https://satijalab.r-universe.dev>

RemoteUrl <https://github.com/wjawaid/enrichR>

RemoteRef HEAD

RemoteSha 79fad70a8c1c1ae2150025d616de434aa2bef05b

Contents

.add_background	2
.add_list	3
.enrichment_prep_df	3
.formatGenes	4
.get_backgroundenrich	5

.onAttach	5
.proxyOpts	6
.read_gmt	6
background	7
enrichr	7
genes790	9
getEnrichr	9
input	10
listEnrichrDbs	10
listEnrichrSites	11
plotEnrich	11
printEnrich	13
setEnrichrSite	14
Index	15

<code>.add_background</code>	<i>Upload background list using Speedrichr API</i>
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Description

Upload background list using Speedrichr API

Usage

```
.add_background(genes)
```

Arguments

`genes` gene list

Details

Upload background list using Speedrichr API

Value

R object from JSON

Author(s)

I-Hsuan Lin <i-hsuan.lin@manchester.ac.uk>

Details

Given a Enrichr output, order and subset criteria, returns a data frame accordingly

Value

Data frame

Author(s)

I-Hsuan Lin <i-hsuan.lin@manchester.ac.uk>

.formatGenes

FormatGenes

Description

Given an input, check format and return a character vector

Usage

```
.formatGenes(x, type = c("standard", "background"))
```

Arguments

x	Vector or dataframe of genes with or without score
type	Depends on type of gene input

Details

In standard analysis without background, crisp (symbols only) and fuzzy (with scores) gene sets are acceptable In analysis with background, only crisp gene sets are acceptable

Value

Character vector

Author(s)

I-Hsuan Lin <i-hsuan.lin@manchester.ac.uk>

`.get_backgroundenrich` *Get enrichment result using Speedrichr API*

Description

Get enrichment result using Speedrichr API

Usage

```
.get_backgroundenrich(uId, bId, db)
```

Arguments

<code>uId</code>	user List ID
<code>bId</code>	background ID
<code>db</code>	background Type

Details

Get enrichment result using Speedrichr API

Value

R object from JSON

Author(s)

I-Hsuan Lin <i-hsuan.lin@manchester.ac.uk>

`.onAttach` *onLoad hook to setup package options*

Description

onLoad hook to setup package options

Usage

```
.onAttach(libname, pkgname)
```

Arguments

<code>libname</code>	(Required). Library name
<code>pkgname</code>	(Required). Package name

Details

onLoad hook to setup package options and to check connection to website

Author(s)

Wajid Jawaid <wajid.jawaid@gmail.com>

.proxyOpts	<i>Internal function to check RCurlOptions</i>
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Description

Internal function to check RCurlOptions

Usage

```
.proxyOpts()
```

Details

Internal function to check RCurlOptions

Value

Named vector

Author(s)

I-Hsuan Lin <i-hsuan.lin@manchester.ac.uk>

.read_gmt	<i>Download and parse GMT files from Enrichr</i>
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Description

Download and parse GMT files from Enrichr

Usage

```
.read_gmt(db)
```

Arguments

db	library
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Details

Download and parse GMT files from Enrichr

Value

List object

Author(s)

I-Hsuan Lin <i-hsuan.lin@manchester.ac.uk>

background	<i>Example background genes</i>
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Description

This is a character vector which consists of 20,625 gene symbols taken from the Enrichr website.

Usage

```
data(background)
```

Format

vector

Examples

```
data(background)
length(background)
```

enrichr	<i>Gene enrichment using Enrichr</i>
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Description

Gene enrichment using Enrichr

Usage

```
enrichr(
  genes,
  databases = NULL,
  background = NULL,
  include_overlap = FALSE,
  sleepTime = 1
)
```

Arguments

genes	(Required). Character vector of Entrez gene symbols as input. A data.frame of gene symbols in first column is also acceptable, optionally a score denoting the degree of membership between 0 and 1 in the second column.
databases	(Required). Character vector of databases to search. See https://maayanlab.cloud/Enrichr/ for available databases.
background	(Optional). Character vector of Entrez gene symbols to be used as background. A data.frame of gene symbols in first column is also acceptable. Default is "NULL". Enrichment analysis with background genes is only available on the main site (Enrichr). Also, it is using a different API service (Speedrichr), hence it is a little slower to complete and return the results.
include_overlap	(Optional). Download database in GMT format to include 'Overlap' in the resulting data.frame when analysing with a background. Default is "FALSE".
sleepTime	(Optional) Time to wait (in seconds) between sending requests to the server to prevent the same results being returned as the previous request. Default is 1.

Details

Gene enrichment using Enrichr, also, you can now try adding a background.

Value

Returns a list of data.frame of enrichment terms, p-values, ...

Author(s)

Wajid Jawaid <wajid.jawaid@gmail.com>

Examples

```
# data(input) # Load example input genes
# data(background) # Load example background genes
# dbs <- c("GO_Molecular_Function_2023", "GO_Cellular_Component_2023",
#         "GO_Biological_Process_2023")
# if (getOption("enrichR.live")) {
#   enriched1 <- enrichr(input, dbs)
#   print(head(enriched1[[1]]))

#   # Include background
#   enriched2 <- enrichr(input, dbs, background = background)
#   print(head(enriched2[[1]]))

#   # Include background and add 'Overlap' info
#   enriched3 <- enrichr(input, dbs, background = background, include_overlap = TRUE)
#   print(head(enriched3[[1]]))
# }
```

genes790	<i>790 gene symbols</i>
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Description

This is a character vector which consists of randomly selected 790 genes.

Usage

```
data(genes790)
```

Format

vector

Examples

```
data(genes790)
length(genes790)
```

getEnrichr	<i>Helper function for HTTP methods GET and POST</i>
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Description

Helper function

Usage

```
getEnrichr(method = "GET", url, ...)
```

Arguments

method	(Required). HTTP method. Default is "GET"
url	(Required). URL address requested
...	(Optional). Additional parameters to pass to GET

Details

Helper function for HTTP methods GET and POST

Value

same as GET

Author(s)

Wajid Jawaid <wajid.jawaid@gmail.com>
I-Hsuan Lin <i-hsuan.lin@manchester.ac.uk>

input

Example input genes

Description

This is a character vector which consists of 375 gene symbols taken from the Enrichr website.

Usage

```
data(input)
```

Format

vector

Examples

```
data(input)  
length(input)
```

listEnrichrDbs

Look up available databases on Enrichr

Description

Look up available databases on Enrichr

Usage

```
listEnrichrDbs()
```

Details

Look up available databases on Enrichr

Value

A data.frame of available Enrichr databases

Author(s)

Wajid Jawaid <wajid.jawaid@gmail.com>

Examples

```
dbs <- listEnrichDbs()
```

listEnrichSites	<i>List Enrich Websites</i>
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Description

List modEnrich Websites

Usage

```
listEnrichSites()
```

Details

List Enrich Websites

Value

print Enrich Website status

Author(s)

Alexander Blume

plotEnrich	<i>plotEnrich</i>
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Description

Visualise a Enrich output as barplot

Usage

```
plotEnrich(  
  df,  
  showTerms = 20,  
  numChar = 40,  
  y = "Count",  
  orderBy = "P.value",  
  xlab = NULL,  
  ylab = NULL,  
  title = NULL  
)
```

Arguments

df	(Required). A single data.frame from a list of Enrichr output.
showTerms	(Optional). Number of terms to show. Default is 20.
numChar	(Optional). A single integer. Default is 40. Indicates the number characters to keep in the term description.
y	(Optional). A character string. Default is "Count". Indicates the variable that should be mapped to the y-axis. It can be either "Count" or "Ratio". Results that includes background genes in the analysis can only show "Count".
orderBy	(Optional). A character string. Default is "P.value". Indicates how to order the Enrichr results before subsetting to keep top N terms. It can be one of these: <ul style="list-style-type: none"> • "P.value" • "Adjusted.P.value" (or "FDR") • "Combined.Score" (or "Score")
xlab	(Optional). A character string. Default is NULL. Indicates the x-axis label.
ylab	(Optional). A character string. Default is NULL. Indicates the y-axis label.
title	(Optional). A character string. Default is NULL. Indicates the main title for the graphic.

Details

Visualise Enrichr result from a selected gene-set library as barplot.

Value

A [ggplot](#) plot object

Author(s)

I-Hsuan Lin <i-hsuan.lin@manchester.ac.uk>

See Also

[ggplot](#)

Examples

```
# data(input) # Load example input genes
# dbs <- c("GO_Molecular_Function_2023", "GO_Cellular_Component_2023",
#         "GO_Biological_Process_2023")
# if (getOption("enrichR.live")) {
#   enriched <- enrichr(input, dbs)
#   print(head(enriched[[1]]))
#   # Plot top 20 terms from "GO_Biological_Process_2023" and ordered by P-value
#   plotEnrich(enriched[[3]], showTerms = 20, numChar = 50, y = "Count",
#             orderBy = "P.value")
# }
```

printEnrich	<i>printEnrich</i>
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Description

Print Enrichr results

Usage

```
printEnrich(  
  data,  
  prefix = "enrichr",  
  showTerms = NULL,  
  columns = c(1:9),  
  outFile = c("txt", "excel")  
)
```

Arguments

data	(Required). Output list object from the "enrichr" function.
prefix	(Optional). Prefix of output file. Default is "enrichr".
showTerms	(Optional). Number of terms to show. Default is NULL to print all terms.
columns	(Optional). Columns from each entry of data. Default is c(1:9) to print all columns. * Results without background: 1-"Term", 2-"Overlap", 3-"P.value", 4-"Adjusted.P.value", 5-"Old.P.value", 6-"Old.Adjusted.P.value", 7-"Odds.Ratio", 8-"Combined.Score", 9-"Combined.Score". * In results with background, the second column is "Rank" if terms are not identical with those annotated in the Enrichr GMT files
outFile	(Optional). Output file format, choose from "txt" and "excel". Default is "txt".

Details

Print Enrichr results from the selected gene-set libraries to individual text files or a Excel spreadsheet.

Author(s)

Wajid Jawaid <wajid.jawaid@gmail.com>
I-Hsuan Lin <i-hsuan.lin@manchester.ac.uk>

Examples

```
# data(input) # Load example input genes  
# if (getOption("enrichR.live")) {  
#   enrichRLive <- TRUE  
#   dbs <- listEnrichrDbs()
```

```
# if(is.null(dbs)) enrichRLive <- FALSE
# dbs <- c("GO_Molecular_Function_2023", "GO_Cellular_Component_2023",
#         "GO_Biological_Process_2023")
# enriched <- enrichr(input, dbs)
# print(head(enriched[[1]]))
# # if (enrichRLive) printEnrich(enriched, outFile = "excel")
# }
```

setEnrichrSite

Set Enrichr Website

Description

Set Enrichr Website

Usage

```
setEnrichrSite(site)
```

Arguments

site site requested

Details

Set Enrichr Website

Value

Changes Enrichr Website connection

Author(s)

Alexander Blume

Index

* datasets

- background, [7](#)
- genes790, [9](#)
- input, [10](#)
- .add_background, [2](#)
- .add_list, [3](#)
- .enrichment_prep_df, [3](#)
- .formatGenes, [4](#)
- .get_backgroundenrich, [5](#)
- .onAttach, [5](#)
- .proxyOpts, [6](#)
- .read_gmt, [6](#)

background, [7](#)

enrichr, [7](#)

genes790, [9](#)

getEnrichr, [9](#)

ggplot, [12](#)

input, [10](#)

listEnrichrDbs, [10](#)

listEnrichrSites, [11](#)

plotEnrich, [11](#)

printEnrich, [13](#)

setEnrichrSite, [14](#)