

Package: enrichR (via r-universe)

December 12, 2024

Title Provides an R Interface to 'Enrichr'

Version 3.2

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/>](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://cogdisreslab.r-universe.dev>

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

RemoteRef HEAD

RemoteSha a7bc48f0d66d2ede3ecfcee6428fdb47fa2faeeb

Contents

.onAttach	2
background	2
enrichr	3
genes790	4
getEnrichr	5

input	5
listEnrichrDbs	6
listEnrichrSites	6
plotEnrich	7
printEnrich	8
setEnrichrSite	9

Index 11

<code>.onAttach</code>	<i>onLoad hook to setup package options</i>
------------------------	---

Description

onLoad hook to setup package options

Usage

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

Arguments

libname	(Required). Library name
pkgname	(Required). Package name

Details

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

Author(s)

Wajid Jawaid <wj241@alumni.cam.ac.uk>

background	<i>Example background genes</i>
------------	---------------------------------

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 *Gene enrichment using Enrichr*

Description

Gene enrichment using Enrichr

Usage

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

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".

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 <wj241@alumni.cam.ac.uk>

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

790 gene symbols

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>
------------	--

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/POST

Details

Helper function for HTTP methods GET and POST

Value

same as GET/POST

Author(s)

Wajid Jawaid <wj241@alumni.cam.ac.uk>
I-Hsuan Lin <i-hsuan.lin@manchester.ac.uk>

input	<i>Example input genes</i>
-------	----------------------------

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	<i>Look up available databases on Enrichr</i>
----------------	---

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 <wj241@alumni.cam.ac.uk>

Examples

```
dbs <- listEnrichrDbs()
```

listEnrichrSites	<i>List Enrichr Websites</i>
------------------	------------------------------

Description

List modEnrichr Websites

Usage

```
listEnrichrSites()
```

Details

List Enrichr Websites

Value

print Enrichr Website status

Author(s)

Alexander Blume

plotEnrich

plotEnrich

Description

Visualise a Enrichr 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 `ggplot2` 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

printEnrich

Description

Print Enrichr results

Usage

```
printEnrich(
  data,
  prefix = "enrichr",
  showTerms = NULL,
  columns = c(1:9),
  outFile = c("txt", "excel"),
  write2file = NULL
)
```


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".
write2file	(Optional). Deprecated argument. Always print to text or Excel file(s).

Details

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

Author(s)

Wajid Jawaid <wj241@alumni.cam.ac.uk>

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, write2file = FALSE)
}
```

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, 2
- genes790, 4
- input, 5
- .onAttach, 2

background, 2

enrichr, 3

genes790, 4

getEnrichr, 5

ggplot, 8

input, 5

listEnrichrDbs, 6

listEnrichrSites, 6

plotEnrich, 7

printEnrich, 8

setEnrichrSite, 9