Package 'enrichR'

April 14, 2023

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 biologi-
cal features. Quoting from their website 'Enrichment analysis is a computational method for in-
ferring knowledge about an input gene set by comparing it to annotated gene sets represent-
ing prior biological knowledge.' See <https://maayanlab.cloud/Enrichr/> for further de-
tails.

Depends R (>= 3.0.0)

License GPL (>= 2)

Encoding UTF-8

LazyData true

Imports httr, curl, rjson, ggplot2, WriteXLS

RoxygenNote 7.2.3

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

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enrichR-package   *enrichR package*

Description

The enrichR package provides an R interface to all enrichR (https://maayanlab.cloud/Enrichr/) databases.

Author(s)

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

.onAttach   *onLoad hook to setup package options*

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>

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enrichr	*Gene enrichment using Enrichr*

Description

Gene enrichment using Enrichr

Usage

```
enrichr(genes, databases = NULL)
```

Arguments

genes	(Required). Character vector of gene names or data.frame of gene names in in first column and a score between 0 and 1 in the other.
databases	(Required). Character vector of databases to search. See https://maayanlab.cloud/Enrichr/ for available databases.

Details

Gene enrichment using Enrichr

Value

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

Author(s)

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

Examples

```
dbs <- listEnrichrDbs()
dbs <- c("GO_Molecular_Function_2018", "GO_Cellular_Component_2018",
         "GO_Biological_Process_2018")
enriched <- enrichr(c("Runx1", "Gfi1", "Gfi1b", "Spi1", "Gata1", "Kdr"), dbs)
```

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genes790	*790 gene symbols*

Description

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

Format

vector

Examples

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

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getEnrichr	*Helper function for GET*

Description

Helper function

Usage

```
getEnrichr(url, ...)
```

Arguments

url	(Required). URL address requested
...	(Optional). Additional parameters to pass to GET

Details

Helper function for GET

Value

same as GET

Author(s)

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

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

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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 <wj241@alumni.cam.ac.uk>

Examples

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

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listEnrichrSites *List Enrichr Websites*

Description

List modEnrichr Websites

Usage

```
listEnrichrSites(...)
```

Arguments

... (Optional Additional parameters)

Details

List Enrichr Websites

Value

print Enrichr Website status

Author(s)

Alexander Blume

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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".
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 either "P.value" or "Combined.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](#)2 plot object

Author(s)

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

See Also

[ggplot](#)

Examples

```
if (getOption("enrichR.live")) {
  dbs <- listEnrichrDbs()
  enrichRLive <- TRUE
  if (is.null(dbs)) enrichRLive <- FALSE
  dbs <- c("GO_Molecular_Function_2018", "GO_Cellular_Component_2018",
           "GO_Biological_Process_2018")
  enriched <- enrichr(c("Runx1", "Gfi1", "Gfi1b", "Spi1", "Gata1", "Kdr"), dbs)
  # Plot top 20 terms from "GO_Biological_Process_2018" and ordered by P-value
  if (enrichRLive) {
    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),
  write2file = TRUE,
  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. 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"
`write2file`	(Optional). Set to TRUE if you would like this functino to output a file
`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.

Author(s)

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

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

Examples

```
if (getOption("enrichR.live")) {
  enrichRLive <- TRUE
  dbs <- listEnrichrDbs()
  if(is.null(dbs)) enrichRLive <- FALSE
  dbs <- c("GO_Molecular_Function_2018", "GO_Cellular_Component_2018",
           "GO_Biological_Process_2018")
  enriched <- enrichr(c("Runx1", "Gfi1", "Gfi1b", "Spi1", "Gata1", "Kdr"), dbs)
  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

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