Package ‘enrichR’

October 13, 2022

Title Provides an R Interface to 'Enrichr'

Version 3.1

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 (>= 3.0.0)

License GPL (>= 2)

Encoding UTF-8

LazyData true

Imports httr, curl, rjson, ggplot2

RoxygenNote 7.2.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

Date/Publication 2022-08-10 16:10:12 UTC

R topics documented:

`.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`>

`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)
```

`genes790` *790 gene symbols*

Description

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

Usage

```
genes790
```

Format

A vector.

`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`>

`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()
```

`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

`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

Print Enrichr output to text file.

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 GO-BP results ordered by P-value
  if (enrichRLive) {
    plotEnrich(enriched[[3]], showTerms = 20, numChar = 50, y = "Count",
               orderBy = "P.value")
  }
}
```

`printEnrich` *printEnrich*

Description

Print Enrichr output.

Usage

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

Arguments

`data`	(Required). Output from 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"

Details

Print Enrichr output to text file.

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)
}
```

`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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