

Package ‘enrichR’

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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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.onAttach	<i>onLoad hook to setup package options</i>
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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	<i>Gene enrichment using Enrichr</i>
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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()
```

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

List modEnrichr Websites

Usage

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

Arguments

... (Optional Additional parameters)

Details

List Enrichr Websites

Value

print Enrichr Website status

Author(s)

Alexander Blume

plotEnrich	<i>plotEnrich</i>
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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 `ggplot2` 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	<i>Set Enrichr Website</i>
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Description

Set Enrichr Website

Usage

```
setEnrichrSite(site)
```

Arguments

site	site requested
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Details

Set Enrichr Website

Value

Changes Enrichr Website connection

Author(s)

Alexander Blume

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