

Package ‘enrichR’

August 29, 2019

Title Provides an R Interface to 'Enrichr'

Version 2.1

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 (<http://amp.pharm.mssm.edu/Enrichr/>) for further details.

Depends R (>= 3.0.0)

License GPL (>= 2)

Encoding UTF-8

LazyData true

Imports httr, rjson

RoxygenNote 6.1.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Author Wajid Jawaid [aut, cre]

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

Repository CRAN

Date/Publication 2019-08-29 16:00:02 UTC

R topics documented:

.onAttach	2
enrichr	2
genes790	3
getEnrichr	3
listEnrichrDbs	4
printEnrich	4
Index	6

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

Description

onLoad hook to setup package options

Usage

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

Arguments

libname	Library name
pkgname	Package name

Details

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

Value

Nil

Author(s)

Wajid Jawaid

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

Description

Gene enrichment using Enrichr

Usage

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

Arguments

genes	Character vector of gene names or dataframe of gene names in first column and a score between 0 and 1 in the other.
databases	Character vector of databases to search. See http://amp.pharm.mssm.edu/Enrichr/ for available databases.

Details

Gene enrichment using Enrichr

Value

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

Author(s)

Wajid Jawaid

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

Description

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

Usage

```
genes790
```

Format

A vector.

getEnrichr	<i>Helper function for GET</i>
------------	--------------------------------

Description

Helper function

Usage

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

Arguments

url	url address requested
...	Additional parameters to pass to GET

Details

Helper function for GET

Value

same as GET

Author(s)

Wajid Jawaid

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

dataframe of available Enrichr databases

Author(s)

Wajid Jawaid

printEnrich	<i>Print Enrichr output to text file.</i>
-------------	---

Description

Print Enrichr output.

Usage

```
printEnrich(data, file, sep = "\t", columns = c(2, 3, 6))
```

Arguments

data	Output from Enrichr function.
file	Name of output file.
sep	Default TAB. How to separate fields.
columns	Columns from each entry of data. 1-"Index", 2-"Name", 3-"Adjusted_P-value", 4-"Z-score" 5-"Combined_Score", 6-"Genes", 7-"Overlap_P-value"

Details

Print Enrichr output to text file.

Value

Produces file.

Author(s)

Wajid Jawaid

Index

*Topic **datasets**

genes790, 3

.onAttach, 2

enrichr, 2

genes790, 3

getEnrichr, 3

listEnrichrDbs, 4

printEnrich, 4