

# Package: enrichR (via r-universe)

November 5, 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/> for further details.

**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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**Config/pak/sysreqs** libssl-dev perl

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enrichR-package	<i>enrichR package</i>
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### 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>

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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>

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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 first column and a score between 0 and 1 in the other.
databases	(Required). Character vector of databases to search. See <a href="https://maayanlab.cloud/Enrichr/">https://maayanlab.cloud/Enrichr/</a> 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](mailto: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	<i>790 gene symbols</i>
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**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	<i>Helper function for GET</i>
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**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*

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**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*

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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

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plotEnrich

*plotEnrich*

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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**

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**

```
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")
  }
}
```

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`printEnrich`

*printEnrich*

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**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 function 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)
}
```

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setEnrichrSite

*Set Enrichr Website*

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**Description**

Set Enrichr Website

**Usage**

```
setEnrichrSite(site)
```

**Arguments**

site	site requested
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*setEnrichrSite*

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**Details**

Set Enrichr Website

**Value**

Changes Enrichr Website connection

**Author(s)**

Alexander Blume

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