

# Package: enrichR (via r-universe)

March 5, 2025

**Title** Provides an R Interface to 'Enrichr'

**Version** 3.4

**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 (>= 3.5.0)

**License** GPL (>=2)

**Encoding** UTF-8

**LazyData** true

**Imports** httr, curl, rjson, ggplot2, WriteXLS

**RoxygenNote** 7.3.2

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

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

**Repository** <https://wjawaid.r-universe.dev>

**RemoteUrl** <https://github.com/wjawaid/enrichr>

**RemoteRef** HEAD

**RemoteSha** 79fad70a8c1c1ae2150025d616de434aa2bef05b

## Contents

.add_background	2
.add_list	3
.enrichment_prep_df	3
.formatGenes	4
.get_backgroundenrich	5

.onAttach . . . . .	5
.proxyOpts . . . . .	6
.read_gmt . . . . .	6
background . . . . .	7
enrichr . . . . .	7
genes790 . . . . .	9
getEnrichr . . . . .	9
input . . . . .	10
listEnrichrDbs . . . . .	10
listEnrichrSites . . . . .	11
plotEnrich . . . . .	11
printEnrich . . . . .	13
setEnrichrSite . . . . .	14
<b>Index</b>	<b>15</b>

---

<code>.add_background</code>	<i>Upload background list using Speedrichr API</i>
------------------------------	--

---

## Description

Upload background list using Speedrichr API

## Usage

```
.add_background(genes)
```

## Arguments

genes            gene list

## Details

Upload background list using Speedrichr API

## Value

R object from JSON

## Author(s)

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



**Details**

Given a Enrichr output, order and subset criteria, returns a data frame accordingly

**Value**

Data frame

**Author(s)**

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

---

*.formatGenes*

*FormatGenes*

---

**Description**

Given an input, check format and return a character vector

**Usage**

```
.formatGenes(x, type = c("standard", "background"))
```

**Arguments**

x	Vector or dataframe of genes with or without score
type	Depends on type of gene input

**Details**

In standard analysis without background, crisp (symbols only) and fuzzy (with scores) gene sets are acceptable In analysis with background, only crisp gene sets are acceptable

**Value**

Character vector

**Author(s)**

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

---

.get\_backgroundenrich *Get enrichment result using Speedrichr API*

---

### **Description**

Get enrichment result using Speedrichr API

### **Usage**

```
.get_backgroundenrich(uId, bId, db)
```

### **Arguments**

uId	user List ID
bId	background ID
db	background Type

### **Details**

Get enrichment result using Speedrichr API

### **Value**

R object from JSON

### **Author(s)**

I-Hsuan Lin <i-hsuan.lin@manchester.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 <wajid.jawaid@gmail.com>

---

.proxyOpts	<i>Internal function to check RCurlOptions</i>
------------	--

---

**Description**

Internal function to check RCurlOptions

**Usage**

```
.proxyOpts()
```

**Details**

Internal function to check RCurlOptions

**Value**

Named vector

**Author(s)**

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

---

.read_gmt	<i>Download and parse GMT files from Enrichr</i>
-----------	--

---

**Description**

Download and parse GMT files from Enrichr

**Usage**

```
.read_gmt(db)
```

**Arguments**

db	library
----	---------

**Details**

Download and parse GMT files from Enrichr

**Value**

List object

**Author(s)**

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

---

background	<i>Example background genes</i>
------------	---------------------------------

---

**Description**

This is a character vector which consists of 20,625 gene symbols taken from the Enrichr website.

**Usage**

```
data(background)
```

**Format**

vector

**Examples**

```
data(background)
length(background)
```

---

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

---

**Description**

Gene enrichment using Enrichr

**Usage**

```
enrichr(
  genes,
  databases = NULL,
  background = NULL,
  include_overlap = FALSE,
  sleepTime = 1
)
```

**Arguments**

genes	(Required). Character vector of Entrez gene symbols as input. A data.frame of gene symbols in first column is also acceptable, optionally a score denoting the degree of membership between 0 and 1 in the second column.
databases	(Required). Character vector of databases to search. See <a href="https://maayanlab.cloud/Enrichr/">https://maayanlab.cloud/Enrichr/</a> for available databases.
background	(Optional). Character vector of Entrez gene symbols to be used as background. A data.frame of gene symbols in first column is also acceptable. Default is "NULL". Enrichment analysis with background genes is only available on the main site (Enrichr). Also, it is using a different API service (Speedrichr), hence it is a little slower to complete and return the results.
include_overlap	(Optional). Download database in GMT format to include 'Overlap' in the resulting data.frame when analysing with a background. Default is "FALSE".
sleepTime	(Optional) Time to wait (in seconds) between sending requests to the server to prevent the same results being returned as the previous request. Default is 1.

**Details**

Gene enrichment using Enrichr, also, you can now try adding a background.

**Value**

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

**Author(s)**

Wajid Jawaid <[wajid.jawaid@gmail.com](mailto:wajid.jawaid@gmail.com)>

**Examples**

```
# data(input) # Load example input genes
# data(background) # Load example background genes
# dbs <- c("GO_Molecular_Function_2023", "GO_Cellular_Component_2023",
#         "GO_Biological_Process_2023")
# if (getOption("enrichR.live")) {
#   enriched1 <- enrichr(input, dbs)
#   print(head(enriched1[[1]]))

#   # Include background
#   enriched2 <- enrichr(input, dbs, background = background)
#   print(head(enriched2[[1]]))

#   # Include background and add 'Overlap' info
#   enriched3 <- enrichr(input, dbs, background = background, include_overlap = TRUE)
#   print(head(enriched3[[1]]))
# }
```



---

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

---

**Description**

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

**Usage**

```
data(genes790)
```

**Format**

vector

**Examples**

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

---

getEnrichr	<i>Helper function for HTTP methods GET and POST</i>
------------	--

---

**Description**

Helper function

**Usage**

```
getEnrichr(method = "GET", url, ...)
```

**Arguments**

method	(Required). HTTP method. Default is "GET"
url	(Required). URL address requested
...	(Optional). Additional parameters to pass to GET

**Details**

Helper function for HTTP methods GET and POST

**Value**

same as GET

**Author(s)**

Wajid Jawaid <wajid.jawaid@gmail.com>  
I-Hsuan Lin <i-hsuan.lin@manchester.ac.uk>

---

input	<i>Example input genes</i>
-------	----------------------------

---

**Description**

This is a character vector which consists of 375 gene symbols taken from the Enrichr website.

**Usage**

```
data(input)
```

**Format**

vector

**Examples**

```
data(input)  
length(input)
```

---

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**

A data.frame of available Enrichr databases

**Author(s)**

Wajid Jawaid <wajid.jawaid@gmail.com>

**Examples**

```
dbs <- listEnrichDbs()
```

---

listEnrichSites	<i>List Enrich Websites</i>
-----------------	-----------------------------

---

**Description**

List modEnrich Websites

**Usage**

```
listEnrichSites()
```

**Details**

List Enrich Websites

**Value**

print Enrich Website status

**Author(s)**

Alexander Blume

---

plotEnrich	<i>plotEnrich</i>
------------	-------------------

---

**Description**

Visualise a Enrich 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". Results that includes background genes in the analysis can only show "Count".
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 one of these: <ul style="list-style-type: none"> <li>• "P.value"</li> <li>• "Adjusted.P.value" (or "FDR")</li> <li>• "Combined.Score" (or "Score")</li> </ul>
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](#) plot object

**Author(s)**

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

**See Also**

[ggplot](#)

**Examples**

```
# data(input) # Load example input genes
# dbs <- c("GO_Molecular_Function_2023", "GO_Cellular_Component_2023",
#         "GO_Biological_Process_2023")
# if (getOption("enrichR.live")) {
#   enriched <- enrichr(input, dbs)
#   print(head(enriched[[1]]))
#   # Plot top 20 terms from "GO_Biological_Process_2023" and ordered by P-value
#   plotEnrich(enriched[[3]], showTerms = 20, numChar = 50, y = "Count",
#             orderBy = "P.value")
# }
```

---

printEnrich	<i>printEnrich</i>
-------------	--------------------

---

## Description

Print Enrichr results

## Usage

```
printEnrich(  
  data,  
  prefix = "enrichr",  
  showTerms = NULL,  
  columns = c(1:9),  
  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. * Results without background: 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". * In results with background, the second column is "Rank" if terms are not identical with those annotated in the Enrichr GMT files
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 or a Excel spreadsheet.

## Author(s)

Wajid Jawaid <wajid.jawaid@gmail.com>  
I-Hsuan Lin <i-hsuan.lin@manchester.ac.uk>

## Examples

```
# data(input) # Load example input genes  
# if (getOption("enrichR.live")) {  
#   enrichRLive <- TRUE  
#   dbs <- listEnrichrDbs()
```

```
# if(is.null(dbs)) enrichRLive <- FALSE
# dbs <- c("GO_Molecular_Function_2023", "GO_Cellular_Component_2023",
#         "GO_Biological_Process_2023")
# enriched <- enrichr(input, dbs)
# print(head(enriched[[1]]))
# # if (enrichRLive) printEnrich(enriched, outFile = "excel")
# }
```

---

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

# Index

## \* datasets

- background, [7](#)
- genes790, [9](#)
- input, [10](#)
- .add\_background, [2](#)
- .add\_list, [3](#)
- .enrichment\_prep\_df, [3](#)
- .formatGenes, [4](#)
- .get\_backgroundenrich, [5](#)
- .onAttach, [5](#)
- .proxyOpts, [6](#)
- .read\_gmt, [6](#)

background, [7](#)

enrichr, [7](#)

genes790, [9](#)

getEnrichr, [9](#)

ggplot, [12](#)

input, [10](#)

listEnrichrDbs, [10](#)

listEnrichrSites, [11](#)

plotEnrich, [11](#)

printEnrich, [13](#)

setEnrichrSite, [14](#)