Package ‘msig’

October 13, 2022

Title An R Package for Exploring Molecular Signatures Database

Version 1.0

Description The Molecular Signatures Database ('MSigDB') is one of the most widely used and comprehensive databases of gene sets for performing gene set enrichment analysis <doi:10.1016/j.cels.2015.12.004>. The 'msig' package provides you with powerful, easy-to-use and flexible query functions for the 'MsigDB' database.

There are 2 query modes in the 'msig' package: online query and local query. Both queries contain 2 steps: gene set name and gene.

The online search is divided into 2 modes: registered search and non-registered browse. For registered search, email that you registered should be provided.

Local queries can be made from local database, which can be updated by msig_update() function.

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Encoding UTF-8

RoxygenNote 7.1.1

Imports do, rvest, xml2, set, plyr, httr, jsonlite, utils, kableExtra, tmcn, crayon, dplyr, stringr, sqldf

Depends R (>= 4.1.0)

NeedsCompilation no

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Repository CRAN

Date/Publication 2021-06-29 07:50:02 UTC

R topics documented:

`browse_msig` *Retrieve Gene set Names from MSigDB database Retrieve gene set names from MSigDB database by the gene set name and collection. the search filed is gene name.*

Description

Retrieve Gene set Names from MSigDB database Retrieve gene set names from MSigDB database by the gene set name and collection. the search filed is gene name.

Usage

```
browse_msig(geneSetName = "", collection = "")
```

Arguments

`geneSetName`	one keyword for gene set name, default is empty
`collection`	one collection, default is empty

Value

gene set names

Examples

```
# missing genSetName and collection to get all gene set names
x <- browse_msig()
# search for gene names include immune
x <- browse_msig('immune')

x |>
    msig_view('cells','response','to','m')

# search for gene names include immune in c8
browse_msig('immune','c8')

# gene names in c8
browse_msig('immune','c8')
```

`browse_show_collection` *Show collection of MSigDB database*

Description

Show collection of MSigDB database

Usage

```
browse_show_collection()
```

Value

show all collection in MSigDB in web page http://www.gsea-msigdb.org/gsea/msigdb/genesets.jsp. For chromosome, we should treat as collection together.

Examples

```
browse_show_collection()
```

`local_msig` *Query gene set names from local data*

Description

Query gene set names from local data

Usage

```
local_msig(
  geneset = NULL,
  description = NULL,
  collection = NULL,
  sub_collection = NULL,
  organism = NULL,
  contributor = NULL,
  contributor_org = NULL,
  author = NULL,
  chip = NULL,
  gene = NULL,
  geneset_fuzzy = NULL,
  collection_fuzzy = NULL,
  sub_collection_fuzzy = NULL,
  organism_fuzzy = NULL,
  contributor_fuzzy = NULL,
  contributor_org_fuzzy = NULL,
  author_fuzzy = NULL,
  chip_fuzzy = NULL,
  gene_fuzzy = NULL
)
```

Arguments

`geneset`	one sql format character for exact match
`description`	one sql format character for exact match
`collection`	one sql format character for exact match
`sub_collection`	one sql format character for exact match
`organism`	one sql format character for exact match
`contributor`	one sql format character for exact match
`contributor_org`	one sql format character for exact match
`author`	one sql format character for exact match
`chip`	one sql format character for exact match
`gene`	one sql format character for exact match

`geneset_fuzzy`	fuzzy match
`collection_fuzzy`	fuzzy match
`sub_collection_fuzzy`	fuzzy match
`organism_fuzzy`	fuzzy match
`contributor_fuzzy`	fuzzy match
`contributor_org_fuzzy`	fuzzy match
`author_fuzzy`	fuzzy match
`chip_fuzzy`	fuzzy match
`gene_fuzzy`	fuzzy match

Value

one dataframe with attribute of msig_local.

Examples

```
x <- local_msig('IMMUNE_RESPONSE')
x <- local_msig('IMMUNE_RESPONSE|IMMUNE_SYSTEM_PROCESS')
```

`local_version` *Local database version*

Description

Local database version

Usage

```
local_version()
```

Value

version of local database

Examples

```
local_version()
```

`msig_detail` *Retrieve detail information of gene set*

Description

Retrieve detail information of gene set

Usage

```
msig_detail(...)
```

Arguments

`...`	one or more gene set names, which can be little or capital.

Value

Print detail information about the geneset, number of genes and return all gene names.

Examples

```
d <- msig_detail('izadpanah_stem_cell_adipose_vs_bone_dn',
                 'AAACCAC_MIR140')
```

`msig_download` *Download MsigDB database*

Description

Download MsigDB database

Usage

```
msig_download(version)
```

Arguments

`version`	version

Value

dowanload the data to local PC

`msig_filt` *Filt data by key words Case insensitive*

Description

Filt data by key words Case insensitive

Usage

```
msig_filt(x, ...)
```

Arguments

`x`	data from msig package
`...`	one or more key words

Value

filted results with high light information.

Examples

```
browse_msig('immune') |>
    msig_filt('response')
```

`msig_gene` *Retrieve gene by Gene set Name*

Description

Retrieve gene by Gene set Name

Usage

```
msig_gene(..., list = TRUE, info = TRUE)

## S3 method for class 'character'
msig_gene(..., list = TRUE, info = TRUE)

## S3 method for class 'data.frame'
msig_gene(..., list = TRUE, info = TRUE)
```

Arguments

`...`	one or more geneset names, which can be little or capital.
`list`	logical, default is FALSE, whether to show result by list.
`info`	logical, whether to show information about gene set.

Value

Print detail information about the geneset, number of genes and return all gene names.

Examples

```
genes <- msig_gene('izadpanah_stem_cell_adipose_vs_bone_dn',
                   'REACTOME_DEGRADATION_OF_AXIN')
genes |>
    msig_view()
```

`msig_geneSymbol` *Retrieve gene by Gene Symbol from MsigDB*

Description

Retrieve gene by Gene Symbol from MsigDB

Usage

```
msig_geneSymbol(..., local = FALSE)

## S3 method for class 'list'
msig_geneSymbol(..., local = FALSE)

## S3 method for class 'data.frame'
msig_geneSymbol(..., local = FALSE)

## S3 method for class 'character'
msig_geneSymbol(..., local = FALSE)
```

Arguments

`...`	one or more geneset names, which can be little or capital.
`local`	logical, default is FALSE, whether to extract gene symbol from local database

Value

gene symbol

Examples

```
genes <- msig_geneSymbol('izadpanah_stem_cell_adipose_vs_bone_dn')
genes <- msig_geneSymbol('izadpanah_stem_cell_adipose_vs_bone_dn',
                         'REACTOME_DEGRADATION_OF_AXIN')
```

`msig_update` *Update local MsigDB database*

Description

Update local MsigDB database

Usage

```
msig_update(xml = NULL, version = NULL)
```

Arguments

`xml`	msigdb xml file
`version`	version, if missing, the latest version will be used

Value

update local MsigDB database

`msig_version` *version information of MSigDB database*

Description

version information of MSigDB database

Usage

```
msig_version()
```

Value

version dataframe

`msig_view` *View data in viewer panel*

Description

View data in viewer panel

Usage

```
msig_view(x, ...)
```

Arguments

`x`	dataframe
`...`	one or more hightliht words

Value

open data in view panel in rstudio

Examples

```
#' browse_msig('immune') |>
    msig_view('response')
```

`NewMsigDB` *Create NewMsigDB object for new versions of MsigDB database*

Description

Create NewMsigDB object for new versions of MsigDB database

Usage

```
NewMsigDB(xml)
```

Arguments

`xml`	path of xml msigdb file path

Value

dataframe which can be used inner package

`read_msigdb_xml` *read MSigDB xml data*

Description

read MSigDB xml data

Usage

```
read_msigdb_xml(xml)
```

Arguments

`xml`	xml data path

Value

one dataframe contains gene infomation

`related_geneset` *Query related gene sets*

Description

Query related gene sets

Usage

```
related_geneset(geneSetName)
```

Arguments

`geneSetName`	one gene set name

Value

related gene sets from gene set detailed information table

Examples

```
x <- related_geneset('AAANWWTGC_UNKNOWN')
x |>
    msig_filt('unknown') |>
    msig_view('ttt')
```

`search_msig` *Query MSigDB database by cookie*

Description

Query MSigDB database by cookie

Usage

```
search_msig(keywords, collection = "", organism = "", contributor = "", email)
```

Arguments

`keywords`	one keywords see Detail field
`collection`	one or more collections
`organism`	one or more organisms
`contributor`	one or more contributors
`email`	email that registered for MSigDB database.

Value

dataframe contains name, description and so on.

Examples

```
email <- 'your email'
x <- search_msig('immune & response')
x |>
    msig_filt('system') |>
    msig_view('C2')
```

`search_show_collection` *Show collctions for msigdb_search()*

Description

Show collctions for msigdb_search()

Usage

```
search_show_collection(email)
```

Arguments

`email`	email that registered for MSigDB database.

Value

collections from MsigDB website.

Examples

```
search_show_collection("your email")
# or
email <- 'your email'
search_show_collection()
```

`search_show_contributor` *Show contributor for msigdb_search()*

Description

Show contributor for msigdb_search()

Usage

```
search_show_contributor(email)
```

Arguments

`email`	email that registered for MSigDB database.

Value

contributors from MsigDB website.

Examples

```
search_show_contributor("your email")
# or
email <- 'your email'
search_show_contributor()
```

`search_show_organism` *Show organism for msigdb_search()*

Description

Show organism for msigdb_search()

Usage

```
search_show_organism(email)
```

Arguments

`email`	email that registered for MSigDB database.

Value

organisms from MsigDB website.

Examples

```
search_show_organism("your email")
# or
email <- 'your email'
search_show_organism()
```

`show_local_collection` *Show collections of local MsigDB database*

Description

Show collections of local MsigDB database

Usage

```
show_local_collection()
```

Value

A dataframe contains 2 columns. The first column is the name of the collection. The second column is the number of frequencies it has.

Examples

```
show_local_collection()
```

`show_local_contributor`

Show contributors of local MsigDB database

Description

Show contributors of local MsigDB database

Usage

```
show_local_contributor()
```

Value

A dataframe contains 2 columns. The first column is the name of the contributor. The second column is the number of frequencies it has.

Examples

```
show_local_contributor()
```

`show_local_contributor_org`

Show contributor_orgs of local MsigDB database

Description

Show contributor_orgs of local MsigDB database

Usage

```
show_local_contributor_org()
```

Value

A dataframe contains 2 columns. The first column is the name of the contributor_org. The second column is the number of frequencies it has.

Examples

```
show_local_contributor_org()
```

`show_local_data` *Show local data used in this package*

Description

Show local data used in this package

Usage

```
show_local_data()
```

Value

data used inner this package

Examples

```
show_local_data()
```

`show_local_sub_collection` *Show sub_collections of local MsigDB database*

Description

Show sub_collections of local MsigDB database

Show sub_collections of local MsigDB database

Usage

```
show_local_sub_collection()

show_local_sub_collection()
```

Value

A dataframe contains 2 columns. The first column is the name of the sub_collection. The second column is the number of frequencies it has.

A dataframe contains 2 columns. The first column is the name of the sub_collection. The second column is the number of frequencies it has.

Examples

```
show_local_sub_collection()

show_local_sub_collection()
```

`similarity_geneset` *Query similarity gene sets*

Description

Query similarity gene sets

Usage

```
similarity_geneset(geneSetName)
```

Arguments

`geneSetName`	one gene set name

Value

similarity gene sets

Examples

```
x <- similarity_geneset('REACTOME_DEGRADATION_OF_AXIN')
x |>
    msig_view()
```

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