

Package ‘msigdb’

May 14, 2020

Type Package

Title MSigDB Gene Sets for Multiple Organisms in a Tidy Data Format

Version 7.1.1

Description Provides the 'Molecular Signatures Database' (MSigDB) gene sets typically used with the 'Gene Set Enrichment Analysis' (GSEA) software (Subramanian et al. 2005 <doi:10.1073/pnas.0506580102>, Liberzon et al. 2015 <doi:10.1016/j.cels.2015.12.004>) in a standard R data frame with key-value pairs. The package includes the original human gene symbols and NCBI/Entrez IDs as well as the equivalents for frequently studied model organisms such as mouse, rat, pig, fly, and yeast.

License MIT + file LICENSE

Encoding UTF-8

URL <https://github.com/igordot/msigdb>

BugReports <https://github.com/igordot/msigdb/issues>

LazyData true

Depends R (>= 3.2.0)

Imports magrittr, rlang, dplyr (>= 0.7.0), tibble

Suggests testthat, knitr, rmarkdown

RoxygenNote 7.1.0

VignetteBuilder knitr

NeedsCompilation no

Author Igor Dolgalev [aut, cre]

Maintainer Igor Dolgalev <igor.dolgalev@nyumc.org>

Repository CRAN

Date/Publication 2020-05-14 05:30:03 UTC

R topics documented:

msigdb	2
msigdb_show_species	3

msigdbr	<i>Retrieve the msigdbr data frame</i>
---------	--

Description

Retrieve the msigdbr data frame

Usage

```
msigdbr(species = "Homo sapiens", category = NULL, subcategory = NULL)
```

Arguments

species	Species name, such as Homo sapiens or Mus musculus. The available species can be retrieved with <code>msigdbr_show_species()</code> .
category	MSigDB collection abbreviation, such as H, C1, C2, C3, C4, C5, C6, C7.
subcategory	MSigDB sub-collection abbreviation, such as CGP or BP.

Value

A data frame of gene sets with one gene per row.

References

<https://www.gsea-msigdb.org/gsea/msigdb/collections.jsp>

Examples

```
# get all human gene sets
msigdbr(species = "Homo sapiens")

# get mouse C2 (curated) CGP (chemical and genetic perturbations) gene sets
msigdbr(species = "Mus musculus", category = "C2", subcategory = "CGP")

# check all the available categories and sub-categories
msigdbr() %>% dplyr::distinct(gs_cat, gs_subcat) %>% dplyr::arrange(gs_cat, gs_subcat)
```

`msigdbr_show_species` *List the species available in the msigdbr package*

Description

List the species available in the msigdbr package

Usage

```
msigdbr_show_species()
```

Value

A vector of possible species.

Examples

```
msigdbr_show_species()
```

Index

`msigdb`, [2](#)

`msigdb_show_species`, [3](#)