Package ‘msigdbr’

October 2, 2020

Type Package

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

Version 7.2.1

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.

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Encoding UTF-8

URL https://igordot.github.io/msigdbr,
     https://github.com/igordot/msigdbr

BugReports https://github.com/igordot/msigdbr/issues

LazyData true

Depends R (>= 3.3.0)

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

Suggests testthat, knitr, rmarkdown

RoxygenNote 7.1.1

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

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msigdb | Retrieve the gene sets data frame

Description

Retrieve a data frame of gene sets and their member genes. The available species and collections can be checked with msigdb_species() and msigdb_collections().

Usage

msigdb(species = "Homo sapiens", category = NULL, subcategory = NULL)

Arguments

species Species name, such as Homo sapiens or Mus musculus.
category MSigDB collection abbreviation, such as H or C1.
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
msigdb(species = "Homo sapiens")

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

*List the collections available in the msigdbr package*

**Description**

List the collections available in the msigdbr package

**Usage**

`msigdbr_collections()`

**Value**

A data frame of the available collections.

**Examples**

`msigdbr_collections()`

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**msigdbr_show_species**

*List the species available in the msigdbr package*

**Description**

This function is being deprecated and replaced by `msigdbr_species()`.

**Usage**

`msigdbr_show_species()`

**Value**

A vector of possible species.
msigdbr_species

List the species available in the msigdbr package

Description

List the species available in the msigdbr package

Usage

msigdbr_species()

Value

A data frame of the available species.

Examples

msigdbr_species()
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