

Package ‘msigdb’

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

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

Author Igor Dolgalev [aut, cre]

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

Repository CRAN

Date/Publication 2020-10-02 07:00:03 UTC

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msigdb	<i>Retrieve the gene sets data frame</i>
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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()
```

`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	<i>List the species available in the msigdbr package</i>
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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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