Package ‘msigdb’

May 5, 2021

Type Package

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

Version 7.4.1

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 human genes as listed in MSigDB as well as the corresponding symbols and IDs for frequently studied model organisms such as mouse, rat, pig, fly, and yeast.

License MIT + file LICENSE

Encoding UTF-8

URL https://igordot.github.io/msigdb/

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

Depends R (>= 3.3.0)

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

Suggests knitr, rmarkdown, testthat

RoxygenNote 7.1.1

VignetteBuilder knitr

NeedsCompilation no

Author Igor Dolgalev [aut, cre]

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

Repository CRAN

Date/Publication 2021-05-05 16:10:02 UTC
R topics documented:

  msigdb  .................................................................  2
  msigdb_collections ..................................................  3
  msigdb_show_species ..................................................  3
  msigdb_species ........................................................  4

Index  5

---

**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**

```r
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](https://www.gsea-msigdb.org/gsea/msigdb/collections.jsp)

**Examples**

```r
# 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")
```
msigdbrcollections

List the collections available in the msigdbrc package

Description

List the collections available in the msigdbrc package

Usage

msigdbrcollections()

Value

A data frame of the available collections.

Examples

msigdbrcollections()

msigdbrshowspecies

List the species available in the msigdbrc package

Description

This function is being deprecated and replaced by msigdbrspecies().

Usage

msigdbrshowspecies()

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**

```r
msigdbr_species()
```

**Value**

A data frame of the available species.

**Examples**

```r
msigdbr_species()
```
Index

msigdb, 2
msigdb_collections, 3
msigdb_show_species, 3
msigdb_species, 4