Package ‘msigdb’

September 4, 2019

Type Package
Title MSigDB Gene Sets for Multiple Organisms in a Tidy Data Format
Version 7.0.1
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://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 6.1.1
VignetteBuilder knitr
NeedsCompilation no
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Retrieve the msigdb data frame

Description

Retrieve the msigdb data frame

Usage

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

Arguments

- **species**: species name, such as Homo sapiens, Mus musculus, etc.
- **category**: collection, such as H, C1, C2, C3, C4, C5, C6, C7.
- **subcategory**: sub-collection, such as CGP, MIR, BP, etc.

Value

a data frame of gene sets with one gene per row

Examples

```
# all human gene sets
m = msigdb(species = "Homo sapiens")

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

msigdb_show_species

List the species available in the msigdb package

Description

List the species available in the msigdb package

Usage

```
msigdb_show_species()
```

Value

a vector of possible species
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