Package 'MOFAdata'

November 10, 2026

Type Package

Title Data package for Multi-Omics Factor Analysis (MOFA)

Version 1.28.0

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Date 2018-06-26

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Depends R (>= 3.5)

Description A collection of datasets to accompany the R package MOFA and illustrate running and analysing MOFA models.

Encoding UTF-8

Suggests knitr, MultiAssayExperiment, rmarkdown, BiocStyle

biocViews ReproducibleResearch

VignetteBuilder knitr

LazyData false

NeedsCompilation yes

RoxygenNote 6.1.1

git_url https://git.bioconductor.org/packages/MOFAdata

git_branch RELEASE_3_23

git_last_commit 6f2fbe4

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-10

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`CLL_covariates` *CLL_covariates*

Description

Data frame containing additional information on the patient samples, i.e. diagnosis and gender.

Usage

```
data(CLL_covariates)
```

Format

A data frame diagnosis and gender for the n=200 patient samples in CLL_data

Source

https://www.ncbi.nlm.nih.gov/pubmed/29227286

`CLL_data` *CLL_data*

Description

A list containing different omic measurements for Chronic lymphocytic leukaemia (CLL) patient samples.
The data set was originally published in https://www.ncbi.nlm.nih.gov/pubmed/29227286.
The MOFA analysis for this data set can be found in http://msb.embopress.org/content/14/6/e8124

Usage

```
data(CLL_data)
```

Format

A list of matrices, with the following -omics:

- mRNA: normalized expression values for the 5000 most variable genes
- Methylation: methylation M-values for the 4248 most variable CpG sites
- Drugs: viability values in response to 310 different drugs and concentrations
- Mutations: Mutation status for 69 selected genes

Source

https://www.ncbi.nlm.nih.gov/pubmed/29227286

MOFAdata *MOFAdata: Data package for Multi-Omics Factor Analysis (MOFA)*

Description

The MOFAdata package provides a collection of datasets to accompany the R package MOFA, where they are used to illustrate how to run MOFA and analyse its results. Briefly, it contains multi-omics data for a bulk study on chronic lymphocytic leukemia and a single cell scMT-seq study. For these two data sets, we also provide pretrained MOFA objects to be used in downstream analysis with MOFA. In addition, various gene sets are stored here, that can be useful when performing feature set enrichment analysis in MOFA.

Details

An overview of the datasets contained in this package can be found in the vignette "MOFAdata".

MSigDB_v6.0_C2_human *MSigDB_v6.0_C2_human*

Description

A matrix containing human gene sets from the MSigDB 6.0 data base (http://software.broadinstitute.org/gsea/msigdb).

species: Homo sapiens

Gene IDs: Ensembl IDs from version 75 (i.e. ENSG00000125798)

Collection: C2, curated gene sets from online pathway databases, publications in PubMed, and knowledge of domain experts.

Usage

```
data(MSigDB_v6.0_C2_human)
```

Format

Matrix containing 1329 biological pathways in rows and 20086 genes in columns

Source

http://software.broadinstitute.org/gsea/msigdb

`MSigDB_v6.0_C2_mouse` *MSigDB_v6.0_C2_mouse*

Description

A matrix containing mouse gene sets from the MSigDB 6.0 data base (http://software.broadinstitute.org/gsea/msigdb).

species: Mus musculus

Gene IDs: Gene symbol/name (i.e. FOXA2)

Collection: C2, curated gene sets from online pathway databases, publications in PubMed, and knowledge of domain experts.

Usage

```
data(MSigDB_v6.0_C2_mouse)
```

Format

Matrix containing 4731 biological pathways in rows and 18360 genes in columns

Source

http://software.broadinstitute.org/gsea/msigdb

`MSigDB_v6.0_C5_human` *MSigDB_v6.0_C5_human*

Description

A matrix containing human gene sets from the MSigDB 6.0 data base (http://software.broadinstitute.org/gsea/msigdb).

species: Homo sapiens

Gene IDs: Ensembl IDs from version 75 (i.e. ENSG00000125798)

Collection: C5, consist of genes annotated by GO Biological Process terms.

Usage

```
data(MSigDB_v6.0_C5_human)
```

Format

Matrix containing 4436 biological pathways in rows and 20086 genes in columns

Source

http://software.broadinstitute.org/gsea/msigdb

MSigDB_v6.0_C5_mouse *MSigDB_v6.0_C5_mouse*

Description

A matrix containing mouse gene sets from the MSigDB 6.0 data base (http://software.broadinstitute.org/gsea/msigdb).

species: Mus musculus

Gene IDs: Gene symbol/name (i.e. FOXA2)

Collection: C5, consist of genes annotated by GO Biological Process terms.

Usage

```
data(MSigDB_v6.0_C5_mouse)
```

Format

Matrix containing 4436 biological pathways in rows and 18360 genes in columns.

Source

http://software.broadinstitute.org/gsea/msigdb

reactomeGS *reactomeGS*

Description

A matrix containing human gene sets from the Reactome v59 Pathway data base (https://reactome.org).

species: Homo sapiens

Gene IDs: Ensembl IDs from version 75 (i.e. ENSG00000125798)

Usage

```
data(reactomeGS)
```

Format

Matrix containing 1304 biological pathways in rows and 18818 genes (ensemble IDs) in columns.

Source

https://reactome.org

scMT_data *scMT_data*

Description

A MultiAssayExperiment containing data from a single cell multi-omics study (scMT-seq) on mouse embryonic stem cells (mESCs).
The data set was originally published in https://www.ncbi.nlm.nih.gov/pubmed/26752769.
The MOFA analysis for this data set can be found in http://msb.embopress.org/content/14/6/e8124

Usage

```
data(scMT_data)
```

Format

A MultiAssayExperiment containing four Experiments:

- RNA expression: ExpressionSet with normalized expression values of the 5000 most variable genes
- Met Enhancers: Methylation values for 5000 CpGs overlapping enhancer elements
- Met CpG Islands: Methylation values for 5000 CpGs overlapping CpG Islands
- Met Promoters: Methylation values for 5000 CpGs overlapping promoters

Source

https://www.ncbi.nlm.nih.gov/pubmed/26752769

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