Package ‘MOFAdataset’

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Type Package

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

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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

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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


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)
MOFAdata

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


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

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

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**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)

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**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.
**Description**

A matrix containing mouse gene sets from the MSigDB 6.0 data base ([http://software.broadinstitute.org/gsea/msigdb](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 20086 genes in columns.

**Source**

[http://software.broadinstitute.org/gsea/msigdb](http://software.broadinstitute.org/gsea/msigdb)
reactomeGS  reactomeGS

Description

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
scMT_data

Source

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