

# Package ‘MOFAdata’

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**Type** Package

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

**Version** 1.20.0

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**License** LGPL-3

**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>

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**git\_last\_commit** ce76f9b

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CLL_covariates	<i>CLL_covariates</i>
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### 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>

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CLL_data	<i>CLL_data</i>
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### 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>

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MOFAdata

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

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**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".

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MSigDB\_v6.0\_C2\_human    *MSigDB\_v6.0\_C2\_human*

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**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    *MSigDB\_v6.0\_C2\_mouse*

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**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>

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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>

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MSigDB\_v6.0\_C5\_mouse    *MSigDB\_v6.0\_C5\_mouse*

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**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>

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reactomeGS	<i>reactomeGS</i>
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**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>

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scMT_data	<i>scMT_data</i>
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**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*

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**Source**

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

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