# Package 'MouseAgingData'

January 28, 2025

**Title** Multi-omics data access for studies investigating the effects of
aging

**Version** 1.2.0

**Description** The MouseAgingData package provides analysis-ready data
resources from different studies focused on aging and rejuvenation in
mice. The package currently provides two 10x Genomics single-cell RNA-seq
datasets. The first study profiled the aging mouse brain measured across
37,089 cells (Ximerakis et al., 2019). The second study investigated
parabiosis by profiling a total of 105,329 cells (Ximerakis & Holton et al., 2023).
The datasets are provided as SingleCellExperiment objects and provide raw
UMI counts and cell metadata.

**License** Artistic-2.0

**URL** https://github.com/ccb-hms/MouseAgingData

**BugReports** https://github.com/ccb-hms/MouseAgingData/issues

**Depends** R (>= 4.4.0), SingleCellExperiment

**Imports** AnnotationHub, ExperimentHub

**Suggests** BiocStyle, knitr, rmarkdown, scater

**VignetteBuilder** knitr

**biocViews** ExperimentData, ExpressionData, SequencingData, RNASeqData,
SingleCellData, ExperimentHub, PackageTypeData,
Mus_musculus_Data

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.1

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AgingBrain10x                *Load mouse 2019 Nature Neuroscience aging brain data*

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### Description

Obtain the processed data set for the mouse aging brain 10x Genomics RNA-seq dataset from Ximerakis et al. 2019.

### Usage

```
AgingBrain10x(metadata = FALSE)
```

### Arguments

metadata          Logical, whether only experiment metadata should be returned. Default behavior is to return processed data with metadata included.

### Format

SingleCellExperiment

### Details

This function downloads the data for the mouse aging brain study from Ximerakis et al. (2019).

The processed dataset contains 37,089 cells and 14,699 features for 25 cell types. Low quality cells and animals were removed following Ximerakis et al. (2019) resulting in data for 8 young and 8 old mice. The row metadata contains MGI symbol for each gene.

### Value

Returns a SingleCellExperiment() object.

## Metadata

The `colData` slot contains information about the cells and samples.

The column metadata for called cells contains:

`barcode`: Character, unique cell identifier.

`nCount_RNA`: Numeric, number of RNA transcripts.

`nFeature_RNA`: Integer, number of RNA features.

`animal`: Factor, unique animal identifier.

`batch`: Factor, batch identifier.

`animal_type`: Factor, young (YX) or old (OX) conditions of the animal.

`percent_mito`: Numeric, percentage of mitochondrial content.

`percent_ribo`: Numeric, percentage of ribosomal content.

`cell_type`: Factor, cell type to which the cell was assigned.

`cell_ontology_class`: Factor, Cell Ontology label.

`cell_ontology_id`: Factor, Cell Ontology identifier

## Author(s)

Tram Nguyen

## References

Ximerakis et al. (2019) Single-cell transcriptomic profiling of the aging mouse brain. *Nat Neurosci* 22, 1696–1708. DOI:https://doi.org/10.1038/s41593-019-0491-3.

## Examples

```
data <- AgingBrain10x()
data_meta <- AgingBrain10x(metadata = TRUE)
```

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parabiosis10x                    *Load mouse aging parabiosis data*

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## Description

Obtain the processed data set for the mouse aging parabiosis 10x Genomics RNA-seq dataset from Ximerakis & Holton et al. 2023.

## Usage

```
parabiosis10x(metadata = FALSE)
```

## Arguments

metadata          Logical, whether only experiment metadata should be returned. Default behavior is to return processed data with metadata included.

## Format

SingleCellExperiment

## Details

This function downloads the data for the mouse aging parabiosis study from Ximerakis & Holton et al (2023).

The processed dataset contains 105,329 cells and 20905 features for 31 cell types. Low quality cells and animals were removed following Ximerakis & Holton et al. (2023) resulting in 8 OX, 8 YX, 7 YY, 9 YO, 7 OO, 11 OY animals. The row metadata contains MGI symbol for each gene.

## Value

Returns a `SingleCellExperiment()` object.

## Metadata

The `colData` slot contains information about the cells and samples.

The column metadata for called cells contains:

`barcode`: Character, unique cell identifier.

`nCount_RNA`: Numeric, number of RNA transcripts.

`nFeature_RNA`: Integer, number of RNA features.

`animal`: Factor, unique animal identifier, includes heterochronic or isochronic condition.

`batch`: Factor, sequencing batch identifier.

`animal_type`: Factor, isochronic or heterochronic conditions of the animal.

`percent_mito`: Numeric, percentage of mitochondrial content.

`percent_ribo`: Numeric, percentage of ribosomal content.

`cell_type`: Factor, cell type to which the cell was assigned.

`subpopulation`: Factor, cell subpopulation.

`cell_ontology_class`: Factor, Cell Ontology label.

`cell_ontology_id`: Factor, Cell Ontology identifier

## Author(s)

Tram Nguyen

## References

Ximerakis & Holton et al. (2023) Heterochronic parabiosis reprograms the mouse brain transcriptome by shifting aging signatures in multiple cell types. *Nat Aging* 3, 327–345. DOI:https://doi.org/10.1038/s43587-023-00373-6.

## Examples

```
data <- parabiosis10x()
data_meta <- parabiosis10x(metadata = TRUE)
```

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