Package ‘MouseAgingData’

January 23, 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

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

git_branch RELEASE_3_20

git_last_commit f710868

git_last_commit_date 2024-10-29

Repository Bioconductor 3.20

Date/Publication 2025-01-23

Author Tram Nguyen [aut, cre] (<`https://orcid.org/0000-0003-4809-6227`>),
Kris Holton [aut],
Tyrone Lee [aut],

Nitesh Turaga [ctb],
Ludwig Geistlinger [aut],
Robert Gentleman [aut]

Maintainer Tram Nguyen `<Tram_Nguyen@hms.harvard.edu>`

Contents

`AgingBrain10x` *Load mouse 2019 Nature Neuroscience aging brain data*

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)
```

`parabiosis10x` *Load mouse aging parabiosis data*

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)
```

Index