Package 'MouseThymusAgeing'

November 10, 2026

Type Package

Title Single-cell Transcriptomics Data of the Ageing Mouse Thymus

Version 1.20.0

Description This package provides data access to counts matrices and meta-data for single-cell RNA sequencing data of
thymic epithlial cells across mouse ageing using SMARTseq2 and 10X Genomics chemistries. Access is provided
as a data package via ExperimentHub. It is designed to facilitate the re-use of data from Baran-Gale _et al._
in a consistent format that includes relevant and informative meta-data.

License GPL-3

Encoding UTF-8

biocViews ExperimentHub, SingleCellData, ExpressionData, ExperimentData

LazyData true

Depends SingleCellExperiment, SummarizedExperiment

Imports ExperimentHub, methods, BiocGenerics, S4Vectors

Suggests knitr, scuttle, rmarkdown, BiocStyle

VignetteBuilder knitr

NeedsCompilation no

Collate 'getProcOrRaw.R' 'DropletMetadata.R' 'SMARTseqMetadata.R' 'MouseDropletData.R' 'MouseSMARTseqData.R'

BugReports https://github.com/MarioniLab/MouseThymusAgeing/issues

RoxygenNote 7.1.1.9000

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`DropletMetadata` *Sample metadata from the Baran-Gale et al. ageing mouse thymus droplet experiments A data frame containing mouse age and sort-type information for the droplet single-cell RNA-sequencing experiment data sets*

Description

Sample metadata from the Baran-Gale et al. ageing mouse thymus droplet experiments

A data frame containing mouse age and sort-type information for the droplet single-cell RNA-sequencing experiment data sets

Usage

```
DropletMetadata
```

Format

A data frame containing information for each replicate sample

The object contains:

`sample`**:** Character, sample IDs.

`Gender`**:** Character, gender of mouse - all female.

`HTO`**:** Character, hashtag oligo assignments.

`ncells`**:** Integer, number of cells (post-QC) per sample.

Author(s)

Mike Morgan

References

Baran-Gale J, Morgan MD, et al. (2020) Ageing compromises mouse thymus function and remodels epithelial cell differentiation *eLife* 9:e56221.

Examples

```
head(DropletMetadata)
```

`MouseDropletData` *Mouse ageing thymus droplet single-cell RNA-sequencing data*

Description

Obtain the processed counts for the mouse ageing thymus droplet scRNA-seq data set.

Usage

```
MouseDropletData(samples = NULL)
```

Arguments

`samples`	Integer or character vector specifying the samples for which data should be obtained. If `NULL` (default), data are returned for all (6) samples.

Details

This function downloads the data for the mouse ageing thymus droplet scRNA-seq data from Baran-Gale et al. (2020).

The dataset contains 6 10X Genomics samples. The available samples are: `ZsG_1stRun1`, `ZsG_1stRun2`, `ZsG_2ndRun1`, `ZsG_2ndRun2`, `ZsG_3rdRun1`, `ZsG_3rdRun2`.

In the data, cell-containing libraries have already been identified in each sample using the `emptyDrops` function from **DropletUtils**. The count matrix contains the raw count vectors for the cells called from all samples in this manner. Size factors were computed using the `computeSumFactors` function from **scran**. The column metadata for called cells contains:

`CellID`: Character, unique cell identifier across all samples.

`SampID`: Character, Short unique identified for the experimental sample.

`Class`: Character, Either Singlet or Multiplet Identifies cells called as a multiplet from hash-tag demultiplexing.

`HTO`: Character, Hashtag oligo (HTO) character identifier, used for multiplexing experimental samples.

`Age`: Character, Age of mouse at the time of doxycycline treatment. Age at time of data acquisition is +4weeks.

`SortType`: Character, Flow cytometry sorting group, either ZsGreen+ (ZsGp) or ZsGreen- (ZsGn).

`Cluster`: Integer, Cluster to which cells were assigned based on using the Walktrap community detection algorithm on a k-NN graph.

`ClusterAnnot`: Character, Annotation assigned to cluster.

`SizeFactor`: Numeric, Estimated normalized factor across all cells and experimental samples.

Reduced dimension representations of the data are also available in the `reducedDims` slot of the SingleCellExperiment object. The `SingleCellExperiment` object has row metadata that contains the Ensembl ID `ensembl_gene_id` and Gene symbols `external_gene_name` for each gene, as well as gene chromosome, strand and both start and end positions.

Value

A SingleCellExperiment is returned containing processed data from selected samples.

List elements are named after the corresponding sample.

Author(s)

Mike Morgan, based on original code by Aaron Lun & Jonathan Griffiths

Mike Morgan

References

Baran-Gale J, Morgan MD, et al. (2020) Ageing compromises mouse thymus function and remodels epithelial cell differentiation *eLife* 9:e56221.

Examples

```
drop.data <- MouseDropletData(samples = "ZsG_1stRun1")
drop.data
```

`MouseSMARTseqData` *Mouse ageing thymus SMART-seq2 single-cell RNA-sequencing data*

Description

Obtain the processed counts for the mouse ageing thymus SMART-seq2 scRNA-seq data set.

Usage

```
MouseSMARTseqData(samples = NULL)
```

Arguments

`samples`	Integer or character vector specifying the samples for which data should be obtained. If `NULL` (default), data are returned for all (5) samples.

Details

This function downloads the data for the mouse ageing thymus droplet scRNA-seq data from Baran-Gale et al. (2020).

The dataset contains 5 different SMART-seq2 samples, split by the day of acquisition. The available samples are: `day1`, `day2`, `day3`, `day4`, `day5`.

In the data, poor-quality cells have already been removed based on insufficient sequencing depth, high mitochondrial content, excessive proportion of expression from ERCC spike-in and ribosomal genes. Exact details can be found in the methods section of Baran-Gale et al. (2020).

The count matrix contains the raw count vectors for the cells that pass QC. Size factors were computed using the `computeSumFactors` function from **scran**. The column metadata for called cells contains:

`CellID`: Character, unique cell identifier across all samples.

`ClusterID`: Numeric, The cluster to which cells were assigned based on community detection on a shared-NN grpah.

`Position`: Character, Plate position of the index-sorted cell (384 well plate format).

`PlateID`: Character, A unique ID for the 384-well plate into which each cell was index-sorted.

`Column`: Integer, A value from 1-24 corresponding to the plate column.

`Row`: Character, A value from A-P corresponding to the plate row.

`SortType`: Character, Flow cytometry sorting group, mTEClo, mTEChi, gmTEC or cTEC.

`SortDay`: Integer, Day on which cells were sorted - corresponds to the sample IDs for downloading data and replicate.

`Age`: Character, Mouse age at the time of data acquisition.

`SubType`: Character, Annotation assigned to clusters.

`SizeFactor`: Numeric, Estimated normalized factor across all cells and experimental samples.

Reduced dimension representations of the data are also available in the `reducedDims` slot of the SingleCellExperiment object. The `SingleCellExperiment` object has row metadata that contains the Ensembl ID `ensembl_gene_id` and Gene symbols `external_gene_name` for each gene, as well as gene chromosome, strand and both start and end positions.

Value

A SingleCellExperiment is returned containing processed data from selected samples.

List elements are named after the corresponding sample.

Author(s)

Mike Morgan, based on original code by Aaron Lun & Jonathan Griffiths

Mike Morgan

References

Baran-Gale J, Morgan MD, et al. (2020) Ageing compromises mouse thymus function and remodels epithelial cell differentiation *eLife* 9:e56221.

Examples

```
smart.data <- MouseSMARTseqData(samples = "day1")
smart.data
```

`SMARTseqMetadata` *Sample metadata from the Baran-Gale et al. ageing mouse thymus*

Description

A data frame containing mouse age and sort-type information for the SMARTseq experiment data sets

Usage

```
SMARTseqMetadata
```

Format

A data frame containing information for each replicate sample

The object contains:

`sample`: Character, day<1:5>.

`Age`: Character, age of mouse cells acquired from.

`Gender`: Character, gender of mouse - all female.

`ncells`: Integer, number of cells (post-QC) per sample.

Author(s)

Mike Morgan

References

Baran-Gale J, Morgan MD, et al. (2020) Ageing compromises mouse thymus function and remodels epithelial cell differentiation *eLife* 9:e56221.

Examples

```
head(SMARTseqMetadata)
```

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