

# Package ‘MouseThymusAgeing’

November 4, 2025

**Type** Package

**Title** Single-cell Transcriptomics Data of the Ageing Mouse Thymus

**Version** 1.19.0

**Description** This package provides data access to counts matrices and meta-data for single-cell RNA sequencing data of thymic epithelial 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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|                 |                                                                                                                                                                                                                       |
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| DropletMetadata | <i>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</i> |
|-----------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|

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**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 | <i>Mouse ageing thymus droplet single-cell RNA-sequencing data</i> |
|------------------|--------------------------------------------------------------------|

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## 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
```

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|                   |                                                                       |
|-------------------|-----------------------------------------------------------------------|
| MouseSMARTseqData | <i>Mouse ageing thymus SMART-seq2 single-cell RNA-sequencing data</i> |
|-------------------|-----------------------------------------------------------------------|

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### Description

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

### Usage

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

### Arguments

|                      |                                                                                                                                                 |
|----------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>samples</code> | 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 graph.

**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
```

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

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**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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