

# Package ‘TabulaMurisSenisData’

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**Type** Package

**Title** Bulk and single-cell RNA-seq data from the Tabula Muris Senis project

**Version** 1.0.0

**Description** This package provides access to RNA-seq data generated by the Tabula Muris Senis project via the Bioconductor project. The data is made available without restrictions by the Chan Zuckerberg Biohub. It is provided here without further processing, collected in the form of SingleCellExperiment objects.

**License** MIT + file LICENSE

**Encoding** UTF-8

**RoxygenNote** 7.1.1

**Imports** ExperimentHub, SingleCellExperiment, HDF5Array, SummarizedExperiment, gdata, AnnotationHub

**URL** <https://github.com/fmicompbio/TabulaMurisSenisData>

**BugReports** <https://github.com/fmicompbio/TabulaMurisSenisData/issues>

**VignetteBuilder** knitr

**biocViews** SingleCellData, ExperimentData, RNASeqData, ExperimentHub

**Suggests** ggplot2, testthat, knitr, rmarkdown, iSEE, BiocStyle

**git\_url** <https://git.bioconductor.org/packages/TabulaMurisSenisData>

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## R topics documented:

<code>listTabulaMurisSenisTissues</code> . . . . .	2
<code>TabulaMurisSenisBulk</code> . . . . .	2
<code>TabulaMurisSenisData-pkg</code> . . . . .	3
<code>TabulaMurisSenisDroplet</code> . . . . .	4
<code>TabulaMurisSenisFACS</code> . . . . .	5

<b>Index</b>	<b>7</b>
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`listTabulaMurisSenisTissues`

*List available tissues for the Tabula Muris Senis datasets*

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### Description

List available tissues for the Tabula Muris Senis datasets

### Usage

```
listTabulaMurisSenisTissues(dataset)
```

### Arguments

`dataset`            Either 'Droplet' or 'FACS'

### Value

A character vector with the available tissues for the indicated dataset.

### Examples

```
listTabulaMurisSenisTissues(dataset = "Droplet")
```

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`TabulaMurisSenisBulk`    *Access the Tabula Muris Senis bulk RNA-seq data*

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### Description

Access the bulk RNA-seq data from the Tabula Muris Senis consortium.

### Usage

```
TabulaMurisSenisBulk(infoOnly = FALSE)
```

## Arguments

`infoOnly` Logical scalar. If TRUE, only print the total size of the files that will be downloaded to and/or retrieved from the cache.

## Details

The data set was downloaded from GEO (accession number GSE132040). The summary statistics from HTSeq-count were combined with the provided sample metadata and included in the `colData` of the object. In addition, gene annotations from GENCODE vM19 were downloaded and included in the `rowRanges` of the object.

## Value

If `infoOnly` is FALSE, return a [SingleCellExperiment](#) object with a single matrix of counts. Otherwise, returns 'NULL'.

## Author(s)

Charlotte Soneson

## References

Schaum et al (2019): The murine transcriptome reveals global aging nodes with organ-specific phase and amplitude. bioRxiv doi:10.1101/662254.

The Tabula Muris Consortium (2020): A single-cell transcriptomic atlas characterizes ageing tissues in the mouse. Nature 583:590–595.

## Examples

```
if (interactive()) {  
  sce <- TabulaMurisSenisBulk()  
}
```

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TabulaMurisSenisData-pkg

*TabulaMurisSenisData*

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## Description

The TabulaMurisSenisData package provides access to the bulk RNA-seq data as well as the droplet and FACS single-cell RNA-seq data from the Tabula Muris Senis consortium. The data was downloaded from GEO (bulk) and figshare (single-cell) and is provided in the form of `SingleCellExperiment` objects.

## References

Tabula Muris Consortium (2020): A single-cell transcriptomic atlas characterizes ageing tissues in the mouse. *Nature* 583(7817): 590-595.

Schaum et al (2019): The murine transcriptome reveals global aging nodes with organ-specific phase and amplitude. *bioRxiv* doi:10.1101/662254

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TabulaMurisSenisDroplet

*Access the Tabula Muris Senis droplet single-cell RNA-seq data*

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## Description

Access the droplet (10x Genomics) RNA-seq data from the Tabula Muris Senis consortium.

## Usage

```
TabulaMurisSenisDroplet(
  tissues = "All",
  processedCounts = FALSE,
  reducedDims = TRUE,
  infoOnly = FALSE
)
```

## Arguments

tissues	A character vector with the tissues to retrieve objects for. A list of available tissues can be obtained using <code>listTabulaMurisSenisTissues("Droplet")</code> .
processedCounts	Logical scalar. If TRUE, include the processed counts in addition to the raw counts in the <code>SingleCellExperiment</code> object.
reducedDims	Logical scalar. If TRUE, include the PCA, tSNE and UMAP representations in the <code>SingleCellExperiment</code> object (the tSNE representation is not available for the full dataset ('All' tissue)).
infoOnly	Logical scalar. If TRUE, only print the total size of the files that will be downloaded to and/or retrieved from the cache.

## Details

The data set was downloaded from figshare ([https://figshare.com/articles/dataset/Processed\\_files\\_to\\_use\\_with\\_scanpy\\_/8273](https://figshare.com/articles/dataset/Processed_files_to_use_with_scanpy_/8273) for the full data set, [https://figshare.com/articles/dataset/Tabula\\_Muris\\_Senis\\_Data\\_Objects/12654728](https://figshare.com/articles/dataset/Tabula_Muris_Senis_Data_Objects/12654728) for the individual tissue ones).

## Value

If `infoOnly` is FALSE, returns a named list of `SingleCellExperiment` objects (one per tissue requested via `tissues`). Otherwise, each element in the list is 'NULL'.

**Author(s)**

Charlotte Soneson

**References**

Schaum et al (2019): The murine transcriptome reveals global aging nodes with organ-specific phase and amplitude. bioRxiv doi:10.1101/662254.

The Tabula Muris Consortium (2020): A single-cell transcriptomic atlas characterizes ageing tissues in the mouse. Nature 583:590–595.

**Examples**

```
if (interactive()) {  
  sce <- TabulaMurisSenisDroplet(tissues = "All")  
}
```

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TabulaMurisSenisFACS *Get the Tabula Muris Senis FACS single-cell RNA-seq data*

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**Description**

Access the FACS (Smart-Seq2) RNA-seq data from the Tabula Muris Senis consortium.

**Usage**

```
TabulaMurisSenisFACS(  
  tissues = "All",  
  processedCounts = FALSE,  
  reducedDims = TRUE,  
  infoOnly = FALSE  
)
```

**Arguments**

tissues	A character vector with the tissues to retrieve objects for. A list of available tissues can be obtained using <code>listTabulaMurisSenisTissues("FACS")</code> .
processedCounts	Logical scalar. If TRUE, include the processed counts in addition to the raw counts in the <code>SingleCellExperiment</code> object.
reducedDims	Logical scalar. If TRUE, include the PCA, tSNE and UMAP representations in the <code>SingleCellExperiment</code> object (the tSNE representation is not available for the full dataset ('All' tissue)).
infoOnly	Logical scalar. If TRUE, only print the total size of the files that will be downloaded to and/or retrieved from the cache.

**Details**

The data set was downloaded from figshare ([https://figshare.com/articles/dataset/Processed\\_files\\_to\\_use\\_with\\_scanpy\\_/8273](https://figshare.com/articles/dataset/Processed_files_to_use_with_scanpy_/8273) for the full data set, [https://figshare.com/articles/dataset/Tabula\\_Muris\\_Senis\\_Data\\_Objects/12654728](https://figshare.com/articles/dataset/Tabula_Muris_Senis_Data_Objects/12654728) for the individual tissue ones).

**Value**

If `infoOnly` is `FALSE`, returns a named list of `SingleCellExperiment` objects (one per tissue requested via `tissues`). Otherwise, each element in the list is `'NULL'`.

**Author(s)**

Charlotte Soneson

**References**

Schaum et al (2019): The murine transcriptome reveals global aging nodes with organ-specific phase and amplitude. bioRxiv doi:10.1101/662254.

The Tabula Muris Consortium (2020): A single-cell transcriptomic atlas characterizes ageing tissues in the mouse. Nature 583:590–595.

**Examples**

```
if (interactive()) {  
  sce <- TabulaMurisSenisFACS(tissues = "All")  
}
```

# Index

`listTabulaMurisSenisTissues`, [2](#)

`SingleCellExperiment`, [3](#), [4](#), [6](#)

`TabulaMurisSenisBulk`, [2](#)

`TabulaMurisSenisData-pkg`, [3](#)

`TabulaMurisSenisDroplet`, [4](#)

`TabulaMurisSenisFACS`, [5](#)