Package 'TabulaMurisSenisData'

November 10, 2026

Type Package

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

Version 1.18.0

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.

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Encoding UTF-8

RoxygenNote 7.3.3

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

git_branch RELEASE_3_23

git_last_commit dd55f51

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-10

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`TabulaMurisSenisData-package`
TabulaMurisSenisData

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.

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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 withorgan-specific phase and amplitude. bioRxiv doi:10.1101/662254

See Also

Useful links:

- https://github.com/fmicompbio/TabulaMurisSenisData
- Report bugs at https://github.com/fmicompbio/TabulaMurisSenisData/issues

listTabulaMurisSenisTissues *List available tissues for the Tabula Muris Senis datasets*

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")
```

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

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, return '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()
}
```

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 `listTabulaMurisSenisTissues("Droplet")`.
`processedCounts`	Logical scalar. If `TRUE`, include the processed counts in addition to the raw counts in the SingleCellExperiment object.

reducedDims	Logical scalar. If TRUE, include the PCA, tSNE and UMAP representations in the SingleCellExperiment 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
for the full data set, 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")
}
```

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

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 `listTabulaMurisSenisTissues("FACS")`.
`processedCounts`	Logical scalar. If `TRUE`, include the processed counts in addition to the raw counts in the SingleCellExperiment object.
`reducedDims`	Logical scalar. If `TRUE`, include the PCA, tSNE and UMAP representations in the SingleCellExperiment 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
for the full data set, 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")
}
```

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