Package ‘TabulaMurisSenisData’
March 28, 2024

Type Package
Title Bulk and single-cell RNA-seq data from the Tabula Muris Senis project
Version 1.8.0
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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**R topics documented:**

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**listTabulaMurisSenisTissues**

*List available tissues for the Tabula Muris Senis datasets*

**Description**

List available tissues for the Tabula Muris Senis datasets

**Usage**

```r
listTabulaMurisSenisTissues(dataset)
```

**Arguments**

- `dataset` Either 'Droplet' or 'FACS'

**Value**

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

**Examples**

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

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

**Description**

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

**Usage**

```r
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


Examples

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

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


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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

```r
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_/8273102?file=23938934 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’.
TabulaMurisSenisFACS

Author(s)
Charlotte Soneson

References

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_/8273102 for the full data set, https://figshare.com/articles/dataset/Tabula_Muris_Senis_Data_Obects/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


Examples

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