Package ‘scRNAseq’

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provided as SingleCellExperiment objects with cell- and gene-level metadata.

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**Description**

Gene-level counts for a collection of public scRNA-seq datasets, provided as SingleCellExperiment objects with cell- and gene-level metadata.

**Details**

This package contains a collection of three publicly available single-cell RNA-seq datasets.

The dataset `fluidigm` contains 65 cells from Pollen et al. (2014), each sequenced at high and low coverage.

The dataset `th2` contains 96 T helper cells from Mahata et al. (2014).

The dataset `allen` contains 379 cells from the mouse visual cortex. This is a subset of the data published in Tasic et al. (2016).

See the package vignette for details on the pre-processing of the data.
Author(s)

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References


AztekinTailData

Obtain the Aztekin tail data

Description

Obtain the Xenopus tail single-cell RNA-seq data from Aztekin et al. (2019).

Usage

AztekinTailData(legacy = FALSE)

Arguments

legacy Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata is provided in the same form as supplied in E-MTAB-7761. This contains information such as the treatment condition, batch, putative cell type, putative cell cycle phase.

The UMAP results are available as the "UMAP" entry in the reducedDims.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/aztekin-tail.
**BacherTCellData**

**Value**

A SingleCellExperiment object with a single matrix of UMI counts.

**Author(s)**

Aaron Lun

**References**


**Examples**

```r
sce <- AztekinTailData()
```

---

**Description**

Obtain the human COVID T cell single-cell RNA-seq dataset from Bacher et al. (2020).

**Usage**

```r
BacherTCellData(
  filtered = TRUE,
  ensembl = FALSE,
  location = TRUE,
  legacy = FALSE
)
```

**Arguments**

- `filtered`: Logical scalar indicating whether to filter out cells that were not used by the authors.
- `ensembl`: Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- `location`: Logical scalar indicating whether genomic coordinates should be returned.
- `legacy`: Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.
Details

Column metadata is scraped from GEO, using both the author-supplied TSV of per-cell annotations and the sample-level metadata. This contains information such as the diagnosis, severity, WHO class, clustering and clonotype.

If `filtered=TRUE`, only the cells used by the authors in their final analysis are returned. Otherwise, an additional `filtered` field will be present in the `colData`, indicating whether the cell was retained by the authors.

If `ensembl=TRUE`, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/bacher-tcell.

Value

A `SingleCellExperiment` object with a single matrix of UMI counts.

Author(s)

Aaron Lun

References

Bacher P et al. (2020). Low avidity T cell responses to SARS-CoV-2 in unexposed individuals and severe COVID-19 *Immunity* 53, 1258-1271

Examples

```r
if (.Machine$title > 4L) { # too large for 32-bit machines!
  sce <- BacherTCellData()
}
```

---

**BachMammaryData**

Obtain the Bach mammary data

Description

Obtain the mouse mammary gland single-cell RNA-seq data from Bach et al. (2017).
BachMammaryData

Usage

BachMammaryData(
  samples = c("NP_1", "NP_2", "G_1", "G_2", "L_1", "L_2", "PI_1", "PI_2"),
  location = TRUE,
  legacy = FALSE
)

Arguments

samples A character vector with at least one element, specifying which samples(s) to retrieve.
location Logical scalar indicating whether genomic coordinates should be returned.
legacy Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata is extracted from the sample annotation in GSE106273, and refers to the developmental stage of the mammary gland.

If multiple samples are specified in samples, the count matrices will be cbinded together. Cells originating from different samples are identifiable by the "Sample" field in the column metadata.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/bach-mammary.

Value

A SingleCellExperiment object with a single matrix of UMI counts.

Author(s)

Aaron Lun

References

Bach K et al. (2017). Differentiation dynamics of mammary epithelial cells revealed by single-cell RNA sequencing. Nat Commun. 8(1), 2128

Examples

sce <- BachMammaryData(samples="NP_1")
BaronPancreasData

Obtain the Baron pancreas data

Description

Obtain the human/mouse pancreas single-cell RNA-seq data from Baron et al. (2017).

Usage

BaronPancreasData(
  which = c("human", "mouse"),
  ensembl = FALSE,
  location = TRUE,
  legacy = FALSE
)

Arguments

which
  String specifying the species to get data for.
ensemb1
  Logical scalar indicating whether the output row names should contain Ensembl identifiers.
location
  Logical scalar indicating whether genomic coordinates should be returned.
legacy
  Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata is provided in the same form as supplied in GSE84133. This contains information such as the cell type labels and donor ID (for humans) or strain (for mouse).

If ensembl=TRUE, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output. Note that this is only performed if ensembl=TRUE.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/baron-pancreas.

Value

A SingleCellExperiment object with a single matrix of read counts.

Author(s)

Aaron Lun
References


Examples

```r
sce.human <- BaronPancreasData()
sce.mouse <- BaronPancreasData("mouse")
```

**BhaduriOrganoidData**

*Obtain the Bhaduri cortical organoid data*

**Description**

Obtain the human cortical organoid single-cell RNA-seq dataset from Bhaduri et al. (2020).

**Usage**

```r
BhaduriOrganoidData(ensembl = FALSE, location = TRUE, legacy = FALSE)
```

**Arguments**

- `ensembl` Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- `location` Logical scalar indicating whether genomic coordinates should be returned.
- `legacy` Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

**Details**

Column data contains sample-level information. In theory, there is also cell-level metadata for this dataset but it could not be unambiguously mapped to the column names.

If `ensembl=TRUE`, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output. Note that this is only performed if `ensembl=TRUE`.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for `scRNAseq/bhaduri-organoid`.

**Value**

A `SingleCellExperiment` object with a single matrix of normalized expression values.
Obtain the Buettner ESC data

Description
Obtain the mouse embryonic stem cell single-cell RNA-seq data from Buettner et al. (2015).

Usage
BuettnerESCData(remove.htseq = TRUE, location = TRUE, legacy = FALSE)

Arguments
remove.htseq Logical scalar indicating whether HT-seq alignment statistics should be removed.
location Logical scalar indicating whether genomic coordinates should be returned.
legacy Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details
Rows corresponding to HT-seq’s alignment statistics are removed by default. These can be retained by setting remove.htseq=FALSE.
Column metadata contains the experimentally determined cell cycle phase for each cell.
Counts for ERCC spike-ins are stored in the "ERCC" entry in the altExps.
If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output.
All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/buettner-esc.

Value
A SingleCellExperiment object with a single matrix of read counts.
Author(s)
Aaron Lun

References

Examples
sce <- BuettnerESCData()

---

BunisHSPCData

Obtain the Bunis haematopoietic stem and progenitor cell data

Description
Obtain the human fetal, newborn, and adult haematopoietic stem and progenitor cell single-cell RNA-seq dataset from Bunis et al. (2021).

Usage
BunisHSPCData(filtered = TRUE, legacy = FALSE)

Arguments
- filtered Logical scalar or "cells" indicating whether to:
  - TRUE: filter out cells that were not used by the authors.
  - "cells": filter out empty droplets as filtered out by cell ranger.
  - FALSE: no filtering
- legacy Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details
Column metadata is recreated from GEO using the author-supplied TSV of per-cell annotations, or retrieved from a processed version of the data shared by authors via figshare. This contains information such as the tissue & sample of origin, age group, likely cell type, and Developmental Stage Scoring. Within DevStageScoring element of the column metadata are the applied results ("<cell_type>_scores") of random forest regression trained on the fetal (score = 0) and adult (score = 1) cells of individual cell types indicated by ("<cell_type>_inTraining").

If filtered=TRUE, only the cells used by the authors in their final analysis are returned. Otherwise, an additional retained field will be present in the colData, indicating whether the cell was retained by the authors.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/bunis-hspc.
Value

A SingleCellExperiment object with a single matrix of UMI counts.

Author(s)

Daniel Bunis

References


Examples

sce <- BunisHSPCData()

---

CampbellBrainData

Obtain the Campbell brain data

Description

Obtain the mouse brain single-cell RNA-seq data from Campbell et al. (2017).

Usage

CampbellBrainData(ensembl = FALSE, location = TRUE, legacy = FALSE)

Arguments

ensembl Logical scalar indicating whether the row names of the returned object should contain Ensembl identifiers.
location Logical scalar indicating whether genomic coordinates should be returned.
legacy Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata is provided in the same form as supplied in GSE93374. This contains information such as the diet of the mice, sex and proposed cell type for each cell.

If ensembl=TRUE, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output. Note that this is only performed if ensembl=TRUE.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/campbell-brain.
**ChenBrainData**

**Value**

A `SingleCellExperiment` object with a single matrix of UMI counts.

**Author(s)**

Aaron Lun

**References**


**Examples**

```r
sce <- CampbellBrainData()
```

---

**ChenBrainData**

*Obtain the Chen brain data*

**Description**

Obtain the mouse brain single-cell RNA-seq data from Chen et al. (2017).

**Usage**

```r
ChenBrainData(ensembl = FALSE, location = TRUE, legacy = FALSE)
```

**Arguments**

- `ensembl` Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- `location` Logical scalar indicating whether genomic coordinates should be returned.
- `legacy` Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

**Details**

Column metadata is provided in the same form as supplied in GSE87544. This contains the putative cell type assigned by the original authors.

If `ensembl=TRUE`, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output. Note that this is only performed if `ensembl=TRUE`.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for `scRNAseq/chen-brain`. 
countErccMolecules

Value

A SingleCellExperiment object with a single matrix of UMI counts.

Author(s)

Aaron Lun

References


Examples

sce <- ChenBrainData()

```
countErccMolecules

Description

Compute the number of molecules for each transcript in the ERCC spike-in mixture, based on their published concentration as well as the volume of the diluted mixture added to each cell.

Usage

countErccMolecules(volume, dilution, mix = c("1", "2"), ...)

Arguments

volume Numeric scalar specifying the added volume (in microliters) of ERCC spike-in mixture.

dilution Numeric scalar specifying the dilution factor used for the added volume of the spike-in mixture.

mix String specifying whether to compute the number of molecules for mix 1 or 2.

... Further arguments to pass to fetchDataset.

Value

A DataFrame object with one row per ERCC spike-in transcript. This contains the estimated concentration and molecule count for each transcript.

Author(s)

Aaron Lun, based on code from Alan O’Callaghan
**Examples**

```r
countErccMolecules(volume = 9, dilution = 300000)
```

**Description**

Obtain the human brain single-cell RNA-seq dataset from Darmanis et al. (2015).

**Usage**

```r
DarmanisBrainData(
  ensembl = FALSE,
  location = TRUE,
  remove.htseq = TRUE,
  legacy = FALSE
)
```

**Arguments**

- `ensembl` Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- `location` Logical scalar indicating whether genomic coordinates should be returned.
- `remove.htseq` Logical scalar indicating whether HT-seq alignment statistics should be removed.
- `legacy` Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

**Details**

Column metadata is scraped from GEO and includes patient information, tissue of origin and likely cell type.

If `ensembl=TRUE`, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output. This is only performed when `ensembl=TRUE`.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for `scRNAseq/darmanis-brain`.

**Value**

A `SingleCellExperiment` object with a single matrix of UMI counts.
**Author(s)**

Aaron Lun

**References**


**Examples**

```r
sce <- DarmanisBrainData()
```

---

**ERCCSpikeInConcentrations**

*Obtain ERCC concentrations*

**Description**

Obtain ERCC spike-in concentrations from the Thermo Fisher Scientific website.

**Usage**

```r
ERCCSpikeInConcentrations(
  volume = NULL,
  dilution = NULL,
  mix = c("1", "2"),
  legacy = FALSE
)
```

**Arguments**

- `volume` Numeric scalar specifying the added volume (in nanoliters) of ERCC spike-in mixture. Only used if `dilution` is specified.
- `dilution` Numeric scalar specifying the dilution factor used for the added volume of the spike-in mixture. Only used if `volume` is specified.
- `mix` String specifying whether to compute the number of molecules for mix 1 or 2. Only used if both `dilution` and `volume` are specified.
- `legacy` Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

**Details**

If `volume` and `dilution` are specified, an additional column is added to the output specifying the number of molecules of spike-in transcript for the specified mix.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for `scRNAseq/ercc-concentrations`. 
Value

A DataFrame object with one row per ERCC spike-in transcript. This contains information such as the spike-in concentration in each mix.

Author(s)

Alan O’Callaghan

Examples

df <- ERCCSpikeInConcentrations()

 Obtained the Ernst spermatogenesis data

Description

Obtain the mouse spermatogenesis single-cell RNA-seq dataset from Ernst et al. (2019).

Usage

ErnstSpermatogenesisData(
  method = c("emptyDrops", "Cellranger"),
  location = TRUE,
  legacy = FALSE
)

Arguments

method String indicating which cell caller to obtain results for.
location Logical scalar indicating whether genomic coordinates should be returned.
legacy Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

This study contains two analyses done with datasets from different cell calling algorithms. One uses Cellranger version 2 while the other uses emptyDrops from DropletUtils.

Column metadata includes sample information, per-cell QC metrics and cell type labels. In particular, the sample label specifies the developmental stage of the mouse.

Note that method="Cellranger" contains additional data for Tc1 mice. These mice have an additional human chromosome 21 inserted alongside the usual mouse chromosomes.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/ernst-spermatogenesis.
Value

A **SingleCellExperiment** object with a single matrix of UMI counts.

Author(s)

Aaron Lun

References


Examples

```r
if (.Machine$sizeof.pointer > 4) { # too large for 32-bit machines!
  sce <- ErnstSpermatogenesisData()
}
```

---

**fetchDataset**

*Fetch a dataset from the gypsum backend*

**Description**

Fetch a dataset (or its metadata) from the gypsum backend.

**Usage**

```r
fetchDataset(
  name,
  version,
  path = NA,
  package = "scRNAseq",
  cache = cacheDirectory(),
  overwrite = FALSE,
  realize.assays = FALSE,
  realize.reduced.dims = TRUE,
  ...
)
```

```r
fetchMetadata(
  name,
  version,
  path = NA,
  package = "scRNAseq",
  cache = cacheDirectory(),
  overwrite = FALSE
)
```
**FletcherOlfactoryData**

**Obtain the Fletcher Olfactory data**

**Description**

Obtain the mouse olfactory epithelial HBC stem cell differentiation dataset from Fletcher et al. (2017).

**Arguments**

- **name**: String containing the name of the dataset.
- **version**: String containing the version of the dataset.
- **path**: String containing the path to a subdataset, if `name` contains multiple datasets. Defaults to `NA` if no subdatasets are present.
- **package**: String containing the name of the package.
- **cache, overwrite**: Arguments to pass to `saveVersion` or `saveFile`.
- **realize.assays, realize.reduced.dims**: Logical scalars indicating whether to realize assays and reduced dimensions into memory. Dense and sparse `ReloadedArray` objects are converted into ordinary arrays and `dgCMatrix` objects, respectively.
- **...**: Further arguments to pass to `readObject`.

**Value**

- `fetchDataset` returns the dataset as a `SummarizedExperiment` or one of its subclasses.
- `fetchMetadata` returns a named list of metadata for the specified dataset.

**Author(s)**

Aaron Lun

**See Also**

- [https://github.com/ArtifactDB/bioconductor-metadata-index](https://github.com/ArtifactDB/bioconductor-metadata-index), on the expected schema for the metadata.
- `saveDataset` and `uploadDirectory`, to save and upload a dataset.
- `surveyDatasets` and `listVersions`, to get possible values for `name` and `version`.

**Examples**

```r
fetchDataset("zeisel-brain-2015", "2023-12-14")
fetchMetadata("zeisel-brain-2015", "2023-12-14")
```
Usage

FletcherOlfactoryData(
  filtered = TRUE,
  ensembl = FALSE,
  location = TRUE,
  legacy = FALSE
)

Arguments

  filtered  Logical scalar indicating whether to filter out cells that were not used by the authors.
  ensembl  Logical scalar indicating whether the output row names should contain Ensembl identifiers.
  location  Logical scalar indicating whether genomic coordinates should be returned.
  legacy  Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata is scraped from GEO, using both the author-supplied “phenoData” per-cell annotations and the author-supplied “protocolData” per-cell annotations. The former includes information about the animals and the instruments, while the latter contains QC statistics.

We also included the clustering results from the authors’ analysis.

If filtered=TRUE, only the cells used by the authors in their cluster analysis are returned. Otherwise, the cells not used by the authors will have NA in the clustering columns of the colData.

If ensembl=TRUE, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/fletcher-olfactory.

Value

A SingleCellExperiment object with a single matrix of read counts.

Author(s)

Davide Risso

References

**Description**

Obtain the mouse haematopoietic stem cell single-cell RNA-seq and CRISPR-seq dataset from Giladi et al. (2018).

**Usage**

```r
GiladiHSCData(
  mode = c("rna", "crispr"),
  filtered = TRUE,
  ensembl = FALSE,
  location = TRUE,
  legacy = FALSE
)
```

**Arguments**

- `mode`: Character vector specifying which modalities should be returned.
- `filtered`: Logical scalar indicating whether to filter out cells that were not used by the authors.
- `ensembl`: Logical scalar indicating whether the output row names should contain Ensembl identifiers, when `mode` contains "rna".
- `location`: Logical scalar indicating whether genomic coordinates should be returned, when `mode` contains "rna".
- `legacy`: Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

**Details**

Column metadata is scraped from GEO using the author-supplied TSV of per-cell annotations. This contains information such as the batch of origin for each cell plus an array of FACS measurements per cell.

If `filtered=TRUE`, only the cells used by the authors in their final analysis are returned. Otherwise, an additional `filtered` field will be present in the `colData`, indicating whether the cell was retained by the authors.

If `ensembl=TRUE`, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated
IDs is retained. For row names with multiple semi-colon-delimited symbols, the last symbol is used for matching against the Ensembl annotation.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output. This is only relevant when `ensembl=TRUE`.

If `mode` contains multiple modalities, the intersection of cells that are present in both modalities is returned. This is because not all cells have data across both modalities. If `mode` contains only one modality, all cells for that modality are returned.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for `scRNAseq/giladi-hsc`.

**Value**

A `SingleCellExperiment` object with a matrix of UMI counts for the scRNA-seq or CRISPR-seq data. Alternatively, an object with both count matrices, where the second modality is stored as an alternative Experiment.

**Author(s)**

Aaron Lun

**References**


**Examples**

```r
if (.Machine$sizeof.pointer > 4) { # too large for 32-bit machines!
  sce <- GiladiHSCData()
}
```

---

**GrunHSCData**

**Obtain the Grun HSC data**

**Description**

Obtain the mouse haematopoietic stem cell single-cell RNA-seq data from Grun et al. (2016).

**Usage**

`GrunHSCData(ensembl = FALSE, location = TRUE, legacy = FALSE)`

**Arguments**

- `ensembl` Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- `location` Logical scalar indicating whether genomic coordinates should be returned.
- `legacy` Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.
Details

Row metadata contains the symbol and chromosomal location for each gene. Column metadata contains the extraction protocol used for each sample, as described in GSE76983.

If `ensembl=TRUE`, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output. Note that this is only performed if `ensembl=TRUE`.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for `scRNAseq/grun-hsc`.

Value

A `SingleCellExperiment` object with a single matrix of UMI counts.

Author(s)

Aaron Lun

References


Examples

```r
sce <- GrunHSCData()
```

Description

Obtain the human pancreas single-cell RNA-seq data from Grun et al. (2016).

Usage

`GrunPancreasData(ensembl = FALSE, location = TRUE, legacy = FALSE)`

Arguments

- `ensembl` Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- `location` Logical scalar indicating whether genomic coordinates should be returned.
- `legacy` Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.
Details

Row metadata contains fields for the symbol and chromosomal location of each gene, as derived from the row names.

Column metadata is derived from the column names of the count matrix with the sample annotations in GSE81076. This includes the donor identity for each cell and the type of sample.

The "ERCC" entry in the altExps contains count data for the ERCC spike-in transcripts.

If ensembl=TRUE, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output. Note that this is only performed if ensembl=TRUE.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/grun-pancreas.

Value

A SingleCellExperiment object with a single matrix of UMI counts.

Author(s)

Aaron Lun, using additional metadata obtained by Vladimir Kiselev.

References


Examples

sce <- GrunPancreasData()
HeOrganAtlasData

Usage

HeOrganAtlasData(
            "Stomach", "Trachea"),
  ensembl = FALSE,
  location = TRUE,
  legacy = FALSE
)

Arguments

tissue Character vector specifying the tissues to return.

ensemb1 Logical scalar indicating whether the output row names should contain Ensembl
        identifiers.

location Logical scalar indicating whether genomic coordinates should be returned.

legacy Logical scalar indicating whether to pull data from ExperimentHub. By default,
        we use data from the gypsum backend.

Details

Column data contains the tissue of origin, a variety of per-cell QC metrics as well as some cell
        type annotations. The reclustered annotations required some assembly:

- reclustered.broad was generated based on whether the barcode was present in each
  *_meta.data.txt
  file at https://github.com/bei-lab/scRNA-AHCA.

- For each barcode that was present in one of those files, reclustered.fine was generated
  based on the label in the annotation field inside that file.

If multiple tissues are requested, counts are only reported for the intersection of genes across all
        tissues. This is because the gene annotation in the original count matrices differs across
        tissues.

If ensembl=TRUE, the gene symbols are converted to Ensembl IDs in the row names of the output
        object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated
        IDs is retained.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of
        the output. Note that this is only performed if ensembl=TRUE.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can
        be retrieved by searching for scRNAseq/he-organ-atlas.

Value

A SingleCellExperiment object with a single matrix of UMI counts.

Author(s)

Aaron Lun
References


Examples

```r
if (.Machine$sizeof.pointer > 4) { # too large for 32-bit machines!
  sce <- HeOrganAtlasData()
}
```

HermannSpermatogenesisData

*Obtain the Hermann spermatogenesis data*

Description

Obtain the mouse spermatogenesis single-cell RNA-seq data from Hermann et al. (2018).

Usage

```r
HermannSpermatogenesisData(strip = FALSE, location = TRUE, legacy = FALSE)
```

Arguments

- `strip` Logical scalar indicating whether to strip the .X notation from the row names.
- `location` Logical scalar indicating whether genomic coordinates should be returned. Only used if `strip=TRUE`.
- `legacy` Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata contains cell types provided by the data generators at [https://data.mendeley.com/datasets/kxd5f8vpt4/1#file-fe79c10b-c42e-472e-9c7e-9a9873d9b3d8](https://data.mendeley.com/datasets/kxd5f8vpt4/1#file-fe79c10b-c42e-472e-9c7e-9a9873d9b3d8).

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/hermann-spermatogenesis.

Value

A `SingleCellExperiment` object with two matrices, containing spliced and unspliced counts, respectively.

Author(s)

Charlotte Soneson
References


Examples

sce <- HermannSpermatogenesisData()

---

HuCortexData

**Obtain the Hu cortex data**

Description

Obtain the mouse cortex single-nuclei RNA-seq data from Hu et al. (2017).

Usage

HuCortexData(
  mode = c("ctx", "3T3"),
  samples = NULL,
  ensembl = FALSE,
  location = TRUE,
  legacy = FALSE
)

Arguments

- **mode** Character vector indicating whether to return data for the 3T3 cells or the mouse cortex.
- **samples** Character vector indicating whether to return data for specific samples, see Details. If specified, this overrides mode.
- **ensembl** Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- **location** Logical scalar indicating whether genomic coordinates should be returned.
- **legacy** Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata includes the mode and sample corresponding to each cell/nuclei. Available samples are:

- "cell-3T3" and "nuclei-3T3", generated from the 3T3 cell line.
- "nuclei-ctx-X", nuclei generated from the cortex of animal number X (from 1 to 13).
• "nuclei-ctx-salineX" or "nuclei-ctx-PTZX", nuclei generated from the cortex of saline- or PTZ-treated mice. X represents the replicate number and can be 1 or 2.

If multiple modes are requested, counts are only reported for the intersection of genes across all modes. This is because the gene annotation in the original count matrices differs across modes.

If ensembl=TRUE, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output. Note that this is only performed if ensembl=TRUE.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/wu-kidney.

Value

A SingleCellExperiment object with a single matrix of read counts.

Author(s)

Aaron Lun

References


Examples

sce <- HuCortexData("3T3")

---

JessaBrainData

Obtain the Jessa brain data

Description

Obtain the mouse brain single-cell RNA-seq dataset from Jessa et al. (2019).

Usage

JessaBrainData(filtered = TRUE, location = TRUE, legacy = FALSE)

Arguments

| filtered   | Logical scalar indicating whether to filter out cells that were not used by the authors. |
| location   | Logical scalar indicating whether genomic coordinates should be returned.               |
| legacy     | Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend. |
Details

If `filtered=TRUE`, only the cells used by the authors in their final analysis are returned. Otherwise, an additional `filtered` field will be present in the `colData`, indicating whether the cell was retained by the authors.

The column data contains sample of origin, some QC metrics and various cluster assignments for each cell. Cluster assignments starting with `Sample_*` are derived from per-sample analyses and cannot be compared sensibly across samples. Other clusterings (`Forebrain_*` and `Pons_*`) are derived from joint analyses across all samples involving the named tissue.

The `reducedDims` of the output contains various dimensionality reduction results. Coordinates for entries prefixed with `Sample_*` were generated from per-sample analyses and cannot be compared across samples. Coordinates for entries prefixed with `Forebrain_*` and `Pons_*` were generated from joint analyses from the corresponding tissue.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for `scRNAseq/jessa-brain`.

Value

A `SingleCellExperiment` object with a single matrix of UMI counts.

Author(s)

Aaron Lun

References

Jessa S et al. (2019). Stalled developmental programs at the root of pediatric brain tumors *Nat Genet* 51, 1702-1713

Examples

```r
if (.Machine$sizeof.pointer > 4) { # too large for 32-bit machines!
  sce <- JessaBrainData()
}
```

KolodziejczykESCData Obtain the Kolodziejczyk ESC data

Description

Obtain the mouse embryonic stem cell single-cell RNA-seq data from Kolodziejczyk et al. (2015).

Usage

```
KolodziejczykESCData(remove.htseq = TRUE, location = TRUE, legacy = FALSE)
```
Arguments

- **remove.htseq**: Logical scalar indicating whether HT-seq alignment statistics should be removed.
- **location**: Logical scalar indicating whether genomic coordinates should be returned.
- **legacy**: Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata is generated from the column names, and contains the culture conditions and the plate of origin for each cell.

Count data for ERCC spike-ins are stored in the "ERCC" entry in the `altExps`.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for `scRNAseq/kolodziejczyk-esc`.

Value

A `SingleCellExperiment` object with a single matrix of read counts.

Author(s)

Aaron Lun

References


Examples

```r
sce <- KolodziejczykESCData()
```

---

**KotliarovPBMCData**

Obtain the Kotliarov CITE-seq data

Description

Obtain the Kotliarov PBMC CITE-seq data from Kotliarov et al. (2020).
KotliarovPBMCData

Usage

KotliarovPBMCData(
  mode = c("rna", "adt"),
  ensembl = FALSE,
  location = TRUE,
  legacy = FALSE
)

Arguments

mode          Character vector specifying whether to return either or both the RNA and ADT
counts.
ensembl       Logical scalar indicating whether the output row names should contain Ensembl
identifiers.
location      Logical scalar indicating whether genomic coordinates should be returned.
legacy        Logical scalar indicating whether to pull data from ExperimentHub. By default,
we use data from the gypsum backend.

Details

This dataset contains 20 samples from 2 experimental batches, where each batch contains 5 high
and 5 low responders. The 10 samples per batch were mixed and distributed across the 6 lanes using
a cell hashing approach.

The column metadata contains the following fields:

- sample*: identifiers for the sample of origin for each cell.
- adjmfc.time: type of responder for each sample.
- tenx_lane: 10X lane from which each cell was collected.
- batch: the batch of origin.
- barcode_check: barcode identifier.
- hash_* and hto_* columns: HTOdemux outputs.
- DEMUXLET.* columns: demuxlet outputs.
- joint_classification_global: HTOdemux and demuxlet joint classification.
- nGene: number of genes as defined from Seurat’s CreateSeuratObject.
- nUMI: number of UMIs as defined from Seurat’s CreateSeuratObject.
- pctMT: percent of mitochondrial reads as defined from Seurat’s CreateSeuratObject.

Note, no filtering has been performed based on the quality control metrics.

If ensembl=TRUE, the gene symbols in the RNA data are converted to Ensembl IDs in the row names
of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence
of duplicated IDs is retained.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges for the
RNA data. Note that this is only performed if ensembl=TRUE.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can
be retrieved by searching for scRNAseq/kotliarov-pbmc.
**Value**

A `SingleCellExperiment` object with a single matrix of UMI counts corresponding to the first mode, with an optional alternative Experiment if there is a second mode.

**Author(s)**

Stephany Orjuela, with modifications from Aaron Lun

**References**


**Examples**

```r
sce <- KotliarovPBMCData()
```

---

**LaMannoBrainData**  
*Obtain the La Manno brain data*

**Description**

Obtain the mouse/human brain scRNA-seq data from La Manno et al. (2016).

**Usage**

```r
LaMannoBrainData(
  which = c("human-es", "human-embryo", "human-ips", "mouse-adult", "mouse-embryo"),
  ensembl = FALSE,
  location = TRUE,
  legacy = FALSE
)
```

**Arguments**

- `which` A string specifying which dataset should be obtained.
- `ensembl` Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- `location` Logical scalar indicating whether genomic coordinates should be returned.
- `legacy` Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.
Details

Column metadata is provided in the same form as supplied in the supplementary tables in GSE71585. This contains information such as the time point and cell type.

The various settings of which will obtain different data sets.

- "human-es", human embryonic stem cells.
- "human-embryo", human embryo midbrain.
- "human-ips", human induced pluripotent stem cells.
- "mouse-adult", mouse adult dopaminergic neurons.
- "mouse-embryo", mouse embryo midbrain.

Unfortunately, each of these datasets uses a different set of features. If multiple datasets are to be used simultaneously, users will have to decide how to merge them, e.g., by taking the intersection of common features across all datasets.

If ensembl=TRUE, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output. Note that this is only performed if ensembl=TRUE.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/lamanno-brain.

Value

A SingleCellExperiment object with a single matrix of UMI counts.

Author(s)

Aaron Lun

References


Examples

sce.h.es <- LaMannoBrainData()

sce.h.em <- LaMannoBrainData("human-embryo")

sce.h.ip <- LaMannoBrainData("human-ips")

sce.m.ad <- LaMannoBrainData("mouse-adult")

sce.m.em <- LaMannoBrainData("mouse-embryo")
LawlorPancreasData

Obtain the Lawlor pancreas data

Description

Provides the human pancreas single-cell RNA-seq data from Lawlor et al. (2017).

Usage

LawlorPancreasData(legacy = FALSE)

Arguments

- **legacy**: Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata is provided in the same form as supplied in GSE86469. This contains information such as the cell type labels and patient status.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/lawlor-pancreas.

Value

A SingleCellExperiment object with a single matrix of read counts.

Author(s)

Aaron Lun

References


Examples

sce <- LawlorPancreasData()
**LedergorMyelomaData**  

*Obtain the Ledergor Myeloma data*

**Description**

Obtain the human multiple myeloma single-cell RNA-seq data from Ledergor et al. (2018).

**Usage**

```r
LedergorMyelomaData(ensembl = FALSE, location = TRUE, legacy = FALSE)
```

**Arguments**

- `ensembl` Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- `location` Logical scalar indicating whether genomic coordinates should be returned.
- `legacy` Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

**Details**

Column metadata was created from the sample metadata file in GSE117156. It contains an 'Experiment_ID' column, from which the tissue and subject of origin were extracted, as well as the condition and treatment status of the subject.

If `ensembl=TRUE`, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output. Note that this is only performed if `ensembl=TRUE`.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for `scRNAseq/ledergor-myeloma`.

**Value**

A `SingleCellExperiment` object with a single matrix of read counts.

**Author(s)**

Milan Malfait

**References**

Examples

```r
sce <- LedegorMyelomaData()
```

Description

Obtain the human embryonic stem cell single-cell RNA-seq data from Leng et al. (2015).

Usage

```r
LengESCData(ensembl = FALSE, location = TRUE, legacy = FALSE)
```

Arguments

- `ensembl` Logical scalar indicating whether gene symbols should be converted to Ensembl annotation.
- `location` Logical scalar indicating whether genomic coordinates should be returned.
- `legacy` Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata contains the cell line, experiment number and experimentally determined cell cycle phase for each cell.

If `ensembl=TRUE`, the gene symbols in the published annotation are converted to Ensembl. If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for `scRNAseq/leng-esc`.

Value

A `SingleCellExperiment` object with a single matrix of normalized expected read counts.

Author(s)

Aaron Lun

References

**Examples**

```r
cse <- LengESCData()
```

---

## listDatasets

**List all available datasets**

### Description

Summary information for all available datasets in the `scRNAseq` package.

### Usage

```r
listDatasets()
```

### Details

A study may contribute multiple datasets if they cannot be reasonably combined (e.g., different species). The reported number of cells refers only to the dataset as it is stored in `scRNAseq`; this may be different to the number of cells used by the authors in their analysis, e.g., due to filtering.

### Value

A `DataFrame` where each row corresponds to a dataset, containing the fields:

- Reference, a Markdown-formatted citation to `scripts/ref.bib` in the `scRNAseq` installation directory.
- Taxonomy, an identifier for the organism.
- Part, the part of the organism being studied.
- Number, the total number of cells in the dataset.
- Call, the relevant R call required to construct the dataset.

### Author(s)

Aaron Lun

### Examples

```r
listDatasets()
```
listVersions  
List available versions

Description
List the available and latest versions for an asset (i.e., datasets or collections of datasets).

Usage

```r
listVersions(name)
fetchLatestVersion(name)
```

Arguments

- `name`  
  String containing the name of the asset.

Value

For `listVersions`, a character vector containing the names of the available versions of the `name` asset.  
For `fetchLatestVersion`, a string containing the name of the latest version.

Author(s)

Aaron Lun

Examples

```r
listVersions("zeisel-brain-2015")
fetchLatestVersion("zeisel-brain-2015")
```

LunSpikeInData  
Obtain the Lun spike-in data

Description
Obtain the spike-in single-cell RNA-seq data from Lun et al. (2017).

Usage

```r
LunSpikeInData(
  which = c("416b", "tropho"),
  split.oncogene = FALSE,
  location = TRUE,
  legacy = FALSE
)
```
LunSpikeInData

Arguments

- **which**: String specifying whether the 416B or trophoblast data should be obtained.
- **split.oncogene**: Logical scalar indicating whether the oncogene should be split to a separate altExp.
- **location**: Logical scalar indicating whether genomic coordinates should be returned.
- **legacy**: Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Row data contains a single "Length" field describing the total exonic length of each feature.

Column metadata is provided in the same form as supplied in E-MTAB-5522. This contains information such as the cell type, plate of origin, spike-in addition order and oncogene induction.

Two sets of spike-ins were added to each cell in each dataset. These are available as the "SIRV" and "ERCC" entries in the altExps.

If `split.oncogene=TRUE` and `which="416b"`, the CBFB-MYH11-mcherry oncogene is moved to extra "oncogene" entry in the altExps.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the rowRanges of the output.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/lun-spikein.

Value

A SingleCellExperiment object with a single matrix of read counts.

Author(s)

Aaron Lun

References


Examples

```r
sce <- LunSpikeInData()
sce <- LunSpikeInData("tropho")
```
Obtain the Macosko retina data

Description

Obtain the mouse retina single-cell RNA-seq data from Macosko et al. (2016).

Usage

MacoskoRetinaData(ensembl = FALSE, location = TRUE, legacy = FALSE)

Arguments

- ensembl: Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- location: Logical scalar indicating whether genomic coordinates should be returned.
- legacy: Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata contains the cluster identity as reported in the paper. Note that some cells will have NA identities as they are present in the count matrix but not in the metadata file. These are presumably low-quality cells that were discarded prior to clustering.

If ensembl=TRUE, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output. Note that this is only performed if ensembl=TRUE.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/macosko-retina.

Value

A SingleCellExperiment object with a single matrix of UMI counts.

Author(s)

Aaron Lun

References

MairPBMCData

Examples

sce <- MacoskoRetinaData()

Description

Obtain the Mair PBMC targeted CITE-seq data from Mair et al. (2020).

Usage

MairPBMCData(
  mode = c("rna", "adt"),
  ensembl = FALSE,
  location = TRUE,
  legacy = FALSE
)

Arguments

mode Character vector specifying whether to return either or both the RNA and ADT counts.
ensembl Logical scalar indicating whether the output row names should contain Ensembl identifiers.
location Logical scalar indicating whether genomic coordinates should be returned.
legacy Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata contains the donor identity and cartridge of origin. Some libraries may also be classified as multiplets or have undeterminate origins after hash tag debarcoding.

If ensembl=TRUE, the gene symbols in the RNA data are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges for the RNA data. Note that this is only performed if ensembl=TRUE.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/mair-pbmc.

Value

A SingleCellExperiment object with a single matrix of UMI counts corresponding to the first mode, with an optional alternative Experiment if there is a second mode.
MarquesBrainData

Author(s)

Stephany Orjuela, with modifications from Aaron Lun

References


Examples

sce <- MairPBMCData()

MarquesBrainData

Obtain the Marques brain data

Description

Obtain the mouse brain single-cell RNA-seq data from Marques et al. (2016).

Usage

MarquesBrainData(ensembl = FALSE, location = TRUE, legacy = FALSE)

Arguments

ensembl Logical scalar indicating whether the output row names should contain Ensembl identifiers.

location Logical scalar indicating whether genomic coordinates should be returned.

legacy Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata is provided in the same form as supplied in GSE75330. This contains information such as the cell type and age/sex of the mouse of origin for each cell.

Note that some genes may be present in multiple rows corresponding to different genomic locations. These additional rows are identified by a _loc[2-9] suffix in their row names. Users may wish to consider either removing them or merging them, e.g., with scater::sumCountsAcrossFeatures.

If ensembl=TRUE, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained. All searching is performed after removing the _loc[2-9] suffix.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output. Note that this is only performed if ensembl=TRUE.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/marques-brain.
Value

A SingleCellExperiment object with a single matrix of UMI counts.

Author(s)

Aaron Lun

References


Examples

sce <- MarquesBrainData()

---

Obtain the Messmer ESC data

Description

Obtain the human embryonic stem cell single-cell RNA-seq data from Messmer et al. (2019).

Usage

MessmerESCData(location = TRUE, legacy = FALSE)

Arguments

  location Logical scalar indicating whether genomic coordinates should be returned.
  legacy Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Row data contains a single "Length" field describing the total exonic length of each feature.

Column metadata is provided in the same form as supplied in E-MTAB-6819. This contains information such as the cell phenotype (naive or primed) and the batch of origin. Note that counts for technical replicates have already been summed together.

Count data for ERCC spike-ins are stored in the "ERCC" entry of the altExps. If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNaseq/messmer-esc.
MuraroPancreasData

Value

A `SingleCellExperiment` object with a single matrix of read counts.

Author(s)

Aaron Lun

References


Examples

```r
sce <- MessmerESCData()
```

---

MuraroPancreasData  Obtain the Muraro pancreas data

Description

Obtain the human pancreas single-cell RNA-seq data from Muraro et al. (2016).

Usage

```r
MuraroPancreasData(ensembl = FALSE, location = TRUE, legacy = FALSE)
```

Arguments

- `ensembl` Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- `location` Logical scalar indicating whether genomic coordinates should be returned.
- `legacy` Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Row data contains fields for the symbol and chromosomal location of each gene. Column metadata is derived from the columns of the count matrix provided in GSE85241, with additional cell type labels obtained from the authors (indirectly, via the Hemberg group). Some cells have NA labels and were presumably removed prior to downstream analyses. Count data for ERCC spike-ins are stored in the "ERCC" entry of the `altExps`. If `ensembl=TRUE`, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.
**NestorowaHSCData**

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output. Note that this is only performed if `ensembl=TRUE`.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for `scRNAseq/muraro-pancreas`.

**Value**

A `SingleCellExperiment` object with a single matrix of UMI counts.

**Author(s)**

Aaron Lun, using additional metadata obtained by Vladimir Kiselev.

**References**


**Examples**

```r
sce <- MuraroPancreasData()
```

---

**NestorowaHSCData** *Obtain the Nestorowa HSC data*

**Description**

Obtain the mouse haematopoietic stem cell single-cell RNA-seq data from Nestorowa et al. (2015).

**Usage**

`NestorowaHSCData(remove.htseq = TRUE, location = TRUE, legacy = FALSE)`

**Arguments**

- `remove.htseq` Logical scalar indicating whether HT-seq alignment statistics should be removed.
- `location` Logical scalar indicating whether genomic coordinates should be returned.
- `legacy` Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.
Details

Rows corresponding to HT-seq’s alignment statistics are removed by default. These can be retained by setting `remove.htseq=FALSE`.

Column metadata includes the cell type mapping, as described on the website (see References), and the FACS expression levels of selected markers. Note that these are stored as nested matrices within the `colData`.

Diffusion map components are provided as the "diffusion" entry in the `reducedDims`.

Counts for ERCC spike-ins are stored in the "ERCC" entry in the `altExps`.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for `scRNAseq/nestorowa-hsc`.

Value

A `SingleCellExperiment` object with a single matrix of read counts.

Author(s)

Aaron Lun

References


Examples

```r
sce <- NestorowaHSCData()
```

Description

Obtain the human cortex single-cell RNA-seq dataset from Nowakowski et al. (2017).

Usage

```r
NowakowskiCortexData(ensembl = FALSE, location = TRUE, legacy = FALSE)
```
Arguments

- **ensembl**: Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- **location**: Logical scalar indicating whether genomic coordinates should be returned.
- **legacy**: Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata includes the presumed cell type (`WGCNAcluster`), patient and tissue region of origin. A variety of dimensionality reduction results are also provided.

If `ensembl=TRUE`, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output. This is only performed when `ensembl=TRUE`.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for `scRNAseq/nowakowski-cortex`.

Value

A `SingleCellExperiment` object with a single matrix of TPMs. The `reducedDims` contains an assortment of dimensionality reduction results.

Author(s)

Aaron Lun

References


Examples

```r
c <- NowakowskiCortexData()
```
PaulHSCData

Obtain the Paul HSC data

Description

Obtain the mouse haematopoietic stem cell single-cell RNA-seq data from Paul et al. (2015).

Usage

PaulHSCData(
  ensembl = FALSE,
  discard.multiple = TRUE,
  location = TRUE,
  legacy = FALSE
)

Arguments

- ensembl: Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- discard.multiple: Logical scalar indicating whether ambiguous rows should be discarded.
- location: Logical scalar indicating whether genomic coordinates should be returned.
- legacy: Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata includes the plate and the mouse of origin, fluorescence intensities from indexed sorting and the number of cells in each well.

Some of the original rownames are concatenated symbols from multiple genes. We consider these rows to represent ambiguously assigned counts and discard them if discard.multiple=TRUE.

If ensembl=TRUE, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output. Note that this is only performed if ensembl=TRUE.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNaseq/nesrorowa-hsc.

Value

A SingleCellExperiment object with a single matrix of read counts.
polishDataset

Author(s)
Aaron Lun

References

Examples
sce <- PaulHSCData()

polishDataset  Polish dataset for saving

Description
Prepare a SummarizedExperiment or SingleCellExperiment to be saved with saveDataset. This performs some minor changes to improve storage efficiency.

Usage
polishDataset(
x,       
strip.inner.names = TRUE,  
reformat.assay.by.density = 0.3,  
attempt.integer.conversion = TRUE,  
remove.altexp.coldata = TRUE,  
forbid.nested.altexp = TRUE
)

Arguments
x                     A SummarizedExperiment or one of its subclasses.
strip.inner.names     Logical scalar indicating whether to strip redundant names from internal objects, e.g., dimnames of the assays, row names of reduced dimensions, column names of alternative experiments. This saves some space in the on-disk representation.
reformat.assay.by.density   Numeric scalar indicating whether to optimize assay formats based on the density of non-zero values. Assays with densities above this number are converted to ordinary dense arrays (if they are not already), while those with lower densities are converted to sparse matrices. This can be disabled by setting it to NULL.
attempt.integer.conversion
Logical scalar indicating whether to convert double-precision assays containing integer values to actually have the integer type. This can improve efficiency of downstream applications by avoiding the need to operate in double precision.

remove.altexp.coldata
Logical scalar indicating whether column data for alternative experiments should be removed. This defaults to TRUE as the alternative experiment column data is usually redundant with that of the main experiment.

forbid.nested.altexp
Logical scalar indicating whether nested alternative experiments (i.e., alternative experiments of alternative experiments) should be forbidden. This defaults to TRUE as nested alternative experiments are usually the result of some mistake in altExp preparation.

Value
A modified copy of x.

Author(s)
Aaron Lun

Examples
```r
mat <- matrix(rpois(1000, lambda=0.2), 100, 10) * 1.0
rownames(mat) <- sprintf("GENE_%i", seq_len(nrow(mat)))
colnames(mat) <- head(LETTERS, 10)

library(SingleCellExperiment)
sce <- SingleCellExperiment(list(counts=mat))
str(assay(sce, withDimnames=FALSE))

polished <- polishDataset(sce)
str(assay(polished, withDimnames=FALSE))
```

Obtain the Pollen radial glia data

Obtain the human radial glia single-cell RNA-seq dataset from Pollen et al. (2017).

Usage
```
PollenGliaData(ensembl = FALSE, location = TRUE, legacy = FALSE)
```
reexports

Arguments

ensemb1 Logical scalar indicating whether the output row names should contain Ensembl identifiers.
location Logical scalar indicating whether genomic coordinates should be returned.
legacy Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata includes the anatomical source, sample of origin, presumed cell type and assorted alignment statistics.

If ensembl=TRUE, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output. This is only performed when ensembl=TRUE.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/pollen-glia.

Value

A SingleCellExperiment object with a single matrix of read counts.

Author(s)

Aaron Lun

References


Examples

sce <- PollenGliaData()
Reprocessed single-cell data sets

Description

Obtain the legacy count matrices for three publicly available single-cell RNA-seq datasets. Raw sequencing data were downloaded from NCBI's SRA or from EBI's ArrayExpress, aligned to the relevant genome build and used to quantify gene expression.

Usage

ReprocessedAllenData(  
  assays = NULL,  
  ensembl = FALSE,  
  location = TRUE,  
  legacy = FALSE  
)

ReprocessedTh2Data(  
  assays = NULL,  
  ensembl = FALSE,  
  location = TRUE,  
  legacy = FALSE  
)

ReprocessedFluidigmData(  
  assays = NULL,  
  ensembl = FALSE,  
  location = TRUE,  
  legacy = FALSE  
)

Arguments

assays Character vector specifying one or more assays to return. Choices are "tophat_counts", "cufflinks_fpkm", "rsem_counts" and "rsem_tpm". If NULL, all assays are returned.

ensemb1 Logical scalar indicating whether the output row names should contain Ensembl identifiers.

location Logical scalar indicating whether genomic coordinates should be returned.

legacy Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.
ReprocessedAllenData

Details

ReprocessedFluidigmData returns a dataset of 65 human neural cells from Pollen et al. (2014), each sequenced at high and low coverage (SRA accession SRP041736).

ReprocessedTh2Data returns a dataset of 96 mouse T helper cells from Mahata et al. (2014), obtained from ArrayExpress accession E-MTAB-2512. Spike-in counts are stored in the "ERCC" entry of the altExps.

ReprocessedAllenData return a dataset of 379 mouse brain cells from Tasic et al. (2016). This is a re-processed subset of the data from TasicBrainData, and contains spike-in information stored as in the altExps.

In each dataset, the first columns of the colData are sample quality metrics from FastQC and Picard. The remaining fields were obtained from the original study in their GEO/SRA submission and/or as Supplementary files in the associated publication. These two categories of colData are distinguished by a which_qc element in the metadata, which contains the names of the quality-related columns in each object.

If ensembl=TRUE, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output. Note that this is only performed if ensembl=TRUE.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/legacy-allen, scRNAseq/legacy-fluidigm or scRNAseq/legacy-th2.

Value

A SingleCellExperiment object containing one or more expression matrices of counts and/or TPMs, depending on assays.

Pre-processing details

FASTQ files were either obtained directly from ArrayExpress, or converted from SRA files (downloaded from the Sequence Read Archive) using the SRA Toolkit.

Reads were aligned with TopHat (v. 2.0.11) to the appropriate reference genome (GRCh38 for human samples, GRCm38 for mouse). RefSeq mouse gene annotation (GCF_000001635.23_GRCm38.p3) was downloaded from NCBI on Dec. 28, 2014. RefSeq human gene annotation (GCF_000001405.28) was downloaded from NCBI on Jun. 22, 2015.

featureCounts (v. 1.4.6-p3) was used to compute gene-level read counts. Cufflinks (v. 2.2.0) was used to compute gene-level FPKMs. Reads were also mapped to the transcriptome using RSEM (v. 1.2.19) to compute read counts and TPM's.

FastQC (v. 0.10.1) and Picard (v. 1.128) were used to compute sample quality control (QC) metrics. However, no filtering on the QC metrics has been performed for any dataset.

References


**Examples**

```r
sce <- ReprocessedAllenData()
```

---

**RichardTCellData**

*Obtain the Richard T cell data*

**Description**

Obtain the mouse CD8+ T cell single-cell RNA-seq data from Richard et al. (2018).

**Usage**

```r
RichardTCellData(location = TRUE, legacy = FALSE)
```

**Arguments**

- `location`: Logical scalar indicating whether genomic coordinates should be returned.
- `legacy`: Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

**Details**

Column metadata is provided in the same form as supplied in E-MTAB-6051. This contains information such as the stimulus, time after stimulation, age of the mice and sequencing batch.

Count data for ERCC spike-ins are stored in the "ERCC" entry of the `altExps`.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/richard-tcell.

**Value**

A `SingleCellExperiment` object with a single matrix of read counts.

**Author(s)**

Aaron Lun
References


Examples

```r
sce <- RichardTCellData()
```

---

**RomanovBrainData**

*Obtain the Romanov brain data*

**Description**

Obtain the mouse brain single-cell RNA-seq dataset from Romanov et al. (2017).

**Usage**

```r
RomanovBrainData(ensembl = FALSE, location = TRUE, legacy = FALSE)
```

**Arguments**

- `ensembl` Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- `location` Logical scalar indicating whether genomic coordinates should be returned.
- `legacy` Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

**Details**

Column metadata is provided in the same form as supplied in GSE74672. This contains information such as the reporter gene expressed in each cell, the mouse line, dissection type and so on.

Counts for ERCC spike-ins are stored in the "ERCC" entry of the `altExps`. Note that some of the spike-in rows have NA observations for some (but not all) cells.

If `ensembl=TRUE`, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output. Note that this is only performed if `ensembl=TRUE`.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for `scRNAseq/romanov-brain`.

**Value**

A `SingleCellExperiment` object with a single matrix of UMI counts.
Author(s)

Aaron Lun, based on code by Vladimir Kiselev and Tallulah Andrews.

References


Examples

sce <- RomanovBrainData()

saveDataset

Save a dataset to disk

Description

Save a single-cell dataset to disk, usually in preparation for upload.

Usage

saveDataset(x, path, metadata)

Arguments

x A SummarizedExperiment or one of its subclasses.
path String containing the path to a new directory in which to save x. Any existing directory is removed before saving x.
metadata Named list containing metadata for this dataset, see the schema returned by fetchMetadataSchema(). Note that the applications.takane property will be automatically added by this function and does not have to be supplied.

Value

x and its metadata are saved into path, and NULL is invisibly returned.

Author(s)

Aaron Lun

See Also

https://github.com/ArtifactDB/bioconductor-metadata-index, on the expected schema for the metadata.

polishDataset, to polish x before saving it.

uploadDirectory, to upload the saved contents.
searchDatasets

Examples

```r
library(SingleCellExperiment)
sce <- SingleCellExperiment(list(counts=matrix(rpois(1000, lambda=1), 100, 10)))
rownames(sce) <- sprintf("GENE_%i", seq_len(nrow(sce)))
colnames(sce) <- head(LETTERS, 10)

meta <- list(
  title="My dataset",
  description="This is my dataset",
  taxonomy_id="10090",
  genome="GRCh38",
  sources=list(list(provider="GEO", id="GSE12345")),
  maintainer_name="Shizuka Mogami",
  maintainer_email="mogami.shizuka@765pro.com"
)

tmp <- tempfile()
saveDataset(sce, tmp, meta)
list.files(tmp, recursive=TRUE)
alabaster.base::readObject(tmp)
```

searchDatasets

**Search dataset metadata**

Description

Search for datasets of interest based on matching text in the associated metadata.

Usage

```r
searchDatasets(
  query,
  cache = cacheDirectory(),
  overwrite = FALSE,
  latest = TRUE
)
```

Arguments

- **query**: String or a gypsum.search.object, see Examples.
- **cache, overwrite**: Arguments to pass to `fetchMetadataDatabase`.
- **latest**: Whether to only consider the latest version of each dataset.
Details

The returned DataFrame contains the usual suspects like the title and description for each dataset, the number of rows and columns, the organisms and genome builds involved, whether the dataset has any pre-computed reduced dimensions, and so on. More details can be found in the Bioconductor metadata schema at https://github.com/ArtifactDB/bioconductor-metadata-index.

Value

A DataFrame where each row corresponds to a dataset, containing various columns of metadata. Some columns may be lists to capture 1:many mappings.

Author(s)

Aaron Lun

See Also

surveyDatasets, to easily obtain a listing of all available datasets.

Examples

searchDatasets("brain")[,c("name", "title")]
searchDatasets(defineTextQuery("Neuro%", partial=TRUE))[,c("name", "title")]
searchDatasets(defineTextQuery("10090", field="taxonomy_id"))[,c("name", "title")]
searchDatasets(
  defineTextQuery("GRCm38", field="genome") &
  (defineTextQuery("neuro%", partial=TRUE) |
  defineTextQuery("pancrea%", partial=TRUE))
)][,c("name", "title")]

SegerstolpePancreasData

Obtain the Segerstolpe pancreas data

Description

Download the human pancreas single-cell RNA-seq (scRNA-seq) dataset from Segerstolpe et al. (2016)

Usage

SegerstolpePancreasData(ensembl = FALSE, location = TRUE, legacy = FALSE)
Arguments

- **ensembl**: Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- **location**: Logical scalar indicating whether genomic coordinates should be returned.
- **legacy**: Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Row data contains fields for the gene symbol and RefSeq transcript IDs corresponding to each gene. The rows of the output object are named with the symbol, but note that these are not unique.

Column metadata were extracted from the Characteristics fields of the SDRF file for ArrayExpress E-MTAB-5061. This contains information such as the cell type labels and patient status.

Count data for ERCC spike-ins are stored in the “ERCC” entry of the `altExps`. Estimated numbers of spike-in molecules are provided in the `rowData` of this entry. Note that these concentrations are incorrect for donor H1, as 100 uL of spike-in mixture were added for this donor, rather than 25 uL for all others.

If `ensembl=TRUE`, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output. Note that this is only performed if `ensembl=TRUE`.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for `scRNAseq/segerstolpe-pancreas`.

Value

A `SingleCellExperiment` object with a single matrix of read counts.

Author(s)

Aaron Lun

References


Examples

```r
sce <- SegerstolpePancreasData()
```
Obtain the mouse retina single-cell RNA-seq dataset from Shekhar et al. (2016).

**Usage**

```r
ShekharRetinaData(ensembl = FALSE, location = TRUE, legacy = FALSE)
```

**Arguments**

- `ensembl` Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- `location` Logical scalar indicating whether genomic coordinates should be returned.
- `legacy` Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

**Details**

Column metadata contains the cluster identities as reported in the paper. Note that some cells will have NA identities as they are present in the count matrix but not in the metadata file. These are presumably low-quality cells that were discarded prior to clustering.

If `ensembl=TRUE`, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output. Note that this is only performed if `ensembl=TRUE`.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for `scRNAseq/shekhar-retina`.

**Value**

A `SingleCellExperiment` object with a single matrix of UMI counts.

**Author(s)**

Aaron Lun

**References**

Obtain the Stoeckius cell hashing data

Obtain the (mostly human) cell hashing single-cell RNA-seq data from Stoeckius et al. (2018).

Usage

StoeckiusHashingData(
  type = c("pbmc", "mixed"),
  mode = NULL,
  ensembl = FALSE,
  location = TRUE,
  strip.metrics = TRUE,
  legacy = FALSE
)

Arguments

type String specifying the dataset to obtain.
mode String specifying the data modalities to obtain, see Details.
enssembl Logical scalar indicating whether the output row names should contain Ensembl identifiers.
location Logical scalar indicating whether genomic coordinates should be returned.
strip.metrics Logical scalar indicating whether quality control metrics should be removed from the HTO/ADT counts.
legacy Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

When type="pbmc", the mode can be one or more of:

- "human", the RNA counts for human genes.
- "mouse", the RNA counts for mouse genes. Present as the PBMC dataset is actually a mixture of human PBMCs and unlabelled mouse cells.
- "hto", the HTO counts.
- "adt1", counts for the first set of ADTs (immunoglobulin controls).
- "adt2", counts for the second set of ADTs (cell type-specific markers).
If mode=NULL, the default is to use "human", "mouse" and "hto".

When type="mixed", the mode can be one or more of:

- "rna", the RNA counts for the genes;
- "hto", the HTO counts.

If mode=NULL, the default is to use "rna" and "hto".

If ensembl=TRUE, gene symbols for the RNA counts are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output. Note that this is only performed if ensembl=TRUE and only for the RNA counts.

For the HTO and ADT matrices, some rows correspond to quality control metrics. If strip.metrics=TRUE, these rows are removed so that only data for actual HTOs or ADTs are present.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/nestorowa-hsc.

Value

A SingleCellExperiment object with a matrix of UMI counts corresponding to the first mode, plus any number of alternative Experiments containing the remaining modes. If multiple modes are specified, the output object only contains the intersection of their column names.

Author(s)

Aaron Lun

References


Examples

sce.pbmc <- StoeckiusHashingData()
sce.pbmc

sce.mixed <- StoeckiusHashingData(type="mixed")
sce.mixed
surveyDatasets  

Survey of dataset metadata

Description

Metadata survey for all available datasets in the scRNAsseq package.

Usage

surveyDatasets(cache = cacheDirectory(), overwrite = FALSE, latest = TRUE)

Arguments

cache, overwrite
Arguments to pass to fetchMetadataDatabase.

latest  Whether to only consider the latest version of each dataset.

Details

The returned DataFrame contains the usual suspects like the title and description for each dataset, the number of rows and columns, the organisms and genome builds involved, whether the dataset has any pre-computed reduced dimensions, and so on. More details can be found in the Bioconductor metadata schema at https://github.com/ArtifactDB/bioconductor-metadata-index.

Value

A DataFrame where each row corresponds to a dataset, containing various columns of metadata. Some columns may be lists to capture 1:many mappings.

Author(s)

Aaron Lun

See Also

searchDatasets, to search on the metadata for specific datasets.

Examples

surveyDatasets()
Obtain the Tasic brain data

Description

Obtain the mouse brain single-cell RNA-seq data from Tasic et al. (2015).

Usage

TasicBrainData(ensembl = FALSE, location = TRUE, legacy = FALSE)

Arguments

- `ensembl` Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- `location` Logical scalar indicating whether genomic coordinates should be returned.
- `legacy` Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata is provided in the same form as supplied in GSE71585. This contains information such as the reporter gene expressed in each cell, the mouse line, dissection type and so on.

Count data for ERCC spike-ins are stored in the "ERCC" entry of the `altExps`. Note that some of the spike-in rows have NA observations for some (but not all) cells.

The last 9 columns (containing _CTX_ in their names) correspond to no-cell control libraries.

If `ensembl=TRUE`, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output. Note that this is only performed if `ensembl=TRUE`.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/tasic-brain.

Value

A `SingleCellExperiment` object with a single matrix of read counts.

Author(s)

Aaron Lun

References

Obtain the Usoskin brain data

Usage

UsoskinBrainData(ensembl = FALSE, location = TRUE, legacy = FALSE)

Arguments

ensembl Logical scalar indicating whether the output row names should contain Ensembl identifiers.
location Logical scalar indicating whether genomic coordinates should be returned.
legacy Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata is provided in the same form as supplied in External Table 2 of http://linnarssonlab.org/drg/. This contains information such as the library of origin and the cell type.

The count matrix contains information for repeats, marked with r_ prefixes in the row names; as well as mitochondrial transcripts, marked with mt- prefixes.

If ensembl=TRUE, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output. Note that this is only performed if ensembl=TRUE.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/usoskin-brain.

Value

A SingleCellExperiment object with a single matrix of RPMs.

Author(s)

Aaron Lun
References


Examples

```r
sce <- UsoskinBrainData()
```

**WuKidneyData**

*Obtain the Wu kidney data*

**Description**

Obtain the mouse kidney single-nuclei RNA-seq data from Wu et al. (2019).

**Usage**

```r
WuKidneyData(
  mode = c("healthy", "disease"),
  ensembl = FALSE,
  location = TRUE,
  legacy = FALSE
)
```

**Arguments**

- **mode** String indicating whether to return data for healthy and/or diseased donors.
- **ensembl** Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- **location** Logical scalar indicating whether genomic coordinates should be returned.
- **legacy** Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

**Details**

Column metadata includes the single-cell technology and whether they came from a diseased or healthy individual.

If `mode` specifies both healthy and disease donors, counts are only reported for the intersection of genes that are present for both donors. This is because the original count matrices had differences in their annotation.

If `ensembl=TRUE`, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output. Note that this is only performed if `ensembl=TRUE`. 
All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/wu-kidney.

Value

A `SingleCellExperiment` object with a single matrix of read counts.

Author(s)

Aaron Lun

References


Examples

```r
sce <- WuKidneyData("disease")
```

---

**XinPancreasData**

*Obtain the Xin pancreas data*

**Description**

Obtain the human pancreas single-cell RNA-seq dataset from Xin et al. (2016).

**Usage**

```r
XinPancreasData(ensembl = FALSE, location = TRUE, legacy = FALSE)
```

**Arguments**

- `ensembl` Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- `location` Logical scalar indicating whether genomic coordinates should be returned.
- `legacy` Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.
ZeiselBrainData

Details
Row data contains fields for the Entrez ID and symbol for each gene. Column metadata was obtained from the authors (indirectly, via the Hemberg group) and contains information such as the cell type labels and donor status.

If `ensembl=TRUE`, the Entrez IDs are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output. Note that this is only performed if `ensembl=TRUE`.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for `scRNAseq/xin-pancreas`.

Value
A SingleCellExperiment object with a single matrix of RPKMs.

Author(s)
Aaron Lun, using additional metadata obtained by Vladimir Kiselev.

References

Examples
```r
sce <- XinPancreasData()
```

---

Obtain the Zeisel brain data

Description
Obtain the mouse brain single-cell RNA-seq dataset from Zeisel et al. (2015).

Usage
```r
ZeiselBrainData(ensembl = FALSE, location = TRUE, legacy = FALSE)
```

Arguments
- `ensembl` Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- `location` Logical scalar indicating whether genomic coordinates should be returned.
- `legacy` Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.
Details
Row data contains a single "featureType" field describing the type of each feature (endogenous genes, mitochondrial genes, spike-in transcripts and repeats). Spike-ins and repeats are stored as separate entries in the altExps.

Column metadata is provided in the same form as supplied in http://linnarssonlab.org/cortex/. This contains information such as the cell diameter and the published cell type annotations.

If ensembl=TRUE, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output.

Spike-in metadata is added using ERCCSpikeInConcentrations, with molecule counts computed using a volume of 9 nL per cell at a dilution of 1:20000.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/zeisel-brain.

Value
A SingleCellExperiment object with a single matrix of UMI counts.

Author(s)
Aaron Lun

References

Examples
	sce <- ZeiselBrainData()

---

ZeiselNervousData

Obtain the Zeisel nervous system data

Description
Obtain the mouse nervous system single-cell RNA-seq dataset from Zeisel et al. (2018).

Usage
ZeiselNervousData(location = TRUE, legacy = FALSE)
ZhaoImmuneLiverData

**Arguments**

- location: Logical scalar indicating whether genomic coordinates should be returned.
- legacy: Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

**Details**

Row data contains the gene symbol as well as some relevant per-gene statistics, e.g., the squared coefficient of variance, mean, and whether it was selected for downstream analyses.

Column data contains a wide variety of fields including patient-level information, sample-level sequencing statistics and many flavors of cell type classification. Note that many numeric columns may have NA values if they could not be successfully parsed form the source file.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/zeisel-nervous.

**Value**

A SingleCellExperiment object with a single matrix of UMI counts.

**Author(s)**

Aaron Lun

**References**


**Examples**

```r
if (.Machine$sizeof.pointer > 4) { # too large for 32-bit machines!
  sce <- ZeiselNervousData()
}
```

---

**ZhaoImmuneLiverData**

Obtain the Zhao immune liver data

**Description**

Obtain the human liver immune single-cell RNA-seq data from Zhao et al. (2020).

**Usage**

```r
ZhaoImmuneLiverData(location = TRUE, filter = FALSE, legacy = FALSE)
```
Arguments

- **location**: Logical scalar indicating whether genomic coordinates should be returned.
- **filter**: Logical scalar indicating if the filtered subset should be returned.
- **legacy**: Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata contains various cell labels as provided by the authors. Some of these labels required assembly on our part:

- The broad label was assigned to each barcode based on whether that barcode was present in each *_identities.tsv.gz in GSE125188’s supplementary files.
- For each cell barcode that was present in one of these files, the fine label was generated from the Group annotations inside that file.

We guessed the sample for each cell by assuming that the GEM group numbers match the order of samples in GSE125188. We also assumed that “donor 4” is a typo, given that the paper only mentions 3 donors.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the output. Note that this is only performed if ensembl=TRUE.

If filter=TRUE, only cells that have been used in the original analysis are returned. Otherwise, the cells used are specified in the retained column of the colData.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for scRNAseq/zhao-immune-liver.

Value

A SingleCellExperiment object with a single matrix of UMI counts.

Author(s)

Aaron Lun

References


Examples

sce.zhao <- ZhaoImmuneLiverData()
ZhongPrefrontalData

Obtain the Zhong prefrontal cortex data

Description

Obtain the human prefrontal cortex single-cell RNA-seq dataset from Zhong et al. (2018).

Usage

ZhongPrefrontalData(ensembl = FALSE, location = TRUE, legacy = FALSE)

Arguments

- `ensembl`: Logical scalar indicating whether the output row names should contain Ensembl identifiers.
- `location`: Logical scalar indicating whether genomic coordinates should be returned.
- `legacy`: Logical scalar indicating whether to pull data from ExperimentHub. By default, we use data from the gypsum backend.

Details

Column metadata is scraped from GEO and includes week of gestation, gender and likely cell type.

If `ensembl=TRUE`, the gene symbols are converted to Ensembl IDs in the row names of the output object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated IDs is retained.

If `location=TRUE`, the coordinates of the Ensembl gene models are stored in the `rowRanges` of the output. This is only performed when `ensembl=TRUE`.

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can be retrieved by searching for `scRNAseq/zhong-prefrontal`.

Value

A `SingleCellExperiment` object with a single matrix of UMI counts.

Author(s)

Aaron Lun

References


Examples

sce <- ZhongPrefrontalData()
ZilionisLungData

Obtain the Zilionis lung cancer data

Description

Obtain the human/mouse lung cancer single-cell RNA-seq data from Zilionis et al. (2019).

Usage

ZilionisLungData(
  which = c("human", "mouse"),
  ensembl = FALSE,
  location = TRUE,
  filter = FALSE,
  legacy = FALSE
)

Arguments

which       String specifying the species to get data for.
ensemb1     Logical scalar indicating whether the output row names should contain Ensembl
            identifiers.
location    Logical scalar indicating whether genomic coordinates should be returned.
filter      Logical scalar indicating if the filtered subset should be returned.
legacy      Logical scalar indicating whether to pull data from ExperimentHub. By default,
            we use data from the gypsum backend.

Details

Column metadata is provided and contains information on the library, donor ID/animal ID, replicate
and tissue.

If ensembl=TRUE, the gene symbols are converted to Ensembl IDs in the row names of the output
object. Rows with missing Ensembl IDs are discarded, and only the first occurrence of duplicated
IDs is retained.

If location=TRUE, the coordinates of the Ensembl gene models are stored in the rowRanges of the
output. Note that this is only performed if ensembl=TRUE.

If filter=TRUE, only cells that have been used in the original analysis are returned. The cells used
are specified in the Used column of the colData.

The reducedDim contains coordinates of SPRING representations. This may be filled with NAs for
SPRING coordinates computed on a subset of cells (specified in colData).

All data are downloaded from ExperimentHub and cached for local re-use. Specific resources can
be retrieved by searching for scRNAseq/zilionis-lung.
Value

A `SingleCellExperiment` object with a single matrix of read counts.

Author(s)

Jens Preussner

References


Examples

```r
sce.human <- ZilionisLungData()
sce.mouse <- ZilionisLungData("mouse")
```
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