

Package ‘TENxPBMCData’

July 9, 2024

Title PBMC data from 10X Genomics

Version 1.23.0

Description Single-cell RNA-seq data for on PBMC cells, generated by 10X Genomics.

License CC BY 4.0

Depends SingleCellExperiment, HDF5Array

Imports AnnotationHub, ExperimentHub

Suggests rmarkdown, knitr, BiocStyle, snow, BiocFileCache,
BiocParallel

VignetteBuilder knitr

biocViews SequencingData, RNASeqData, ExpressionData, ExperimentHub,
ExperimentData, SingleCellData

NeedsCompilation no

git_url <https://git.bioconductor.org/packages/TENxPBMCData>

git_branch devel

git_last_commit 585a645

git_last_commit_date 2024-04-30

Repository Bioconductor 3.20

Date/Publication 2024-07-09

Author Kasper D. Hansen [aut],
Davide Risso [aut],
Milan Malfait [ctb],
Jeroen Gilis [ctb],
Theodore Killian [ctb],
Murat Cem Kose [ctb],
Chong Tang [ctb],
Teun van den Brand [ctb],
Dania Machlab [ctb],
Stephanie Hicks [aut, cre]

Maintainer Stephanie Hicks <shicks19@jhu.edu>

Contents

TENxPBMCData	2
Index	4

TENxPBMCData	<i>10X PBMC Data</i>
--------------	----------------------

Description

Various single-cell RNA-seq data on PBMC, generated by 10X Genomics.

Usage

```
TENxPBMCData(dataset = c("pbmc4k", "pbmc68k",
                          "frozen_pbmc_donor_a", "frozen_pbmc_donor_b",
                          "frozen_pbmc_donor_c", "pbmc33k", "pbmc3k",
                          "pbmc6k", "pbmc8k", "pbmc5k-CITEseq"),
              as.sparse = TRUE)
```

Arguments

dataset	Which PBMC dataset from 10X Genomics should be retrieved?
as.sparse	Logical, specifies whether the underlying HDF5 dataset should be treated as sparse or not - will be passed to the call to <code>HDF5Array()</code> . Defaults to TRUE, i.e. by using the <code>DelayedArray</code> infrastructure.

Details

Single-cell RNA-seq and CITE-seq data were generated by 10X Genomics at various times, using different versions of CellRanger, different chemistries and different genome builds. For details, see the 10X website.

We obtained 'filtered' data and generated `SingleCellExperiment` containers with data stored as an HDF5 Assay.

As `rowData` we include `ENSEMBL` and `Symbol_TENx` which are ENSEMBL gene ID and gene symbol provided by TENx genomics and a remapping of the Ensembl identifier to a Hugo gene symbol as columns `Symbol` using the `org.Hs.eg.db` package. The difference between `Symbol` and `Symbol_TENx` is that the former has many missing values (for non-protein coding genes) whereas the later is technically not a Hugo gene symbol. In case of CITE-seq data, the `rowData` has an additional column `Type` specifying if the counts are "Gene Expression" or "Antibody Capture". Note that there is a separate `rowData` for the `altExp`.

Value

A SingleCellExperiment object with a HDF5Matrix in the counts assay, which contains UMI counts for each gene in each cell. Row- and column-level metadata are also provided. In case of CITE-seq data, the "Antibody Capture" counts are stored in the altExp of the SingleCellExperiment.

Author(s)

Kasper D. Hansen, Stephanie Hicks, Davide Risso

References

10X Genomics (2017). 1.3 Million PBMC Cells from E18 Mice. https://support.10xgenomics.com/single-cell-gene-expression/datasets/1.3.0/1M_neurons

See Also

[SingleCellExperiment](#)

Examples

```
sce <- TENxPBMCData()
sce
lib.size <- colSums(assay(sce))
hist(log10(lib.size))

# CITE-seq data
sce <- TENxPBMCData(dataset = "pbmc5k-CITEseq")
sce
altExp(sce)
```

Index

SingleCellExperiment, [3](#)

TENxPBMCData, [2](#)