Package 'TENxPBMCData'

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Title PBMC data from 10X Genomics

Version 1.28.0

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

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Depends SingleCellExperiment, HDF5Array

Imports AnnotationHub, ExperimentHub

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

VignetteBuilder knitr

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

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Contents

1

TENxPBMCData   *10X PBMC Data*

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 HDF5Array(). Defaults to TRUE, i.e. by using the DelayedArray 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