Package ‘TENxPBMCData’

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

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

Usage

```r
TENxPBMCData(dataset = c("pbmc4k", "pbmc68k", "frozen_pbmc_donors.a", "frozen_pbmc_donors.b", "frozen_pbmc_donors.c", "pbmc33k", "pbmc5k", "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.eh.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)**

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**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](https://support.10xgenomics.com/single-cell-gene-expression/datasets/1.3.0/1M_neurons)

**See Also**

`SingleCellExperiment`

**Examples**

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

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