Package ‘TENxBrainData’

October 14, 2018

Title Data from the 10X 1.3 Million Brain Cell Study

Version 1.0.0

Description Single-cell RNA-seq data for 1.3 million brain cells from E18 mice, generated by 10X Genomics.

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Depends SingleCellExperiment, HDF5Array

Imports AnnotationHub (>= 2.9.22), ExperimentHub

Suggests knitr, BiocStyle, snow, BiocFileCache, BiocParallel, data.table

VignetteBuilder knitr

biocViews SequencingData, RNASeqData, ExpressionData, SingleCellData

NeedsCompilation no

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R topics documented:

`TENxBrainData` *10X Brain Data*

Description

Single-cell RNA-seq data for 1.3 million brain cells from E18 mice, generated by 10X Genomics.

Usage

```
TENxBrainData()
```

Details

Single-cell RNA-seq data were generated by 10X Genomics using the Cromium Megacell technology and processed using CellRanger 1.3.0. Cells were obtained from the cortex, hippocampus and subventricular zone of two E18 mice (1306127 cells in total). Each count represents the number of unique molecular identifiers (UMIs) assigned to each gene in the Ensembl annotation (27998 genes in total).

The Ensembl ID and gene symbol are provided in the row-level metadata. The barcode sequence, sequencing library ID and mouse of origin are provided in the column-level metadata.

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.

Author(s)

Aaron Lun

References

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

See Also

`SingleCellExperiment`

Examples

```
sce <- TENxBrainData()
sce
sce[, 10000 + seq_len(10000)]
lib.size.10k <- colSums(assay(sce)[,seq_len(10000)])
hist(log10(lib.size.10k))
```

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