Package 'TENxBrainData'

November 26, 2024

Title Data from the 10X 1.3 Million Brain Cell Study

Version 1.27.0

Date 2018-09-08

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, rmarkdown

VignetteBuilder knitr

biocViews SequencingData, RNASeqData, ExpressionData, SingleCellData

NeedsCompilation no

RoxygenNote 6.1.0

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Description

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

Usage

```
TENxBrainData()

TENxBrainData20k()
```

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. Each count represents the number of unique molecular identifiers (UMIs) assigned to each gene in the Ensembl annotation (27998 genes in total).

The `TENxBrainData` will return a SingleCellExperiment object containing the full data set, i.e., 1306127 cells. The `TENxBrainData20k` will return a subset of 20,000 cells from this full data set, as described on the 10X Genomics website. The latter is often useful for quickly testing scripts prior to running them on the full data set.

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. All libraries with IDs greater than 69 are derived from the second mouse.

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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