Package ‘TENxBrainData’

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Title  Data from the 10X 1.3 Million Brain Cell Study
Version  1.22.0
Date  2018-09-08
Description  Single-cell RNA-seq data for 1.3 million brain
cells from E18 mice, generated by 10X Genomics.
License  CC BY 4.0
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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TENxBrainData

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 Chromium 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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