Package ‘tenXplore’

May 17, 2024

Title  ontological exploration of scRNA-seq of 1.3 million mouse neurons from 10x genomics

Description

Perform ontological exploration of scRNA-seq of 1.3 million mouse neurons from 10x genomics.

Version  1.26.0

Author  Vince Carey

Suggests  org.Hs.eg.db, testthat, knitr, rmarkdown, BiocStyle

Depends  R (>= 4.0), shiny, restfulSE (>= 0.99.12)

Imports  methods, ontoProc (>= 0.99.7), SummarizedExperiment,
          AnnotationDbi, matrixStats, org.Mm.eg.db, stats, utils

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License  Artistic-2.0

LazyLoad  yes

BiocViews  ImmunoOncology, DimensionReduction, PrincipalComponent,
           Transcriptomics, SingleCell

VignetteBuilder  knitr

RoxygenNote  7.2.3

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CellTypes

Description

cellTypes: data.frame with ids and terms

Usage

CellTypes

Format

TermSet instance

Source

efo.owl, August 2017, subclasses of http://www.ebi.ac.uk/efo/EFO_0000324

Examples

data(CellTypes)
head(slot(CellTypes, "cleanFrame"))

tenx500

Description

tenx500: serialized full SummarizedExperiment for demonstration

Usage

tenx500

Format

SummarizedExperiment instance

Source

restfulSE se1.3M pared down to 500 samples, assay materialized and assigned

Examples

data(tenx500)
tenx500
tenXplore

Description
basic shiny interface to 10x data with ontological setup for cell selection

Usage
tenXplore()

Value
shiny app invocation

Note
Starts slowly as it sets up connection to HDF Server.

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