Package ‘tenXplore’
March 21, 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  1.24.0

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**

*cellTypes: data.frame with ids and terms*

**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](http://www.ebi.ac.uk/efo/EFO_0000324)

**Examples**

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

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**tenx500**

*tenx500: serialized full SummarizedExperiment for demonstration*

**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**

```r
data(tenx500)
tenx500
```
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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