

Package ‘tenXplore’

November 15, 2019

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 1.8.0

Author Vince Carey

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

Depends R (>= 3.4), shiny, restfulSE (>= 0.99.12)

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

Maintainer VJ Carey <stvjc@channing.harvard.edu>

License Artistic-2.0

LazyLoad yes

biocViews ImmunoOncology, DimensionReduction, PrincipalComponent, Transcriptomics, SingleCell

VignetteBuilder knitr

RoxygenNote 6.1.0

git_url <https://git.bioconductor.org/packages/tenXplore>

git_branch RELEASE_3_10

git_last_commit 8748ad4

git_last_commit_date 2019-10-29

Date/Publication 2019-11-14

R topics documented:

CellTypes	2
tenx500	2
tenXplore	3

Index	4
--------------	----------

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

Examples

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

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

```
data(tenx500)
tenx500
```

tenXplore	<i>basic shiny interface to 10x data with ontological setup for cell selection</i>
-----------	--

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.

Examples

```
tenXplore
```

Index

*Topic **datasets**

CellTypes, [2](#)

tenx500, [2](#)

CellTypes, [2](#)

tenx500, [2](#)

tenXplore, [3](#)