Package 'tenXplore'

April 12, 2018

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 1.0.0

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>

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LazyLoad yes

biocViews DimensionReduction, PrincipalComponent, Transcriptomics, SingleCell

VignetteBuilder knitr

RoxygenNote 6.0.1.9000

NeedsCompilation no

R topics documented:

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"))
```

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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

```
data(tenx500)
tenx500
```

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

Description

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

Usage

```
tenXplore(remouse)
```

Arguments

remouse   optional SummarizedExperiment instance, assay data in memory

Value

shiny app invocation

Examples

```
tenXplore
```

Index