Package ‘STexampleData’

March 16, 2022

Version 1.2.0

Title Collection of spatially resolved transcriptomics datasets in SpatialExperiment Bioconductor format

Description Collection of spatially resolved transcriptomics datasets in SpatialExperiment Bioconductor format, for use in examples, demonstrations, tutorials, and other purposes. The datasets have been sourced from various publicly available sources, and cover several technological platforms.

URL `https://github.com/lmweber/STexampleData`

BugReports `https://github.com/lmweber/STexampleData/issues`

License MIT + file LICENSE

biocViews ExperimentHub, ExperimentData, ReproducibleResearch, ExpressionData, SingleCellData, Homo_sapiens_Data, Mus_musculus_Data

Depends ExperimentHub, SpatialExperiment

Imports utils

VignetteBuilder knitr

Suggests BiocStyle, knitr, rmarkdown

RoxygenNote 7.1.1

git_url https://git.bioconductor.org/packages/STexampleData

git_branch RELEASE_3_14

git_last_commit 8b317cd

git_last_commit_date 2021-10-26

Date/Publication 2022-03-16

Author Lukas M. Weber [aut, cre] (<`https://orcid.org/0000-0002-3282-1730`>)

Maintainer Lukas M. Weber <`lukas.weber.edu@gmail.com`>

R topics documented:

`STexampleData` *Collection of spatially resolved transcriptomics datasets in SpatialExperiment Bioconductor format*

Description

Collection of spatially resolved transcriptomics datasets in SpatialExperiment Bioconductor format, for use in examples, demonstrations, tutorials, and other purposes. The datasets have been sourced from various publicly available sources, and cover several technological platforms.

Details

The `STexampleData` package provides access to a collection of spatially resolved transcriptomics datasets, which have been formatted into the `SpatialExperiment` Bioconductor object class.

These datasets have been collected from various publicly available sources, and cover several technological platforms. We provide them in the form of `SpatialExperiment` objects to make them easier to access, so that we and others can use them for examples, demonstrations, tutorials, and other purposes.

The `SpatialExperiment` class is an extension of `SingleCellExperiment`, adapted for the properties of spatially resolved transcriptomics data. For more details, see the `SpatialExperiment` documentation.

Datasets

The `STexampleData` package contains the following datasets:

- Visium_humanDLPFC (10x Genomics Visium): A single sample (sample 151673) of human brain dorsolateral prefrontal cortex (DLPFC) in the human brain, measured using the 10x Genomics Visium platform. This is a subset of the full dataset containing 12 samples from 3 neurotypical donors, published by Maynard and Collado-Torres et al. (2021). The full dataset is available from the `spatialLIBD` Bioconductor package.
- Visium_mouseCoronal (10x Genomics Visium): A single coronal section from the mouse brain spanning one hemisphere, measured using the 10x Genomics Visium platform. This dataset was publicly released by 10x Genomics.
- seqFISH_mouseEmbryo (seqFISH): A subset of cells (embryo 1, z-slice 2) from a dataset investigating mouse embryogenesis by Lohoff and Ghazanfar et al. (2020), generated using the seqFISH platform. The full dataset is available from the original publication.

Examples

```
# load using dataset name
spe <- Visium_humanDLPFC()
spe
```

Index