Package 'STexampleData'

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Version 1.0.8

- 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

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

Depends ExperimentHub, SpatialExperiment

Imports utils

VignetteBuilder knitr

Suggests BiocStyle, knitr

RoxygenNote 7.1.1

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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:

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STexampleData
```

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.

Note that objects in Bioconductor version 3.13 have names ending with _3_13, and have been kept for backward compatibility. The latest versions of the objects are available in Bioconductor version 3.14 onwards.

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
# note objects in Bioc version 3.13 have names ending in "_3_13"
spe <- Visium_humanDLPFC_3_13()
spe
```

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