

# Package ‘STexampleData’

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**Version** 1.7.0

**Title** Collection of spatially-resolved transcriptomics datasets in SpatialExperiment Bioconductor format

**Description** Collection of spatially-resolved transcriptomics (SRT) datasets in SpatialExperiment Bioconductor format, for use in examples, demonstrations, and tutorials. The datasets are from several different SRT platforms and have been sourced from various publicly available sources. Several datasets include images and/or ground truth annotation labels.

**URL** <https://github.com/lmweber/STexampleData>

**BugReports** <https://github.com/lmweber/STexampleData/issues>

**License** MIT + file LICENSE

**biocViews** ExperimentData, ExperimentHub, ReproducibleResearch, ExpressionData, SingleCellData, SpatialData, Homo\_sapiens\_Data, Mus\_musculus\_Data

**Depends** ExperimentHub, SpatialExperiment

**Imports** utils

**VignetteBuilder** knitr

**Suggests** BiocStyle, knitr, rmarkdown, BumpyMatrix

**RoxygenNote** 7.1.2

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STexampleData	<i>Collection of spatially-resolved transcriptomics datasets in SpatialExperiment Bioconductor format</i>
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## Description

Collection of spatially-resolved transcriptomics (SRT) datasets in SpatialExperiment Bioconductor format, for use in examples, demonstrations, and tutorials. The datasets are from several different SRT platforms and have been sourced from various publicly available sources. Several datasets include images and/or ground truth annotation labels.

## Details

The STexampleData package contains a collection of spatially-resolved transcriptomics (SRT) datasets, which have been formatted into the SpatialExperiment Bioconductor class, for use in examples, demonstrations, and tutorials.

The datasets are from several different SRT platforms and have been sourced from various publicly available sources. Several datasets include images and/or ground truth annotation labels.

Additional examples and documentation are provided in the package vignette.

### *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. This dataset was previously released by 10x Genomics on their website.
- seqFISH\_mouseEmbryo (seqFISH): A subset of cells (embryo 1, z-slice 2) from a previously published 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.
- ST\_mouseOB (Spatial Transcriptomics): A single sample from the mouse brain olfactory bulb (OB), measured with the Spatial Transcriptomics platform (Stahl et al. 2016). This dataset contains annotations for five cell layers from the original authors.
- SlideSeqV2\_mouseHPC (Slide-seqV2): A single sample of mouse brain from the hippocampus (HPC) and surrounding regions, measured with the Slide-seqV2 platform (Stickels et al. 2020). This dataset contains cell type annotations generated by Cable et al. (2021).

**Examples**

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

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