

# Package ‘STexampleData’

January 23, 2025

**Version** 1.14.0

**Title** Collection of spatial transcriptomics datasets in  
SpatialExperiment Bioconductor format

**Description** Collection of spatial transcriptomics datasets stored in  
SpatialExperiment Bioconductor format, for use in examples, demonstrations,  
and tutorials. The datasets are from several different platforms and  
have been sourced from various publicly available sources. Several datasets  
include images and/or reference 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, SingleCellExperiment, SpatialExperiment

**Imports** utils

**VignetteBuilder** knitr

**Suggests** BiocStyle, knitr, rmarkdown, BumpyMatrix, HDF5Array

**RoxygenNote** 7.1.2

**git\_url** <https://git.bioconductor.org/packages/STexampleData>

**git\_branch** RELEASE\_3\_20

**git\_last\_commit** 75ad233

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.20

**Date/Publication** 2025-01-23

**Author** Lukas M. Weber [aut, cre] (<<https://orcid.org/0000-0002-3282-1730>>),  
Yixing E. Dong [aut] (<<https://orcid.org/0009-0003-5115-5686>>)

**Maintainer** Lukas M. Weber <lmweberedu@gmail.com>

## Contents

STexampleData . . . . .	2
<b>Index</b>	<b>4</b>

---

STexampleData

*Collection of spatial transcriptomics datasets in SpatialExperiment  
Bioconductor format*

---

## Description

Collection of spatial transcriptomics datasets in SpatialExperiment Bioconductor format, for use in examples, demonstrations, and tutorials. The datasets are from several different technological platforms and have been sourced from various publicly available sources. Several datasets include images and/or reference annotation labels.

## Details

The STexampleData package contains a collection of spatial transcriptomics datasets, which have been formatted into the SpatialExperiment Bioconductor class, for use in examples, demonstrations, and tutorials.

The datasets are from several different technological platforms and have been sourced from various publicly available sources. Several datasets include images and/or reference 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. (2022), 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. 2021). This dataset contains cell type annotations generated by Cable et al. (2022).
- Janesick\_breastCancer\_Chromium (10x Genomics Chromium): 10x Genomics Chromium single-cell RNA sequencing data from human breast cancer dataset by Janesick et al. (2023). High resolution mapping of the breast cancer tumor microenvironment using integrated single-cell, spatial, and in situ analysis of FFPE tissue. Contains annotations for cell type from the original authors.
- Janesick\_breastCancer\_Visium (10x Genomics Visium): 10x Genomics Visium spatial transcriptomics data from human breast cancer dataset by Janesick et al. (2023). High resolution mapping of the breast cancer tumor microenvironment using integrated single-cell, spatial, and in situ analysis of FFPE tissue.

- `Janesick_breastCancer_Xenium_rep1` (10x Genomics Xenium): 10x Genomics Xenium in situ spatial data (sample 1, replicate 1) from human breast cancer dataset by Janesick et al. (2023). High resolution mapping of the breast cancer tumor microenvironment using integrated single-cell, spatial, and in situ analysis of FFPE tissue.
- `Janesick_breastCancer_Xenium_rep2` (10x Genomics Xenium): 10x Genomics Xenium in situ spatial data (sample 1, replicate 2) from human breast cancer dataset by Janesick et al. (2023). High resolution mapping of the breast cancer tumor microenvironment using integrated single-cell, spatial, and in situ analysis of FFPE tissue.
- `CosMx_lungCancer` (NanoString CosMx): NanoString CosMx human non-small cell lung cancer (NSCLC) dataset. Contains data from one sample (patient 9, slice 1). This dataset was previously released by NanoString on their website.
- `MERSCOPE_ovarianCancer` (Vizgen MERSCOPE): Vizgen MERSCOPE human ovarian cancer dataset. Contains data from one sample (patient 2, sample 1). This dataset was previously released by Vizgen on their website.
- `STARmapPLUS_mouseBrain` (STARmap PLUS): STARmap PLUS mouse brain data by Shi et al. (2023). Contains data from one sample (well 05), including annotations for cell type and tissue regions from the original authors.

### Examples

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

# Index

CosMx\_lungCancer (STexampleData), [2](#)

Janesick\_breastCancer\_Chromium  
(STexampleData), [2](#)

Janesick\_breastCancer\_Visium  
(STexampleData), [2](#)

Janesick\_breastCancer\_Xenium\_rep1  
(STexampleData), [2](#)

Janesick\_breastCancer\_Xenium\_rep2  
(STexampleData), [2](#)

MERSCOPE\_ovarianCancer (STexampleData),  
[2](#)

seqFISH\_mouseEmbryo (STexampleData), [2](#)

SlideSeqV2\_mouseHPC (STexampleData), [2](#)

ST\_mouseOB (STexampleData), [2](#)

STARmapPLUS\_mouseBrain (STexampleData),  
[2](#)

STexampleData, [2](#)

STexampleData-package (STexampleData), [2](#)

Visium\_humanDLPFC (STexampleData), [2](#)

Visium\_mouseCoronal (STexampleData), [2](#)