Package ‘TENxXeniumData’

April 9, 2026

Version 1.6.0

Title Collection of Xenium spatial data by 10X genomics

Description Collection of Xenium spatial transcriptomics datasets provided by 10x Genomics, formatted into the Bioconductor classes, the SpatialExperiment or SpatialFeatureExperiment (SFE), to facilitate seamless integration into various applications, including examples, demonstrations, and tutorials. The constructed data objects include gene expression profiles, per-transcript location data, centroid, segmentation boundaries (e.g., cell or nucleus boundaries), and image.

URL `https://github.com/mrbakhsh/TENxXeniumData`

BugReports `https://github.com/mrbakhsh/TENxXeniumData/issues`

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Encoding UTF-8

biocViews ExperimentData, ExperimentHub, SpatialData

Depends ExperimentHub

Imports SpatialExperiment, SpatialFeatureExperiment, BumpyMatrix, SummarizedExperiment, utils

VignetteBuilder knitr

Suggests BiocStyle, knitr, rmarkdown

RoxygenNote 7.2.3

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

git_branch RELEASE_3_22

git_last_commit ce89f83

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-04-09

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Description

Collection of Xenium spatial transcriptomics datasets from 10X Genomics, formatted into the Bioconductor classes, the SpatialExperiment or SpatialFeatureExperiment (SFE). Such Datasets can be used as examples in packages, tutorials, or for testing purposes.

Details

The following Xenium Spatial Transcriptomics datasets by 10X Genomics are currently available:

- spe_mouse_brain
- sfe_mouse_brain
- spe_human_pancreas
- sfe_human_pancreas

Value

a `SpatialExperiment` or a `SpatialFeatureExperiment` data objects.

Author(s)

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Examples

```
# initialize hub instance
eh <- ExperimentHub()

# query for TENxXenium datasets
(q <- query(eh, "TENxXenium"))
```

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