

Package ‘muSpaData’

May 14, 2026

Version 1.5.0

Title Multi-sample multi-group spatially resolved transcriptomic data

Description Data package containing a multi-sample multi-group spatial dataset in SpatialExperiment Bioconductor object format.

URL <https://github.com/peicai/muSpaData>

BugReports <https://github.com/peicai/muSpaData/issues>

License MIT + file LICENSE

Depends R (>= 4.5.0), ExperimentHub

Suggests SpatialExperiment, ggplot2, BiocStyle, knitr, rmarkdown, R.utils

biocViews ExperimentHub, ExperimentData, ExpressionData, SpatialData, SingleCellData

VignetteBuilder knitr

RoxygenNote 7.3.2

Encoding UTF-8

NeedsCompilation no

git_url <https://git.bioconductor.org/packages/muSpaData>

git_branch devel

git_last_commit 0d7cb48

git_last_commit_date 2026-04-28

Repository Bioconductor 3.24

Date/Publication 2026-05-14

Author Peiyong Cai [aut, cre] (ORCID: <<https://orcid.org/0009-0001-9229-2244>>)

Maintainer Peiyong Cai <peiyong.cai@uzh.ch>

Contents

| | |
|-------------------------|----------|
| Wei22_example | 2 |
| Wei22_full | 3 |
| Index | 4 |

`Wei22_example``Wei22_example dataset`

Description

- A subset of the Wei22_full dataset, focusing on fewer regeneration stages.
- It includes 2 (2 sections), 10 (2 sections), and 20 (2 sections) days post injury (DPI).
- The original data is deposited in the Spatial Transcript Omics DataBase (STOmics DB) under dataset id STDS0000056.

Usage

```
Wei22_example(metadata = FALSE)
```

Arguments

| | |
|-----------------------|---|
| <code>metadata</code> | A logical value indicating whether to return only the ExperimentHub meta-data, which describes the overall dataset, or to load the entire dataset. Defaults to FALSE. |
|-----------------------|---|

Details

link to reference: <https://www.science.org/doi/10.1126/science.abp9444>

link to raw data: <https://db.cngb.org/stomics/artista/download/>

Value

an object of class `SpatialExperiment`.

Author(s)

Peiying Cai <peiyong.cai@uzh.ch>

References

Wei et al. (2022). "Single-cell Stereo-seq reveals induced progenitor cells involved in axolotl brain regeneration", *Science*, **377**(6610).

Examples

```
# load metadata only
Wei22_example(metadata = TRUE)

# load SpatialExperiment
Wei22_example(metadata = FALSE)
```

`Wei22_full``Wei22_full dataset`

Description

- Single-cell Stereo-seq spatial transcriptomics data includes axolotl brain tissues collected from multiple sections across five regeneration stages (16 samples in total)
- The dataset contains 13890 features across 147432 cells, and preprocessing has been applied.
- The original data is deposited in the Spatial Transcript Omics DataBase (STOmics DB) under dataset id STDS0000056.

Usage

```
Wei22_full(metadata = FALSE)
```

Arguments

| | |
|-----------------------|--|
| <code>metadata</code> | A logical value indicating whether to return only the ExperimentHub metadata, which describes the overall dataset, or to load the entire dataset. Defaults to FALSE. |
|-----------------------|--|

Details

link to reference: <https://www.science.org/doi/10.1126/science.abp9444>

link to raw data: <https://db.cngb.org/stomics/artista/download/>

Value

an object of class `SpatialExperiment`.

Author(s)

Peiying Cai <peiying.cai@uzh.ch>

References

Wei et al. (2022). "Single-cell Stereo-seq reveals induced progenitor cells involved in axolotl brain regeneration", *Science*, **377**(6610).

Examples

```
# load metadata only
Wei22_full(metadata = TRUE)

# load SpatialExperiment
Wei22_full(metadata = FALSE)
```

Index

Wei22_example, [2](#)

Wei22_full, [3](#)