Package 'muSpaData'

October 27, 2026

Version 1.4.0

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 RELEASE_3_23

git_last_commit cd5c92a

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-10-27

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

Maintainer Peiying Cai <peiying.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

`metadata`	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_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

metadata	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