Package ‘muSpaData’

April 2, 2026

Version 1.3.0

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

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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 cfc96e3

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Repository Bioconductor 3.23

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`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)
```

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