Package ‘WeberDivechaLCdata’

February 27, 2024

Version 1.4.0

Title Spatially-resolved transcriptomics and single-nucleus RNA-sequencing data from the locus coeruleus (LC) in postmortem human brain samples

Description Spatially-resolved transcriptomics (SRT) and single-nucleus RNA-sequencing (snRNA-seq) data from the locus coeruleus (LC) in postmortem human brain samples. Data were generated with the 10x Genomics Visium SRT and 10x Genomics Chromium snRNA-seq platforms. Datasets are stored in SpatialExperiment and SingleCellExperiment formats.

URL https://github.com/lmweber/WeberDivechaLCdata

BugReports https://github.com/lmweber/WeberDivechaLCdata/issues

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biocViews ExperimentData, ExperimentHub, ReproducibleResearch, ExpressionData, SequencingData, RNASeqData, SingleCellData, SpatialData, Homo_sapiens_Data

Depends ExperimentHub, SpatialExperiment, SingleCellExperiment

Imports utils

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Suggests BiocStyle, knitr, rmarkdown

RoxygenNote 7.1.2

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**R topics documented:**

- WeberDivechaLCdata

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**Description**

Spatially-resolved transcriptomics (SRT) and single-nucleus RNA-sequencing (snRNA-seq) data from the locus coeruleus (LC) in postmortem human brain samples. Data were generated with the 10x Genomics Visium SRT and 10x Genomics Chromium snRNA-seq platforms. Datasets are stored in SpatialExperiment and SingleCellExperiment formats.

**Details**

This dataset is described in our paper on the gene expression landscape of the human locus coeruleus (LC). The data are provided as R/Bioconductor objects in this package, and in online web apps (Shiny and iSEE) for interactive exploration. The R/Bioconductor objects in this package are stored in SpatialExperiment (Visium data) and SingleCellExperiment (snRNA-seq data) formats.

**Datasets**

The package contains the following objects:

- **WeberDivechaLCdata_Visium**: SRT (Visium) dataset
- **WeberDivechaLCdata_singleNucleus**: snRNA-seq dataset

The objects can be loaded using the dataset names, i.e. WeberDivechaLCdata_Visium() and WeberDivechaLCdata_singleNucleus(), or by accessing the ExperimentHub IDs (see vignette).

**Examples**

```r
# Load objects using dataset names
spe <- WeberDivechaLCdata_Visium()
sce <- WeberDivechaLCdata_singleNucleus()

# Show objects
spe
sce
```
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