Package ‘WeberDivechaLCdata’

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

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

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

# Show objects
spe
sce
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