Package 'WeberDivechaLCdata'

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Version 1.10.0

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

VignetteBuilder knitr

Suggests BiocStyle, knitr, rmarkdown

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`WeberDivechaLCdata` *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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