# Package ‘WeberDivechaLCdata’

May 26, 2026

**Version** 1.14.0

**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`

**License** MIT + file LICENSE

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

**Depends** ExperimentHub, SpatialExperiment, SingleCellExperiment

**Imports** utils

**VignetteBuilder** knitr

**Suggests** BiocStyle, knitr, rmarkdown

**RoxygenNote** 7.1.2

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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

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

# Show objects
spe
sce
```

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