Package 'muscData'

November 10, 2026

Version 1.26.0

Title Multi-sample multi-group scRNA-seq data

Description Data package containing a collection of multi-sample multi-group scRNA-seq datasets in SingleCellExperiment Bioconductor object format.

URL https://github.com/HelenaLC/muscData

BugReports https://github.com/HelenaLC/muscData/issues

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Depends R (>= 3.6), ExperimentHub, SingleCellExperiment

Imports utils

Suggests BiocStyle, dplyr, DropletUtils, knitr, GEOquery, Matrix, matrixStats, methods, muscat, rmarkdown, R.utils, readxl, scater, scds, Seurat

biocViews ExperimentHub, ExperimentData, ExpressionData, GEO, Homo_sapiens_Data, ImmunoOncologyData, SingleCellData

VignetteBuilder knitr

RoxygenNote 6.1.1

git_url https://git.bioconductor.org/packages/muscData

git_branch RELEASE_3_23

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Kang18_8vs8 Kang18_8vs8 *dataset*

Description

- 10x droplet-based scRNA-seq PBMC data from 8 Lupus patients before and after 6h-treatment with INF-beta.
- The dataset contains 35635 features across 29065 cells, and no filtering or preprocessing has been applied.
- The original data is deposited in the Gene Expression Ombnibus (GEO) under accession number GSE96583.

Usage

```
Kang18_8vs8(metadata = FALSE)
```

Arguments

metadata	logical value indicating whether ExperimentHub metadata (describing the overall dataset) should be returned only, or if the whole dataset should be loaded. Defaults to FALSE.

Details

link to reference: https://www.ncbi.nlm.nih.gov/pubmed/29227470

link to raw data: https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE96583

Value

an object of class SingleCellExperiment.

Author(s)

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References

Kang et al. (2019). "Multiplexed droplet single-cell RNA-sequencing using natural genetic variation", *Nature Biotechnology* **36**, 89-94.

Examples

```
# load metadata only
Kang18_8vs8(metadata = TRUE)

# load SingleCellExperiment
Kang18_8vs8(metadata = FALSE)
```

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