Package ‘muscData’

June 18, 2024

Version 1.19.0

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

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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)

Helena L. Crowell <`helena.crowell@uzh.ch`>

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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