Package ‘muscData’

May 21, 2024

Version 1.18.0
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
License MIT + file LICENSE
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

Repository Bioconductor 3.19
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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 Omnibus (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


Examples

# load metadata only
Kang18_8vs8(metadata = TRUE)

# load SingleCellExperiment
Kang18_8vs8(metadata = FALSE)
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