

Package: scrapbook (via r-universe)

October 10, 2026

Title Single-cell RNA-seq analyses with scrapper

Version 1.0.0

Date 2026-02-11

Description Demonstrates some basic analysis of single-cell RNA-seq data with scrapper. This includes quality control, normalization, feature selection, various forms of dimensionality reduction, clustering into subpopulations, and detection of marker genes. It is intended for users who already have some familiarity with R and want to get hands-on with some basic single-cell analyses.

Depends AnnotationHub, BiocStyle, bluster, cluster, DropletTestFiles, DropletUtils, dynamicTreeCut, edgeR, ggplot2, gridExtra, msigdbr, pheatmap, scater, scrapper, scRNAseq, TENxPBMCDData

Suggests rmarkdown, bookdown, knitr

VignetteBuilder knitr

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URL <https://github.com/libscran/scrapbook>

BugReports <https://github.com/libscran/scrapbook/issues>

biocViews Workflow, SingleCellWorkflow

BiocType book

RoxygenNote 7.3.3

Config/pak/sysreqs cmake libglpk-dev make libbz2-dev libicu-dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev libnode-dev xz-utils zlib1g-dev

Repository Bioconductor 3.23

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RemoteUrl <https://github.com/bioc/scrapbook>

RemoteRef RELEASE_3_23

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Description

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Author(s)

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See Also

Useful links:

- <https://github.com/libscranscrapbook>
- Report bugs at <https://github.com/libscranscrapbook/issues>

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