

Package: OSCA.multisample (via r-universe)

October 10, 2026

Title OSCA for Multiple Samples

Version 1.20.0

Date 2025-01-20

Description Deploys the multi-sample analysis chapters for the
``Orchestrating Single Cell Analysis with Bioconductor" book.
This describes the handling of multiple samples in a
single-cell RNA-seq analysis, starting with integration of
multiple datasets into a common space for consistent analyses,
differential expression comparisons between conditions based on
pseudo-bulk samples, and differential abundance analyses for
cell subpopulations. It is intended for readers who are already
familiar with basic single-cell analyses, possibly after
reading some of the prior books in this collection.

Depends batchelor, BiocSingular, bluster, DropletUtils, edgeR,
gridExtra, igraph, MouseGastrulationData, pheatmap, rebook,
rmarkdown, Rtsne, scater, scran, scuttle, SingleR,
TENxPBMCDData, TSCAN, uwot, viridis

Imports OSCA.workflows

Suggests OSCA.basic, rmarkdown, knitr

VignetteBuilder knitr

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URL <https://github.com/OSCA-source/OSCA.multisample>

biocViews ImmunoOncologyWorkflow, Workflow, SingleCellWorkflow

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

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RemoteUrl <https://github.com/bioc/OSCA.multisample>

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