

Package: OSCA.basic (via r-universe)

May 28, 2026

Title Single-Cell Analysis Basics

Version 1.21.0

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Description Deploys basic analysis chapters for the "Orchestrating Single Cell Analysis with Bioconductor" book. This describes the steps of a simple single-cell RNA-seq analysis, involving quality control, normalization, various forms of dimensionality reduction, clustering into subpopulations, detection of marker genes, and annotation of cell types. 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, apcluster, AUCell, BiocFileCache, BiocSingular, bluster, celldex, cluster, dendextend, dynamicTreeCut, GO.db, gridExtra, GSEABase, igraph, limma, mbkmeans, org.Mm.eg.db, pheatmap, rebook, rmarkdown, RMTstat, robustbase, Rtsne, scater, scran, scrapper, scRNAseq, scuttle, SingleR, statmod, viridis

Imports OSCA.workflows

Suggests rmarkdown, knitr, OSCA.advanced

VignetteBuilder knitr

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

biocViews ImmunoOncologyWorkflow, Workflow, SingleCellWorkflow

Config/pak/sysreqs libcairo2-dev cmake libfontconfig1-dev libfreetype6-dev libfridi-dev libglpk-dev libgmp3-dev libharfbuzz-dev libbz2-dev libicu-dev libjpeg-dev liblzma-dev libpng-dev libtiff-dev libuv1-dev libwebp-dev libxml2-dev libssl-dev libnode-dev xz-utils zlib1g-dev

Repository <https://tempbioc.r-universe.dev>

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

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