

Package: OSCA.basic (via r-universe)

October 10, 2026

Title Single-Cell Analysis Basics

Version 1.20.0

Date 2025-09-29

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, scan, 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 cmake libglpk-dev libgmp3-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/OSCA.basic>

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