Package: OSCA.advanced (via r-universe)

May 28, 2026

Title Advanced Single-Cell Analysis

Version 1.21.0

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Description Deploys the advanced analysis chapters for the ``Orchestrating Single Cell Analysis with Bioconductor'' book. This describes the more complex steps of a single-cell RNA-seq analysis ranging from doublet detection, cell cycle assignment, specific steps for processing droplet data, nuclei-specific analyses, trajectory analyses, integrated analyses with protein abundances, and interactive visualization. It also elaborates on some of the basic analysis steps, focusing on alternative strategies and theoretical considerations. 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 AnnotationHub, batchelor, BiocFileCache, BiocNeighbors, BiocParallel, BiocSingular, bluster, clustree, corral, densvis, DropletTestFiles, DropletUtils, edgeR, ggbeeswarm, ggplot2, gridExtra, igraph, iSEE, limma, msigdbr, mumosa, org.Mm.eg.db, pheatmap, rebook, rmarkdown, Rtsne, scater, scDblFinder, scPCA, scran, scrapper, scRNAseq (>= 2.17.9), scuttle, SingleR, slingshot, snifter, TENxBrainData, tradeSeq, TSCAN, velociraptor, viridis

Imports OSCA.workflows, OSCA.basic, OSCA.multisample

Suggests rmarkdown, knitr

VignetteBuilder knitr

URL https://github.com/OSCA-source/OSCA.advanced

biocViews ImmunoOncologyWorkflow, Workflow, SingleCellWorkflow

Config/pak/sysreqs libcairo2-dev cmake libfontconfig1-dev libfreetype6-dev libfribidi-dev libglpk-dev libgmp3-dev make libharfbuzz-dev libmagick++-dev gsfonts libbz2-dev libicu-dev libjpeg-dev liblzma-dev libpng-dev libtiff-dev libuv1-dev libwebp-dev libxml2-dev libssl-dev perl python3 libnode-dev xz-utils zlib1g-dev

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

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RemoteUrl https://github.com/bioc/OSCA.advanced

RemoteRef HEAD

RemoteSha 84c44efb72cfed29ab9e66d68ae4ea0763c02910