Package: OSCA.intro (via r-universe)

May 29, 2026

Title Introduction to OSCA

Version 1.21.0

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Description Deploys the introduction to the ``Orchestrating Single Cell Analysis with Bioconductor'' book. This describes how to install R and Bioconductor packages, links out to some resources to learn R, describes how to load datasets into an R session, provides an overview of the SingleCellExperiment class, and performs a ``quick start'' demonstration for basic single-cell RNA-seq analyses. It is intended for readers with little-to-no computational background who are just getting started with analyses in R.

Depends batchelor, BiocFileCache, BiocManager, bluster, DropletTestFiles, DropletUtils, gridExtra, knitr, LoomExperiment, R.utils, readxl, rebook, rmarkdown, rtracklayer, scater, scran, scRNAseq, scuttle, SingleCellExperiment, uwot, zellkonverter

Suggests BiocManager, rmarkdown, knitr

VignetteBuilder knitr

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

biocViews ImmunoOncologyWorkflow, Workflow, SingleCellWorkflow

RoxygenNote 7.1.1

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

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

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

RemoteRef HEAD

RemoteSha 2a2b6c57f4cec61d5ca751c2db83f812320e3eba