Package: OSCA.workflows (via r-universe)

May 29, 2026

Title OSCA Workflows

Version 1.21.0

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Description Deploys the workflows of the ``Orchestrating Single Cell Analysis with Bioconductor'' book. This contains worked case studies of analyses of a variety of single-cell datasets, each proceeding from a SingleCellExperiment object. Exposition is generally minimal other than for dataset-specific justifications for parameter tweaks; refer to the other books in the OCSA collection for a detailed explanation of the theoretical basis of each step. It is intended for readers who already know the background and just want some code to copy and paste into their own analyses.

Depends AnnotationHub, batchelor, BiocFileCache, BiocNeighbors, BiocParallel, BiocSingular, bluster, celldex, cluster, DropletTestFiles, DropletUtils, dynamicTreeCut, edgeR, EnsDb.Hsapiens.v86, gridExtra, HCAData, igraph, limma, org.Hs.eg.db, org.Mm.eg.db, pheatmap, rebook, rmarkdown, scater, scPCA, scran, scRNAseq, scuttle, SingleR, viridis

Suggests BiocManager, rmarkdown, knitr

VignetteBuilder knitr

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

biocViews ImmunoOncologyWorkflow, Workflow, SingleCellWorkflow

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 libnode-dev xz-utils zlib1g-dev

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

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

RemoteRef HEAD

RemoteSha b4be006c213b7d0f93a78e490088ba890d641fab