

Package: csawUsersGuide (via r-universe)

October 4, 2026

Version 1.28.0

Date 2020-11-25

Title csaw User's Guide

Suggests knitr, BiocStyle, BiocManager

biocViews Workflow, EpigeneticsWorkflow

Description A user's guide for the csaw package for detecting differentially bound regions in ChIP-seq data. Describes how to read in BAM files to obtain a per-window count matrix, filtering to obtain high-abundance windows of interest, normalization of sample-specific biases, testing for differential binding, consolidation of per-window results to obtain per-region statistics, and annotation and visualization of the DB results.

License GPL-3

VignetteBuilder knitr

Workflow true

Repository Bioconductor 3.23

Date/Publication 2026-04-28 12:43:28 UTC

RemoteUrl <https://github.com/bioc/csawUsersGuide>

RemoteRef RELEASE_3_23

RemoteSha 6e76902445ef16da818f0620b6676ea71d45915e