

Package: csawBook (via r-universe)

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Title The Book of csaw

Depends BiocFileCache, ChIPpeakAnno, chipseqDBData, csaw, edgeR, Gviz,
org.Mm.eg.db, rebook, rmarkdown, Rsamtools, rtracklayer,
TxDb.Mmusculus.UCSC.mm10.knownGene

biocViews Workflow, EpigeneticsWorkflow

Description Describes how to use the csaw package to detect differentially bound regions in ChIP-seq data. This provides instructions on 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.

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VignetteBuilder knitr

BiocType Book

Config/pak/sysreqs cmake make libbz2-dev libicu-dev libjpeg-dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

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