

Package: chipseqDB (via r-universe)

October 4, 2026

Title A Bioconductor Workflow to Detect Differential Binding in ChIP-seq Data

Version 1.36.0

Date 2020-11-25

Description Describes a computational workflow for performing a DB analysis with sliding windows. The aim is to facilitate the practical implementation of window-based DB analyses by providing detailed code and expected output. The workflow described here applies to any ChIP-seq experiment with multiple experimental conditions and multiple biological samples in one or more of the conditions. It detects and summarizes DB regions between conditions in a de novo manner, i.e., without making any prior assumptions about the location or width of bound regions. Detected regions are then annotated according to their proximity to genes.

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

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Encoding UTF-8

LazyData true

VignetteBuilder knitr

biocViews ImmunoOncologyWorkflow, Workflow, EpigeneticsWorkflow

Workflow true

NeedsCompilation no

URL <https://www.bioconductor.org/help/workflows/chipseqDB/>

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