

Package: generegulation (via r-universe)

October 9, 2026

Title Finding Candidate Binding Sites for Known Transcription Factors
via Sequence Matching

Version 1.36.0

Date 2017-09-05

Description The binding of transcription factor proteins (TFs) to DNA promoter regions upstream of gene transcription start sites (TSSs) is one of the most important mechanisms by which gene expression, and thus many cellular processes, are controlled. Though in recent years many new kinds of data have become available for identifying transcription factor binding sites (TFBSs) -- ChIP-seq and DNase I hypersensitivity regions among them -- sequence matching continues to play an important role. In this workflow we demonstrate Bioconductor techniques for finding candidate TF binding sites in DNA sequence using the model organism *Saccharomyces cerevisiae*. The methods demonstrated here apply equally well to other organisms.

Depends R (>= 3.3.0), BSgenome.Scerevisiae.UCSC.sacCer3, Biostrings, GenomicFeatures, MotifDb, S4Vectors, TxDb.Scerevisiae.UCSC.sacCer3.sgdGene, motifStack, org.Sc.sgd.db, seqLogo

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Encoding UTF-8

LazyData true

VignetteBuilder knitr

biocViews Workflow, EpigeneticsWorkflow

Suggests knitr, rmarkdown, BiocStyle

NeedsCompilation no

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

Config/pak/sysreqs cmake make libgsl0-dev libbz2-dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

Repository Bioconductor 3.23

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

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