Resource Summary Report

Generated by dkNET on Apr 30, 2025

GEM

RRID:SCR_005339
Type: Tool

Proper Citation

GEM (RRID:SCR_005339)

Resource Information

URL: http://cgs.csail.mit.edu/gem/

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Description: Java software for studying protein-DNA interaction using ChIP-seq / ChIP-exo data. It links binding event discovery and motif discovery with positional priors in the context of a generative probabilistic model of ChIP data and genome sequence, resolves ChIP data into explanatory motifs and binding events at unsurpassed spatial resolution. GEM reciprocally improves motif discovery using binding event locations, and binding event predictions using discovered motifs.

Abbreviations: GEM

Synonyms: Genome wide Event finding and Motif discovery, GEM: ChIP-Seq and ChIP-exo analysis tool

Resource Type: software resource

Defining Citation: PMID:22912568

Keywords: chip-seq, chip-exo, genome, event, motif, protein-dna interaction, java, transcription factor, genome sequence, motif discovery, binding event calling

Funding:

Resource Name: GEM

Resource ID: SCR_005339

Alternate IDs: OMICS_00441

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250420T014249+0000

Ratings and Alerts

No rating or validation information has been found for GEM.

No alerts have been found for GEM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Gonzalez-Teran B, et al. (2022) Transcription factor protein interactomes reveal genetic determinants in heart disease. Cell, 185(5), 794.

Landeras-Bueno S, et al. (2021) Cellular mRNA triggers structural transformation of Ebola virus matrix protein VP40 to its essential regulatory form. Cell reports, 35(2), 108986.

Kluge M, et al. (2020) Watchdog 2.0: New developments for reusability, reproducibility, and workflow execution. GigaScience, 9(6).

Morgulis A, et al. (2020) SRPRISM (Single Read Paired Read Indel Substitution Minimizer): an efficient aligner for assemblies with explicit guarantees. GigaScience, 9(4).

Kurylo CM, et al. (2018) Endogenous rRNA Sequence Variation Can Regulate Stress Response Gene Expression and Phenotype. Cell reports, 25(1), 236.

Mak SST, et al. (2017) Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. GigaScience, 6(8), 1.

Iwata S, et al. (2017) The Transcription Factor T-bet Limits Amplification of Type I IFN Transcriptome and Circuitry in T Helper 1 Cells. Immunity, 46(6), 983.

He BZ, et al. (2017) Evolution of reduced co-activator dependence led to target expansion of a starvation response pathway. eLife, 6.

Gould GM, et al. (2016) Identification of new branch points and unconventional introns in Saccharomyces cerevisiae. RNA (New York, N.Y.), 22(10), 1522.

Tran NT, et al. (2014) A survey of motif finding Web tools for detecting binding site motifs in ChIP-Seq data. Biology direct, 9, 4.

Chung D, et al. (2013) dPeak: high resolution identification of transcription factor binding sites from PET and SET ChIP-Seq data. PLoS computational biology, 9(10), e1003246.

Guo Y, et al. (2012) High resolution genome wide binding event finding and motif discovery reveals transcription factor spatial binding constraints. PLoS computational biology, 8(8), e1002638.