Resource Summary Report

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Dynamic Regulatory Events Miner

RRID:SCR_003080
Type: Tool

Proper Citation

Dynamic Regulatory Events Miner (RRID:SCR_003080)

Resource Information

URL: http://www.sb.cs.cmu.edu/drem

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Description: The Dynamic Regulatory Events Miner (DREM) allows one to model, analyze, and visualize transcriptional gene regulation dynamics. The method of DREM takes as input time series gene expression data and static transcription factor-gene interaction data (e.g. ChIP-chip data), and produces as output a dynamic regulatory map. The dynamic regulatory map highlights major bifurcation events in the time series expression data and transcription factors potentially responsible for them. DREM 2.0 was released and supports a number of new features including: * new static binding data for mouse, human, D. melanogaster, A. thaliana * a new and more flexible implementation of the IOHMM supports dynamic binding data for each time point or as a mix of static/dynamic TF input * expression levels of TFs can be used to improve the models learned by DREM * the motif finder DECOD can be used in conjuction with DREM and help find DNA motifs for unannotated splits * new features for the visualization of expressed TFs, dragging boxes in the model view, and switching between representations

Abbreviations: DREM

Synonyms: Dynamic Regulatory Events Miner (DREM)

Resource Type: software resource, software application, data processing software

Defining Citation: PMID:22897824

Keywords: transcription, gene regulation, dynamics, time series, gene expression, static, dynamic, transcription factor-gene interaction, chip-chip, transcription factor, regulatory network, hidden markov model, systems biology, gene regulatory network, times series expression data, dynamic network, chip-seq

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Resource Name: Dynamic Regulatory Events Miner

Resource ID: SCR_003080

Alternate IDs: nif-0000-30478

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250519T204459+0000

Ratings and Alerts

No rating or validation information has been found for Dynamic Regulatory Events Miner.

No alerts have been found for Dynamic Regulatory Events Miner.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Gérard D, et al. (2019) Temporal enhancer profiling of parallel lineages identifies AHR and GLIS1 as regulators of mesenchymal multipotency. Nucleic acids research, 47(3), 1141.

Chasman D, et al. (2019) Inferring Regulatory Programs Governing Region Specificity of Neuroepithelial Stem Cells during Early Hindbrain and Spinal Cord Development. Cell systems, 9(2), 167.

Abernathy DG, et al. (2017) MicroRNAs Induce a Permissive Chromatin Environment that Enables Neuronal Subtype-Specific Reprogramming of Adult Human Fibroblasts. Cell stem cell, 21(3), 332.

Xiao Y, et al. (2009) Identification of yeast transcriptional regulation networks using multivariate random forests. PLoS computational biology, 5(6), e1000414.

Ernst J, et al. (2007) Reconstructing dynamic regulatory maps. Molecular systems biology, 3, 74.