Identification of functional transcription factor binding motifs in the *Arabidopsis thaliana* ChIP-seq data

Dolgikh V.A., Zemlyanskaya E.V., Levitsky V.G.

Institute of Cytology and Genetics of the Siberian Branch of the Russian Academy of Sciences & Novosibirsk State University, Novosibirsk, Russia
E-mail: dolgikh@bionet.nsc.ru

Transcription factors (TFs) regulate the expression of target genes by binding to cis-regulatory elements (CREs) in their promoters. Such regulation is controlled by several types of mechanisms, including (I) physical interactions between TF and DNA and oligo-/multimerization of TFs. For correct binding of TF complexes with DNA, gene promoters contain complex CREs. Thus, promoters contain cis-regulatory modules (CREs) of two or more CREs. In addition, one TF can bind several alternative CREs. The intricate structure of CRMs makes it difficult to systematic experimental research. Bioinformatics integration of ChIP-seq data (that represents the CRE of the TF under study and its partners) with RNA-seq data (reflecting the transcriptional response of potential TF targets) can facilitate such researches. In this work, we have developed a pipeline SFMotif for identifying functional CREs and CRMs based on the integration of ChIP-seq and RNA-seq data. We used genome-wide ChIP-seq data on binding the key phytohormone ethylene TF EIN3, and the ethylene-induced transcriptome data, to assess the functionality of the pipeline.

This work was supported by the RSF grant no. 20-14-00140

The main publications of authors on the subject of the abstract:

Dolgikh VA, Wiebe DS, Levitsky VG, Zemlyanskaya EV Integration of ChIP-seq and RNA-seq data in structure-function analysis of cis-regulatory elements // Bioinformatics of Genome Regulation and Structure/Systems Biology (BGRS/SB-2022) Abstracts – Novosibirsk: ICG SB RAS, 2022. – 599 p DOI 10.18699/BGRS/SB-2022-000.

Take-home message:

Our pipeline SFMotif is able to determine the major transcription factor binding motif, its alternative structural variants, binding motifs of potential partner transcription factors, and functional cis-regulatory modules between them.

DOI 10.18699/PlantGen2023-18