ISMARA: Completely Automated Inference of Gene Regulatory Networks from High-Throughput Data

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Abstract : Understanding the key players and interactions in the regulatory networks that control gene expression and chromatin state across different cell types and tissues in metazoans remains one of the central challenges in systems biology. Our laboratory has pioneered a number of methods for automatically inferring core gene regulatory networks directly from high-throughput data by modeling gene expression (RNA-seq) and chromatin state (ChIP-seq) measurements in terms of genome-wide computational predictions of regulatory sites for hundreds of transcription factors and micro-RNAs. These methods have now been completely automated in an integrated webserver called ISMARA that allows researchers to analyze their own data by simply uploading RNA-seq or ChIP-seq data sets and provides results in an integrated web interface as well as in downloadable flat form. For any data set, ISMARA infers the key regulators in the system, their activities across the input samples, the genes and pathways they target, and the core interactions between the regulators. We believe that by empowering experimental researchers to apply cutting-edge computational systems biology tools to their data in a completely automated manner, ISMARA can play an important role in developing our understanding of regulatory networks across metazoans.

Keywords : gene expression analysis, high-throughput sequencing analysis, transcription factor activity, transcription regulation

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