

# Identification of gene regulatory networks using a biclustering method

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## ABSTRACT

We present an integrative approach for identifying context-specific transcription networks. Using a composite gene-set analysis method, we combine the information of transcription factor binding sites, Gene Ontology or pathway gene sets, and gene expression fold-change profiles for a variety of cell conditions. As a result, context-specific roles of transcription factors as well as their functional targets are readily identified. We validated some of the predicted networks. Among nine candidate targets of E2F1 in HeLa cells, five (*Gadd45b*, *Dusp6*, *Mil5*, *Bmp2* and *E2f3*) were identified as novel targets using a chromatin immunoprecipitation assay. We also validated c-JUN targets and the EMT transcription networks from literature. We also present an ongoing result for identifying gene regulatory networks by transcription factors and microRNAs using a bicluster analysis method.