

Topological Importance of Transcriptional Regulatory Network Revealed by Genetic Perturbation in Yeast

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Abstract

The topological structure of transcriptional regulatory network (TRN) is important for controlling progressive events such as the cell cycle; however, whether it is also important to other biological processes is unclear. Using the genome-wide gene expression data from yeast strains deficient of each of the 263 transcription factor (TF) genes, we found that the effect of a TF gene deletion and the response of a gene to a TF deletion depends on the topological locations of the TF and the responding gene (Figure 1, 2). All yeast genes can be classified into three groups based on their responses to TF deletions: robust, normal, and sensitive. Genes regulated by more TFs have larger responses to TF deletions. Our analysis also reveals the role of non-transcriptional regulation in the response of a gene to TF deletions. To model the possible interactions between transcriptional and non-transcriptional regulations will be an interesting topic.

Figures in Abstract

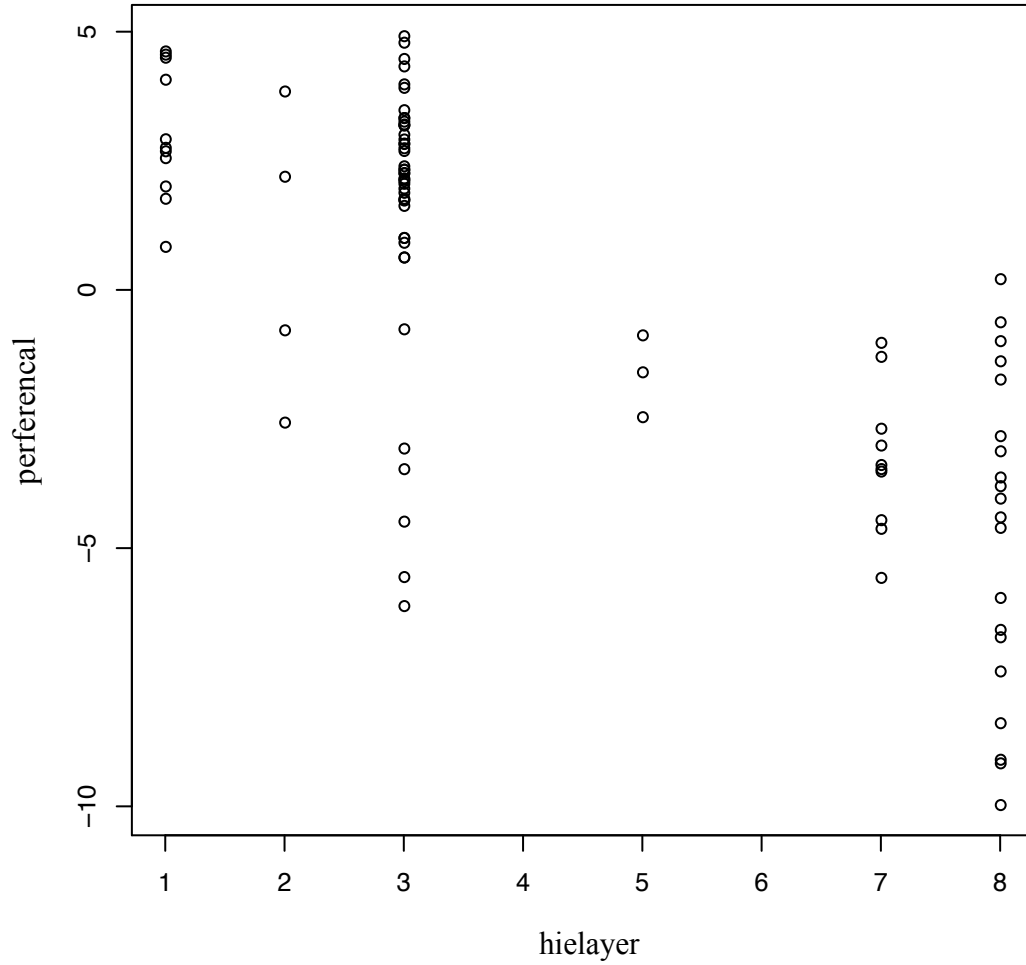


Figure 1. The distribution of TFs' preference among different layers. Each dots representing the TFs in the TRN.

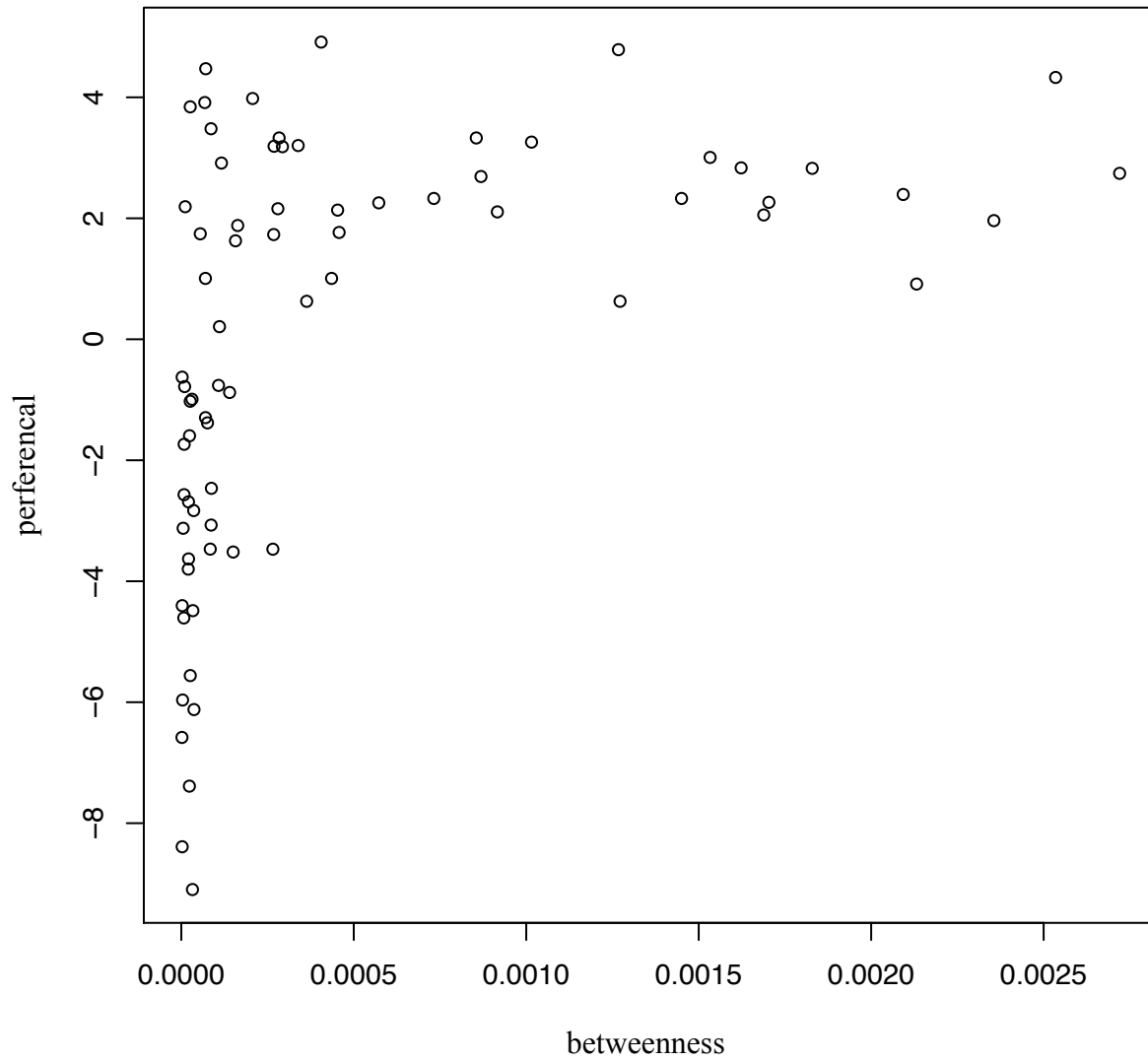


Figure 2. The correlation between TFs' preference and betweenness centrality.