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Loyola Marymount University. **Modeling of Gene Regulatory Network Dynamics Predicts which Regulatory Relationships are Important for Controlling the Cold Shock Response in *Saccharomyces cerevisiae***

A gene regulatory network (GRN) is a set of transcription factors which regulate the level of expression of genes encoding other transcription factors. The dynamics of a GRN show how gene expression in the network changes over time. Microarray data were obtained from the wild type strain and five transcription factor deletion strains (Δcin5, Δgln3, Δhap4, Δhmo1, Δzap1) before cold shock at 13°C and 15, 30, and 60 minutes after cold shock. A modified ANOVA showed that for all networks a large number of genes had a log2 fold change significantly different than zero at any time point. These genes were submitted to the YEASTRACT database to determine which transcription factors regulated them. Data from each strain were used to generate a candidate GRN of 15 nodes and 28 edges. The edges of this network were then systematically deleted, to determine the significance of each edge in the network. We used mathematical modeling through the open source software GRNmap to estimate the production rates, expression thresholds, mean squared error, least squared error and regulatory weights for these networks. After the parameter estimation, we determined that based on the least squared error and mean squared error results, certain edge-deletion networks performed better than the candidate network, and some edge-deletion networks performed more poorly than the candidate network. Furthermore, the edge deletions led to changes in the production rates and expression threshold values of certain genes. They also caused downstream regulatory weight changes. These findings suggest that some edges are more important to the regulation of cold shock than others.