**Systems modeling and statistical analysis allows comparison in the response to cold shock in *Saccharomyces cerevisiae* between Hap4 and a randomly generated network**

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A gene regulatory network (GRN) is a set of transcription factors which regulates 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. A MATLAB software package called GRNmap uses ordinary differential equations to model the dynamics of medium-scale GRNs and estimates production rates, expression thresholds, and regulatory weights for each transcription factor in the network based on DNA microarray data. Microarray data were obtained from a *Saccharomyces cerevisiae* strain deleted for the Hap4 transcription factor subjected to cold shock at 13°C for 15, 30, and 60 minutes. A modified ANOVA showed that 1794 genes had a log2 fold change significantly different than zero at any of the time points. These genes were submitted to the YEASTRACT database to determine which transcription factors regulated them. From this, we generated a candidate GRN of 15 genes and 28 edges and random network of similar size based on the Hap4 deletion strain family was created using Excel. GRNmap was used to estimate the production rates, expression thresholds, and regulatory weights for these networks. Gephi was used to analyze the networks’ structures in terms of the node in- and out-degrees, eccentricity, and betweenness centrality. From this analysis, Hap4’s role in the gene regulatory network can be analyzed and compared to the randomly generated network to help further understand the cold shock response in yeast.

Keywords: *Saccharomyces cerevisiae*, Hap4, gene regulatory network, dynamical systems modeling