**Dynamical systems modeling and gene regulatory network structure analysis of two generated networks reveal's Hap4's role in regulating the response to cold shock in Saccharomyces cerevisiae**

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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. We then estimated and compared the parameter values for production rates, expression thresholds, and regulatory weights for the GRN using GRNmap. Gephi was used to analyze the graph properties of each network in terms of the in and out degrees, and centrality measures focusing specifically on betweenness centrality, eccentricity and closeness centrality. From this analysis we have gained insight into Hap4's role in the gene regulatory network that controls the cold shock response in yeast

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