**Using Graph Statistics to Investigate the Properties of Six Candidate Gene Regulatory Networks for Controlling the Cold Shock Response in *Saccharomyces cerevisiae***

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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 30°C and after 15, 30, and 60 minutes of cold shock at 13°C. 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 six candidate GRN’s of between 14 to 17 nodes and 25 to 36 edges, depending on the specific network. The open source software Gephi was used to analyze the graph properties of each network in terms of the in- and out-degree, distance between nodes, and centrality measures, focusing on betweenness centrality, eccentricity and closeness centrality. The centrality measures indicate which nodes are most easily accessed in each network, how central a node is in a network, and which nodes most frequently appear in the shortest paths of a network. Based on these measures, we observed that Msn2 and Yhp1 seem to play central roles across all the candidate networks, making them good candidates for further testing in the lab.

Required word count: 250 Actual Word Count: 240