**Dynamical systems modeling of six related small gene regulatory networks suggest that the transcription factors Cin5, Gln3, Hmo1, and Yhp1 play a role in controlling the cold shock response in *Saccharomyces cerevisiae***

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A gene regulatory network (GRN) is a group of transcription factors that control the level of expression of genes encoding other transcription factors. Dynamics of GRNs illustrate how expression in the network changes over time. GRNmap, a MATLAB software package, uses differential equations to model the dynamics of medium-scale GRNs. The software estimates production rates, expression thresholds, and regulatory weights for each transcription factor in the network based on microarray data. Microarray data was obtained from a cold shock experiment where wild type budding yeast, *Saccharomyces cerevisiae*, and five strains from which the transcription factors Cin5, Gln3, Hap4, Hmo1, and Zap1 were subjected to cold shock at 13°C for 15, 30, and 60 minutes. Six related GRNs, which ranged from 15-20 genes and 27-36 edges, were constructed using data from the YEASTRACT database. GRNmap was then used to estimate production rates, expression thresholds, and regulatory weights for each of these GRNs.

Forward simulation of the model showed a good fit to the experimental data, as compared to random networks with the same genes and number of edges. The transcription factors Cin5, Gln3, Hmo1, and Yhp1 comprised a regulatory chain that stood out because its dynamics were consistently conserved across five of the six GRNs. These transcription factors also had among the highest total degree (in- plus out-degree) and betweenness centrality values of all the genes in the networks, suggesting that they play an important role in regulating the cold shock response in yeast.

Keywords: *Saccharomyces cerevisiae*, Cin5, Gln3, Hmo1, Yhp1, gene regulatory network, dynamical systems modeling