Comparison of the regulatory dynamics of related small gene regulatory networks that control the cold shock response in *Saccharomyces cerevisiae*

The Dahlquist lab has investigated the global, transcriptional response of *Sacchromyces cerevisiae*, baker’s yeast, to the environmental stress of cold shock using DNA microarrays in the wild type strain and five strains deleted for a particular regulatory transcription factor. Gene regulatory networks (GRNs) consist of transcription factors, genes, and the regulatory connections between them that control the resulting mRNA and protein expression levels. A family of six related GRNs were derived from the YEASTRACT database which ranged in size from 15 to 20 genes and 27 to 36 edges. We used mathematical modeling to determine the dynamics of these GRNs to determine the relative influence of each transcription factor in the network. We then compared the modeling results from the database-derived network to random networks with the same number of genes and edges. An initial sample of ten random networks were generated. After performing parameter estimation, we found that the database-derived networks performed better with smaller least-squares error values than seven of the ten random networks. To perform a more robust analysis, a larger collection of random networks was generated. Comparisons made between the random networks and the database-derived networks consistently showed better modeling of the database-derived networks. These comparisons also revealed key network motifs in both the database-derived and random networks that correlated with better fits to the data.