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

The Dahlquist Lab investigates the global, transcriptional response of *Sacchromyces cerevisiae*, baker’s yeast, to the environmental stress of cold shock, using DNA microarrays for the wild type strain and strains deleted for a particular regulatory transcription factor. Gene regulatory networks (GRNs) consist of transcription factors (TF), genes, and the regulatory connections between them that control the resulting mRNA and protein expression levels. We used mathematical modeling to determine the dynamics of the GRN controlling the cold shock response to determine the relative influence of each transcription factor in the network. A family of GRNs was derived from the YEASTRACT TF database with approximately 15 genes and 30 edges. To determine which of these models best explains the observed response to cold shock, we compared the modeling results from this database(DB)-derived network with random networks with the same number of genes and edges. Previously in the lab, ten sample random networks were generated. After performing parameter estimation, we found that the DB-derived network performed better than seven of the ten random networks with smaller least-squares error values. To perform a more robust analysis, a large collection of random networks was generated. Comparisons made between the random networks and the DB-derived network consistently saw better modeling of the DB-derived network. Through analysis, we determined key features of the DB-derived network that better predicted yeast cell behavior. This in turn validated our predictions as to the relative influence of each transcription factor that can be tested in the lab.