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 use 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 has been 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 will compare 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 will be generated via an R script. Comparisons will be made between the random networks and the DB-derived network. We predict that we will see a significant difference between the random network and the DB-derived network. We will analyze the network to determine which features better predict yeast cell behavior. This in turn will validate our predictions as to the relative influence of each transcription factor that can be tested in the lab.