

**HONORS THESIS PROSPECTUS**

The purpose of this form is to inform the University Honors Program about the intended research or creative activity that will comprise your Honors Thesis and to confirm that your Thesis Advisor has endorsed your project.

**PROSPECTIVE ABSTRACT**

Please supply a brief abstract of your intended project (maximum 250 words). Plans for your project may change under the supervision of your Advisor. If project aims or methods change ***substantially***, please submit a revised form with your advisor’s signature. If this project represents a collaboration with your advisor’s research group, please make sure to specify your particular contributions.

**TITLE: TBD**

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 (TFs), 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 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-derived network with random networks with the same number of genes and the same number of edges. Previously in the lab, ten sample random networks were generated. After performing parameter estimation, we found that the database-derived network performed better than seven of the ten random networks, as indicated by smaller least-squares error values. To perform a more robust analysis, I will generate code to automate the generation of random networks to amass a large collection to feed into the model. Comparisons will be made between the random networks and the database-derived network. We predict that we will see a significant difference between the random network and the database-derived network. We will analyze the collection of networks to determine which features better predict yeast cell behavior. This investigation, in turn, will validate our predictions as to the relative influence of each transcription factor that can be tested in the lab.

Thesis Advisor’s Name: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Thesis Advisor’s Signature: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Date: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_