Title: *Need write a correct title for your summer projects*

{{Please also read Parnell’s thesis for background}}

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Abstract:

Understanding the intricate process of biological aging is an essential question that science seeks to answer. In efforts of biologically and computationally understanding the complexity of aging specifically under caloric restriction and reactive oxidative species within eukaryotes, we utilized the model organism *S. cerevisiae* in order to provide scientific findings that aid in deducing this phenomenon. Through this experiment we believe that low glucose levels induce heterogeneity in cell populations that may partially change the reported changes of average glucose signals.

Conducted as a parallel study within Dr. Hong Qin’s proposal, the measure of robustness within various strains of yeast allowed us to test the hypothesis that an increased amount of strength in the robustness signal has a proportional relationship to the rate of aging within cells. This hypothesis was formulated through the quantitative definition of biological aging- Gompertz model as well as the network reliability model of cellular aging, which work in conjunction in order mathematically depict the amount of active interactions per gene that occur within in a cell- the amount of interactions per gene is what is known the a cell’s network robustness.

The ‘free radical theory of aging’ plays an integral part in understanding robustness. This theory states that aging occurs because cells collect free radicals that cause damage and ultimately cause the cell to age. As cells grow antioxidants are released which are useful in defending the cell from quickly aging and dying. Among those antioxidants is superoxide dismutase (SOD). SOD aids as an enzyme that helps in reducing the harmful effects of oxidative stress within the yeast cell by catalyzing the dismutation of superoxide, which is a known harmful anion that causes aging, which breaks down into oxygen and hydrogen peroxide, which also causes aging in cells.

It is widely accepted that CR (0.5% glucose) extends CLS by inducing H2O2 and superoxide dismutase. Knowing that superoxide and hydrogen peroxide are causes of aging within yeast cells we wanted to test the yeast strains robustness under different concentrations (i.e. 2%, 1%, 0.5%, 0.25%, 0.1%, 0.01% and 0%) of these stressors with an ultimate goal of seeing how the cells behave when their external environment is undergoing a change and therefore this change represents stress. In order to conduct this experiment we used various concentrations of artificial stressors that resembled both superoxide (DHE) and hydrogen peroxide (DHR) as well as a blank of yeast cells and using the R programming computational tool in order to analyze and compare the results of each concentration.

The results gathered suggest that glucose can lead to cell populations with different levels of H2O2 and superoxide. Based off of these findings we plan to characterize these changes in great detail and in more strains and also develop a prototype mathematical model to study its mechanisms.