**Introduction**

For the past 5 years, the career goal of Dr. Hong Qin has been to continue to contribute to the current knowledge of cellular aging. The topic of cellular aging still holds great ambiguity within the world of biology. Several models, including the Gempertz model, have made attempts to accurately define cellular aging. The most commonly used and seemingly accurate definition of aging currently states that aging is an exponential increase of mortality rate over time. An organism commonly used to study this idea of aging in the lab is yeast cells. Yeast cells have the ability to live to different ages despite each cell’s extremely similar genotype.

Currently, there is no specific gene that has been found to directly influence cellular aging. Also, several different pathways are observed during yeast aging. These finding indicate that cellular aging is an emergent property of gene networks. Throughout this course, students were able to study this idea via computer simulations and R and R Studio software.

**Materials and Methods**

This experiment aims to examine statistical associations of the effects of specific genes on aging and robustness, and to experimentally test the link between network robustness and cellular aging rates. It will be important to look for shared characteristics genes associates with aging and phenotypic compacitors. The ultimate goal will be to be able to predict new genes that may be associated with aging.