Lisa Jones February 28, 2012

“Genomic Expression Programs in the Response of Yeast Cells to Environmental Changes”

Purpose:

The purpose of this research was to use DNA microarrays to measure the changes in transcription levels and transcription factors in yeast *Saccharomyces cerevisiae* in response to stress.Multicellular organisms can use a wide array of mechanisms, tissues, and organs to respond to external stress, where unicellular organisms such as yeast do not have that capability. Yeasts on the other hand have evolved a series of autonomous mechanisms to help maintain homeostasis in response to stress. The different environmental stresses that were applied to the yeast were; heat shock (at various temperatures), cell lysis, RNA isolation, Hydrogen Peroxide Treatment, Menadione exposure, DTT exposure, Hyper-osmotic shock, nitrogen depletion, and amino acid starvation.

Microarray:

A DNA microarray is when small amounts of DNA are used in order to measure expression levels of genes. The expression levels can then be used to determine the amount of transcription that is taking place, which influences the amount of a gene, or genes that are expressed in order to combat the environmental changes that are taking place in the cell.

Clustering Analysis:

Clustering analysis was used to examine corregulated genes, promoters, and transcription factors. Genes that are expressed together typically cluster in the same region. Clustering is important because genes it shows all of the genes that work in conjunction with one another; even genes whose specific function is unknown. This is helpful in being able to determine the function of unspecific genes because it can then be studied with the use of known environmental factors.

Results:

The results showed that genes that are corregulated under the conditions examined will cluster together, genes that cluster suggest hypothetical functions for uncharacterized genes in the same cluster, the choreography of expression of the various gene clusters can be related to the various series of events, and that a physiological picture of the cellular response can be sketched by considering the expression of genes that are known and regulation, which suggests the effects of the environmental conditions of the cell.

Qin Proposal:

The Qin proposal argues that data in this paper can be used to estimate robustness because robustness is defined as the ability of cells to continue homeostatic equilibrium while facing damaging environmental, polymorphic, and genetic alterations. The Gasch experiment, implemented many forms of stress on the yeasts. The resulting efficiency of the cell to maintain homeostasis would be robustness. According to the Qin proposal cellular aging is thought to be proportional to the robustness in gene protein interaction networks. The Qin project hypothesizes that cellular aging occurs as a result of the complex interactions that transpire between genes and proteins ; the relationship between robustness and the rate of cellular aging, forecast new genes that are associated with cellular aging, find mutual attributes that are common to genes that are involved with phenotypic capacitors and cellular aging, and to utilize the statistical data of genes involved in aging and to study how they impact robustness.