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**Introduction**

The aging is an essential progress for Saccharomyces cerevisiae or yeast. Why do organism age? Saccharomyces cerevisiae is broken down into two life spans which include replicative and chronological life span. A replicative life span measures the average number of offsprings in a single cell and a chronological life span measures the cells in the stationary phase of growth (Qin). Bioinformatics is used to expand research technics in the biology field. This is used in this experiment by the used of the software called R-studio. By choosing a genetic set and comparing them against other known data sets will aid in the investigation of the aging of cells. The selection of the data set GSE 12221 is used to analyze the aging of yeast. GSE12221 IS known to decay profiles of Sacchamyces cerevisiae mRNAs with the oxidative stress and DNA damage ("GEO Accession Viewer"). The impact of stress can either speed or delay the aging process of a cell. This can convey a correlation on how it affects the aging of cells. With the examination of Saccharomyces cerevisiae and aging, GSE12221 will benefit in the understanding of this process.

**Materials**

R-studio Software

Data Set- GSE12221

Data: fitness, interaction degree of protein network, interaction degree of positive genetic interaction degree, interaction degree of negative genetic interaction degree, and replicative life span

**Methods**

By using the software of R-studio the data set GSE 12221 was observed. The analysis of the data set was done by comparing it to the several data. The following is the data: fitness, interaction degree of protein network, interaction degree of positive genetic interaction degree, interaction degree of negative genetic interaction degree, and replicative life span. With R-studio the working directory was set and the first set of codes were examined. The calculation of standard deviation, mean, and CV was completed for the data set of GSE 12221. Then analysis the correlation between the data from fitness, interaction degree of protein, genetic network, and real life span. In addition this included the running of multiple regressions. To conclude the experiment, the data was permutated by the calculation of the different expression of the protein networks and genetic networks. Then the observation of the graphs, p-value, and standard deviation created by this code were made for a conclusion.

**References**

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