# Red Light Green Light: Microarray Gene Expression Data to Analyze Differences in Healthy and Cancerous Prostate Tissues

Zonnefeld, Jocelyn (School: Unity Christian High School)

Purpose: Cancer is a leading cause of death in the United States. Research has shown that cancer is a genetic disease, and using microarrays to determine the expression levels of genes in tissues is one method to expand available information. Using microarray data, I searched for statistically significant differences between the expression levels of genes in healthy and cancerous prostate tissue. Procedure: Averages of gene expression levels for the cancerous and healthy tissue for each gene were taken, and each gene was labeled as up-regulated or down-regulated. The ratio of the healthy and cancerous means was determined by dividing the larger mean by the smaller mean. The p-value, standard deviation, and confidence interval were calculated for all genes with ratios greater than three. Results: Each gene with a ratio near or greater than three showed p-values that were statistically significant, with values of .0006, .0003, and six of the genes had p-values of .0000. Each of the genes also had confidence intervals that did not include 0. The standard deviations of each up-regulated gene's cancer tissue was much greater than the healthy tissue, with the down-regulated gene showing the inverse. Conclusions: This study showed that there are eight genes that show statistically significant differences in their expression levels and are deserving of further research. Further experiments will compare significant genes across different types of cancer.