Identification of the Impact of Obesity Treatments on Gene Expression using a Novel Statistical Test

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In the United States, obesity is estimated to cause 111,909 to 365,000 deaths per year, while 1 million deaths are linked to obesity in Europe. On average, obesity reduces life expectancy by six to seven years and is linked to a multitude of diseases. DNA microarray technology can simultaneously screen thousands of gene expression profiles, transforming how genetics is applied in medicine. However, the lack of normality in microarray data renders common statistical methods ineffective. We propose a novel statistical method, coined the S-test, which does not require stringent assumptions but is still more powerful than some of its competitors. Using both simulation studies and clinical data, we show that our novel method outperforms previous methods. The limiting distribution is obtained under null and alternative hypotheses. The proposed test will help us better understand the genetic effects of various obesity treatments and how to better these treatments to have minimal side effects. It may also help in the development of a prediction model in genetic profiling studies built on a subset of deferentially expressed genes and the clinical data to assess the accuracy of the clinical prediction.

Awards Won:

Fourth Award of $500