

## Abstract

Microarray technology is extensively used today in many applications. One of its uses is discovering sets of genes that are most likely to be related to cancer. Typically, based on microarray data, a statistical test is conducted for each of thousands of genes simultaneously. In a two-group comparative microarray experiment, an important parameter for controlling the rate of false positives and also for determining the appropriate sample size is the proportion of true null hypotheses ( $\pi_0$ ). This presentation will focus on an improved  $\pi_0$  estimation method we have developed, and some results comparing its performance to that of other methods. Some details and results will also be presented on a formal Likelihood Ratio test for  $\pi_0$ .