

Presentation of Master's Project

A Comparison of Analytical Methods for DNA Microarrays

By

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The ability to measure gene expression and accurately determine whether a gene or a set of genes is differentially expressed has become a popular area of investigation. This is partly a result of the fact that the differential expression of genes can be indicative of the health or changing health of an animal. The use of DNA Microarrays, in particular the Affymetrix oligonucleotide gene chip, to obtain gene expression measurements has become commonplace, but with such technology arises potential roadblocks. One such roadblock is analyzing the overwhelming amount of data that is acquired with any experiment implementing the use of DNA Microarrays. The focus of this paper is, therefore, to develop and compare two methods for analyzing gene expression measurements obtained from oligonucleotide gene chips.

The first of these methods, which has become a standard approach, is a parametric empirical Bayes method in which a mixture model is constructed and then used to estimate the mixing probabilities that correspond to the possible patterns of differential expression. The second method, which is of our design, is a permutation test implementing a multivariate test statistic that is calculated using the probe-level data. Using a range of posterior probabilities for the empirical Bayes method and variety of false discovery rates for our method, the error rates of the two approaches are then compared using a benchmark data set.

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