



The University of Mississippi

Department of Mathematics

Statistics Seminar

A modified approach in statistical significance for genome wide studies

By

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Abstract

Most microarray studies are focused on identifying genes that are differentially expressed between two experimental conditions. One of the well known measures of significance for genome wide studies is the q value based on the false discovery rate. The q value is estimated from a list of p values based on permutation test for equality of means. Permutation test does not control Type I error rate to its nominal value when variances are unequal. Therefore, permutation test can be conservative or liberal. In this study we propose a modified t -test based on jackknife estimator of population variance. The resulting p values are used to estimate q value as given by Storey and Tibshirani (2003). Monte Carlo method is used to show that the estimated q value from the proposed test controls q -value threshold rate better than the q value estimated from permutation test based p values.

Date: Friday, October 15, 2010

Time: 3 PM – 4 PM

Location: Hume 331