

Shuo Jiao

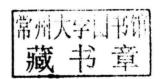
# MICROARRAY DATA ANALYSIS

DETECTING DIFFERENTIALLY EXPRESSED GENES WHILE CONTROLLING THE FALSE DISCOVERY RATE



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by

Shuo Jiao

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# DETECTING DIFFERENTIALLY EXPRESSED GENES WHILE CONTROLLING THE FALSE DISCOVERY RATE FOR MICROARRAY DATA

Shuo Jiao, Ph.D.

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Microarray is an important technology which enables people to investigate the expression levels of thousands of genes at the same time. One common goal of microarray data analysis is to detect differentially expressed genes while controlling the false discovery rate. This dissertation consists with four papers written to address this goal. The dissertation is organized as follows: In Chapter 1, a brief introduction of the Affymetrix GeneChip microarray technology is provided. The concept of differentially expressed genes and the definition of the false discovery rate are also introduced. In Chapter 2, a literature review of the related works on this matter is provided. In Chapter 3, a *t*-mixture model based method is proposed to detect differentially expressed genes. In Chapter 4, a *t*-mixture model based false discovery rate estimator is proposed to overcome several problems of the current empirical false discovery rate estimators. In Chapter 5, a two-step false discovery rate estimation procedure is proposed to correct the overestimation of the false discovery rate caused by differentially expressed genes. In Chapter 6, a novel estimator is developed to estimate the proportion of equivalently expressed genes, which is an important component of the false discovery rate estimators. In Chapter 7, a summary of the dissertation will be given along with some possible directions for the future work.

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