Identifying Differentially Expressed Genes in Microarray Experiment with Dye-swapping Design

連怡斌
彰化師範大學數學系

Abstract

In microarray experiments, there are many inherent variations that make analysis challenging. To address inherent variations, various methods and multiple experimental designs have been proposed. In the present study, an easily implemented statistical method, SARA (Swapping And Regression Analysis), has been proposed to identify differentially expressed genes in a swapped-designed microarray data. Under very general assumptions regarding the structure of channel, scanner, and target effects obtained from the experiment, we showed that SARA removes bias caused by the above effects. Our methods and a few commonly used methods including ANOVA, CAT, fold change and t-test type methods were compared using simulation and real data. Our statistical framework and related simulation results show that SARA has excellent and consistent performance in identifying differentially expressed genes in microarray experiments with dye swapping design and replications.