

# False discovery rate in microarray studies

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*Abstract:* An important aim of DNA microarrays is the identification of differentially expressed genes affected by explanatory variables or covariates of interest: Multiple testing for each gene. The traditional approach to this multiplicity problem controls the familywise error rate(FWER). Control of the FWER is unduly conservative in analyzing large-screening microarray data. The false discovery rate(FDR) may be a promising alternative to the FWER which aims to control the expected proportion of Type I errors among the rejected hypotheses. Many FDR controlling procedures control the FDR under independence or restrictive dependence structures, resulting in an unreliable FDR estimation. For these problems, two-stage FDR controlling procedure under suitable dependence structures are proposed here. This proposed testing procedure is based on a Poisson distributional approximation. It eliminates the need to consider specific dependence structures of genes. We compare the performance of two-stage FDR controlling procedure with that of other FDR controlling procedures. The procedures are studied using Leukemia study of Golub et al. and simulated data. In these examples, proposed FDR procedure has greater power without much elevation of FDR.