

TESTING FOR DIFFERENTIALLY EXPRESSED PATHWAYS IN MICROARRAY EXPERIMENTS

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Due to the rapid development of microarray technology and the increasing popularity of its applications, new statistical methods for analysis of gene expression data are needed. Most of the methods recently introduced are designed to detect differential expression for individual genes between two or more groups. We examine the problem from a slightly different angle, focusing on genetic pathways rather than on individual genes. Our goal is to develop a Bayesian methodology to test whether pathways are significantly different for two or more groups with phenotypic differences. The method is based on a logistic regression model and uses a Metropolis-Hastings algorithm to simulate the posterior distributions of the regression parameters of interest. These parameters are then used as the basis of the test for differential pathway expression. The method is applied to several real data sets.