

“Bayes Error Control for Multiple QTL Mapping”

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Abstract

Genome-wide linkage analysis suffers from multiple, correlated tests, which is exacerbated when mapping multiple quantitative trait loci. Traditional significance thresholds have been set to control the probability of detecting at least one false positive peak, although such thresholds are known to result in excessively low power to detect true positive peaks. Recently, false discovery rate-controlling procedures have been developed that yield more power by relaxing the stringency of the significance threshold. Here, a new procedure is described that extends false discovery rate control to include simultaneous control of the false non-discovery rate. This procedure is developed in the Bayesian framework using a direct posterior probability approach. Significance thresholds are determined by minimizing a function of the overall error rate. Several definitions of the unit of testing are considered. Correlation among tests is also discussed.