Abstract

The effects of genotype and relationship errors on linkage results are evaluated in three of the Genetic Analysis Workshop 12 asthma genome scans. A number of errors are detected in the samples. While the evidence for linkage is not striking in any data set with or without error, in some cases the difference in test statistic could support different conclusions. The results provide empirical evidence for the predicted effects of genotype and relationship error and highlight the need for rigorous detection and elimination of data error in complex trait studies.