

Mapping Epistatic Genes for Complex Traits

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Abstract:

Most complex traits of animals, plants and humans are influenced by multiple genetic and environmental factors. Interactions among multiple genes play fundamental roles in the genetic control and evolution of complex traits. Statistical modeling of interaction effects in quantitative trait loci (QTL) analysis must accommodate a very large number of potential genetic effects, which presents a major challenge to determining the genetic model with respect to the number of QTL and their effects. In this study, we use the methodology of Bayesian model and variable selection to develop strategies for identifying multiple QTL with complex epistatic patterns. Specifically, we develop a reversible jump Markov chain Monte Carlo algorithm to determine the number of QTL and to select significant main and epistatic effects. With the proposed method, we can jointly infer the genetic model of a complex trait and the associated genetic parameters, including the number, positions, and significant main and epistatic effects of the identified QTL.