Mixture Generalized Linear Models for Multiple Interval Mapping of Quantitative Trait Loci in Experimental Crosses

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Abstract

Quantitative trait loci mapping in experimental organisms is experiencing a rapid evolution in genetic studies. The advent of new techniques for genotyping dense markers has made genome-wide quantitative trait loci mapping possible. Statistical methods for mapping normally distributed quantitative traits have been well established. However, methods for mapping non-normally distributed traits, which are common and economically important, have not been fully developed yet. In this article, we formulate a mixture generalized linear model for multiple interval mapping of non-normally distributed traits in experimental crosses. We develop an efficient EM-algorithm for the simultaneous computation of the maximum likelihood estimates of the QTL effects and positions as well as the observed Fisher information matrix of such models. We also deal with the mapping strategy in terms of statistical model selections. Simulation studies are presented for the illustration of the estimation and mapping procedures.

Keywords: Experimental crosses, generalized linear model, mixture models, model selection, multiple interval mapping, quantitative trait loci.