

RANDOM COEFFICIENT REGRESSION MODELS IN QTL INTERVAL MAPPING

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Quantitative trait loci (QTL) analysis has changed the conventional view of polygenic inheritance. Several strategies have been proposed to explore associations between phenotypic values and molecular marker genotypes leading to the identification of loci producing continuous trait variation. Composite interval mapping (CIM) is a common method of QTL analysis in plant genetics. In interval mapping, the phenotypic response is regressed on the expected value of a random variable indicating the putative QTL genotype given the genotype of the molecular markers flanking a target genome interval. A multiple regression approach is used to incorporate several cofactors corresponding to markers on the map which are outside the target interval and probably associated with QTL different than the one at the interval under inspection. The error term distribution is approximated as a mixture of normal distributions depending on the number of genotypes at the putative QTL in the mapping population. ML estimation of full and reduced (putative QTL effect equals zero) models provides statistical support to detect QTL effects and positions. In this framework, variable selection methods need to be run to correctly specify the model. Here, we propose to use a random intercept regression model to account for the genetic background corresponding to different genetic lines that is not captured by the available markers. We use the NLMIXED/SAS procedure to specify a general likelihood yielding estimations of the QTL effect at several interval positions. A simulation study showed that the procedure is able to identify the putative QTL without variable selection. Moreover, the method provides estimation of variance components to explore trait heritability.