A Selective Shrinkage Method for Mapping Multiple Quantitative Trait Loci

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The variance of a quantitative trait is often contributed by the segregation of multiple genetic loci plus an environmental variant. These multiple genes are called quantitative trait loci (QTL). Some QTL may contribute a large proportion of the trait variance but others may contribute little. Conventional statistical methods for QTL mapping only detect and estimate QTL with large effects because the model that includes all QTL (regardless of the sizes) is often oversaturated and cannot be handled with the conventional approaches. We develop a selective shrinkage method under the Bayesian framework to overcome the problem of model saturation so that all QTL (large or small) are simultaneously estimated in the same model. Putative QTL with negligible or no effects are shrunken to zero whereas those with noticeable or large effects are unaffected. This selective shrinkage property is accomplished by using Normal priors with zero mean but variable variance parameters across different QTL. The shrinkage method allows us to include a fixed number of QTL in the model so that model selection is avoided. The fixed number of QTL is chosen as the "maximum" number that a genome can possibly possess for the trait of interest. Superfluous QTL are automatically shrunken to zero by the method. Positions of the actual QTL are estimated from the posterior sample generated via Markov chain Monte Carlo sampling. Simulation studies and real data analyses demonstrate that the new method outperforms existing methods that are currently practiced in QTL mapping experiments.

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