

Bayesian Variable Selection to Identify Quantitative Trait Loci

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Mutiple quantitative trait loci (QTL) regulating a specific phenotype can be approximately identified by using available genotypic markers. Classical approaches are usually developed using multivariate regression models with trait values regressed on marker genotypes. However, missing values of either trait values or marker genotypes and large number of marker genotypes relative to sample size challenge the identification of QTL using classical approaches based on multivariate regression models. We will take advantage of Bayesian inference on small datasets to develop a Bayesian variable selection approach to identify QTL, which is built up on a more natural Bayesian framework than the Bayesian methods in literatures.

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