

Evaluation of the Performance of Maximum Likelihood and Regression Approach in Quantitative Trait Loci Mapping for Trait in Binary Scale

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ABSTRACT

Genes or loci on chromosome underlying a quantitative trait are called Quantitative Trait Loci (QTL). Characterizing genes controlling quantitative trait on their position in chromosome and their effect on trait is through a process called QTL mapping. This research was focusing on the assessment of the performance of Maximum Likelihood (ML) and Regression (REG) approach employed in QTL mapping for binary trait by means of simulation study. The simulation study was conducted by taking into account several factors that may affect the performance of both approaches. The factors are: (1) marker density; (2) QTL effect; (3) sample size; and (4) shape of phenotypic distribution. From simulation study, it was obtained that LB and Piepho method showing similar performance in determining critical value in testing the existence of QTL for binary trait. The simulation study also indicating that both methods could be used in determining critical value in QTL mapping analysis for binary trait. In assessing the performance of ML and REG approach in QTL mapping analysis for binary trait, the two approaches showing comparable performance. As a result, in QTL mapping analysis, ML and REG approach could be used when dealing with binary trait.

Keywords: QTL mapping, binary, maximum likelihood, regression, critical value