

GENETIC ALGORITHM FOR MAPPING EPISTASIS IN CONTROLLED CROSSES

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- **ABSTRACT:** *The identification of epistasis or interactions among genes plays an important step for understanding the genetic regulatory network of complex diseases. When there are more than one genetic locus influencing the phenotype, interaction effects among loci are probably involved. Nevertheless, despite of the advances in genetic mapping studies the analytical detection of epistasis is still considered a challenge. In this work, we apply the genetic algorithm (GA) jointly with different criteria for model selection to search for molecular markers associated with multiple QTL's (Quantitative Trait Loci) and their interaction effects. GA represents a more efficient alternative for searching high dimensional spaces and it is less affected to general problems of identification of epistatic genes. We use simulation studies to compare the performance of GA with the classic search procedures, exhaustive and conditional, under different configurations. Finally, we analyze data from a F2 rats design and the AG found more optimal results when compared to conditional procedure. Two QTL's with epistatic effect on systolic blood pressure were identified, located in chromosomes 5 and 9 of the rat genome.*
- **KEYWORDS:** *Interval mapping, gene interaction, model selection, quantitative trait loci.*

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