

# Combined Linkage and Association Mapping of Quantitative Trait Loci

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## **Abstract:**

In this research, we propose to combine population data and pedigrees of any size and any types of relatives in joint high resolution linkage and linkage disequilibrium (LD or association) mapping of quantitative trait loci (QTL) by variance component models. Multiple markers can be simultaneously used in modeling association with the trait locus, instead of using one marker a time in the analysis. This may avoid the complications of different results obtained from the separate analysis of marker by marker. The models simultaneously incorporate both linkage and LD information. The measures of LD are modeled by mean coefficients, and linkage information is modeled by variance-covariance matrix. Using analytical formulas to calculate the regression coefficients, the genetic effects are shown to be decomposed into additive and dominance components.

The non-centrality parameter approximations of test statistics of LD are provided to make power calculations. Power and type I error rates are explored to investigate the merit of the proposed method by both the analytical formulas and simulations. Compared with the association between-family and association within-family ("AbAw") approach of Fulker and Abecasis et al., it is evident that the method proposed is more powerful. The method is applied to investigate the relation between polymorphisms in the angiotensin-1 converting enzyme (ACE) genes and circulating ACE levels, with a better result than that of the "AbAw" approach.