

# High Resolution Linkage Disequilibrium Mapping of Quantitative Trait Loci by Multiple Markers

Jeesun Jung, Ph.D.  
Texas A&M University

## Abstract:

In recent years, there have been great interests in linkage and linkage disequilibrium mapping between quantitative trait loci (QTL) and multiple markers. Using multiple bi-allelic markers, variance component models are proposed for high resolution linkage disequilibrium mapping of QTL based on nuclear families. The measures of linkage disequilibrium and genetic effects are incorporated in the mean coefficients of linear model, and decomposed into orthogonal additive and dominant effects. The linkage information is modeled in variance covariance matrices. Therefore, the proposed methods explain both association and linkage in the unified model. Based on marker information, multipoint interval mapping is provided to estimate the proportion of allele sharing identical by descent (IBD) and the probability of sharing 2 alleles IBD at a putative QTL for a sib-pair. To test the genetic effects and linkage disequilibrium, the analytical formula for non-centrality parameter approximations of test statistics are derived. By comparing with the "AbAw" approach, it is found that the model proposed is more powerful and advantageous. With power and sample size comparison, it is shown that models using more markers may have higher power than those using less markers. The multiple marker analysis can be more advantageous, and has high power in fine mapping QTL. As an example, the Genetic Analysis Workshop 12 German asthma data are analyzed using the proposed methods.

Key words: QTL;LD mapping;IBD;Variance Component Model.  
*email:* jsjung@stat.tamu.edu