



The University of Mississippi
Department of Mathematics

STATISTICS SEMINAR

Integrating Genome-wide Expression Information into
Genome Scans for Complex Traits

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HUME 331
2:00 P.M.

Abstract:

One of the central goals of genetics is gene mapping: that is, determining which genes are responsible for variation in traits of interest such as diseases. Efforts at gene mapping have been hampered by low statistical power when there are many genes involved in determining the trait. In this talk, I will discuss two procedures that we have developed for integrating expression information into genome scans in order to increase power. In both approaches we use an EM algorithm with the expression data to estimate the parameters for unobserved controlling genotypes. In one approach we use the EM algorithm to test whether the controlling factor for a group of highly correlated genes is disease causative. If it is, then we apply standard gene mapping techniques to identify candidates for that controlling factor. In the other approach, we use a model based on the parameter estimates to infer genotype at unobserved trait causative loci. We then use these inferred genotypes to construct “optimal” samples with reduced heterogeneity for mapping the target locus. We then apply standard gene mapping techniques using these “optimal” samples. We show via simulations that both techniques result in a major improvement in power over standard gene mapping techniques. We also show an application to a mouse obesity data set in which our methods show very promising results.

Faculty, Staff and Students are welcome