



The University of Chicago
Department of Statistics

Ph.D. Seminar

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**A Method for Genetic Mapping of Quantitative Traits
and Related Statistical Problems**

**THURSDAY, May 15, 2008 at 3:30 PM
110 Eckhart Hall, 5734 S. University Avenue**

ABSTRACT

Association mapping of quantitative trait loci is a challenging problem, especially when a lot of the existing variants are not genotyped. In this talk, I will present a new statistical method for this problem. The method is based on monotone regression for independent samples. It can be used to test association between a trait and a genotyped SNP, one or several haplotypes or an untyped SNP. I will also present an application of this method to a genome-wide data set.

The above-mentioned test of association between the trait and the untyped SNPs makes use of information on the joint distribution of genotypes for the genotyped and untyped SNPs, which is estimated using a reference data set where all such SNPs are genotyped. Using an estimate from another data set introduces variability which is ignored in many studies. We study the effect of this variability, and develop a theory for estimation and hypothesis testing in the case when nuisance parameters in the model are estimated from another data set. I will present some asymptotic results derived for this setting.