



The University of Chicago

Department of Statistics

Seminar Series

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**“Multilocus Genetic Association Testing
Using Localized Haplotype Clustering ”**

**WEDNESDAY, November 8, 2006 at 12:00 PM
110 Eckhart Hall, 5734 S. University Avenue**

ABSTRACT

I will describe a new method for association-based gene mapping that makes powerful use of multilocus data, is computationally efficient, and is straightforward to apply over large genomic regions. The approach is based on the fitting of a localized cluster model to haplotype data. The model fitting automatically adapts to the degree of linkage disequilibrium between markers to give a parsimonious model for the linkage disequilibrium structure. After the model is fit, the clusters can be tested for association with trait status. This approach can be thought of as haplotype testing with sophisticated windowing that accounts for extent of linkage disequilibrium to reduce degrees of freedom and number of tests while maximizing information. Analyses of published and simulated data show that this approach can have better power than single marker tests. Whole genome association haplotype data (hundreds of thousands of markers on thousands of individuals) can be analyzed in one day on a desktop PC with our implementation of this method.