



The University of Chicago  
Department of Statistics

Seminars for Fourth Year Ph.D. Students

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**Methods for Detecting Gene-Gene Interaction  
and Single-Locus Association**

**TUESDAY, November 28, 2006 at 10:30 AM  
110 Eckhart Hall, 5734 S. University Avenue**

**ABSTRACT**

Novel statistical designs and testing methods have been developed during the past two decades for identifying genes that are responsible for a number of inherited human diseases. However, success has been largely restricted to simple Mendelian diseases. Because complex traits are typically caused by multiple genes, the common approaches of testing markers one after another fail to capture the substantial information of interactions among disease loci. Recent attention has been focused on genome scans using a large number of marker loci. Hence, the approach using a full interaction model on all possible pairs of markers will be computationally expensive and involve an overwhelming multiple testing problems. As an alternative, new strategies were proposed, such as those including two stages, where the analyses in the second stage are done only on markers associated in the first stage. Here we propose methods which can be applied to this 2-stage strategy.

For association studies, we will show likelihood ratio test(LRT) for models with ordered penetrance is powerful compared to other popular tests for association. For interaction studies, we develop LRTs for models with ordered penetrance. Future research directions and open problems will also be discussed.