



The University of Chicago

Department of Statistics

Seminar Series

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**“Quantifying Correlation with Applications
to Genome-Wide Association Studies”**

MONDAY May 2, 2005 at 4:00 PM
133 Eckhart Hall, 5734 S. University Avenue

Refreshments following the seminar in Eckhart 110.

ABSTRACT

Genome-wide association studies aim to detect the genetic variation responsible for common diseases in humans. The challenges in analyzing the data generated by these studies come from the complexity of both the data and of the phenotypes under investigation. We discuss some of the statistical issues involved including the need for multi-locus analyses and allowing for environmental risk factors. We introduce a framework for quantifying the association between two data structures, for example the genotypes of two mutually exclusive groups of markers. The proposed measures of association are functions of the Fisher information contents in the two data structures. The derived measures are used for investigating how much information is in the markers on the Affymetrix 100K SNP chip relative to the markers in the HapMap database.