



The University of Chicago  
Department of Statistics  
Seminar Series

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**On the Use of General Control Samples for Genome-Wide  
Association Studies: genetic matching highlights causal variants**

**MONDAY, November 5, 2007 at 4:00 PM**  
**133 Eckhart Hall, 5734 S. University Avenue**  
*Refreshments following the seminar in Eckhart 110.*

**ABSTRACT**

Resources being amassed for genome-wide association (GWA) studies include “control databases” genotyped using a large-scale SNP array. How to use these databases effectively is an open question. Unfortunately, population structure can induce false positives. For instance, if cases and controls have different genetic backgrounds, differences in frequencies of distinct forms of variants might be due to differences in ancestral population of origin. We develop a method to match, by genetic ancestry, controls to affected individuals (cases). For complex structure typical of human populations, matching can be essential for highlighting true positives and downplaying false positives. We perform a GWA by matching Americans with Type 1 diabetes (T1D) to controls from Germany. Despite the complex study design, these analyses identify numerous loci known to confer risk for T1D.