



ANNOUNCES A
COLLOQUIUM

Dr. Yu Zhang

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will speak on

**A New Bayesian Variable Selection Method
for Disease Association Mapping**

Time: 3:00 – 4:00 PM

Date: Friday, September 30, 2011

Place: Alter Hall 746

Abstract

Genome-wide association studies identify genetic mutations affecting disease risks. In a case control setting, the response variable is the disease status of individuals, and the predictor variable is single nucleotide polymorphisms (SNPs) measured across the genome. The number of SNPs is typically much larger (in 10^5 - 10^6) than the number of individuals. In this talk, I will present a new Bayesian variable selection method to detect associations between the disease status and the SNPs. The method will not only detect main effects of SNPs, but also detect interaction between multiple SNPs. The huge number of possible interactions among SNPs in the genome-scale presents a daunting task. For high-density SNPs, the problem is further complicated by the arbitrary SNP dependence. Without properly accounting for the dependence among SNPs, interaction mapping could identify a large number of “interactions” that are merely due to SNP dependence. The new method has two major advantages: 1) it constructs a sophisticated interaction graph specific to the disease; and 2) it accounts for the complex and unknown SNP dependence. Using simulation and real disease studies, I demonstrate the superior performance of the new method compared to other popular approaches. If time permits, I will further discuss a modification of the method for rare variant disease association mapping. I will demonstrate its flexibility and extendibility for more general problems.