



The University of Chicago
Department of Statistics

PHD THESIS PRESENTATION

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**Bayesian Analysis of Genetic Association Data,
Accounting for Heterogeneity**

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110 Eckhart Hall, 5734 S. University Avenue

ABSTRACT

In genetic association analysis it is often desired to analyze data from multiple potentially-heterogeneous subgroups. For example,

1. To detect modest genetic association signals that are too weak to be detected in smaller individual studies, meta-analysis of multiple studies are often required. These studies are typically carried out by different investigators, at different centers, which might be expected to exhibit heterogeneity of genetic effects.
2. In analysis of a single study, genuine environmental interactions may cause some genetic variants to have different effects on individuals in different subgroups.

In this presentation, we will discuss a general Bayesian strategy for analyzing potentially heterogeneous genetic association data. Within our proposed statistical framework, we address the problems of *WHETHER* and *HOW* a particular genetic variant acts on the phenotype of interest by Bayesian testing and model comparison in a systematic way. We propose Bayesian models, derive easy-to-compute Bayes Factors for this purpose. Various interesting properties of our Bayesian models and Bayes Factors will be discussed and demonstrated through real data examples.

Finally, we will discuss our ongoing work on mapping tissue-specific expression Quantitative Traits Loci (eQTL) using a novel hierarchical mixture model built on the groundwork laid by our Bayesian meta-analysis approaches.

Information about building access for persons with disabilities may be obtained in advance by calling Sandra Romero at 773.702-0541 or by email (sandra@galton.uchicago.edu).