

STATISTICS COLLOQUIUM

THURSDAY, FEBRUARY 21, 2013

TALK: 4:15 PM — SCIENCE CENTER RM. 705

RECEPTION: 3:50 PM — SCIENCE CENTER, 7TH FLOOR

**“Statistical Methods for Association Analysis:
Multiple Phenotypes, Multiple Variants, Multiple Subgroups”**

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ABSTRACT

Genetic association studies attempt to identify genetic variants that are associated with traits of interest, which might include clinical traits (e.g. lipid levels, heart disease, diabetes) or molecular traits (e.g. gene expression in different cell types). Most analyses of these kinds of data take a stunningly simplistic approach: analyse each genetic variant and each phenotype, one at a time. In cases where the phenotype is measured on multiple subgroups, the multiple subgroups are also usually treated in simplistic ways – either analysed separately, or together assuming that genetic effects are constant across subgroups.

Here we report on our recent attempts to develop improved statistical methods for these problems: either by considering multiple variants, multiple phenotypes, or by allowing for heterogeneity among subgroups. Methodological innovations discussed include methods for large-scale sparse regression, and analysis of multiple phenotypes using ideas from graphical models.