# COLLOQUIUM

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## Detecting and Comprehending Marker-Set Association for Common and Rare Variants

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A405 Wells Hall
10:20 a.m. - 11:10 a.m.
Refreshments: 10:00 a.m.

### Abstract

Modern association analyses of complex traits, such as GWAS or sequencing studies, demand statistical tools that are capable of detecting small effects of common and rare variants, modeling complex interaction effects, and yet are computationally feasible. In this work, we introduce a set of approaches for detecting marker-set association and comprehending the signals identified. To detect the joint effect for a group of loci, we propose a gene-trait similarity regression, which assesses association by regressing trait similarities for pairs of individuals on their genetic similarities. This method uses genetic similarity to aggregate information from multiple loci, and integrates adaptive weights that depend on allele frequencies to accommodate common and rare variants. Collapsing information at the similarity level instead of the genotype level avoids canceling signals with opposite etiological effects, is applicable to any class of genetic variants without having to dichotomize the allele types, and can capture non-additive effects among markers. To comprehend the signal identified at marker-set level, we present a penalized regression approach to evaluate the haplotype effects and haplotype-environment interactions of the set. This method specifies an L1 penalty on the pairwise difference of the haplotype-by-environment effects, simultaneously carries out the effect estimation and effect comparison, and yields desired personalized output. We demonstrate the utility of the methods by simulations and applications in pharmacogenetic studies.

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