Speaker: Po-Ru Loh, Harvard Medical

Title: Fast linear mixed model algorithms for association testing and heritability analysis

Abstract:
The widespread availability of large-scale genetic data sets has engendered a revolution in quantitative genetics. In particular, genome-wide association studies (GWAS) have helped illuminate the heritability of common diseases and identify clinically relevant disease genes and pathways. Yet, at the same time, GWAS have been unsuccessful thus far at finding loci explaining the bulk of known heritability, which remains hidden in rare alleles or variants with very small effects. Continued GWAS discovery will require both the statistical power of very large data sets and advanced methods for analyzing such data. Linear mixed models are the current state of the art approach to modeling GWAS data. However, mixed model analysis is computationally challenging, and existing methods are also limited by suboptimal modeling assumptions. In this talk, I will present a new, much faster algorithm (BOLT-LMM) for performing mixed model computations, which achieves orders-of-magnitude gains in computational speed and also increase statistical power of association analyses. Additionally, I will describe current work applying an extension of this technique to investigate the genetic architecture of schizophrenia as well as several common diseases phenotyped in the 60,000-sample Genetic Epidemiology Research on Aging (GERA) data set.