COLLOQUIUM

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Mixed Model/Score Test Based Methods
for Association Studies of Binary Traits
with Risk Covariates in Populations of Related Individuals

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10:20 a.m. - 11:10 a.m.
Refreshments: 10:00 a.m.

Abstract

Statistical approaches based on mixed models and score tests are increasingly popular for studying the genetic determinants of diseases, such as asthma or hypertension, with non-genetic covariates in populations with family structures or cryptic relatedness. However, there are few such techniques explicitly designed for binary traits. Furthermore, with increasing emphasis on analyzing collections of genetic markers corresponding to individual genes (gene enrichment) and gene x environment (GxE) or gene x gene (GxG) interactions, it is desirable to extend the frameworks proposed for studies of individual markers into those capable of addressing a wider range of applied analyses.

In this talk, we discuss our efforts to develop a system for marker-wise genome-wide association studies (GWAS) of binary traits in populations of related individuals with risk covariates, and expand that system into one that can perform a range of other analyses. We begin by introducing GLOGS (Genome-wide LOGistic mixed model / Score test) a parallelized, efficient and powerful system for such GWAS, and show how it may be applied to marker-wise studies of hypertension in the Hutterites, a population related through a 13-generation pedigree. With these results as context, we describe the development of GLOMS (Genome-wide LOgistic mixed model / Multivariate Score test), a related system that can, in an integrated manner, perform gene enrichment, GxE and GxG studies.

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