COLLOQUIUM

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Statistical Approaches for High-Dimensional Family-Based Genetic Association Studies

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

Abstract

Although family studies were the basis for genetic research before the advent of modern molecular markers, they have been much less developed for association studies of complex diseases using high-dimensional data. Family studies offer many ideal features for large-scale genetic research. For instance, they provide robust protection against confounding bias when dealing with samples from multiple ethnic groups (i.e., population stratification). In this talk, I will discuss two statistical approaches for family-based genetic association studies, and will illustrate these approaches using both simulation studies and empirical data applications. The proposed approaches can be used for family-based association studies on a large ensemble of genetic variants (e.g., 600K genetic markers), taking into account the issues of population stratification and phenotypic heterogeneity.

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