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Department of Statistics and Probability

COLLOQUIUM

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Adjustment for Population Stratification in Genetic Association Analysis with Sequencing Data

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10:20am – 11:10am
Refreshments 10:00am
C405 Wells Hall

Abstract

Several analysis methods have been established as simple and effective approaches to adjusting for population stratification in association analysis of common variants (CVs) for unrelated samples, while it is less clear how they would perform in analysis of low-frequency variants (LFVs) or rare variants (RVs). Furthermore, with next-generation sequencing data, it is unknown whether these methods should be applied to CVs, LFVs, RVs, or their combinations.

In this study, we use real sequencing data to explore these issues.

This is joint work with Yiwei Zhang and Xiaotong Shen.

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