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*Genetic Association Analysis in Admixed Populations*

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**ABSTRACT**

Admixed populations offer a unique opportunity for mapping diseases that have large disease allele frequency differences between ancestral populations. However, association analysis in such populations is challenging because population stratification may lead to association with loci unlinked to the disease locus. In this talk, I will show that local ancestry at a genetic locus may confound with genetic association signal and ignoring it can lead to spurious association. I will demonstrate theoretically that adjustment for local ancestry at the test marker is sufficient to remove the spurious association regardless of the mechanism of population stratification. I will further present statistical methods to test for genetic association for both common and rare variants. Our results suggest that it is important to appropriately control for population stratification induced by local ancestry difference in genetic association analysis in admixed populations.

**4:15 p.m. Tuesday, April 23, 2013**

## **LEPH 115, 60 College Street**