

# **Efficient Multipoint Analysis of Association Studies**

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## **Abstract:**

This talk will describe a new statistical approach to the analysis of association studies. The approach is particularly designed to exploit the availability of dense SNP data on a "panel" of unrelated individuals who are not part of the study group (eg HapMap data, or resequencing data in a candidate region of interest), to allow markers that are not typed in the study group to be tested for association with the phenotype. Specifically, we use patterns of correlation ("Linkage Disequilibrium") in the dense marker set in the panel, together with genotype data on a less dense marker set in the study group, to estimate the genotype data in the study group at the dense set of markers, and then assess association between the phenotype and these estimated genotypes. Compared with standard single-SNP tests, the approach results in an increase in power to detect association, even in cases where the causal variant is typed, with the greatest gain being when multiple functional variants are present in the region of study. In addition, the approach also provides more interpretable explanations for observed associations, including assessing, for each SNP, the strength of the evidence that it (rather than another correlated SNP) has a functional effect on the phenotype.