

Mapping Genes for Complex Human Diseases with Applications to Type 2  
Diabetes

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**Abstract:**

In this talk, I will discuss efficient design and analysis methods for association studies of complex human diseases. I will describe the value of using familial cases and prior linkage information in the selection of cases in a case-control association study, and methods to assess whether an associated variant may explain (in part) an observed linkage signal. I will illustrate these methods with results on the genetics of type 2 diabetes from the Finland-United States Investigation of NIDDM genetics (FUSION) study.