# Case-Control Haplotype-Disease Association Analysis Allowing for Haplotype-Environment Interaction and Correlation

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## Abstract

Detecting the gene-disease association has now been based increasingly on haplotypes, which are specific combinations of genetic markers on a short interval along the chromosomes. Also, for the public health purpose, the study of the gene-environment (G-E) interaction has attracted increasing attentions. In this talk, I will introduce a novel modeling framework for haplotype-based case-control association studies, which facilitates assessing the G-E interaction, and allows environmental variables to be related with haplotypes. A semiparametric estimation procedure is proposed for estimating the gene-disease and haplotype-environment association/interaction parameters, and an EM algorithm is used to handle the ambiguity of genotype data. The proposed method is illustrated with an analysis of the association between colorectal adenoma, NAT-2 haplotype, and smoking.