Test of Parent-of-Origin Effects in Family Studies

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Abstract

Imprinting is an epigenetic phenomenon where the same genetic variants have unequal transcriptions and thus contribute differently to a trait depending on their parent of origin. This mechanism has been found to affect a variety of human disorders. Although various methods for testing parent-of-origin effects have been proposed in classic linkage analysis settings, only a few are available for recent single-nucleotide polymorphism (SNP)–disease association analysis and they are usually restricted to small families and particular study designs. In this presentation, we will talk about newly proposed methods to handle this problem in family studies. The focus will be given to the most powerful maximum likelihood approach that incorporates inter-marker linkage-disequilibrium (LD) information in genome-wide association studies. The advantages of the method will be demonstrated through extensive simulation studies with various allele frequencies, LD structures, family sizes, and missing schemes. The optimal study design will be discussed in terms of family size and number of families. An application to a real genetic study of insulin and glucose will be used for illustration.

***Keywords**:* GWAS; Haplotype method; Imprinting; Statistical genetics.