The Chinese University of Hong Kong
Department of Statistics

Seminar

Single-Marker and Haplotype Analyses for Detecting Parent-of-Origin Effects

By

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Abstract

Genomic imprinting is an important epigenetic factor in complex traits study. Some statistical methods may be ineffective or fail to detect linkage or association for an imprinted gene. Genomic imprinting is generally examined through testing for parent-of-origin effects of alleles prior to fine mapping. For families with both parents, the parental-asymmetry test (PAT) and its haplotype version HAP-PAT are simple and powerful in detecting parent-of-origin effects. In this talk, we focused on the following methods in the frameworks of single-marker and haplotype analyses for detection of parent-of-origin effects based on family and pedigree data: (1) 1-PAT for families with only one parent, (2) C-PAT for the combined data of families with both parents and those with one parent, (3) PPAT and MCPPAT for extended pedigrees with missing genotypes, and (4) HAP-1-PAT and HAP-C-PAT, which are the haplotype versions of 1-PAT and C-PAT, respectively.

The performance of all the methods was verified by simulation studies. The results showed that (1) using the additional information from families with one parent in the analysis greatly improves the power of the tests, compared to that based only on families with both parents, (2) utilizing all affected children in each family will lead to a higher power of the tests than when only one affected child from each family is selected, (3) more power will be gained by using information from extended pedigrees than randomly selecting one two-generation nuclear family from each pedigree, (4) haplotype analysis is advantageous over single-marker analysis. Also, the PPAT and MCPPAT were applied to rheumatoid arthritis data and we found three significant markers showing the maternal imprinting effect.

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