Region-Based Interaction Detection in Genome-Wide Case-Control Studies

by

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Abstract

Genome-wide association study (GWAS) has served as an important tool to investigate the relationship between genomic variants and diseases. Current results from GWAS mainly focus on single nucleotide polymorphisms (SNPs). It’s well known that genetic variants work synergistically, and interactions could play an important role in disease pathways. Researchers have developed various strategies, like BOOST, to detect genomic interactions. However, conventional interaction detection methods for case-control studies are mostly based on SNP-SNP interactions. Although a SNP achieves the finest resolution of human genome, it’s not necessarily the smallest functional unit for complex phenotypes. Region-based strategies have proved successful in studies aimed at marginal effects. In this thesis, we developed a novel region-region interaction detection method named RRIntCC (region-region interaction detection for case-control studies) for case-control studies. RRIntCC uses the correlations between individual SNP-SNP interactions based on linkage disequilibrium (LD) contrast test. The source code and sample data of RRIntCC are available at http://bioinformatics.ust.hk/RRIntCC.html. We performed extensive simulations, with empirical linkage disequilibrium patterns and allele frequencies, to show that our method can achieve higher statistical power than conventional SNP-SNP based methods while maintaining correct type-I-error rates. When applied to two real datasets on myocardial infarction and renal complications in T2D (Type-2-diabetes) patients, RRIntCC was able to find several significant region pairs, while BOOST failed to identify any significant results.

Date: 4 Jun 2018 (Monday)
Time: 10:00 am
Venue: Room 5560 (Lift 27-28)

Examination Committee:
Prof. Hong Xue (Chair)
Prof. Weichuan Yu (Supervisor)
Prof. Jiguang Wang

All are welcome!