Multiple-Variant Association Testing for Quantitative Traits with Application to Dental Caries GWAS Data

Xiaowei Wu

Virginia Tech

Abstract: High-throughput sequencing has often been used in pedigree-based studies to identify genetic risk factors associated with complex traits. The genotype data in such studies exhibit complex correlations attributed to both familial relation and linkage disequilibrium. Accounting for such genotypic correlations can improve power for assessing the contribution of multiple genomic loci. In this study, we propose PC-ABT, a novel principal-component-based adaptive-weight burden test for gene-based association mapping of quantitative traits. This test is able to make efficient use of complex genotypic correlation information, and hence is generally more powerful than other burden tests that allow related individuals. We illustrate the application of PC-ABT to the Gene Environment Association Studies (GENEVA) data to identify genes associated with dental caries. Our proposed method and its application to human dental caries GWAS data provide valuable information to guide the implementation of newer preventive or diagnostic measures and novel therapeutic approaches to dental caries, with a long-term goal to promote precise and personalized oral health care.

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refreshments at 3:30