“Parsing the Effects of Individual SNPs in Candidate Genes with Family Data”

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Abstract:

When there are multiple linked markers in a genetic region which show a significant association with a trait, it is useful to determine whether one or more SNPs can explain this association. To test this hypothesis, one can test the effect of a set of markers conditional on another set of markers. Several previous approaches to this problem have been likelihood based, for particular family structure, or not completely robust to population stratification. We propose two types of tests in a family-based framework that are both applicable to arbitrary family structures and completely robust to population stratification. We first propose an extension of the FBAT main genetic effect test that is completely model-free. Then, for power issues, we introduce model-based tests that do not depend on the error structure of the model for continuous and dichotomous traits. We demonstrate our methodology in the IL10 gene.