Computational and Applied Mathematics 
& Statistics Student Seminar

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Association Analysis of Phenotypes Jointly Influenced by a Pair of Organisms

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ABSTRACT

The virulence of infectious diseases is usually affected by a combination of a host and at least one pathogen organism. Previous experiments have divulged that combining genetic information from different organisms has enabled the identification of more relevant genetic variants than just individually performing an association analysis on each organism. Two main issues may arise when testing for interaction effects between the genotypes of different organisms on a phenotypic trait. First, the presence of any interaction effect between one of the genotypes being tested and some unaccounted factor may lead to heteroskedasticity in the trait, which in turn leads to overinflated type I error rates, so some method to account for this heteroskedasticity is required. Then, the fact that the trait is held fixed while the genotypes vary across different interaction tests may often lead to tangible departures from the known null distribution of the interaction test statistic. We present diagnostic tools to detect such departures and a method to correct them under a wide range of scenarios. We demonstrate the applicability of our methodology on data from a hepatitis C clinical trial and simulated data.