

**A joint regression analysis for genetic association studies
with outcome stratified samples**

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Genetic association studies in practice often involve multiple traits resulting from a common disease mechanism, and samples for such studies are often stratified based on some trait outcomes. In such situations, statistical methods using only one of these traits may be inadequate and lead to under-powered tests for detecting genetic associations. We propose in this paper an estimation and testing procedure for evaluating the shared-association of a genetic marker on the joint distribution of multiple traits of a common disease. Specifically, we assume that the disease mechanism involves both quantitative and qualitative traits, and our samples could be stratified based on one of the qualitative traits. Through a joint likelihood function, we derive a class of estimators and test statistics for evaluating the shared genetic association on both the quantitative and qualitative traits. Our simulation study shows that the joint likelihood test procedure is potentially more powerful than association tests based on univariate traits. Application of our proposed procedure is demonstrated through the rheumatoid arthritis data provided by the Genetic Analysis Workshop 16 (GAW16).

Key Words: Genetic association study, likelihood ratio test, joint regression model, multiple traits, stratified sample, splines