A new modeling framework for multi-trait mapping of binary and quantitative phenotypes

We are working on a problem of joint mapping of small numbers of traits consisting of both binary and quantitative phenotypes, with incorporation of covariates and population structure. One solution to this problem is to use existing LMM methods for multiple phenotypes. However, previous work has found that using LMM to analyze binary traits suffers from substantial power loss if covariate effects are important. We propose a new model for multi-trait mapping of a combination of binary and quantitative phenotypes, which is based on a mixed-effects quasi-likelihood framework. It can incorporate covariates and population structure information and it captures the dichotomous nature of the binary traits. We plan to test for association based on a retrospective approach, which is robust to misspecification of the phenotype model. Parameter estimation for the binary trait(s) in this setting presents additional challenges beyond those for the quantitative trait case. As part of estimating the correlation matrix, we explore a recently proposed parametrization which enforces the positive (semi) definiteness and which can be viewed as a multivariate generalization of Fisher’s Z-transformation of a single correlation.

Yi Wei, PhD candidate

We are working on a problem of joint mapping of small numbers of traits consisting of both binary and quantitative phenotypes, with incorporation of covariates and population structure. One solution to this problem is to use existing LMM methods for multiple phenotypes. However, previous work has found that using LMM to analyze binary traits suffers from substantial power loss if covariate effects are important. We propose a new model for multi-trait mapping of a combination of binary and quantitative phenotypes, which is based on a mixed-effects quasi-likelihood framework. It can incorporate covariates and population structure information and it captures the dichotomous nature of the binary traits. We plan to test for association based on a retrospective approach, which is robust to misspecification of the phenotype model. Parameter estimation for the binary trait(s) in this setting presents additional challenges beyond those for the quantitative trait case. As part of estimating the correlation matrix, we explore a recently proposed parametrization which enforces the positive (semi) definiteness and which can be viewed as a multivariate generalization of Fisher’s Z-transformation of a single correlation.