

**Abstract:**

Multiple correlated traits/phenotypes are often collected in genetic association studies and they may share a common genetic mechanism. Joint analysis of correlated phenotypes has well known advantages over one-at-a-time analysis including gain in power and better understanding of genetic etiology. However, when the phenotypes are of discordant types such as binary and continuous, the joint modeling is more challenging. Another research area of current interest is discovery of rare genetic variants. Currently there is no method available for detecting association of rare (or common) haplotypes with multiple discordant phenotypes jointly. Our goal is to fill this gap specifically for two discordant phenotypes. We consider a rare haplotype association method for a binary phenotype Logistic Bayesian LASSO (univariate LBL) and its extension for two correlated binary phenotypes (bivariate LBL-2B). Under this framework, we propose a haplotype association test with binary and continuous phenotypes jointly (bivariate LBL-BC). Specifically, we use a latent variable to induce correlation between the two phenotypes. We carry out extensive simulations to investigate bivariate LBL-BC and compare it with univariate LBL and bivariate LBL-2B. In most settings, bivariate LBL-BC performs the best. In only two situations, bivariate LBL-BC has similar performance --- when the two phenotypes are (1) weakly or not correlated and the target haplotype affects the binary phenotype only and (2) strongly positively correlated and the target haplotype affects both phenotypes in positive direction. Finally, we apply the method to a dataset on lung cancer and nicotine dependence and detect several haplotypes including a rare one.