

BAYESIAN MULTIPLE REGRESSION METHODS FOR ANALYZING LONGITUDINAL GENETIC DATA

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In genetics, the quantitative trait loci (QTL) mapping aims to identify some particular regions of DNA sequences, which are associated with the phenotype traits. Linear regression is a widely used statistical technique to build the relation between phenotype and genotype data. Many quantitative traits such as height and weight are dynamic in nature, meaning that they are changing or growing during the developmental process of life. When some repeated phenotype measurements over time within each individual are available, it is often beneficial to perform a longitudinal analysis by simultaneously analyzing the data at multiple time points in one model compared to the procedure by separately analyzing the data at each single time point (Wu and Lin 2006). We propose two possible Bayesian multiple regression methods for analyzing longitudinal traits, a two-step multilevel model approach and a linear mixed effects model approach. In the two-step approach, the phenotypic temporal trend of each individual is first estimated and the corresponding parameters are considered as the latent traits, and second the genetic effects on those latent traits are evaluated. While in a mixed effect model, the temporal trends and effects of markers are simultaneously estimated. In both methods, a slab and spike prior is assigned to the coefficient of each marker for variable selection, and an efficient Gibbs sampling method is used for computation. A Bayesian false discovery rate based decision rule is further used for formally judging QTLs. We evaluate and compare the performances of these two approaches on both real and simulation data sets.

References:

- Wu, R., M. Lin (2006). Functional mapping-how to map and study the genetic architecture of dynamical complex traits *Nat. Revs. Genet.* 7, 229–237.