A Bayesian Method for Gene-Gene and Gene-Environment Interactions in Pharmacogenomics

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In the studies of pharmacogenomics, it is essential to address gene-gene and gene-environment interactions for describing the complex traits involving pharmacokinetic and pharmacodynamic mechanisms. In this study, we proposed a Bayesian method for detecting gene-gene and gene-environment interactions in pharmacogenomics. We employed the framework of variable selection and a Markov Chain Monte Carlo (MCMC) based technique to identify significant interactions. The proposed approach was applied to the pharmacogenomics study of interferon treatment for persons with chronic hepatitis C (CHC). Our studies show that the proposed Bayesian algorithm is very effective for deriving models for pharmacogenomics studies and for providing the information of gene-gene and gene-environment interactions.

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