

Comparison of Bayesian variable selection methods for genetic data from different populations

Jing-Lin Cheng* (鄭敬霖) and Miao-Yu Tsai (蔡秒玉)
Institute of Statistics and Information Science,
National Changhua University of Education

Abstract

Many methodologies for variable or model selection are available in statistical researches. In mixed-effects models, a fully Bayesian variable selection allow a flexible method for incorporation of prior knowledge into the selection of the variables to select the fixed and random components simultaneously. In this talk, we focus on comparing two Bayesian variable selection methods, stochastic search variable selection (SSVS) and Holmes and Held algorithm (H-H algorithm) that is a special case of the reversible jump Markov chain Monte Carlo (RJMCMC) for logistic mixed models. Two genetic case-control data from different populations are used to compare the performance of the two Bayesian variable selection methods by assessing the sensitivity of posterior probabilities to prior specifications and the efficiency of the MCMC algorithms. The results indicate that the H-H algorithm is a stable and efficient selection tool in identifying true candidate genes and gene-gene interactions after accounting for the uncertainty in population structures.

Keywords: logistic mixed model, Bayesian variable selection, stochastic search variable selection, reversible jump Markov chain Monte Carlo