

A score-based two-stage Bayesian network method for detecting causal SNPs

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Abstract: With the development of genome-wide association studies, how to gain more meaningful information from the volumes of data has become an issue of common concern, especially when dealing with the problems like identifying the epistatic interactions associated with complex diseases. The huge amount of possible combinations of all SNPs makes the task difficult. Thus, developing powerful and robust methods for detecting epistatic interactions is of great importance. In this paper, we propose a score-based two-stage Bayesian network method to identify genomewide epistatic interactions in a case-control design. This method combines the ideas of constraint-based methods and score-and-search methods to learn the structure of the disease-centred local Bayesian network. We compare our new algorithm with several common epistasis interactions detecting methods in simulation studies. The results show that our method has a good accuracy and stability. Besides, its successful application on SMRI dataset suggests that our algorithm has the ability to handle real GWAS data.