Bayesian Neural Networks for Genetic Association Studies of Complex Phenotypes
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The information return on current generation GWAS studies is diminishing which has lead to several hypotheses to account for this so-called “missing heritability”. One hypothesis suggests the missing heritability may be due to complex gene-gene interaction structures in which several loci have small and potentially non-additive contributions to the phenotype. Several machine learning methods including random forests, support vector machines, multifactor dimensionality reduction (MDR) and grammatically evolved neural networks have had varying degrees of success in modeling phenotypes with complex and unknown genetic interactions. In this work we outline an extension to the standard neural network model, a Bayesian neural network, which allows for simultaneous modeling of arbitrarily complex interaction structures while identifying which loci are involved in the core genetic etiology. We provide a brief overview of existing work in this field, an introduction to Bayesian neural networks, computational considerations, and some preliminary results demonstrating the approach.