

Public Abstract

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Title:Nonlocal Priors for Bayesian Variable Selection in Generalized Linear Models and Generalized Linear Mixed Models and Their Applications in Biology Data

A crucial problem in building a generalized linear model (GLM) or a generalized linear mixed model (GLMM) is to identify which subset of predictors should be included into the model. Hence, the main thrust of this dissertation is aimed to discuss and showcase our promising Bayesian methods that circumvent this problem in both GLMs and GLMMs.

In the first part of the dissertation, we study the hyper-g prior based Bayesian variable selection procedure for generalized linear models. The integrals necessary for the computation of this Bayes factor are performed with Laplace approximation and Gaussian quadrature. We show that, under certain regularity conditions, the resulting Bayes factor is consistent. Furthermore, a simulation study confirms our theoretical results. Finally, we illustrate this model selection procedure with an application to a real ecological dataset.

In the second part of the dissertation, we propose two novel scale mixtures of nonlocal priors (SMNP) for variable selection in generalized linear models (GLMs). We develop a Laplace integration procedure to compute posterior model probabilities. Further, we show that under certain regularity conditions the proposed methods are variable selection consistent. We also show that, when compared to local priors, our SMNP priors lead to faster accumulation of evidence in favor of a true null hypothesis. Simulation studies indicate that our proposed SMNP-based methods select true models with higher success rates than other existing Bayesian methods. Finally, we illustrate the application of our SMNP-based methods with the analyses of two real datasets.

In the last part of the dissertation, we develop nonlocal prior for variable selection in generalized linear mixed models (GLMM) and apply the proposed nonlocal prior and its inference procedure for the whole genome allelic imbalance detection. Allelic imbalance occurs when one of a gene's two parental alleles is expressed unequally. We thus perform the allelic imbalance detection in terms of model selection using nonlocal prior for the parameter of interest. Through the simulation study as well as real data analysis, we demonstrate the great potential of our proposed nonlocal prior variable selection procedure.