

Original Article

Survival prediction and variable selection with simultaneous shrinkage and grouping priors

Kyu Ha Lee , Sounak Chakraborty, Jianguo Sun

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Abstract

The presented work is motivated by the need of reliably estimating and predicting the survival rates for individuals diagnosed with cancer, when gene expression profiles are available for identifying molecular risks factors for cancer. The regression analysis of such data is challenged by three characteristics of data: (i) time - to - event outcome, (ii) high - dimensional covariate space, and (iii) a group structure of genes. One strategy to simultaneously deal with all three of the aforementioned challenges is to build a penalized regression model using special penalty functions such as elastic net, fused lasso, and group lasso. To our knowledge, existing methods are sparse or non - existent, however, when a Bayesian estimation/inference is the goal for the penalized regression models. In this article, we propose a Bayesian semi - parametric framework for the regression analysis of gene expression data with survival outcomes. Our proposed Bayesian methods permit researchers to take advantage of numerous benefits including the ability to incorporate substantive prior information, the straightforward and automated quantification of uncertainty in prediction, and the prescriptive nature of computation. The performance of our proposed models for variable selection and prediction is thoroughly investigated through simulation studies, where we consider four scenarios based on different underlying group structures of covariates and covariate effects. The results generally show the satisfactory variable selection capability and predictability of our methods. Finally, we apply our proposed framework to three different gene expression data sets. We developed an efficient Markov chain Monte Carlo algorithm for the implementation of our proposed framework and provided an easy - to - use R package.

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