Review 3 responses

We thank the reviewer for the time spent reviewing our submission. We have corrected several typos and grammatical mistakes throughout the manuscript. In what follows, we address concerns about novelty of the work, numerical experiments and code availability.

Responses

1. We first address the concerns about novelty and originality of the work. Although many of the techniques are available from the existing work (*e.g.* methods for estimating the marginal likelihoods), incorporating these techniques with the PARNI proposal and applying them to the generalised linear models and survival models are not trivial and straightforward. The main difficulty of extending PARNI to the these models is the lack of analytical expressions for the marginal likelihood and the Rao-Blackwellised estimate of the Posterior Inclusion Probabilities (PIP's). Section 4.2 describes a novel adaptive ALA informed proposal which produces efficient and accurate estimate of the marginal likelihood by exploiting the previous draws of the PARNI algorithm. Figure 1 illustrates the substantial possible improvements of the adaptive ALA informed proposal compared to the LA/ALA informed proposals. The adaptive ALA informed proposal combines the benefits from both LA and ALA informed proposals. Section 4.3 introduces a replacement of the Rao-Blackwellised estimates of the PIP's for the algorithm tuning parameters. The novel scheme provides increased reliability in adapting the tuning parameters, in the sense of avoiding poor exploration of the space which can only occur if simple ergodic averages are used in the PARNI scheme. All these new components are necessary for the PARNI proposal to become a computationally efficient tool, making it available for the variable selection community in generalised linear models and survival models. In addition, we provide valuable insights that can guide future research aimed at improving the performance of the PARNI proposal in some challenging problems, such as "large-n" data, or extending PARNI to a broader range of variable selection problems.

2. We address the concerns about implementing data-augmentation method in `Rcpp` environment which leads to unfair comparisons between the PARNI and add-delete-swap proposals. Both the PARNI-DA and ADS-DA proposals require the `pgdraw` package (coded in `Rcpp`) to sample the Pólya-gamma auxiliary variables from their posterior distributions (which also follow the Pólya-gamma distributions) in every MCMC iteration. The processes of model proposal and MH acceptance step of PARNI-DA and ADS-DA remains implemented in R. Therefore, the use of `pgdraw` does not lead to an unfair comparison between PARNI-DA and ADS-DA. It could potentially lead to biased comparisons between data-augmentation and correlated-pseudo marginal methods. So it is more appropriate to compare PARNI-CPM with ADS-CPM for the results in Table 2. We have an alternative R implementation of the Pólya-gamma sampler as described in Supplement S.1 of Polson et al. (2013) but it results in an increased CPU time that is at least 10 times longer than `pgdraw` when applied to the SLE data-sets.

3. You also raise concerns about the comparison of the mixing time for PARNI and for add-delete-swap proposals in real data-sets. In this study, we use the average MSE as a metric to measure the computational efficiencies of different MCMC algorithms. The average MSE is more comprehensive compared to conventional metrics like the effective sample size (ESS). The key reason is that the MSE can be decomposed into bias and variance of the estimate. While bias measures the speed of attaining to the true value (convergence), the variance reflects the mixing behaviour like ESS. Therefore, while running MCMC schemes for the same amount of CPU time, a lower MSE indicates faster mixing times and a greater computational efficiency. In support of our claim,

we provide additional evidence in Figure 1 to showcase the rapid mixing of the PARNI proposal in comparison to the ADS proposal. Figure 1 presents the trace-plots of log posterior model probability and the bar-plots of CPU time for the PARNI and ADS proposals. The PARNI proposal is more computationally expensive than the ADS proposal, but the chains obtained from the PARNI proposal mix better than the ones obtained from ADS. Notably, the PARNI proposal have attained convergence. It is capable of proposing and accepting large jumps and exploring a wider range of models including models with lower posterior model probabilities. Coupled with Table 4 in the manuscript, this offers clear evidence that the PARNI proposal exhibits faster mixing time and better computational efficiency than the ADS proposal in most of the real data-sets.

4. To address the concern about code availability, we uploaded the R codes of PARNI and add-delete-swap proposals to a GitHub repository (`https://github.com/XitongLiang/The-PARNI-scheme`). The codes are now publicly available for replicating the experiments described in the paper or applying the PARNI proposal to other research topics. We have updated the manuscript accordingly to include a link to the GitHub repository.

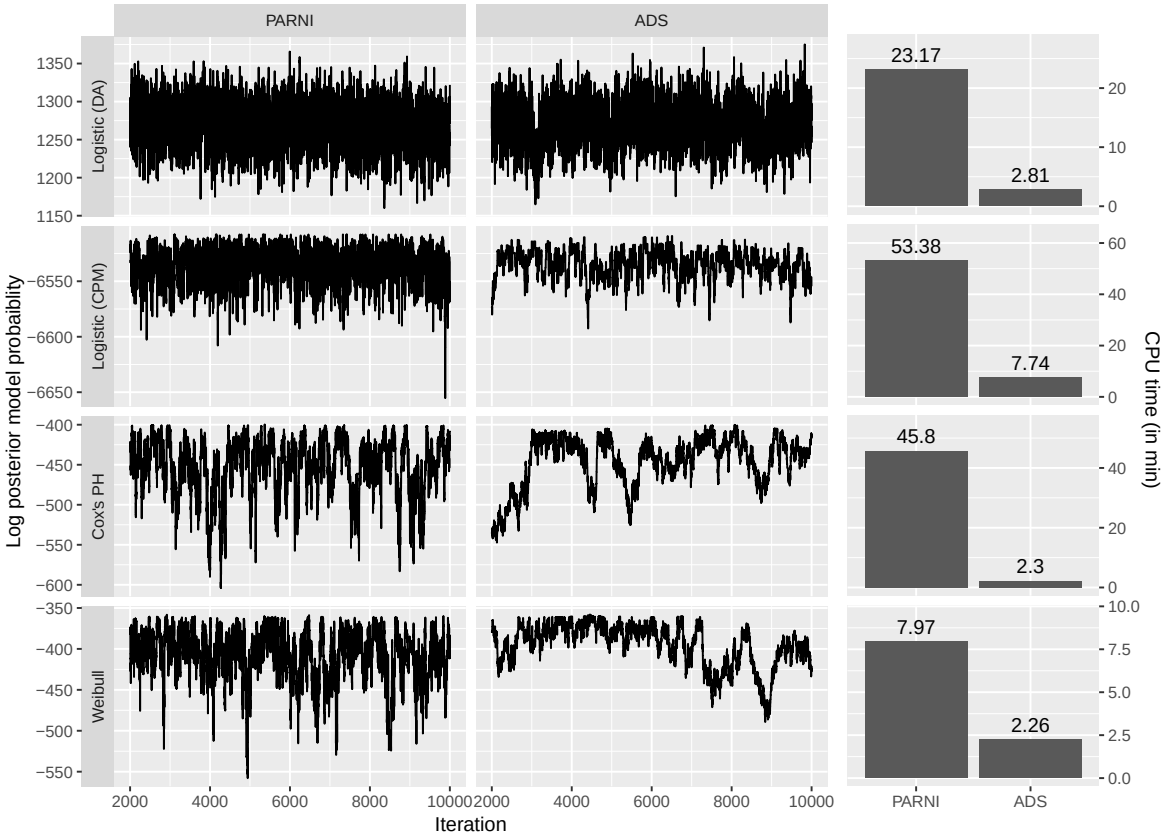


Figure 1: Left two columns: Trace-plots of the log posterior model probability of the PARNI and ADS proposals on two real data-sets (SLE Chromosome 1 for logistic model and NKI for the Cox PH and Weibull models). Right column: The bar-plot of the CPU time of the PARNI and ADS proposals for simulating 10,000 samples on two real data-sets.

References

Polson, N. G., Scott, J. G. and Windle, J. (2013), 'Bayesian inference for logistic models using pólya–gamma latent variables', *Journal of the American Statistical Association* **108**(504), 1339–1349.