



May 20, 2021

Dear Professor Hurley,

We thank you very much for giving us the opportunity to resubmit our revised paper, “BayesSPsurv: An R Package to Estimate Bayesian (Spatial) Split-Population Survival Models” (**R Journal 2021-29**). Per your request, we have endeavored to implement all revisions requested by the reviewers and resubmit our materials before May 28, 2021. To this end, we have submitted a zipped folder that contains the relevant files to the journal’s submission site. The folder specifically includes modified RJwrapper.pdf, RJwrapper.tex, file with the content to produce our revised manuscript in bolte-et-al-spatSP.tex, all references in bolte-et-al-spatSP.bib, all figures in .png or .pdf format, and an R script to reproduce all results and figures in the manuscript. We also include a detailed memo that describes our point-by-point response to each comment raised by both the reviewers.

Our paper, R (and C++) code, and the package’s functionality have improved substantially after incorporating the reviewers’ feedback. We have addressed all comments raised by the reviewers regarding the presentation of some of our results, our MCMC sampling scheme, and enhancements to our R package. We incorporated all code revisions in our updated **BayesSPsurv** package (Version 0.1.3) that was uploaded and accepted to CRAN on May 14<sup>th</sup>, 2021 (<https://cran.r-project.org/web/packages/BayesSPsurv/index.html>). The latest version of the code is also publicly available on its GitHub repository (<https://github.com/Nicolas-Schmidt/BayesSPsurv>). In brief, the revisions we made in response to the reviewers’ suggestions are as follows:

- Both reviewers suggest adding features that permit users to monitor completion of MCMC sampling and reporting the running time for all the presented models.

We incorporated a progress bar for each of the three models in our updated R package, which allows the user to track the completeness of the computation in real time. We also reported the run times for the application examples.

- Reviewer 1 requested that we mention that users can potentially estimate our presented models using STAN in the future, while Reviewer 2 noted that we should comment on shared frailty terms as an avenue for future research.

We mention in our paper’s conclusion that STAN, which employs the Hamiltonian Monte Carlo algorithm for MCMC estimation, would be useful for estimation as we develop the model in future work (**page 16**). We also rationalize our current focus on individual frailties and discuss when shared frailty terms should be employed, and propose a procedure for estimating them (**pages 3 and 16**).

- Reviewer 1 suggested that we introduce separate proposal variance steps for parameters W and V as well as assign Metropolis-Hastings proposal steps for these parameters in our Spatial split-population survival model.

We incorporated the reviewer’s suggestion in two ways. First, our updated code includes separate proposal variance variables (prop.varW and prop.varV) for the parameters W and V in the functions spatialSPsurv() and exchangeSPsurv() and assigns separate proposal steps to estimate these parameters to optimize the Metropolis-Hastings acceptance rates. Second, we emphasize in our revised manuscript (i) the assignment of separate

proposal variance steps for sampling  $W$  and  $V$  for estimating the Spatial SP survival model (**page 6**), and (ii) the use of `prop-varW` and `Prop.varV` in our MCMC routine (**page 9**). These updates are illustrated in the revised application section (see **pages 9-14**).

- Reviewer 2 asked us to comment on how users might utilize multiple chains and examine multi-chain diagnostics.

We addressed this point by updating the available arguments for each of the SP survival model functions by including an option for users to specify an initial value for various parameters of interest. Users can then estimate multiple chains with different starting values and examine convergence diagnostics. We have included this update to the new version of the package, now available on CRAN. Additionally, we present a routine for generating multiple chains (with different starting values) in parallel, and then plotting them and obtaining Gelman-Rubin diagnostics using functions in the **coda** package. Due to space constraints, we present the results obtained from this routine in the revised manuscript (**pages 11-13**), while the routine itself is available in the package's public GitHub repository.

Following your suggestion, we employed the strategy described at <http://matt.might.net/articles/peer-review-rebuttals/> to address all the points raised by the reviewers and prepare our memo. This source was extremely helpful for guiding our revisions. Please do not hesitate to get in touch with us if you need more information regarding our paper and updated R package. We look forward to hearing from you.

With best wishes,

Brandon L. Bolte