August 24, 2014

Editor in Chief. *Systematic Biology*
Department of Zoology
Southern Illinois University
Carbondale, IL 62901 USA

Dear Dr. Anderson,

Please find enclosed our manuscript '*Bayesian Analysis of Partitioned Data*' coauthored by Jim McGuire, Fredrik Ronquist, John Huelsenbeck, and myself. Briefly, the manuscript describes a new Bayesian approach for estimating phylogeny from partitioned sequence alignments under a Dirichlep process prior (DPP) model. This approach is in the spirit of the conventional 'mixed-model' approach for accommodating variation in the substitution process across an alignment, were the biologist first defines a candidate 'partition scheme' (that specifies the number of different substitution models and the assignment of data elements to those models), and then estimates the fit of that mixed model to the dataset by estimating the marginal likelihood, and finally using Bayes factors to chose among candidate mixed-models. Our new approach, however, allows both the number of process partitions and the assignment of data elements (nucleotide sites or sets of sites) to those process partitions as random variables under the DPP model. Accordingly, the phylogeny is estimated while effectively integrating over all possible partition schemes.

This manuscript has a long history: it was previously submitted to *Systematic Biology* (USYB-2010-093), and was accepted with major revisions prior under the previous EIC, Ron DeBry. The revisions included a comprehensive simulation study to validate the statistical behavior of the method. This simulation study was both involved and computationally expensive, requiring ≈ 46 years of computational time. Unfortunately, we were unable to complete the revisions in a timely manner, and so deadline for submitting the revision elapsed.

Nevertheless, we have included our responses to the reviewer comments, which have all been carefully addressed. If you decide that it is necessary to have our manuscript reviewed again, we would be grateful if it could be handled by an AE with expertise in Bayesian inference: we would suggest Mark Holder or Tanja Stadler. Conversely, we wish to declare a conflict with (and so avoid reviews by) Mark Pagel and Andrew Meade.

Given that this is an unusual situation, I would be more than happy to discuss any questions you may have.

Thank you in advance for your kind consideration of our manuscript.

Sincerely,

Brian R. Moore