Dear Editors:

Please find attached a submission to *Systematic Biology* entitled "*Bayesian Analysis of Partitioned Data*" coauthored by Jim McGuire, Fredrik Ronquist, John Huelsenbeck, and myself. As the title suggests, our manuscript presents a novel Bayesian approach for estimating phylogenies from partitioned data.

It is critical that phylogeny estimation is based on a model that adequately captures variation in the substitution process within the sequence data (to avoid biased parameter estimates), while simultaneously preventing the inclusion of superfluous parameters (to avoid inflated error variance of parameter estimates). The prevailing current approach relies on Bayes factors to select a 'mixed model' from a pool of candidate partition schemes by comparing their respective marginal likelihoods. The chosen partition scheme is then accepted as an adequate description of the process heterogeneity in the sequence data, and this partition scheme becomes a fixed assumption of the analysis.

By contrast, we propose an alternative approach for accommodating process heterogeneity that treats the partition scheme as a random variable with a prior probability distribution that is specified by the Dirichlet process prior (DPP) model. The DPP model has recently been applied with great success to several problems in evolutionary biology—these inferences generally involve 'non-parametric clustering' problems, where the number of clusters (partitions) and the assignment of data elements to those clusters are not specified a priori, but are instead treated as random variables.

Accordingly, the DPP model would seem to provide a natural and statistically justified framework for the phylogenetic analysis of partitioned data. The extension of the DPP model to the analysis of partitioned data is quite straightforward: we provide a detailed description of this method, and explore the properties of this approach by means of rigorous analyses of several empirical data sets. The results of these analyses are compared to previous conventional analyses, in which partition schemes were selected by means of Bayes factors.

We are very excited by these results, and sincerely believe that this method will prove to be a very useful solution to an important and fundamental problem in phylogenetic biology. Should you decide to consider our manuscript for peer review, we wish to declare a conflict with (and so avoid reviews by): Mark Pagel and Andrew Meade.

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

Sincerely,
Brian R. Moore