Please accept our submission of a substantially revised manuscript on a comparative method for Brownian motion on a phylogenetic network. This was originally intended for a symposium volume from an SSB symposium years ago. Our first preprint of this was on biorxiv in 2015. Since then, it has been through two rounds of review at *Systematic Biology*: the paper improved substantially from the review process, but in the most recent review Paul Bastide noted a serious mathematical error. We have thus spent the last couple of years (this is a side project for both of us) working to fix that error, recode the approach (we now have 8 models rather than 4, model averaging is built in, we have new ways to visualize results, starting points are much better, matrix conditioning does not seem to be a problem as it was before, it runs in parallel automatically, etc.), and revise the manuscript. We believe this new version is much improved, and unlike previous versions, the parameter estimates are actually pretty good, especially given moderate sample sizes. Past reviewers have been enthusiastic about the approach (though note this was before Bastide et al. (2018)’s similar (and independently developed) approach appeared, though we have additional optional yet biologically compelling parameters in our model), other than poor performance and errors, which we believe has been fixed. However, we do not doubt another round of review will improve it further.

Thank you,

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