# Supplemental Materials

In addition to the tests done by Vasconcelos et al. (2022) and the work for Figure 4, we tested the performance of MiSSE with a model where the speciation rate exponentially increased towards the present. This is another case where there may be multiple congruent models through time and which violates the assumptions used by MiSSE (piecewise constant rates, though the rates can change across taxa and/or over time due to changes of state of a hidden character). Ideally, MiSSE would recover the true speciation rate exactly at the tip and zero extinction rate, with the same rates for all taxa. In theory, one could expect the speciation rate to be estimated to be lower than that at the tip: with an exponentially increasing rate, the rate over the entire tree until the last moment is lower than at the tip, and so the estimate given the available data should be lower than the rate at the final instant. However, we would still hope that extinction rate is estimated correctly, even under this unrealistic model (we know empirically that extinction is substantially high, not zero, for example (Marshall 2017), and exponentially increasing speciation rates would in short order lead to speciation becoming a daily occurrence for every surviving species).

For the simulation, we used castor (Louca and Doebli, 2017), set to simulate 101 taxon trees, then deleted one of the two taxa originating from the most recent simulation event and then deleted half the length of the shortest tip branch (so that simulations did not exactly end with a speciation event). Simulation conditions that resulted in tips 89 to 152 arbitrary time units from the stem of the clades (4 to 120 time units from the crown group). The speciation rate started at 0 and at the tips ranged from 0.07 to 0.18 events per time units. The MiSSEGreedy() function of the R package hisse was used to automatically try models and select the best one for each simulation (multimodel inference is very possible and recommended for a single empirical study,

but for simplicity across simulations we used the single best model for each simulation). The best

models in 366 of 397 simulations had the same net diversification rates for all taxa.

Supplemental Figure 1 shows the results of these simulation (also see discussion in main text).
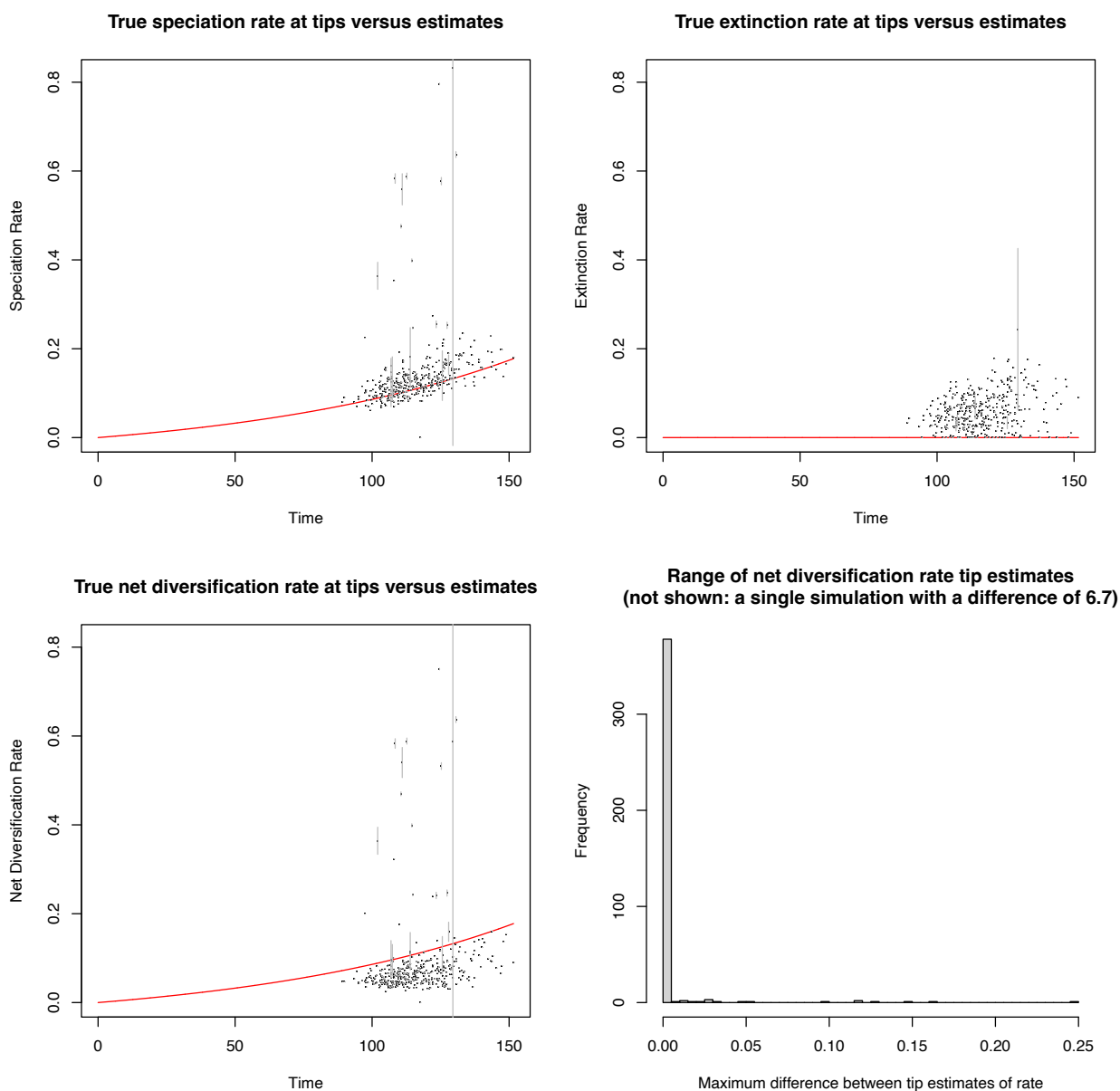
Figure S1. Plots of the speciation, extinction, and net diversification rates, as well as a histogram of the range of estimates across taxa within a single tree. Red lines show the true rates. Dots indicate the phylogenetically uncorrected median of the tips (one dot per simulation); the gray lines are the median ± one standard deviation across the tip estimates.

MiSSE worked fairly well at estimating speciation rates; it estimated extinction rates that were too high and thus an overall net diversification rate that was too low. The median extinction rate was estimated at about half the estimated speciation rate, though with wide variation across replicates: it should have been zero but could have been as high or higher than the speciation rate.