**Supplemental Materials for** “**Detecting hidden diversification shifts in models of trait-dependent speciation and extinction”**

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Figure S1. The uncertainty surrounding estimates of net turnover rate (λ+μ), extinction fraction (μ/λ), and transition rates as a function of tree size. Each row represents a different simulation scenario, all of which are described in detail in Table 1 in the main text. For both turnover rates and extinction fractions the solid green line and green region represent the mean and 95% confidence interval for state 0, the solid blue line and blue region represents the mean and 95% confidence interval for state 1*A*, and the solid red line and red region represents the mean and 95% confidence interval for state 1*B*. In the panels depicting the log-transformed transition rates, the solid purple line and purple region, the solid light purple line and light purple region, represent mean and 95% confidence interval for transition to and from the “hidden” state (i.e., 1*B*), respectively.

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Figure S2. Results from the simulations when transforming the estimates of turnover and extinction fraction depicted in Figure S1 to reflect estimates of speciation (λ) and extinction (μ) rates.

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Figure S3. The uncertainty surrounding estimates of net diversification rate (λ-μ, obtained from backtransforming net turnover rates and extinction fraction; see main text), extinction fraction (μ/λ), and transition rates as a function of tree size, when the generating model does not contain a hidden state (i.e., a BiSSE model). The specifics of the different simulation scenarios are described in detail in Table 1 from the main text. For both net diversification rates and extinction fractions the solid green line represents and green region represent the mean and 95% confidence interval for state 0, and the solid blue line and blue region represents mean and 95% confidence interval for state 1. In the panels depicting the log-transformed transition rates, the solid black line and surrounding region, and the solid gray line and surrounding region, represent the mean and 95% confidence interval for transitions from state 0 to 1, and state 1 to 0, respectively.

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Figure S4. The uncertainty surrounding estimates of net turnover rate (λ+μ) and extinction fraction (μ/λ) when the generating model assumes (a,b) diversification is independent of the observed characters (i.e., null-two model), or (c,d) a hidden state underlies both observed states (i.e., a general HiSSE model). The specifics of the different simulation scenarios are described in detail in Table 2 from the main text. In all panels, the color of dashed line corresponds to the true value under the generating model.

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Figure S5. The model-averaged parameter estimates of net diversification across two empirical examples (Cetacea and Dipsidae). The rates are transformed and ordered to show the proportion of the rate for state 0 relative to the rate state 1 (regardless of the hidden state) to emphasize that although a trait-dependent model may have higher overall weight, the relative difference in rates is minimal. The dots are colored on a black to red scale: red indicates increasing support for trait-dependent diversification models. The horizontal line shows the expectation of equal rates; dotted lines show rates within 10% of the true rate. For the 87-taxon cetacean tree, across simulated trees the model-averaged diversification rate in state 0 was within 10% of the rate for state 1 in 87% of the simulations; for Dipsidae, in 95% of the simulations the estimated diversification rate for state 0 was within 0.5% of the rate for state 1.

Table S1. Summary of the model support for the same simulated scenarios shown in Table 1 (see text), but based on different configurations of the model set. Here we group the models shown in Table 1 into five “classes” of models: we assess the best model based on different configurations of five “classes” of models: equal diversification rate BiSSE, BiSSE, CID-2, CID-4, and a full HiSSE model. We use three measures of support, the average Akaike weight (*wi*), the percentage of time each model had a ΔAIC=0, and the percentage of time each character-dependent (i.e., BiSSE and HiSSE) model had a ΔAIC=0 after culling instances where one of the character-independent models (i.e., equal rates BiSSE, CID-2, and CID-4) had a ΔAIC<2. However, note in the case of the percentages it is incorrect to interpret these values as Type I or Type II errors and, therefore, do not represent statements about confirming or rejecting particular models. All data sets tested contained 400 species.

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|  |  | Assuming BiSSE only | |  | Assuming BiSSE+CID-two | | |  | Full set | | | | |
| Generating model | Measure | Equal rates BiSSE | BiSSE |  | Equal rates BiSSE | BiSSE | CID-two |  | Equal rates BiSSE | BiSSE | CID-two | CID-four | HiSSE |
| BiSSE state 1, 2x speciation | *wi* | 0.017 | 0.982 |  | 0.014 | 0.959 | 0.026 |  | 0.001 | 0.531 | 0.013 | 0.001 | 0.446 |
|  | ΔAIC=0 | 1% | 99% |  | 1% | 98% | 1% |  | 1% | 75% | 1% | 0% | 23% |
|  | ΔAIC<2 model | − | 97% |  | − | 95% | − |  | − | 75% | − | − | 22% |
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| Null-two, state B 2x speciation | *wi* | 0.279 | 0.721 |  | 0.074 | 0.174 | 0.753 |  | 0.051 | 0.101 | 0.494 | 0.072 | 0.282 |
|  | ΔAIC=0 | 26% | 74% |  | 9% | 15% | 76% |  | 9% | 11% | 64% | 1% | 15% |
|  | ΔAIC<2 model | − | 38% |  | − | 7% | − |  | − | 2% | − | − | 8% |
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| HiSSE, state 1B 2x speciation | *wi* | 0.018 | 0.982 |  | 0.013 | 0.766 | 0.221 |  | 0.005 | 0.228 | 0.021 | 0.003 | 0.742 |
|  | ΔAIC=0 | 0% | 100% |  | 0% | 81% | 19% |  | 0% | 25% | 0% | 0% | 75% |
|  | ΔAIC<2 model | − | 97% |  | − | 67% | − |  | − | 24% | − | − | 73% |
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| "Worst-case" trait-independence | *wi* | 0.080 | 0.920 |  | <0.001 | 0.013 | 0.986 |  | <0.001 | 0.001 | 0.246 | 0.454 | 0.299 |
|  | ΔAIC=0 | 6% | 94% |  | 0% | 1% | 99% |  | 0% | 0% | 22% | 49% | 29% |
|  | ΔAIC<2 model | − | 80% |  | − | 1% | − |  | − | 0% | − | − | 16% |

Table S2. Summary of model support for neutral character data simulated on two empirical trees, Cetaceans (i.e., whales and relatives; Steeman et al. 2015) and our own empirical tree of the plant clade Dipsidae (see main text), following the simulation procedures of Rabosky and Goldberg (2015). As in Table S1, we assess the best model based on different configurations of five “classes” of models: equal diversification rate BiSSE, BiSSE, CID-2, CID-4, and a full HiSSE model. We use three measures of support, the average Akaike weight (*wi*), the percentage of time each model had a ΔAIC=0, and the percentage of time each character-dependent (i.e., BiSSE and HiSSE) model had a ΔAIC=0 after culling instances where one of the character-independent models (i.e., equal rates BiSSE, CID-2, and CID-4) had a ΔAIC<2. Again, as in the case of Table S1, it is incorrect to interpret these values as Type I or Type II errors and, therefore, do not represent statements about confirming or rejecting particular models.

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|  |  | Assuming BiSSE only | |  | Assuming BiSSE+CID-2 | | |  | Full set | | | | |
| Empirical dataset | Measure | Equal rates BiSSE | BiSSE |  | Equal rates BiSSE | BiSSE | CID-2 |  | Equal rates BiSSE | BiSSE | CID-2 | CID-4 | HiSSE |
| Cetaceans (*N*=87) | *wi* | 0.047 | 0.953 |  | <0.01 | 0.204 | 0.796 |  | <0.01 | 0.021 | 0.063 | 0.621 | 0.294 |
|  | ΔAIC=0 | 4% | 96% |  | 0% | 17% | 83% |  | 0% | 0% | 0% | 71% | 29% |
|  | ΔAIC<2 | − | 94% |  | − | 12% | − |  | − | 0% | − | − | 20% |
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| Dipsidae (*N*=417) | *wi* | <0.01 | 0.999 |  | <0.01 | <0.01 | 0.998 |  | <0.01 | <0.01 | <0.01 | 0.986 | 0.014 |
|  | ΔAIC=0 | 0% | 100% |  | 0% | 0% | 100% |  | 0% | 0% | 0% | 0% | 1% |
|  | ΔAIC<2 | − | 100% |  | − | 0% | − |  | − | 0% | − | − | 0% |

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Table S3. The sampling frequencies of clades contained within our phylogeny of the Dipsidae clade. The current diversity estimates were taken from the Angiosperm Phylogeny Website (APWeb; Stevens, 2012).

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| Clade | Known diversity | Sampling freq. |
| *Quintinia* | 25 | 0.08 |
| *Paracryphia* | 1 | 1.00 |
| *Sphenostemon* | 10 | 0.10 |
| *Viburnum* | 175 | 0.49 |
| *Sambucus* | 20 | 0.70 |
| *Adoxa* | 1 | 1.00 |
| *Sinadoxa* | 1 | 1.00 |
| *Tetradoxa* | 1 | 1.00 |
| Diervilleae | 16 | 0.81 |
| *Lonicera* | 180 | 0.47 |
| Rest of Caprifolieae | 30 | 0.63 |
| *Heptacodium* | 1 | 1.00 |
| Linnaeeae | 32 | 0.44 |
| *Zabelia* | 5 | 1.00 |
| Morinaceae | 13 | 0.77 |
| *Triplostegia* | 2 | 1.00 |
| Dipsacaceae | 290 | 0.20 |
| Valerianaceae | 350 | 0.34 |

**Supplemental References**

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