Supplementary Material

Figure S1. The (relative) error in estimating the parameters as a function of clade size A) Speciation-initiation rate, B) Extinction rate, C) Incipient diversification rate (speciation-initiation rate minus extinction rate), D) Speciation-completion rate, E) Duration of speciation in species that complete the speciation process (a composite of the speciation-initiation rate, the speciation-completion rate and the extinction rate, Eq. (4)). The scatterplots represent the absolute errors (A-C) or relative errors (D-E) in the estimates for 1000 replicate simulations, and the blue arrow indicates their mean clade size, while the green arrow indicates their median value. The various plots are for different simulation parameter sets: speciation initiation rate is 0.5 (all panels), the extinction rate μ takes the values 0, 0.1, and 0.2 (rows) and the speciation completion rate λ takes the values 0.1, 0.3 and 1 (columns). The simulated trees all had a crown age of 15 My.

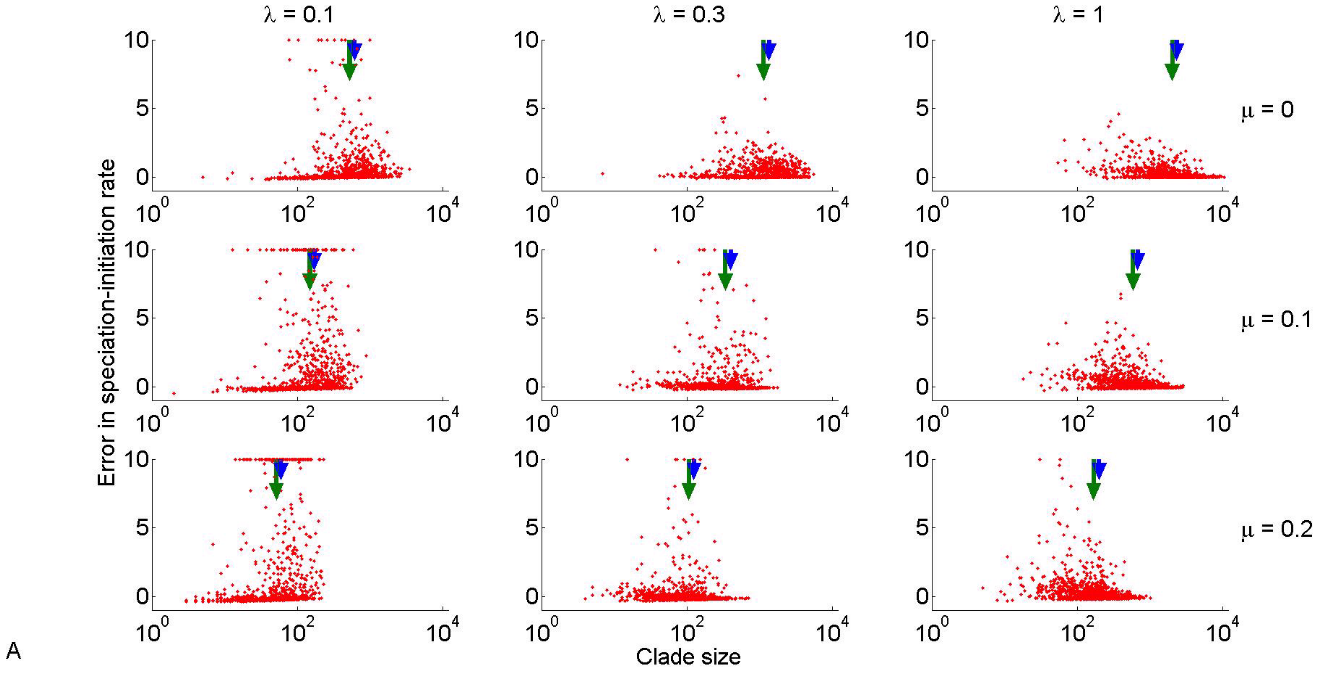

Figure S1A.

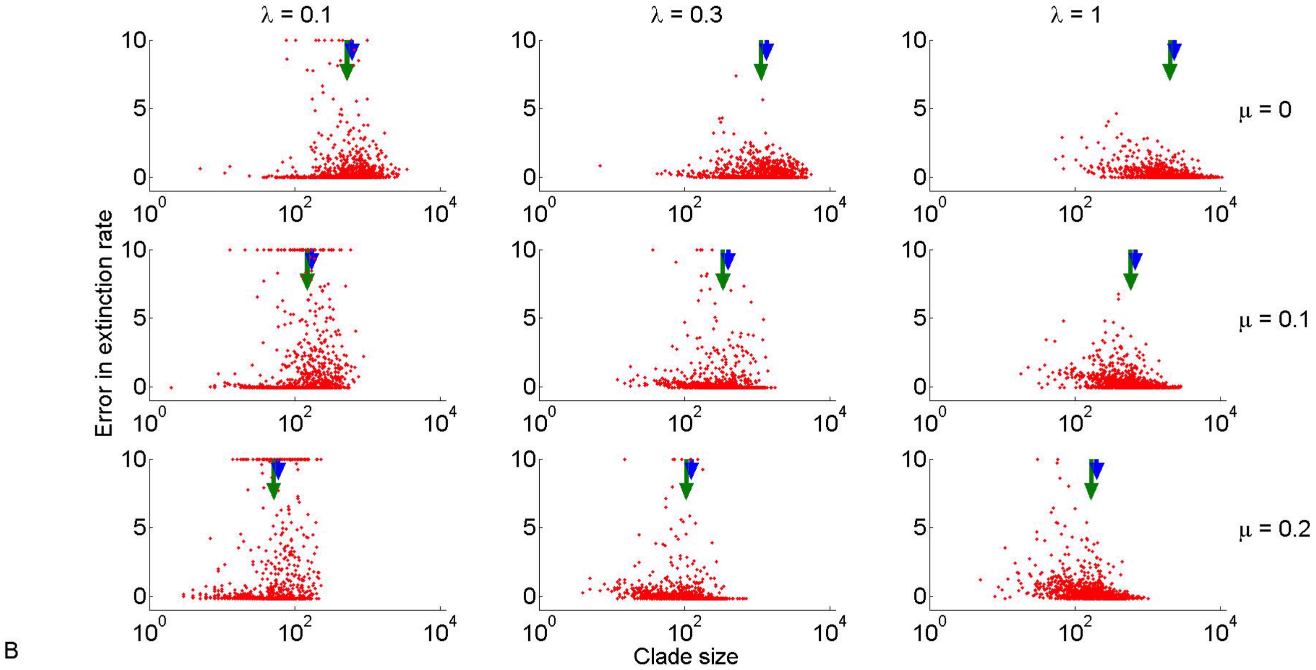

Figure S1B.

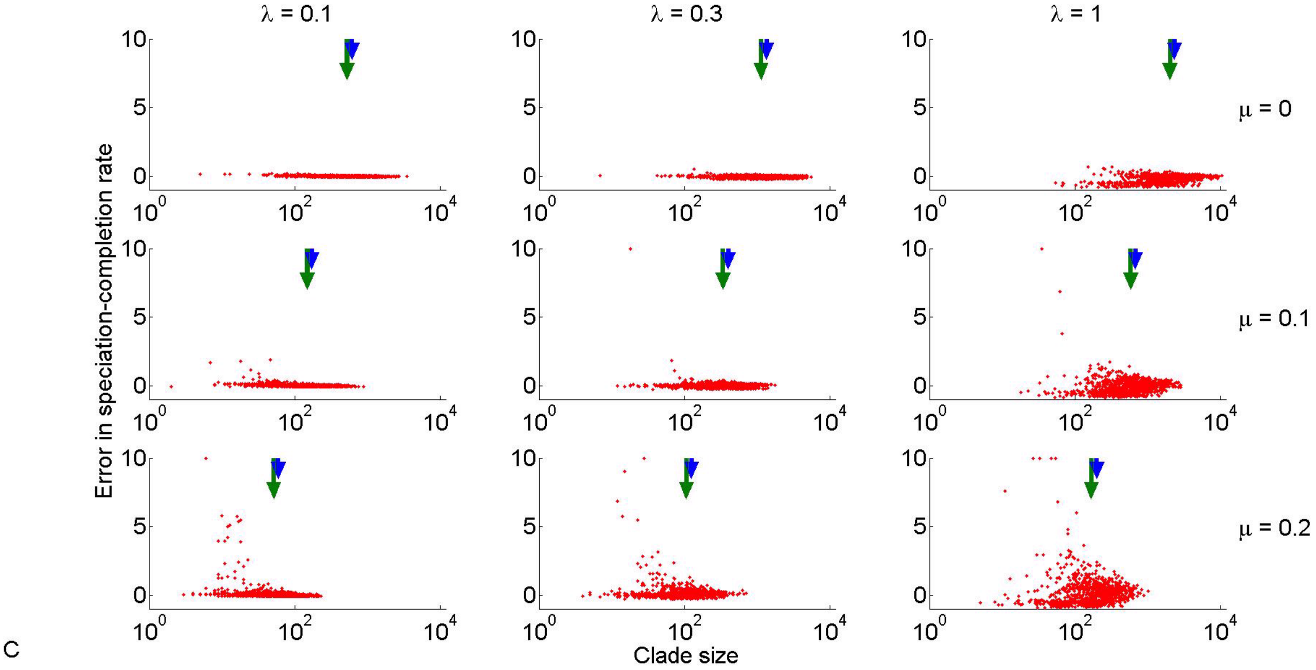

Figure S1C.

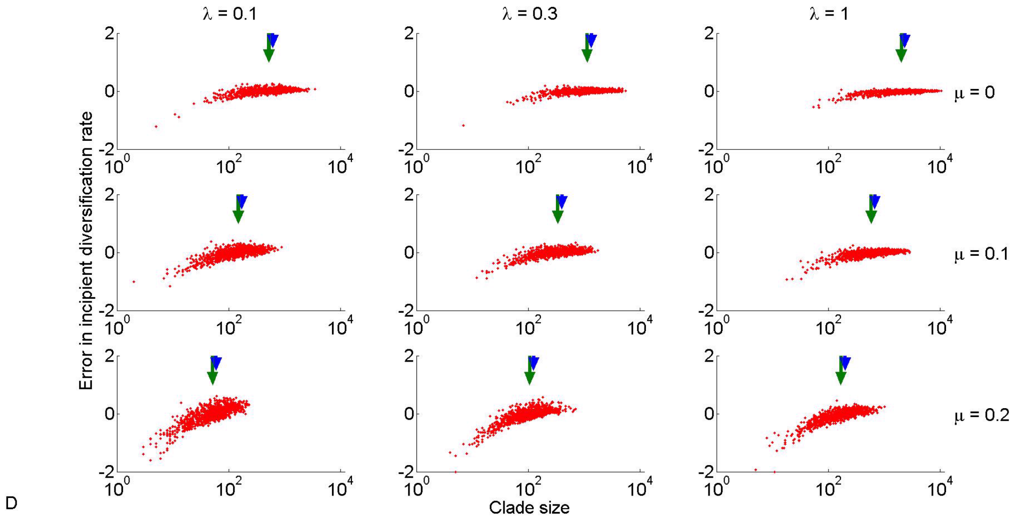

Figure S1D.

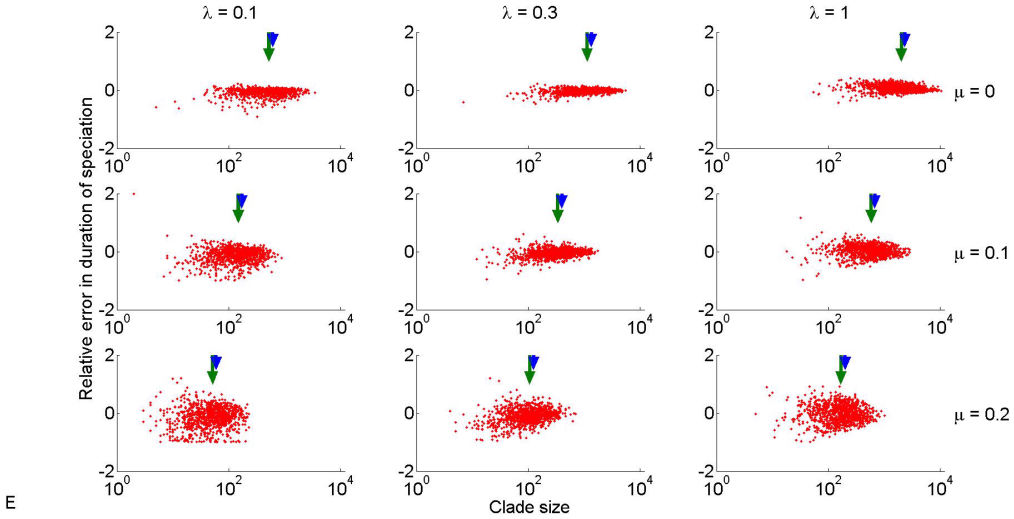

Figure S1E.

Figure S2. Speciation rates estimated with a constant rate birth-death model from phylogenies simulated with the protracted speciation model. The various plots are for different simulation parameter sets: speciation initiation rate is 0.5 (all panels), the extinction rate μ takes the values 0, 0.1, and 0.2 (rows) and the speciation completion rate λ takes the values 0.1, 0.3 and 1 (columns). The simulated trees all had a crown age of 15 My.

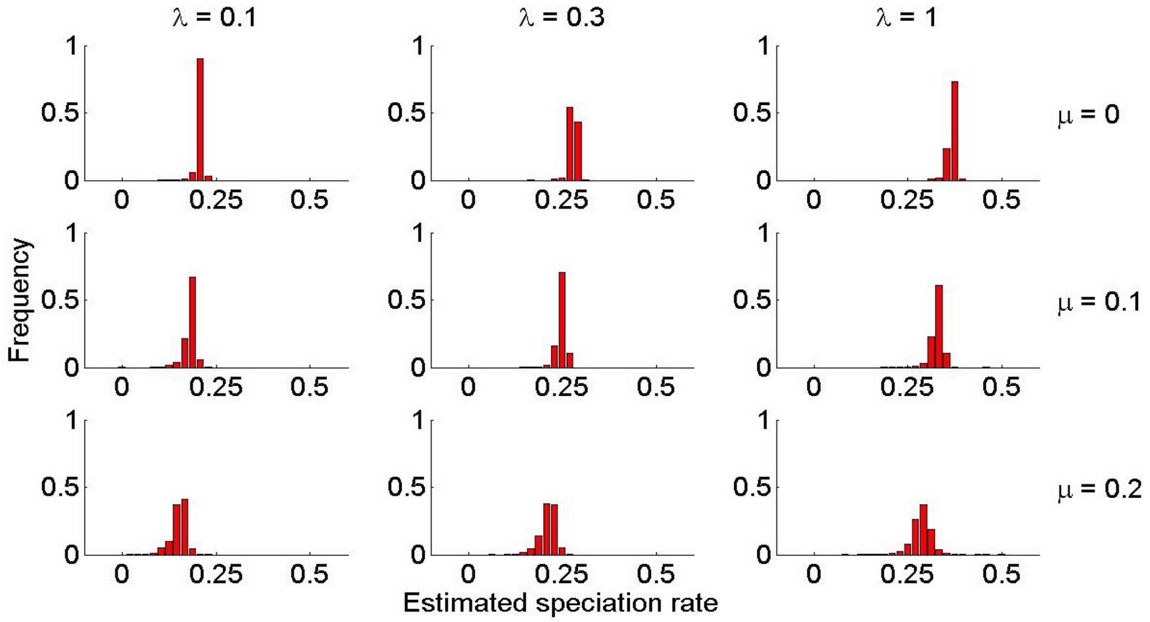

Figure S2.

Figure S3. Speciation rate, estimated using the constant-rate birth-death model, versus the speciation-completion rate, estimated using the protracted speciation model, for 80 avian clades. To obtain these 80 clades we downloaded all stage-1 trees (i.e., including only genetic species) based on the Hackett backbone typology from the posterior distribution of trees available from http://birdtree.org/. We selected 1 tree at random from the posterior distribution for analysis and identified those genera that were monophyletic (we also included clades where together two genera formed a monophyletic group).

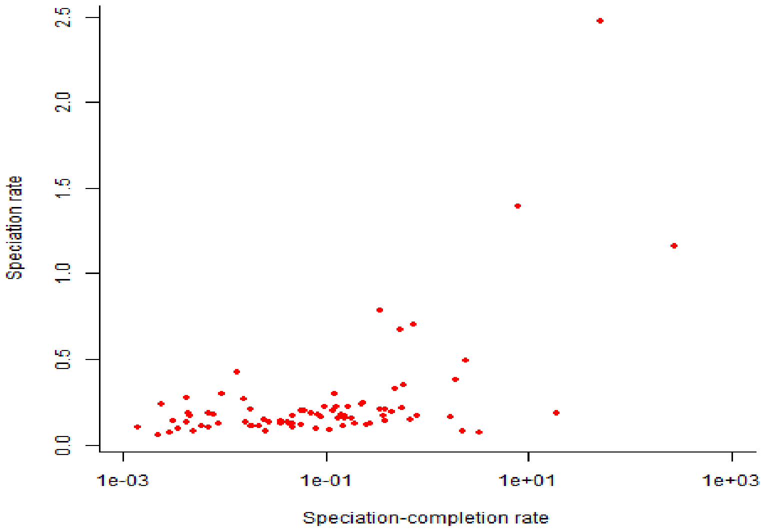

Figure S3.