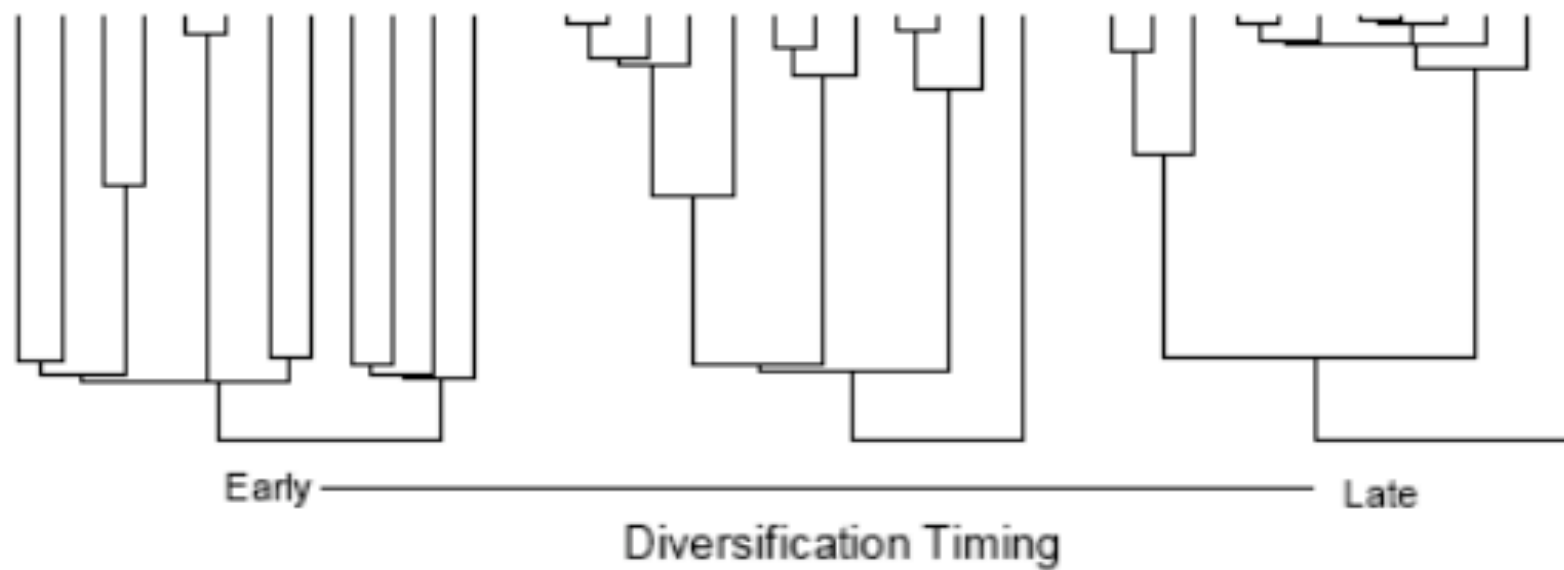
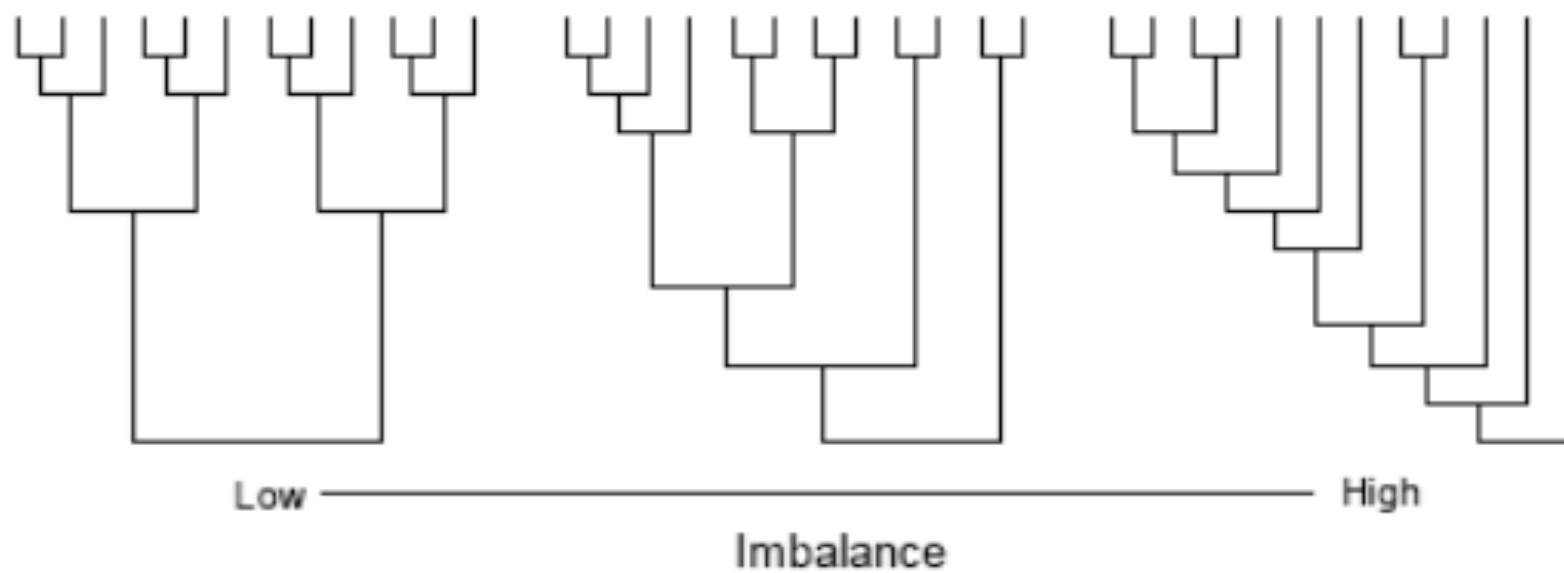


(b) Age and species richness



Magallon and Sanderson 2001. Clade age (crown group) vs. diversity



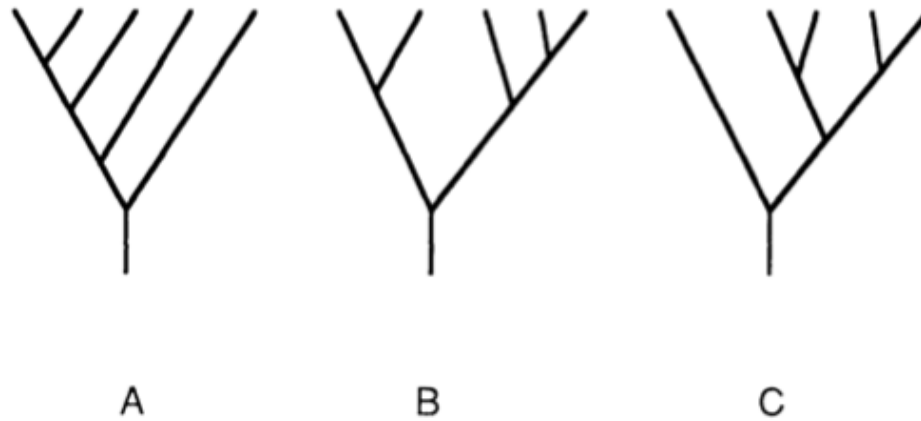


FIG. 1.—The three distinct topological types on five taxa.

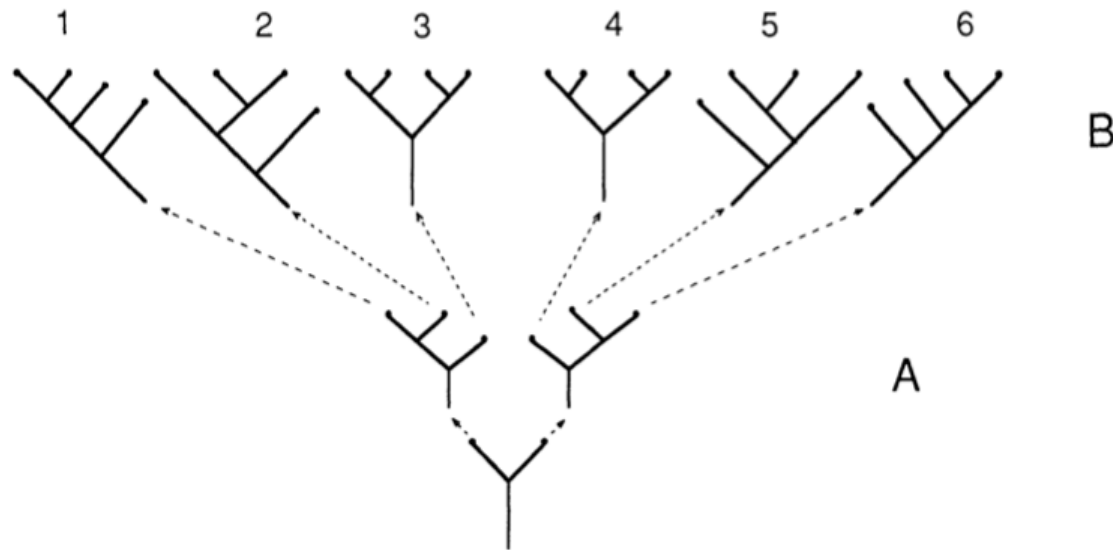
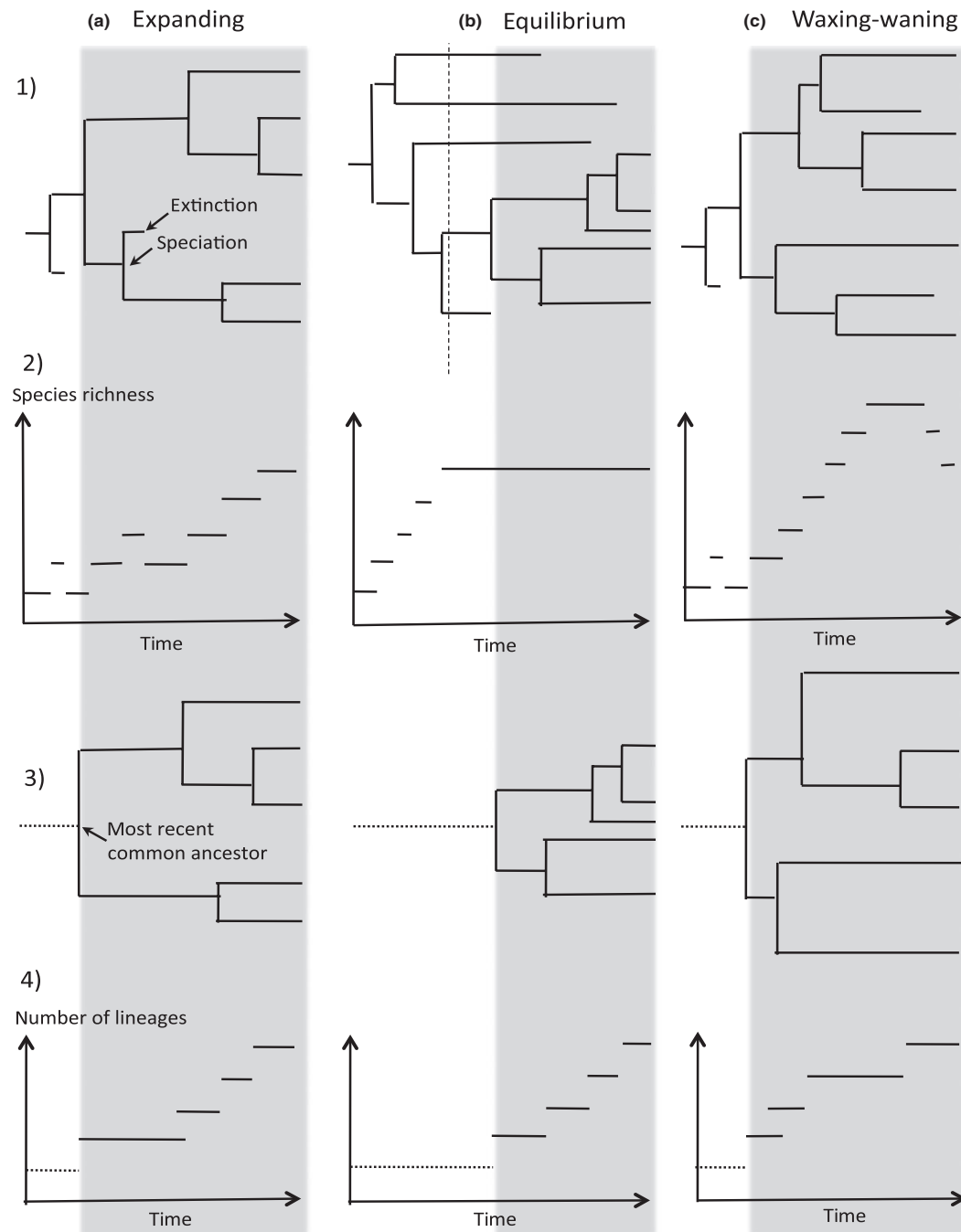
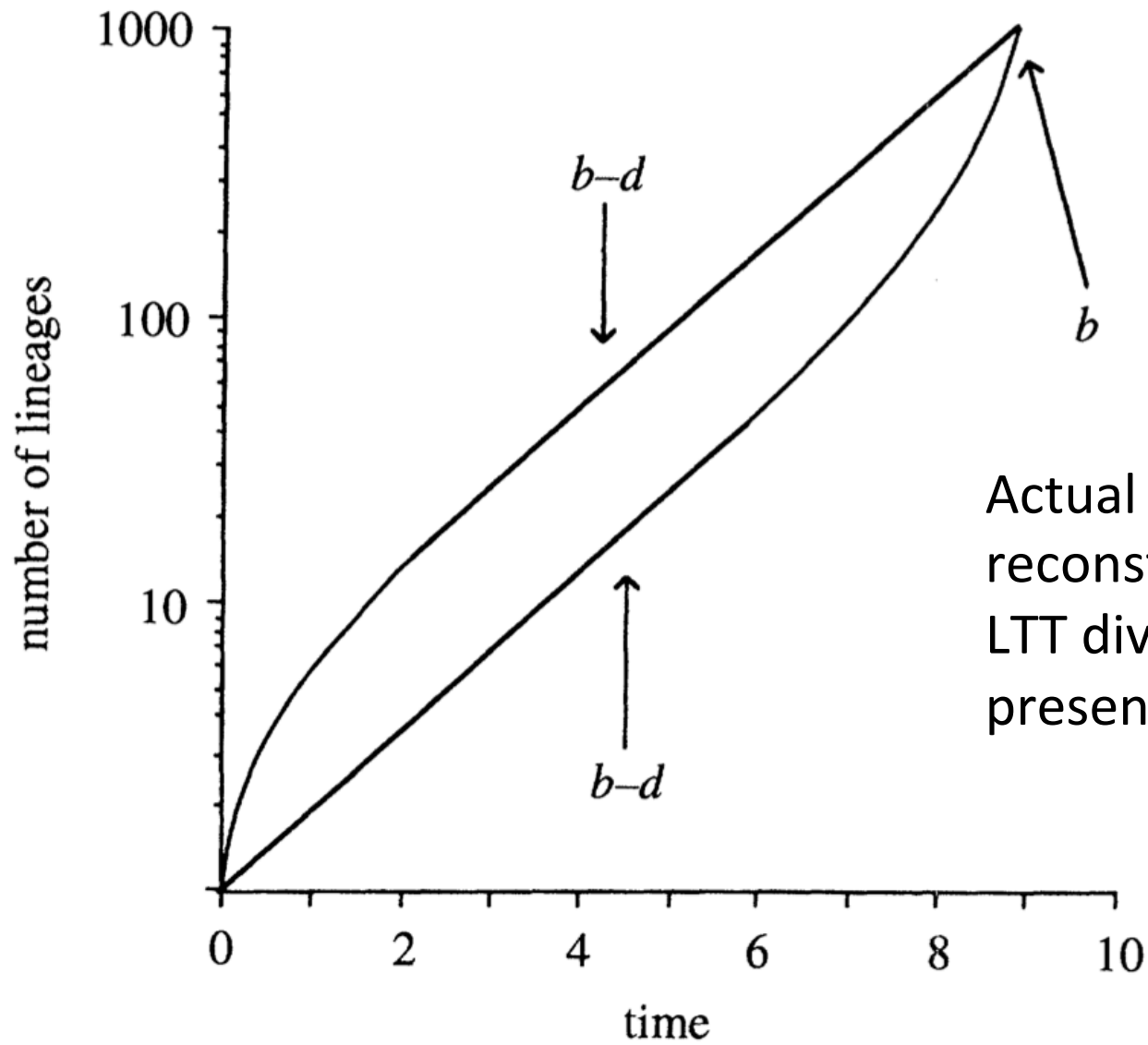


FIG. 2.—A diagrammatic representation of the process of lineage-splitting leading to four taxa.

Figure 1 Analysing diversification with phylogenies. (1) Complete phylogenies representing the birth and death of species; (2) diversity-through-time plot, (3) reconstructed phylogeny and (4) lineage-through-time plot corresponding to scenarios of (a) expanding diversity, meaning that clades' richness increases over time, (b) equilibrium diversity, meaning that clades' richness stay constant over time and (c) waxing-waning diversity dynamics, meaning that clades' richness first increases and then decreases over time. The grey areas correspond to the time period going from the time of the most recent common ancestor in the reconstructed phylogeny to the present. Although the number of lineages in the reconstructed phylogeny always increases from 2 to present-day diversity (4), the corresponding diversity trajectory can be increasing (a), stable (b), or contain periods of diversity decline (c). In (b), starting from the time indicated with the dashed line, each extinction event is immediately followed by a speciation event, resulting in equilibrium dynamics.





Actual (top) and
reconstructed (bottom)
LTT diverge in the
presence of extinction

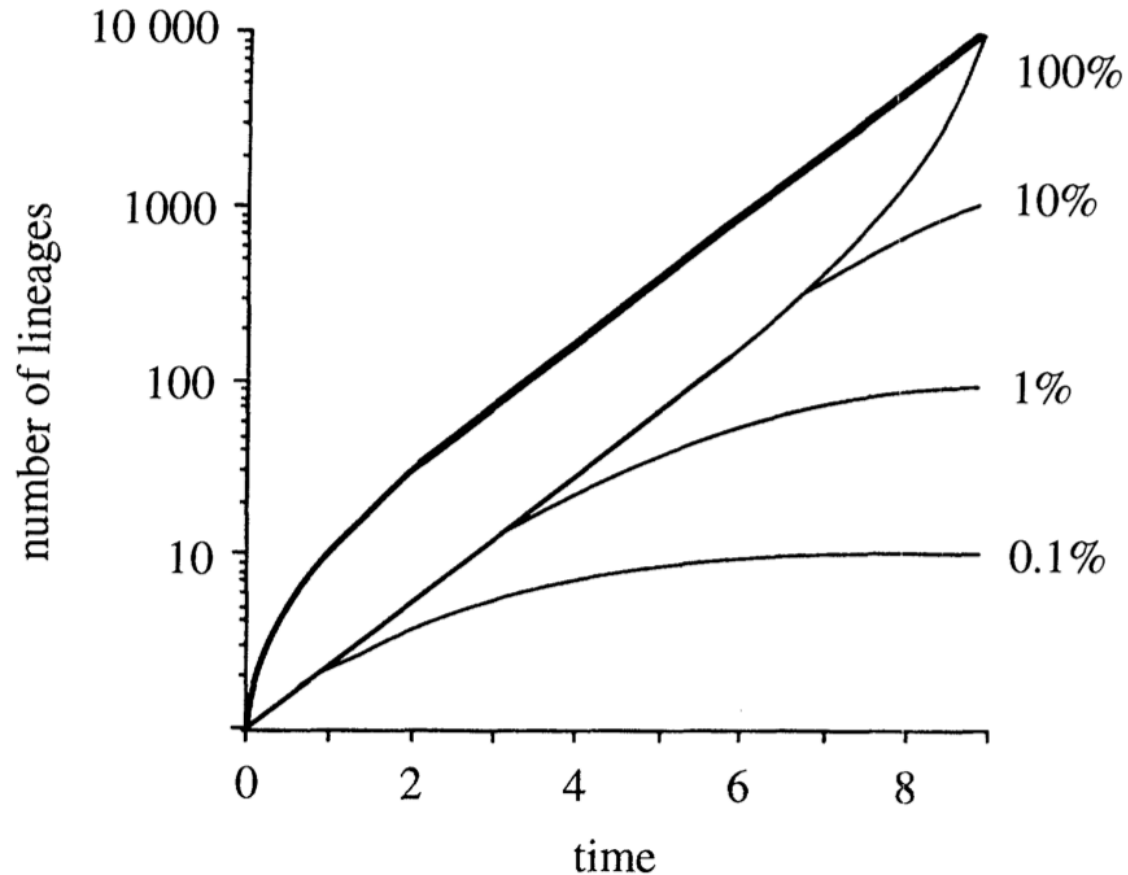


Figure 8. The theoretically expected lineages-through-time plots for reconstructed phylogenies based on successively smaller samples from the actual phylogeny described by the top line.

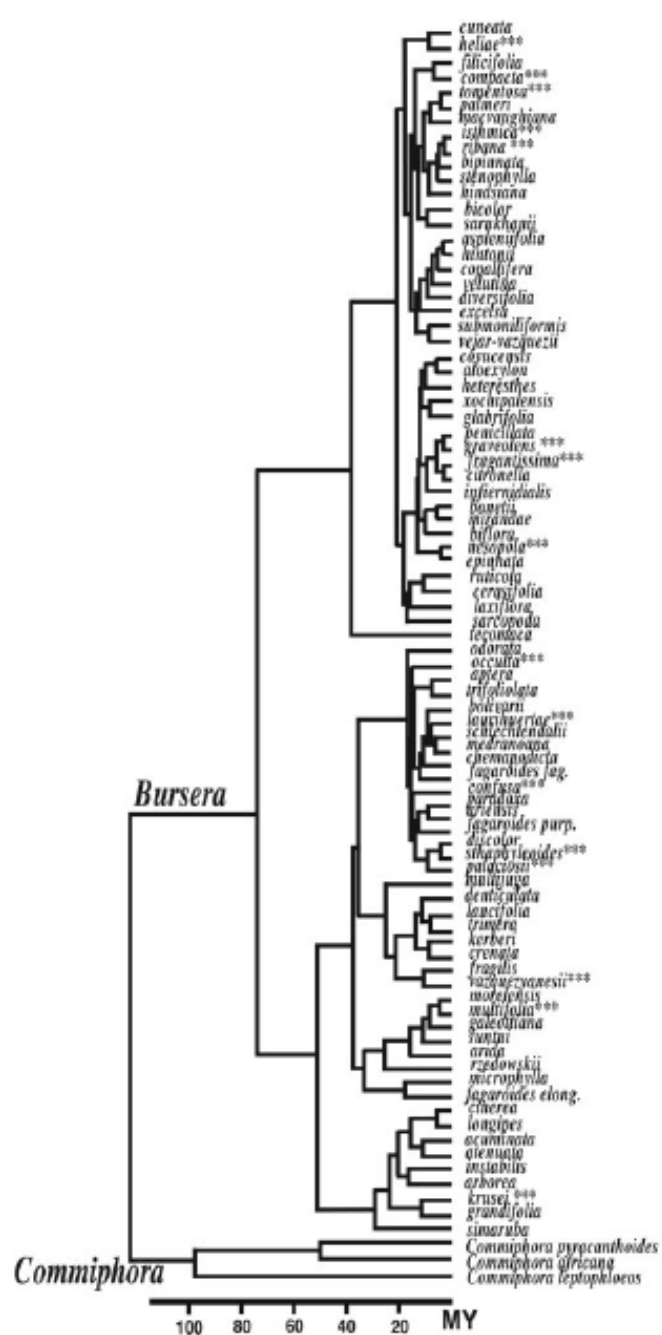


Fig. 2. Time-calibrated phylogeny of *Bursera* (modified from ref. 13). Asterisks indicate species that were added to the phylogeny on the basis of their taxonomic descriptions and for which divergence time is unknown.

Lineages-through-time (LTT) plot

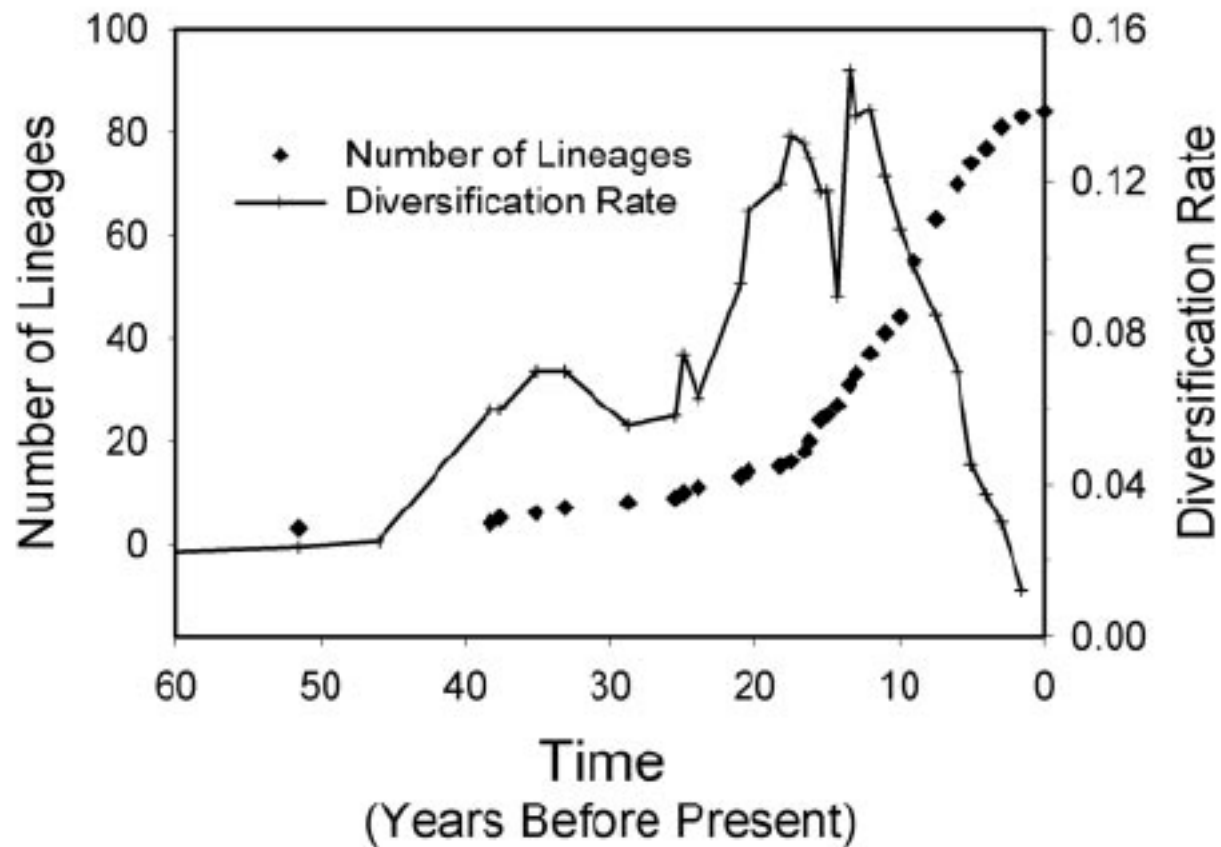


Fig. 3. Number of *Bursera* lineages through time and 10-MY average diversification rates at different times over the last 60 MY.

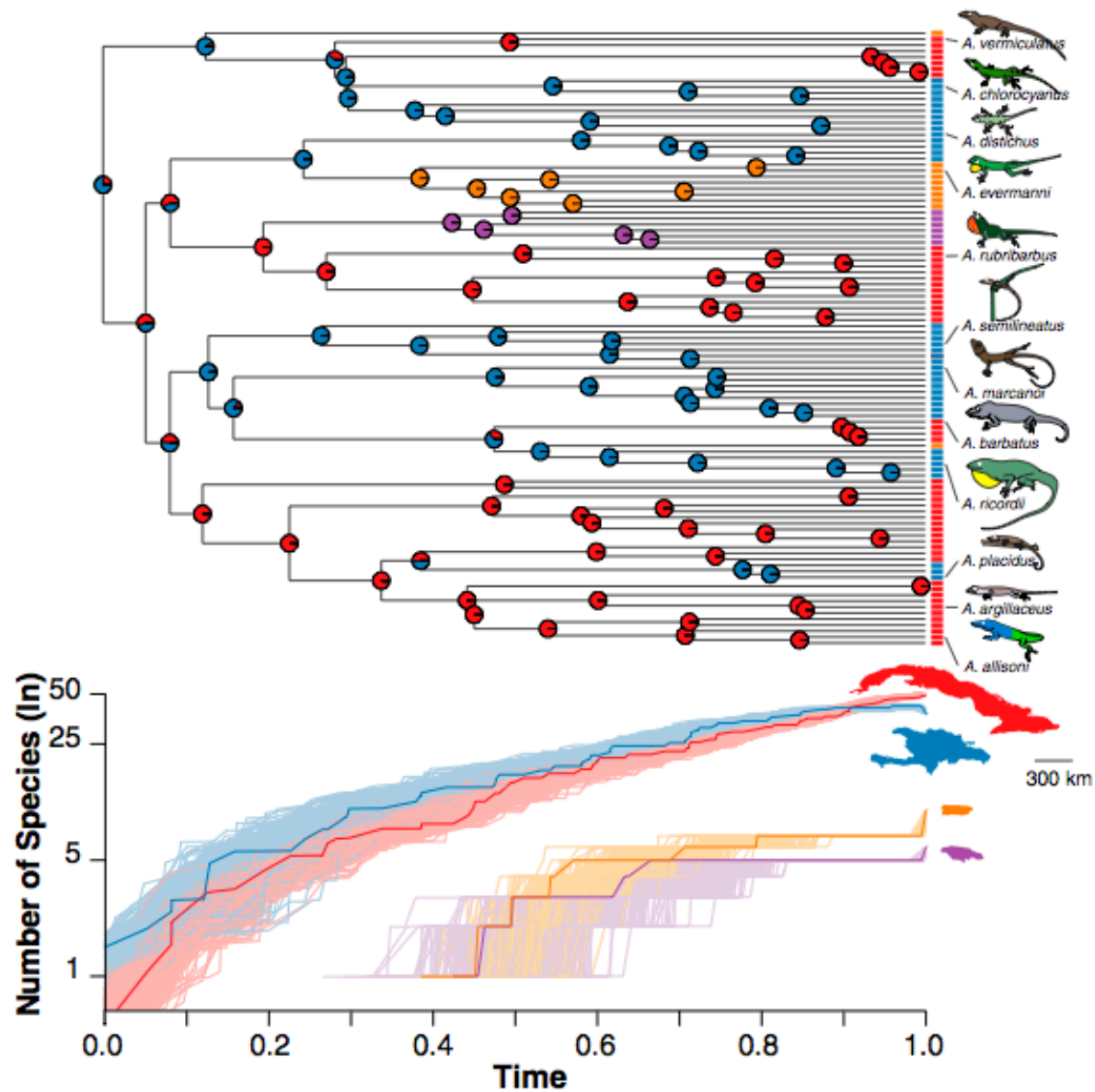


Fig. 2. *Anolis* MCC tree with reconstructed island occupancy probabilities and lineage accumulation curves for Cuba (red), Hispaniola (blue), Jamaica (purple), and Puerto Rico (orange). Occupancy probabilities on internal nodes were estimated under the overall best-fit model (IslandVariable). The MCC tree with all taxon labels is shown in Fig. S1.

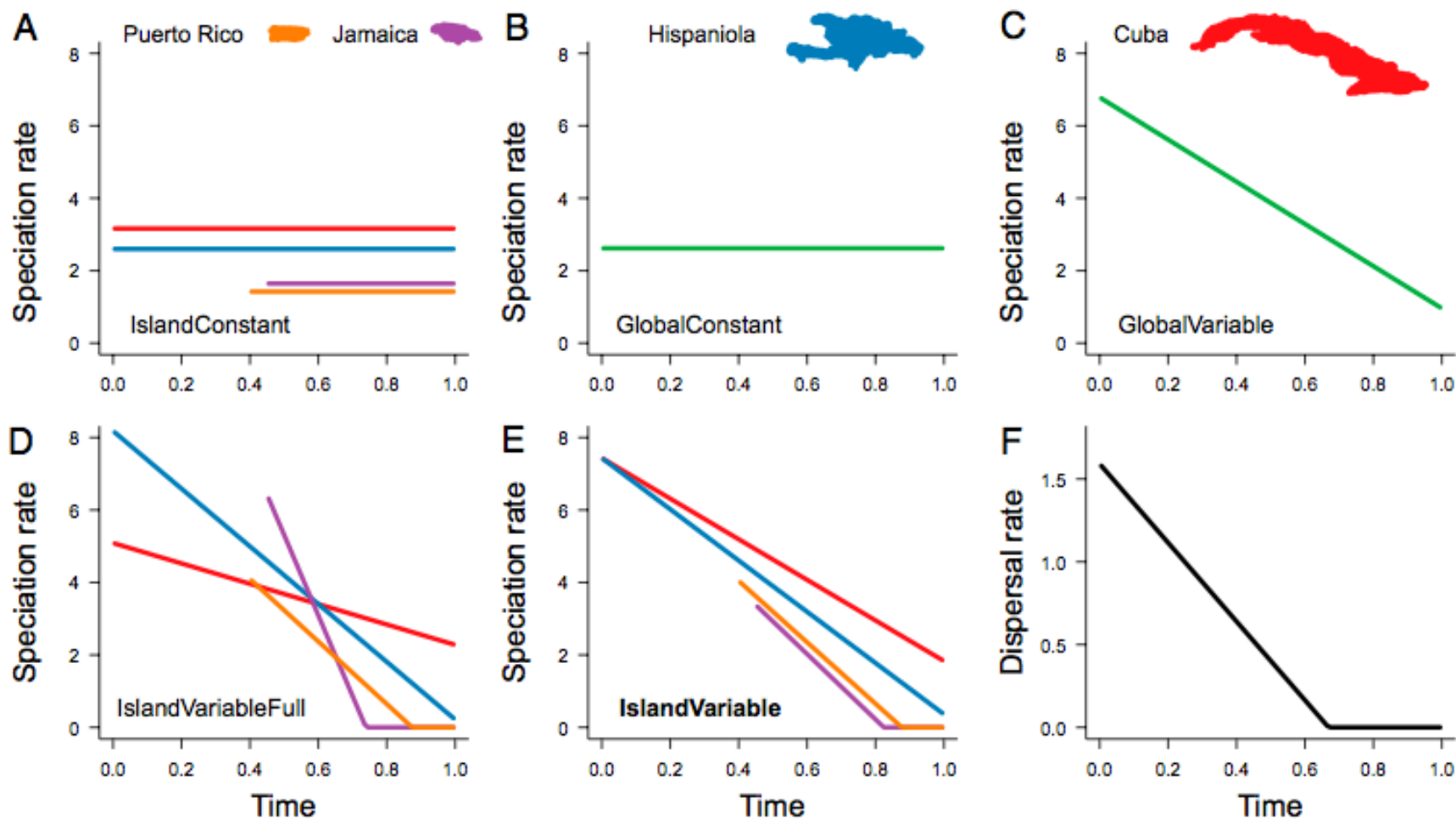


Fig. 1. (A–E) Reconstructed speciation-through-time curves under five diversification models fitted to the *Anolis* phylogeny (Fig. 2, Fig. S1). Green curves denote models without state-dependent diversification; other colors describe speciation dynamics on Cuba, Hispaniola, Jamaica, and Puerto Rico. Models are sorted (left to right, top to bottom) from lowest to highest conditional probability (Table 1). Models with island-specific changes in speciation (D and E) account for $P = 0.995$ of the total probability of the data taken across all models. The maximum-likelihood estimate of the dispersal rate between islands under the IslandVariable model is shown in F. Rates are shown in relative time units, as the tree was scaled to basal divergence of 1.0.

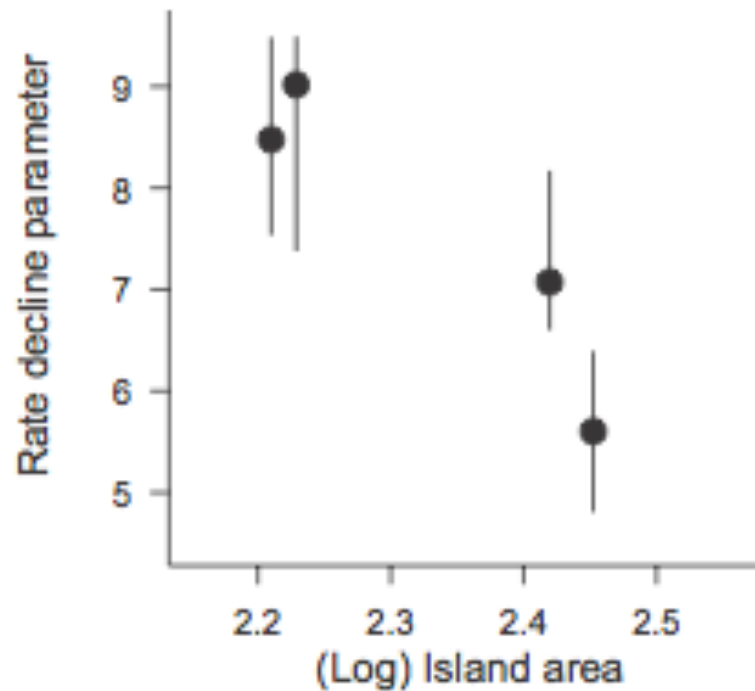


Fig. 3. Island-specific rate-decline parameters as a function of island area for (from left to right) Puerto Rico, Jamaica, Hispaniola, and Cuba. The rate decline parameter is the slope of the relationship between speciation and time ($-\lambda_0/K$). Confidence intervals reflect uncertainty in tree reconstruction and represent the 0.025 and 0.975 percentiles of the distribution of parameter estimates taken across the posterior distribution of trees sampled with BEAST.

c LTT

