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

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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.
Fig. 3. Number of *Bursera* lineages through time and 10-MY average diversification rates at different times over the last 60 MY.
Fig. 1. Two models of the relation between local species richness and regional diversity. According to the saturation model, the coexistence of species is determined by their interactions, which impose a fixed limit whose value depends on the physical conditions of the environment. Variation in regional diversity due to rates of speciation and dispersal is accommodated by habitat specialization and increased geographical turnover of species. According to the regional enrichment model, variation in regional diversity influences local communities, where differences in diversity are accommodated by varying the degree of niche overlap or the degree of resource specialization.
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.
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Figure 3 | Geographic variation in species-level lineage diversification rate and the richness of high-diversification rate species. a–c, Mean assemblage diversification rate (see Fig. 2), calculated as the geometric mean of all species in a grid cell assemblage, weighted by the inverse of their range size. a, All species; b, non-passerines; c, passerines. This visualization limits the overbearing (pseudo-replicating) effect wide-ranging species have on perceived spatial patterns of assemblage summaries. d–f, Relative (d) and absolute (e) richness of top 25% diversification rate species (DR ≥ 0.243 species Myr⁻¹); f shows the richness of all 9,993 bird species for comparison. Grid cell size is 110 × 110 km for all panels (Behrman projection).
Fig. 1. (2 columns) A timetree of 50,632 species synthesized from times of divergence published in 2,274 studies. Evolutionary history is compressed into a narrow strip and then arranged in a spiral with one end in the middle and the other on the outside. Therefore, time progresses across the width of the strip at all places, rather than along the spiral. Time is shown in billions of years on a log scale and indicated throughout by bands of gray. Major taxonomic groups are labeled and the different color ranges correspond to the main taxonomic divisions of our tree.
**Fig. 4.** (1 column) Patterns of lineage diversification. (a) Cumulative lineages-through-time (LTT) curve for eukaryotes (50,455 sp.), in black, showing the number of lineages through time (unsmoothed, dashed; smoothed, solid) and variance (red, 500 replicates). (b) Same LTT curve (black line), but compared with a simulated constant-expansion LTT curve \((\lambda\) (speciation rate) = 0.073 and \(\mu\) (extinction rate) = 0.070) shown as \pm 99\% confidence intervals (red). (c) Diversification rate plot of same data showing only significant changes in rate as determined in maximum-likelihood tests; variance (red, 500 replicates) shown as \pm 99\% intervals.