When biodiversity is examined in the context of species richness, a consistent feature emerges: Most taxonomic groups are species-poor, relatively few are species-rich, and the frequency distribution has the shape of a so-called “hollow curve” (1, 2) (Fig. 1A).

Attempts to explain hollow-curve distributions often compare real data to hollow curves generated from models (2, 3). These approaches focus on the fraction of groups with a single species (monotypes) and the fraction of species in the largest group (dominance). Two such models are the simultaneous broken stick (SBS) and the geometric distribution. Although these models generate hollow curves, they fail to produce the high number of monotypes and the high dominance when compared with real data. Another approach samples various-sized clades randomly from a phylogenetic tree (4), but this fails because clades sampled from a tree are not mutually exclusive. Because geometric, SBS, and other models have been unsuccessful, processes such as adaptive radiation and extinction have been invoked to explain the apparent high dominance and percentage of monotypes in real data (2).

We developed a new “simultaneous broken tree” (SBT) model comprising three distinct elements: (i) It generates trees according to a Yule-type branching process (3). (ii) It contains a model of character evolution in which character changes evolve at a constant rate on this tree. (iii) The character changes are regarded as cues for the recognition of mutually exclusive taxonomic groups. As with real data that have been studied in the context of hollow curves, some fraction of these groups will be nonmonophyletic (5).

The number of species in genera of birds and three families of angiosperms are given in Fig. 1B along with the percentage of monotypic genera and dominance statistics for SBS and SBT models. (The geometric distribution is almost identical to SBS and is not discussed further.) In every case, the SBT model generates a percentage of monotypes and dominance that is greater than for the real data. In contrast, the SBS model generates percentages of monotypes and dominance statistics lower than in real data. Thus, although relative to a broken stick model real data has many small and excessively large groups, compared with our broken tree model the real data contains fewer small and less dominant groups.

To explain the lack of statistical fit between hollow curves from real data and the SBT model is the opposite direction. Our results show that the phenomenon in need of explanation is not the large percentage of monotypic taxa and high number of species in the largest taxon (dominance) seen in real hollow curves but rather the opposite. The high frequency of monotypes generated by the SBT model arises because half of the branches in any phylogenetic tree are terminal. Very large taxa are generated when groups are delimited in regions of the tree where there are the most branches, namely near the tips, leaving large “remainder” taxa. Thus, random variation in the distribution of character changes on a phylogenetic tree is sufficient to generate a high percentage of monotypes and a high dominance statistic—in fact, higher than that observed in real data.

We suggest that the explanation for the lack of fit between hollow curves from real data and the SBT model is taxonomic, not evolutionary. Although there are no objective criteria for recognizing higher taxa, taxonomists are averse to studying genera that are either too large or too small. (Large genera are cumbersome and can be nonmonophyletic, whereas monotypic genera contain no information about relationships.) Observed hollow curves reflect a shortening of the tails of the SBT distribution. Our taxonomic explanation contrasts with evolutionary explanations, which depend on the premise that in real data sets there are many too monotypic taxa and species-rich groups that are too large. Evidence does exist for differences in speciation and extinction rates (4, 6, 7) but it does not come from hollow curves.

References and Notes
5. Materials and Methods are available as supporting material on Science Online.
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Supporting Online Material
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