

Method.—Phylogenetic clustering of extinction is a measure of the strength of phylogenetic signal present in the timings of extinction of taxa. A time bin of interest is chosen and extinction is treated as a binary trait (i.e., the taxon goes extinct within the bin, or the taxon does not go extinct within the bin). We used the metric D , which was originally developed by Fritz and Purvis (2010) to measure phylogenetic signal strength of extinction risk in extant taxa, but it can be used to measure clustering of any binary trait (Hardy et al. 2012). The analysis is powerful for trees with at least 25 terminals (preferably more than 50) and if trait prevalence is not extreme. In addition, performance is consistent only when phylogenetic resolution is greater than 70% (Fritz and Purvis 2010). This analysis was performed with the range data used to time-scale the trees, and did not require simulated data. D assumes lower values when phylogenetic clustering is strong. A phylogenetically random trait distribution is expected to result in $D=1$, and $D=0$ is the trait distribution expected under Brownian motion. For each clade we chose the 20 myr time interval with the most even trait distribution and measured D in that window.

Results.—When all results are reviewed, only one of the datasets that we used falls within the acceptable range of tree size and trait prevalence outlined by Fritz and Purvis (2010) (> 25 taxa in the timeslice, and non-extreme trait prevalence between about 0.2 and 0.8). Many of our datasets contain a low number of tips following removal of taxa that are not shared between the cladogram and taxonomy. Timeslicing also reduces the number of taxa included in the measurement, because only those lineages occurring within a given stratigraphic window are considered. There is good agreement between the result on the TBP and CBP for the one clade that is suitable for analysis (mammals, Supplemental material: Results), but further large datasets would need to be found in order to confirm the utility of taxonomy for such analyses.