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| **Reference** | **Phylogenetic calculation** | **Variables associated** |
| Sonne, J., Dalsgaard, B., Borregaard, M. K., Kennedy, J., Fjeldså, J., & Rahbek, C. (2022). Biodiversity cradles and museums segregating within hotspots of endemism. *Proceedings of the Royal Society B*, *289*(1981), 20221102. | The species most frequently falling into the first branch length quartile were identified as young. Similarly, we identified old endemic species that most frequently felt into the fourth branch length quartile. | Richness and geographical locations |
| Brée, B., Condamine, F. L., & Guinot, G. (2022). Combining palaeontological and neontological data shows a delayed diversification burst of carcharhiniform sharks likely mediated by environmental change. | We extracted from the time-calibrated phylogeny of carcharhiniforms all divergence times leading to extant species. Median ages were obtained for each node. Following several authors, divergence times of extant species are equivalent to the times of species origination. | We performed PyRate analyses over the combined dataset (time for speciation and extinction) using the BDCS model to estimate diversification rates |
| Rahbek, C., Borregaard, M. K., Antonelli, A., Colwell, R. K., Holt, B. G., Nogues-Bravo, D., ... & Fjeldså, J. (2019). Building mountain biodiversity: Geological and evolutionary processes. *Science*, *365*(6458), 1114-1119. | The number of early divergent birds, mammals, and amphibians, defined as the 25% of species that are separated from the crown node of their class in the phylogeny by the smallest, ranked node distance. The number of recently derived species among the 25% with the largest, ranked rood distance from the crown node. | Richness and geographical locations. |
| Tanentzap, A. J., Igea, J., Johnston, M. G., & Larcombe, M. J. (2020). Does evolutionary history correlate with contemporary extinction risk by influencing range size dynamics?. The American Naturalist, 195(3), 569-576. | We used stem ages to estimate taxon age because they require only one species to be sampled within each genus and reflect the entire evolutionary history of clades. Species ages were also generally captured by genus ages. | Extinction status from IUCN and geographical range. |
| Guinot, G., Adnet, S., & Cappetta, H. (2012). An analytical approach for estimating fossil record and diversification events in sharks, skates and rays. | It is necessary that node 2 is older than node 3 and younger than node 1, in order to respect the phylogenetic hypothesis induced by the cladogram. | Phylogenetic reconstruction. |
| Meijaard, E., Sheil, D., Marshall, A. J., & Nasi, R. (2008). Phylogenetic age is positively correlated with sensitivity to timber harvest in Bornean mammals. Biotropica, 40(1), 76-85. | Species age were obtained from published molecular phylogenies in which data on pairwise genetic divergences between species were converted to approximate times since divergence. This approach followed the method used by Webb and Gaston (2000). | Species sensitivity to logging, expressed by Intolerant, Neutral and Tolerant. |
| Lee, W. G., Tanentzap, A. J., & Heenan, P. B. (2012). Plant radiation history affects community assembly: evidence from the New Zealand alpine. Biology Letters, 8(4), 558-561. | We used molecular-based estimates of stem ages (age for divergence from nearest relative outside New Zealand) for 17 monophyletic genera. | Species richness and percentage of cover (as proxy of abundance and dominance). |
| Gaston, K. J. (1997). Evolutionary age and risk of extinction in the global avifauna. *Evolutionary Ecology*, *11*(5), 557-565. | These node ages were used to derive two measures of the persistence of tribes: 1) the time since a tribe split from its closest sister tribe, hereafter called time since origin, and 2) the time since the tribe radiated. | Probability extinction (Collaer et al. 1994; status of threat). |
| Leopold, D. R., Tanentzap, A. J., Lee, W. G., Heenan, P. B., & Fukami, T. (2015). Evolutionary priority effects in New Zealand alpine plants across environmental gradients. *Journal of Biogeography*, *42*(4), 729-737. | We focused our analysis on monophyletic genera with well-documented phylogenies and published divergence time estimates. Immigration timming cannot be known exactly, and estimates of the age of ancestral nodes on time-calibrated phylogenies provide the best available estimate of lineage age. | Relative abundance (% cover) and richness (proxies of dominance) |
| Davies, T. J., Smith, G. F., Bellstedt, D. U., Boatwright, J. S., Bytebier, B., Cowling, R. M., ... & Savolainen, V. (2011). Extinction risk and diversification are linked in a plant biodiversity hotspot. *PLoS biology*, *9*(5), e1000620. | It wasn’t defined. However, they referred to the variable as “taxon age” and their principal source of data was the phylogenies of South African plants | IUCN threat status |
| Verde Arregoitia, L. D., Blomberg, S. P., & Fisher, D. O. (2013). Phylogenetic correlates of extinction risk in mammals: species in older lineages are not at greater risk. *Proceedings of the Royal Society B: Biological Sciences*, *280*(1765), 20131092. | We obtained phylogenetic age estimates defined as branching times from sister taxa, from an update to a dated and calibrated species-level composite supertree of mammals. | IUCN threat status |
| Johnson, C. N., Delean, S., & Balmford, A. (2002). Phylogeny and the selectivity of extinction in Australian marsupials. *Animal Conservation*, *5*(2), 135-142. | Age from phylogenies: the time since divergence from its closest living relative, in millions of years. | IUCN threat status |
| Brandt, A. J., Tanentzap, A. J., Leopold, D. R., Heenan, P. B., Fukami, T., & Lee, W. G. (2016). Precipitation alters the strength of evolutionary priority effects in forest community assembly of pteridophytes and angiosperms. *Journal of Ecology*, *104*(6), 1673-1681. | To estimate immigration timing, we used the divergence time between the most recent common ancestor of the New Zealand clade and its nearest extant relative outside New Zealand (stem age). We compiled these stem age estimates and their uncertainty from sources using a variety of sequence regions and molecular clock methods. | Relative abundance (% cover) and richness (proxies of dominance) |