A phylogenetic and stratigraphic approach to analysing diversification dynamics in deep time

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The fossilised birth-death (FBD) process is a phylogenetic model that incorporates the species diversification and fossil sampling processes explicitly. The model can be applied to the analysis of stratigraphic ranges, defined as the interval between first and last appearance times in the fossil record, and used to estimate speciation and extinction rates during different geological intervals. In this model, fossils are distributed over time according to a uniform Poisson sampling process, and sampling rate may vary across intervals in a piecewise manner. In the initial application of this model, reliable estimates of diversification and sampling rates were demonstrated to depend on the exact number of sampled specimens and the age of first and last appearances times being specified accurately. This is problematic since (i) the number of fossil specimens sampled during different geological intervals may be challenging to constrain and (ii) the uncertainty associated with the age of first and last appearances is often large. We introduce a novel FBD model that relaxes these requirements. Here, we allow for the possibility that we may only know whether a given taxon was sampled or not during each geological interval, but not the frequency or at which precise time points the taxon was sampled (referred to as presence/absence sampling). We assess the performance of our modelling framework using simulations and demonstrate that although precision decreases given presence/absence data, we can still obtain reliable estimates of diversification and sampling parameters. Finally, we apply our new model to the analysis of the Triassic-Jurassic extinction interval, for which presence/absence data only is available at the sub-stage level, and we re-examine the diversification dynamics across this important and turbulent episode in earth's history. Together, our findings demonstrate the importance of explicitly accommodating the diversification and sampling processes in combination. Our new model should be of broad application in palaeodiversity studies, given that many fossil datasets are comprised of presence/absence data only, making it challenging to analyse such datasets using existing phylogenetic models. Future development of phylogenetic models in palaeobiology should continue to consider seriously the nature of the incompleteness of fossil occurrence databases.