The R package divDyn for quantifying diversity dynamics using fossil sampling data

Adam T. Kocsis (1,2), Carl J. Reddin (1), John Alroy (3), and Wolfgang Kiessling (1)
(1) Friedrich-Alexander-Universität, Erlangen-Nürnberg, GeoZentrum Nordbayern, Department of Geography and Geosciences, Erlangen, Germany (adam.kocsis@fau.de), (2) MTA-MTM-ELTE Research Group for Paleontology, POB 137, H-1431 Budapest, Hungary, (3) Department of Biological Sciences, Macquarie University, Sydney NSW 2109, Australia

Methods to calculate accurate estimates of diversity dynamics are in constant development. These include different metrics of global taxonomic richness, extinction and origination rates, as well as sampling standardization protocols. With the increasing size of this toolkit, it becomes more and more difficult to keep track of the different methods, and to compare their performance and applicability.

Depending on their quantitative skills, researchers tend to implement their own solution to create time series of biodiversity dynamics. Students and less quantitatively inclined researchers either rely on snippets of code or collaboration with colleagues. As reconstructed trajectories of biodiversity dynamics are often the basis of hypothesis testing, the community would benefit from an accessible toolkit to calculate diversity dynamics from fossil occurrence data. We hope that a user-friendly implementation will facilitate the distribution and wider application of these approaches.

Here we present the R package ‘divDyn’ that allows the rapid calculation of a large array of raw and sampling-standardized metrics of diversity dynamics. The package is applicable to any sort of time-binned occurrence databases such as the Paleobiology Database, the Neotoma Paleoecology Database, Neptune, or Ammon databases. The ‘divDyn’ package also offers functions to generate environmental affinities, and tests of extinction selectivity, as well as visualization options for fossil data and the package output. The unique subsampling wrapper function allows the application of popular sampling standardization processes such as classical rarefaction, occurrences-weighted by-list subsampling, and shareholder quorum subsampling.

As an example, we demonstrate the Phanerozoic-scale diversity dynamics of marine invertebrates. With the help of the core function and standard subsampling options, we revisit the declining taxonomic rates over time, mass extinctions and equilibrial diversity dynamics and assess their methodological dependency. Our results suggest that rates declined only over the early Phanerozoic, only three mass extinctions stand out clearly, and evidence of equilibrial dynamics is dependent on the used methods.