"HespDiv" method allows to quantify the dark matter of biosystems

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Bretskyan hierarchy of eco-evolutionary entities is a useful theoretical concept that defines hierarchies of communities of species which reside in the same geographical space and are tied together by ecological interactions and evolutionary history. Bretskyan hierarchy can be employed to define and track the evolving hierarchy of bioregions, allowing all sorts of (paleo)biogeographical investigations to be carried out: from finding the causes why bioregions split or fuse and how this happens at many spatial scales, ie. what drives the internal structure of bioregions in Bretskyan hierarchy. Unfortunately, methodical applications of this concept are challenging due to the hybrid nature of Bretskyan hierarchy entities and fuzziness of their boundaries.

In order to help solve the presented problem of explicit subdivision of contiguous spatial regions, which are in our understanding the units of the Bretskyan hierarchy, we propose a new method, within the newly developed R package "HespDiv" which presents a range of functionalities for the determination of spatial structures/bioregions. The method uses fossil taxa distribution data to subdivide a provided territory into hierarchically related (each bioregion is a strict sub-set of larger bioregion) and topologically contiguous bioregional units. It produces split-lines which are used to subdivide bioregions. This subdivision can be done by employing linear or nonlinear divisor lines inside predetermined area polygons. In a latter case, the inferred bioregions can obtain more realistic shapes. The application of "HespDiv" method to Miocene fauna from the contiguous United States was performed in order to demonstrate the potential of the method. Morisita-Horn similarity index was used to measure differences between fossil taxa communities. The results revealed 25 distinct, topologically contiguous and hierarchically related bioregions had the structure dominated by longitudinal and diagonal boundaries, and the three most distinct bioregions were: West Coast, Central Plains and south-east US.

The numerical analyses of real world paleobiogeographical data with newly developed "HespDiv" method indeed show a high potential of the approach in objectively defining the hierarchical units of the Bretskyan hierarchy of (paleo)bioregions in sufficiently densely sampled regions and time bins.