Deep-sea bioregions based on network analyses

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Abstract

The definition of bioregions based on assemblages of species or communities is fundamental in ecology and biogeography but also in evolution and conservation biology where conservation policies often imply spatially based measures such as protected areas. Hence, spatial units should be biologically and ecologically relevant. In the deep sea, the definition of bioregions faces different constraints and limits. First, only a small percentage of the biggest realm on Earth has been explored. Second, species description rates are continuously increasing, highlighting the scarcity of our knowledge on deep-sea marine species. Here, we aimed at delineating bioregions of the Indo-Pacific region, based on two major (and well documented) taxa of the deep sea benthos: the Galatheids and the Ophiuroids. To cope with data of limited quantity and variable spatial coverage, we first tested aggregating of occurrence data at multiple scale to investigate the impact of the scale used for bioregion delimitation and chose the optimal scale. Then, we applied an innovative method to find bioregions based on bipartite networks. This method allows identifying bioregions but also biodiversity hotspots and transitional zones, which represent an interesting and challenging concept in the open marine environment. We compared our results to existing marine regions classifications (shallow, pelagic or deep-sea ones). Finally, we discuss our results under the perspective of the opportunities and caveats of museum data for such applications.

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