The unified neutral theory of biodiversity and biogeography

Understanding the causes and consequences of biological diversity is one of the greatest scientific challenges of our time. This is important not only from a purely academic point of view; the rapid alteration of natural ecosystems by humans makes an understanding of biodiversity of paramount importance. In *The Unified Neutral Theory of Biodiversity and Biogeography*, Stephen Hubbell makes an ambitious attempt to provide a quantitative theory of species diversity that seeks to address key questions in ecology and evolutionary biology.

Hubbell’s theory is based on neutral models of community drift. Because community assembly is partly based on immigration, Hubbell’s theory is conceptually linked to MacArthur and Wilson’s (1967) theory of island biogeography. However, whereas island biogeography theory assumes neutrality (or equivalence) at the species level, Hubbell’s theory does it at the individual level, in the sense that all individuals in the modeled community have equal birth, death, immigration and speciation rates. A major consequence of this assumption is that the application of the theory is largely restricted to within-trophic level species assemblages, making the theory less general than the title of the book implies. Another important difference with island biogeography theory is that Hubbell’s theory also incorporates speciation, which makes it suitable to address evolutionary questions.

The models developed by Hubbell are elegant in being governed by only a few parameters, yet they construct a broad mathematical depiction of a community. For example, a single parameter—a combination of the per capita speciation rate and the total number of individuals in the community — controls both metacommunity species richness and relative species abundance under one of the two assumed speciation modes. With two additional parameters, immigration rate and local community size, the theory also predicts richness and relative species abundance in local communities. These features allow Hubbell’s models to predict not only the number of species and their relative abundances in local communities, but also species–area relationships and phylogenetic dynamics over evolutionary times.

A good scientific theory must be amenable to testing. Hubbell shows that in some cases his models fit real data surprisingly well. However, as he acknowledges, this model-fitting provides no test of the theory. Validating its predictions would involve measuring each of the parameters for particular metacommunities, plugging them into the model, and comparing the predicted species richness and species abundance distribution at the local
and regional levels with the observed ones. Unfortunately, measuring actual metacommunity sizes and speciation rates with reasonable accuracy can, in most cases, be virtually impossible.

Regardless of these and other limitations, we believe Hubbell’s book is a worthy attempt towards understanding important problems in ecology and evolutionary biology. It should spark new avenues of research that will hopefully advance our understanding of the dynamics of ecological systems. We recommend this book to anyone interested in understanding, predicting and managing biodiversity.

References


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