

Preface

The hypotheses that have been derived to explain the distribution, abundance, dynamics, and diversity of species are typically tested using data matrices containing the names and abundances of species in one to many sites. In effect, this research approach treats all species as independent entities. Species, of course, are not independent. They vary in their degree of relatedness and their functional similarity. Aside from being a basic statistical “issue to deal with,” not accounting for the phylogenetic and functional nonindependence of species likely severely limits the ability of an ecologist to adequately test the hypotheses of interest. Indeed the more we analyze the phylogenetic and functional signature in ecological data, the more we realize that the inferences we might have made using only information about species names and abundances would be overturned if we also considered their phylogenetic and functional similarity. I have now seen such instances enough to be wary of any ecological analyses that do not consider where the species came from and how they actually function.

As a young field ecologist working in the rainforest in El Yunque, Puerto Rico, right after earning my undergraduate degree, I was consistently interested in the spatial distributions of individual species. I could tell you where in the forest you are likely to find a certain species and whether or not other species from that same genus or family were also likely to be in that same area. This was satisfying to some degree, but I was always frustrated by not being able to tell someone *why* a species was only found along streams or ridges. My frustrations lead me to seek out institutions where I could perform doctoral research that would investigate the functional ecology of tropical trees. While interviewing for graduate school I was shocked when three potential Ph.D. mentors in a row asked me whether I was familiar with Cam Webb’s research into the phylogenetic structure of tropical tree communities. Admittedly I had not read Cam’s work prior to my first interview, but by the time the second and third interviews came around later that month, I had read almost all of his papers. My master’s research had been focused on evolutionary biology and I was immediately excited to see phylogenetic information being woven into tropical tree ecology. Around this time I was also reading reviews and empirical studies focusing on the evolution of plant function. Suffice it to say that by the time I started

my Ph.D. research that fall at the University of Arizona, I was very excited about the prospect of quantifying function in tropical tree communities and putting that information into a phylogenetic context.

Almost immediately upon arrival in Tucson, I began to analyze the phylogenetic and functional composition of tree assemblages in the Neotropics. Immediately I ran into significant computational challenges both in the form of integrating and formatting enormous forest plot datasets and in the form of synthesizing the output. I had heard of R during my master's research and it was clear many of my new lab mates were using R, but I had yet to dive in and learn. It was at this time when a postdoctoral fellow and a friend of mine named Jason Pither taught me enough basic R and gave me enough books to make me dangerous (and not always in a good way). It is hard to thank Jason enough for his initial help and encouragement. My life as a researcher has never been the same and I still consult him from time to time for sage advice.

Several years have passed now and I have transitioned slowly from a young field ecologist still trying to figure out basic R code to someone leading R workshops around the world focusing on phylogenetic and functional analyses of ecological data. The first of these workshops I conducted at the Chinese Academy of Sciences, Institute of Botany in Beijing. In preparing for that course I generated a short workbook. I continually updated and expanded the workbook prior to new workshops over the years and the result is this book. I am indebted to the students in those workshops for serving as "guinea pigs" and for helping me improve this text.

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