PREFACE

Over the past 15 years, the merging of phylogenetic trees with ecology has led to new questions and insights about how nature is structured around us. But perhaps more importantly, this new field of phylogenetic ecology—*ecophylogenetics*—represents a reunification of the fields of ecology and evolution. Long treated as separate disciplines, the plethora of observations, experiments, and theoretical developments in ecology and evolution reinforce the reality that there are a finite number of mechanisms that shape the distribution and diversity of life on Earth. These mechanisms result in ecological and evolutionary patterns of diversity, and ecophylogenetic approaches offer an opportunity to integrate processes and patterns operating at multiple temporal and spatial scales.

This is not to say that there haven't been missteps, blind alleys, and problematic assumptions during the development of the field. Rather, as with any nascent discipline, the field of ecophylogenetics has had its ups and downs; some researchers have rightfully pointed out that early hypotheses were often unrealistically simplistic and, mirroring the progress of community ecology, others have (rather prematurely) announced the death of the field. However, ecophylogenetic patterns hold more information than measures of species richness and abundance, upon which much of ecology rests. The existence of phylogenetically nonrandom species associations is widespread in nature, and this reality provides an exciting opportunity to understand how communities are structured and assembled.

This book is meant to provide those interested in phylogenetically nonrandom patterns in ecology with the conceptual underpinnings and tools to pursue their own research on the topic. We also carefully highlight problematic assumptions and areas that need further research. In providing these tools, we exclusively use the R statistical programing language. There are other programs and platforms one could use, but we chose R because of our familiarity with it and the fact that it is now the most widely used statistical program in ecology and evolution. Further, since R is open sourced, new functions are contributed to R packages as quickly as they are created, facilitating further advancement. The R package is also freely available. However, despite all these important benefits, there are potential problems. It may be that user-contributed functions have bugs, and the onus is upon the user to ensure that a particular function performs the task asked of it. It is also useful to remember that when writing R scripts, the successful execution of a function or a few lines of code does not guarantee a correct answer. Further, and quite frustratingly, interdependency among packages often means that substantial changes to one package renders others inoperable. It may very well be that shortly after this book is published some of our coded examples fail due to changes in functions, object types, or required arguments. We will do our best to keep code updated in our repository linked here (http://press.princeton.edu/titles/10775.html).

This book has benefited from the help, feedback, and encouragement from a number of people. Firstly, we would like to thank all those researchers who have unselfishly contributed R code and created packages so that others can do better science. In particular, we acknowledge the contribution of a few researchers who have been instrumental in developing many of the methods and libraries we use in the following chapters, including Steve Kembel, Matt Helmus, Liam Revell, Luke Harmon, and William Pearse. We apologize to

the many others we have not named; the length of this list is an indication of the field's strength and depth. Science is truly a cooperative enterprise. We are thankful to those who gave us permission to use their data or R scripts in this book, including Elsa Cleland for the Jasper Ridge data, and Shai Meiri for sharing data on the mammal community at Yotvata. This book greatly benefitted from discussions with Steve Kembel and Pedro Peres-Neto. We wish to thank Jie Liu and Xingfeng Xi for catching errors—though those that remain are completely our fault. We are also extremely grateful to Matthew Leibold and an anonymous reviewer for supplying comments on a draft of the book. For their continuous encouragement and overlooking repeatedly missed deadlines, we are grateful to Alison Kalett and Betsy Blumenthal at Princeton University Press. We are extremely grateful to Sheila Ann Dean for carefully copyediting this book. Finally, Marc would like to thank Shirley Lo-Cadotte for all of her love, patience, and support, but mostly her patience. Three and half years was a long time to have a distracted partner. Jonathan gives thanks to LW.

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