

Preface

Many evolutionary biologists are concerned with the tremendous amount of diversity of species, and their phenotypes, that we can currently observe in nature, and one of the most challenging tasks is to find evolutionary explanations for such interspecific differences. The philosophy of comparing attributes of different species that have undergone different selection regimes has heavily dominated the way we think about evolution since the days of Darwin. Subsequently, a vast number of studies have interpreted inter-specific variations in species-specific traits in the light of parallel variations in certain environmental or social factors.

However, a significant paradigm shift in the application of comparative methods occurred in the 80s, mostly from the influential work of Felsenstein in 1985, when it was recognized that patterns of inter-specific variations cannot be interpreted without taking into account the underlying common descent of species that delineates certain evolutionary constraints and also leads to similarity between species' phenotypes. Statistically, the effect of phylogeny can be regarded as a confounding factor that violates assumptions about non-independence of the unit of analysis, and that potentially introduces spurious correlations across traits. The development of the independent contrast method caused a flourish in the literature, in which most comparative papers adopted the method as an efficient way to get rid of these unwanted effects of phylogeny.

Modern phylogenetic methods go well beyond of this simple task of achieving a simple statistical control for phylogeny. They rather treat the evolutionary history of species as an interesting phenomenon on its own, that allows tracing character states back through time along series of ancestral states. The real value of modern phylogenetic methods is, therefore, the capacity to examine biological diversity in the light of the phylogeny, a perspective that opens up horizons for making inferences about where, when, and how traits have changed over an evolutionary time scale. The phylogenetic comparative framework by today has grown to address a large number of fascinating questions about the correlated evolution of traits, phylogenetic signals in interspecific data, ancestral states, the mode of evolution, evolutionary rates, alternative evolutionary mechanisms, speciation and diversification and between-species interactions. Most of the methods are available for both discrete (like mating system) and continuous (like body size) characters, and have already started to spread into disciplines other than evolutionary biology (e.g., anthropology, genomics, linguistics, law, and sociology). Furthermore, given

that the phylogenetic comparative approach essentially offers a general framework for studying hierarchically structured data of any kind, one must assume that the exploitation of the underlying toolbox it provides has lagged behind its inherent potential.

In the current state of evolutionary biology, when phylogenies and interspecific data are accumulating at an enormous speed, it is becoming crucial that practitioners are armed with a diversity of comparative methods that help them make inferences from such data. However, overseeing these statistical tools becomes particularly challenging because of the richness and mathematical complexity of the relevant literature. In that situation, a secondary source, in which the primarily literature is brought into the attention of the user community in a consumable way may enhance the statistical integration of the discipline. This book has been assembled under this motivation, and aims at providing descriptions about the most recent phylogenetic methods for evolutionary biologist.

There are several other, very useful books on similar topics. Our book is not only novel because it revolves around the most recent developments, but also because this is an edited volume comprising contributions from several authors, each being expert on his/her respective subfield. This extensive collaborative project may, hence, offer a broad focus on a diverse array of topics and perspectives, which could not be covered efficiently by a handful of specialized authors only. The contributors to this book have been working in different fields of evolutionary biology for many years, under the ultimate aim of solving important biological questions. While fulfilling this enthralling mission we are often confronted with the task of broadening existing approaches and exploring new advances in the comparative study of diverse taxonomic systems and communities. In the light of this scientific background and our experiences obtained during teaching and in various statistical courses, we felt that a textbook was needed to provide a broad overview in the field of phylogeny-based evolutionary biology to our students and less experienced colleagues. Therefore, we wanted to compile a wide range of different perspectives and practices in the phylogenetic comparative method: from an introduction to the topic, through the diversity of statistical designs that can powerfully incorporate phylogenetic information, to more enhanced applications that offer studying evolutionary mechanisms. We must note, however, that due to various constraints, we were not able to review the entire literature that might be relevant. We hope that we will be able to adjust for such a shortcoming in the future.

Another extra value we offer is the accompanying online resource (available at <http://www.mpcm-evolution.org>), where we wish to post and permanently update practical materials to help embed methods into practice. As Online Practical Material (OPM), we will provide tutorials, example files and the underlying statistical scripts, with which the users will be able to apply the presented methods to their own data and scientific questions. New approaches appear like mushrooms in the forest, with some of them being implemented in practice at a rapid pace. It is also becoming very common that more than one statistical approach is available for the same evolutionary problem. Being able to select from alternative

approaches also allows researchers to gain better comprehension of biological diversity present in natural systems. Therefore, it is vital to keep these methodologies updated and accessible for the broad user community, and the attributes of an online surface can be fruitfully exploited in that direction.

Statistics is not without mathematics, and the derivation of certain formulas is unavoidable for the appropriate argumentations. In this book, we constrain ourselves to present only the key mathematical formulas that are necessary for understanding the philosophy of different approaches. Doing so should make the reasoning accessible to a broad readership. For those who are interested in the mathematical details, we provide pointers to the primary literature. And for those not interested in the mathematical details, do not fear. The equations herein should be treated as resources if you decide to incorporate these methods into your research.

The quality of this book in large part resides on inputs from several expert reviewers, who provided valuable comments on earlier versions of chapter manuscripts during their review phase. Along that line, we are extremely grateful to David Bapst, Roger Benson, Kierstin K. Catlett, Natalie Cooper, Thomas Currie, Pierre de Villemereuil, Joe Felsenstein, Sive Finlay, Rob Freckleton, Jesualdo Fuentes-Gonzalez, Alejandro Gonzalez-Voyer, Tatiana Giraud, Alan Grafen, Randi Griffin, Jarrod Hadfield, Thomas Hansen, Lam Si Tung Ho, Elisabeth Housworth, Antony Ives, Jason Kamilar, Tom Kraft, Oriol Lapiedra, Jessica Light, Graeme Lloyd, Rafael Maia, Emilia Martins, Nick Matzke, Mark A. McPeck, Magdalena N. Muchlinski, Shinichi Nakagawa, Chris Nasrallah, Charles L. Nunn, Christopher E. Oufiero, Emmanuel Paradis, Sandrine Pavoine, Matt Pennell, Pedro Peres-Neto, Samantha Price, Liam Revell, Aaron Sandel, Holger Schielzeth, William Shipley, Graham Slater, Jeet Sukumaran, Matthew Symonds, Gavin Thomas, Chris Venditti, Jamie Caroline Winternitz and Derrick Zwickl for their constructive assistance in the evaluation process.

Although the list of authors appears male biased, this is completely unintentional. Female scientists were also invited to write chapters, but regretfully they could not make contribution due to various and completely understandable reasons.

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