

PREFACE TO THE SECOND EDITION

It has been over 25 years since the first edition of *Phylogenetics*. During that time, phylogenetic systematics has taken its place as the dominant paradigm of systematic biology and fundamentally influenced how scientists study evolution. Moreover, during the intervening years since that first edition, there have been many theoretical and technical advances and the field of phylogenetics has continued to grow. The great philosopher Marcus Aurelius's recognition that "time is a sort of river of passing events, and strong is its current" is doubly true in this area of scientific research. For instance, there are now new approaches to reconstructing the pattern of evolution designed to take character conflict and the uncertainty of phylogenetic estimates into account. The fallout from the molecular systematics revolution is a prominent part of this. Phylogeneticists have also moved beyond solely employing Hennig's argumentation schemes and now use more formal parsimony analysis or parametric methods such as likelihood and Bayesian inference in an attempt to reconstruct evolutionary relationships among organisms and find a fit between Earth history and descent with modification. We have tried to capture the essence of the evolving discipline that is phylogenetics in this new edition. If current trajectories imply anything, they suggest that the next 25 years of phylogenetic research will continue to prove exciting, with many fascinating theoretical and technical developments yet to come.

We also recognize that this disciplinary growth has not been without acrimony, and there have at times been battles waged between those advocates of parsimony analysis and those who argue for more statistical approaches to estimating phylogenies. We present the view here, however, that there is room for all of these approaches within the phylogenetic community. The principles used in these different approaches are closely similar. Relationship still means genealogical relationship, synapomorphy is still the mark of common ancestry, and monophyletic groups are the only natural groups regardless of whether one uses a parsimony algorithm or a likelihood algorithm to analyze one's data. That make us all phylogeneticists, and if you wish to use a label, it make us all Hennigians.

We have written this book for the practicing systematist and phylogeneticist. Our focus is on both philosophical and technical issues, and the philosophical issues discussed are those that we believe all working systematists need to address; these involve issues of the nature of species, the nature of characters, the nature of names, and the nature of biogeographic areas. While we cover what we think are the basics of parsimony, likelihood, and Bayesian analyses, we do not pretend that our coverage is more than basic. There are other texts, some highly mathematical, others less so, that cover these topics in more depth. We have tried to broadly cite this literature, at least up through 2009, but the field of parametric phylogenetics continues to advance faster than any one book can hope to capture without being out of date before publication. However, we hope that working systematists will be able to understand the basics we present and use these as an entrée to a rapidly evolving discipline.

Over the long course of producing this second edition of *Phylogenetics*, we have greatly benefited from the comments of many colleagues. First and foremost are Mark Holder (University of Kansas) and Peter Midford (now at NESCent) who reviewed, page-by-page, most of the chapters dealing with taxa, characters, and methods of analysis. Mark Holder paid special attention to our chapter on parametric phylogenetics, patiently guiding us through much of the technical literature and attempting to keep us out of trouble in an area where we have no special expertise. We also gratefully acknowledge Mark Holder for his contributions in the area of biogeography. In particular, he helped figure out exactly how Modified Brooks Parsimony could be placed in a formal, algorithmic framework. We are very grateful for all of his insights and help. We also thank Norman MacLeod (Natural History Museum, London) for his insightful comments and suggested revisions on the subject of morphometric analysis. In addition, Francine Abe and Matthew Davis (University of Kansas) helped us understand morphometrics well enough to get a draft of this section to Norman. We thank John Wiens for his insights on missing data. We thank Dr. Randy J. Read for permission to use and adapt his examples illustrating maximum likelihood and Bayesian inference from WWW material that formed part of a course he taught at the University of Cambridge 1999–2000. Special thanks go to two philosophers of science for taking the time to consider philosophical issues with one of us (EOW). David Hull (Northwestern University) has always been willing to discuss issues of individuality and species. Elliott Sober (University of Wisconsin) kindly reviewed an earlier draft of the section on philosophy. We are also grateful to the folks at Wiley-Blackwell, especially our editor Karen Chambers, for helping to bring this project to fruition.

E. O. Wiley
Lawrence, Kansas — Bruce S. Lieberman

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This is a book about systematics and how the results of systematic research can be applied to studying the pattern and processes of evolution. The past twenty or so years have seen tremendous changes in biological systematics. Although some of these changes have occurred because of the discovery of previously unobservable characters, the most profound changes have taken place on the methodological and philosophical levels. Systematists have become more critical about the methods they employ and the biological and philosophical bases for these methods.

The first half of this century saw evolutionary theory march ahead of systematics, but in a rather curious manner. Evolutionary theorists became disinterested in the pattern of organic descent and concentrated on various processes purported to occur on the populational level of analysis. This resulted in the generally accepted theory known as the Synthetic Theory of Evolution, or neo-Darwinism. In itself the neo-Darwinian theory is an admirable accomplishment. However, it is not enough. What is needed now is a better understanding of the origin of species, and, as Waddington (1957) says, why there are tigers and elephants and other such things. To approach such an understanding we must first have something to understand. This something is a phylogenetic tree, a pattern of organismic descent.

Phylogenetic systematics, or simply "phylogenetics," is not just another approach to systematics. It is an approach to systematics designed to estimate the pattern of phylogenetic descent that is needed to deduce the processes of evolution concerned with the origin of species. The classifications that result from phylogenetic analysis are critical tools for evolutionary studies. Phylogenetics is also more than the hand-maiden of evolution, however, for its underlying philosophy provides a way of viewing nature, asking questions and solving problems associated with the evolution of organisms.

I wrote this book to outline what I perceive as the philosophy and methodology of phylogenetics as a systematic discipline. As such, it is not restricted simply to the methods for reconstructing phylogenetic relationships and presenting these relationships in the form of a classification. Rather, it is also directed toward an

understanding of the evolution of species and the biological entities that comprise the history of descent with modification. Further, the phylogeneticist must also be a taxonomic scholar familiar with methods for dealing with specimens and characters, ways of assessing taxonomic literature, and various rules of nomenclature. These subjects are also dealt with.

Phylogenetic systematics is an approach to systematics that accomplishes an ordering of organic diversity in such a way that our ideas concerning the inferred evolutionary relationships among organisms can be scientifically discussed and evaluated. Much reaction has been directed toward this approach from its critics. I believe that most of this reaction stems from a lack of understanding of phylogenetics. My major purpose in writing this book was to clearly and simply present phylogenetic systematics (to the best of my ability) in the hope that others will understand its goals and methods. Only through understanding can profitable criticism and subsequent improvement follow.

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E. O. WILEY