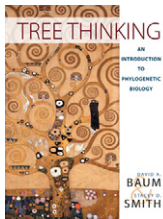


Biology in the light of phylogeny

Tree Thinking: An Introduction to Phylogenetic Biology by David A. Baum and Stacey D. Smith. Roberts and Company Publishers, 2012. US\$75.00/£47.81, hbk (476 pp.) ISBN 978-1-936-22116-5

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The importance of phylogeny to the understanding of patterns of diversity has long been appreciated (indeed, the only figure in Charles Darwin's *Origin* [1] was of a phylogenetic tree). However, only in the past several decades has understanding phylogeny and its consequences become essential across a broad range of evolutionary research topics. Following Felsenstein's prescient paper [2] demon-

strating the non-independence of species in comparative biology and Harvey and Pagel's influential book on comparative methods [3], phylogenetic thinking has percolated into many biological disciplines; the recent development of community phylogenetics, for example, [4], being just one example. This interest has been accompanied by a rapidly expanding body of literature devoted to both the estimation of phylogenies and their application. In his review of Felsenstein's landmark book *Inferring Phylogenies* [5], Fredrik Ronquist wrote 'perhaps the field is now growing too fast for there to ever be [a comparable book]' [6] – a suggestion that seems even more apt today. While using phylogenetic trees has now become commonplace in many fields outside of evolutionary biology, such as ecology, conservation biology and molecular biology, understanding the vast technical literature of phylogeny reconstruction and comparative analyses likely remains a substantial barrier to many researchers and students.

In their new book *Tree Thinking: An Introduction to Phylogenetic Biology* [7], David Baum and Stacey Smith bridge this gap by providing a thorough and comprehensive entry-level text on phylogenetic concepts and methodology. This is undoubtedly an incredibly challenging task – finding the right balance between a rigorous treatment of the methods while still making the material comprehensible to a non-specialized audience – and they pull it off remarkably well. Their book is perhaps the clearest description I have read of what phylogenies actually represent, how to interpret them and how 'tree thinking' is fundamentally different from other ways of (mis)conceiving evolution. The first couple of chapters, in which phylogenetic concepts are introduced, should be mandatory reading for undergraduate biology students.

The authors also do an excellent job at conveying concepts that may be challenging for unfamiliar readers to grasp, often using analogy and plenty of biological examples from the literature. These include relatively extensive coverage of general statistical concepts such as maximum-likelihood

and Bayesian analysis as well as more specific topics such as gene-tree/species-tree incongruence and probabilistic models of sequence evolution. For example, various models of sequence evolution (JC, F81, HKY and GTR) are explained with a scenario of a 'card-flipping' fairy who swaps playing cards on a table, according to some set of rules (the model), unbeknownst to the observer. In this way, the authors are able to present some complex material in an intuitive way.

There are a few topics in the book that I thought were either over- or under-emphasized. I would argue that they give undue attention to parsimony. Several concepts (e.g. optimality criteria for inferring phylogenies, methods for estimating nodal support, and comparative analysis) are introduced with a thorough description of a parsimony-based method. The field has, as Baum and Smith repeatedly emphasize (after explaining the method in question), largely moved beyond these approaches. Despite their historical importance, I question the need to review parsimony-based methods in such detail and think that this may be more confusing than helpful to students first encountering these topics.

A topic that I felt deserved more attention is model selection and model adequacy. With regard to selecting a model of sequence evolution, only hierarchical likelihood ratio tests are discussed in any detail and problems associated with model misspecification are barely mentioned. This applies to both the models of sequence evolution and to comparative methods (e.g. ancestral state reconstruction and models of diversification). It seems to me that inexperienced researchers are often overly confident in the ability of sophisticated models to yield sophisticated results and some (strong) words of caution would probably go a long way.

This book occupies a special niche in the phylogenetics literature and to my mind there is nothing else like it. It is very well-written and well-conceived and will hopefully be widely read by researchers and their students in fields of biology outside of evolution. There are necessarily trade-offs in writing a book intended for such a broad audience. While readers of the book will surely gain a strong grasp of evolutionary thinking and be able to read and understand much of the literature on the topic, those who intend to estimate or to use phylogenetic trees in their own research will need to look elsewhere for details, for example, [5,8]. I imagine that there are many more uses of phylogenies that researchers have not even considered yet. Baum and Smith's book should go a long way to encouraging these developments and fostering 'tree thinking' in young (and old) biologists of all sorts.

Acknowledgments

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