

BOOK REVIEW

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# Phylogenetic biology for both novice and expert learners

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## Book details

*Tree Thinking: An Introduction to Phylogenetic Biology*, by David Baum and Stacey Smith. Greenwood Village, CO: Roberts and Company Publishers, 2013. Pp. xx +476. ISBN:9781936221165. H/b \$75.00.

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Baum and Smith have contributed a thorough explanation of the theory, methodology, and applications of evolutionary relationships in their book *Tree Thinking: An Introduction to Phylogenetic Biology*. These authors have previously contributed to pedagogy in evolutionary biology (e.g., Baum et al., 2005), and this new introduction is a valuable addition to the libraries of both new students and scholars of other scientific fields. Following an introduction framing phylogenetic trees and their basis in biological literacy, the book is divided into three main sections: interpreting trees, inferring trees, and using trees. Resources at the end of the book include appendices which describe the nature and generation of data for phylogenetic analysis as well as a glossary of relevant terms. Each chapter includes two resources at its conclusion: a “Further reading” section and chapter quiz. The questions in the quiz represent a variety of formats (multiple choice, short answer, fill in the blank, etc.) as well as levels of cognition (e.g., knowledge recollection through synthesis), and the answers are available as a resource at the end of the book.

While the format of the book allows readers to learn and assess knowledge independently, a basic understanding of evolutionary theory and genetics is required to easily comprehend the text. Concise definitions for concepts of interest are embedded in the text as well (e.g., speciation, pp. 38–40). Given the propensity of the American population to reject part or all of evolutionary theory (Miller et al., 2006), the authors take a sensible approach to common (but out-of-scope) refutations:

“For our purposes it does not matter whether the cause of the separate origins was by natural or supernatural means...” (p. 15). A few pages later, they emphasize a nuanced but important aspect of the debate by stating, “While science rarely deals with certainty, it is fair to say that evolution from common ancestry is now supported beyond any reasonable doubt” (p. 23).

Following this circumscription of evolutionary theory, the authors continue to identify a number of common student misconceptions. For example, Chapter 5 describes a number of errors that biology students and professionals possess about interpreting relatedness from phylogenetic trees (pp. 111–117), and follows up with sensible, clear ways of correcting these fallacies. A variety of different types of diagrams are used throughout the text to illuminate evolutionary principles, which are essential to ameliorate the effects of misconceptions. Interpretation of phylogenetic trees is cognitively complex, and experts may take tree-thinking skills for granted. Reference to familiar topics, such as transferring pedigrees to phylogeny (pp. 108–109), helps break concepts down into digestible units for students who are struggling or new to the field of study. These same types of diagrams are consistently used in following chapters to highlight more challenging topics, like descent over different timescales (Figures 3.1–3.6, pp. 36–38), fixation of alleles in populations (Figure 4.1, p. 78) and relating gene trees to species trees (Figure 6.7, p. 149).

Following misconceptions about evolutionary theory and interpreting trees, a common barrier to education in biology is student resistance to understanding the mathematical foundations of the methods they use (Bialek and Botstein, 2004). Baum and Smith elegantly explain the

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mathematical basis of phylogenetic inference by providing sufficient detail in an accessible manner. Nonparametric bootstrapping, for example, is illustrated by describing a con artist drawing from a deck of rigged cards (pp. 273–274). The effects of different tree estimation algorithms and datasets (molecular vs. morphological) are illuminated by referencing the same Carnivora dataset (pp. 173 onwards). By offering multiple ways of interpreting mathematical ideas (i.e., clever analogies as well as the equations), *Tree Thinking* promises to diffuse student anxiety associated with these concepts.

Another method consistently used throughout the book is contextualizing important concepts in the history of the field. Students often view taxonomy, for example, as a static set of facts that are infallible and unchanging. Chapter 5 of *Tree Thinking*, however, delves into the reasons behind taxonomic reclassification and what it means for our understanding of evolutionary history (pp. 107–138). Hennigian inference is intuitive and accessible for students to understand, and the authors are explicit in describing this method specifically to highlight its limitations (pp. 180–181). Similarly, generalized parsimony is used as a bridge to explaining maximum likelihood analysis (pp. 202–203), which students may find more intimidating. The development of phylogenetic biology has also spawned a dizzying amount of terminology, but Baum and Smith manage to focus on the most wide-ranging vocabulary, even noting when particular terms are specific to certain areas of study (i.e., complex nomenclature in gene duplication, p. 153).

While the benefits of *Tree Thinking* to novice learners are obvious, the clarity of writing makes the text engaging for experts in evolutionary biology as well. Moreover, there are several notable areas of the book which identify misconceptions commonplace among even professional researchers. Advanced scholars may particularly value Baum and Smith's careful interpretation of what phylogenetic trees represent in relation to biological reality (e.g., hard polytomies, p. 59), especially in the context of contemporary evolutionary biology research. Additionally, they note nuances associated with ancestral vs. derived states early in the book (p. 80), and later expound at length on the inference of adaptation from trait evolution (pp. 306–311). Indeed, the last section of the main text—Using Trees—covers topics that are currently in active and rapid development in the research community. While the specific methods mentioned in the book may be supplanted over the next decade, the conceptual framework around asking such questions will remain valuable.

A final useful perspective represented in the book is a successful reconciliation between how evolutionary theory is presented in textbooks with depictions in primary literature. During a discussion of different tree representations, the authors note that while phylograms are common

in research literature, cladograms and chronograms are frequently used in secondary literature and textbooks (p. 56). Similarly, while discussing types of non-monophyly, Baum and Smith note general that paraphyly and polyphyly are “commonly emphasized, but not very meaningful from a modern, tree-thinking perspective” (p. 125). By filtering out the most important information for students to understand, this text offers a well-rounded understanding of phylogenetic theory without overloading readers with terminology.

On the other hand, there are certainly experienced researchers who will balk at some descriptions and methods described here. Like any circumscription of a rich and nuanced research topic, a plurality of viewpoints exists in the phylogenetics community. For example, the authors describe automated multiple sequence alignment programs as “a good starting point” for manually adjusting the alignment afterwards (p. 200). However, emerging methods for analyzing large phylogenetics datasets preclude subjective curation by hand. Some readers may prefer slight deviations from the methods and theory described in the book based on prevailing usage in their subfield. Moreover, the level of depth with which particular methods or theories are detailed varies throughout the book. In contrast to the nuanced descriptions of early chapters, the last section serves as a more general overview of methods and approaches to tree use.

Despite these slight setbacks, *Tree Thinking* does an admirable job describing the important parts of phylogenetic biology as well as the educational philosophy behind their framework. The quiz questions throughout the text offer readers the opportunity to assess their learning as they progress through material, which should ameliorate common misconceptions in evolutionary biology. The inclusion of analogies and careful use of language makes this an accessible resource for new learners, while the comprehensiveness of the text may appeal to advanced scholars as well.

#### Competing interests

The author declares no competing interests.

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