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Tree Thinking: An Introduction to Phylogenetic Biology. David A. Baum and Stacey D. Smith.

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Emlen has also commented: “We want this book to be fun to read and, more importantly, we want the content to stick in the minds of students.” These are, indeed, 2 distinct goals, as the one does not necessarily imply the other. Perhaps the most obvious approach used by the authors to providing an “engaging read” is to present anecdotes, both about people (at the start of each chapter) and about organisms (during the chapters). However, using anecdotes about each topic is burdened with the possibility that the anecdotes will be the *only* remembered thing. Indeed, there are comments in online review sites that suggest that this has in fact happened: “you’ll never care (or, in my case, remember) what the Buri experiment is, [but] at least you’ll remember what a Harlequin beetle or an okapi looks like” (from Joanna, at GoodReads).

The authors’ approach to providing something that is “gorgeously illustrated” has, I am sorry to say, turned out as far too many illustrations per page. The individual photos are very pleasing, and the graphs and other processed data are clear and informative, but there are simply too many per page for there to be any visual coherence. Sorting out what was what on each and every page became a real challenge after a while. I am not convinced that I will even remember what an okapi looks like, because by the end of the book I had overdosed. So, the content is to some extent buried under the presentation. Even the index is in 4 colors (plus italics). Once again, here I think that less might be more.

The over-whelming nature of the book is also translated into its size, of course. William Goldman, the novelist and scriptwriter, once wrote a large book (*Boys and Girls Together*), about which he later claimed one reviewer wrote: “‘a child of nine could understand this book before he could lift it’ . . . from there the review got really bad.” Zimmer and Emlen are lucky not to have that same reviewer, because their book has 713 pages and weighs 2 kg, even in paperback. If you try to read this book in bed, it is literally life-threatening.

So, do yourself a favor, and get a copy of the app for your iPad Mini, instead, because this is precisely the type of book that Apple had in mind when they designed that device to help with your bedtime reading. At the time of

writing, the *Evolution* app is up to Version 1.3, so most of the bugs have been ironed out.

Importantly, in this case, the app is not simply an adjunct to the printed version of the book but is a stand-alone multimedia “experience” containing images, audio and video clips, and interactive graphics and exercises. For example, when reading about the way male frogs attract females when mating, you can actually listen to the difference between apparently attractive and nonattractive calls. Also, you can highlight text information and make notes in the margins, and then create custom study sheets that incorporate supplemental information.

Zimmer and Emlen are at the forefront of the move to enhanced digital presentation. As Kwok (2012) has noted: “publishers are increasingly placing equal or greater importance on the digital product rather than considering it as an add-on to the printed book.” This kills 2 birds with one stone—authors can focus on “the complete learning experience” rather than trying to do everything with written words, and the readers can stop feeling like they are doing weight training every time they try to learn something. A similar thing can be said about species-identification books, where a printed book is both heavier and less useful than an interactive app, especially in the field (Morrison 2011).

So, the bottom line with *Evolution* is that this is a very well-intentioned book that achieves many laudable aims but simply goes too far in trying to achieve its overall goal—the sum of the parts ends up being more than the whole. I sincerely hope that this can be addressed in a second edition.

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Tree Thinking: An Introduction to Phylogenetic Biology.—David A. Baum and Stacey D. Smith. 2012. Roberts and Co., Greenwood Village, CO. xx+476 pp. ISBN 9978-1-936221-16-5 \$US75 (hardback).

For many years, phylogenetics was a topic confined largely to systematics. However, after the “molecular revolution” phylogenies began to permeate nearly every branch of the biological sciences, and they have since become tools that are common throughout

mainstream biology. Unfortunately, along with this shift came the realization that phylogenetic trees are prone to misinterpretation. A phylogenetic tree provides a particular type of narrative representation of evolutionary history (O’Hara 1992), and one needs to grasp “tree thinking” to correctly interpret this form of narrative.

Systematists tend to take it for granted that a phylogenetic tree is straightforward to interpret. However, in the real world this is clearly not so, and tree

thinking cannot be taken for granted (Sandvik 2008). As David Baum and Stacey Smith have noted in their recent book on *Tree Thinking* (p. xv), the basic issue is that:

tree thinking runs counter to standard perceptions of evolution in popular culture. We do not know why it should be so, but we have learned from working with thousands of students that, without contrary training, people tend to have a one-dimensional and progressive view of evolution. We tend to tell evolution as a story with a beginning, a middle, and an end. Against that backdrop, phylogenetic trees are challenging; they are not linear but branching and fractal, with one beginning and many equally valid ends. Tree thinking is, in short, counterintuitive.

In the past decade, an entire cottage industry has appeared of people studying this phenomenon.

Of particular concern, of course, is educating students. Much progress has been made in comprehending how and why students misunderstand phylogenetic trees, and what we might do about it (Goldsmith 2003; Baum et al. 2005; Meir et al. 2007; Sandvik 2008; Catley et al. 2010; Miesel 2010; Morabito et al. 2010; Novick et al. 2010, 2011; Halverson et al. 2011; Novick and Catley 2013). The message is clear: people seem to easily grasp transformational evolution but not variational evolution, unless a special effort is made to train them (or educate them). One quotation from the internet will illustrate the issue:

Honestly, when I started becoming interested in biology I hated phylogenetic trees. They were annoying to stare at, and impossible to decipher. I knew they showed evolutionary relationships, but I had no idea about the various applications and questions that could be answered using these methods.

People bring certain preconceptions into any educational setting, which may not be appropriate for that setting. These natural preconceptions come from their prior training, their social background, and their own personal experiences. What is being learned will be fitted into their pre-existing thought processes, and what is said and shown to them will be interpreted in the light of those preconceptions. As noted by Henshaw Ward (1925):

the average man . . . thinks evolution is 'the doctrine that man is descended from monkeys', and he is so amused or offended at this theory that his whole mind is occupied with it. His conception is ridiculously false. Until John Doe discards that notion and takes a fresh start, he will never understand the subject.

Of equal concern, however, is the apparent inability of many professional biologists to understand trees

much better than do students (Krell and Cranston 2004; Crisp and Cook 2005; Gregory 2008; Omland et al. 2008; Sandvik 2009). Not only does this cause confusion within the profession but it also causes complications when communicating with nonexperts. A number of people have investigated how well phylogenetics is communicated in various settings, such as in the classroom, in textbooks, and in museums (Clark 2001; Catley and Novick 2008; Hellström 2011; MacDonald and Wiley 2012; Torrens and Barahona 2012), and the news is uniformly dismal. Perhaps the biggest issue is ambiguity in the way that phylogenetic trees are presented and described—understanding phylogenies as representations of evolutionary relatedness is a cognitively complex task, and ambiguity can play no part in that process. The two biggest issues seem to be that (i) people often pay more attention to the order of the taxa at the tips of the phylogeny than they do to the branching order of the lineages, and (ii) they incorrectly emphasize a single lineage in the phylogeny, which they see as the “main branch” of the tree, with the other lineages as side branches (and also some branches as being “basal” and others not).

Clearly, then, we need a textbook for students and nonexperts, and *Tree Thinking: An Introduction to Phylogenetic Biology* is intended to be that book. There are other books available that are either more basic (Hall 2011) or more advanced (Lemey et al. 2009), and even those that are compendious (Felsenstein 2004), but in the broad middle ground there is no real competition. The authors have been working on this book for quite some time, with their initial thoughts about the problem being presented by Baum et al. (2005), along with the associated web page, and more recent contributions from Baum and Offner (2008).

This book is emphatically a textbook, in that it is pedagogically rigorous, with an initial pretest to assess the student's prior understanding of phylogenetic trees and their interpretation, and then with quizzes at the end of each chapter to assess ongoing knowledge acquisition. Such a book is not necessarily readable as a sourcebook for professionals, but it amply achieves its primary aim as an inclusive entry-level book.

The book focuses very much on individuals and their characters. It starts by discussing tree thinking in relation to individuals and species, then proceeds to consider character evolution, and then develops the idea of gene trees within species trees. It ends by discussing the usual tree-inference methods, such as parsimony, minimum distance, maximum likelihood, and Bayesian methodology, and finally presents statistical hypothesis testing. The writing style is very clear, potentially complex concepts are usually introduced by an analogy, and the biological examples that pepper the chapters are appropriate.

The focus on individuals and their characters may seem to some people to give the book a “parsimony” feel, in that character evolution is best introduced by counting character-state changes. However, this is simply an implementation of the idea that Hennigian

logic is a good place to start an understanding of trees—it helps you to think about what trees mean. Molecular biologists, on the other hand, often emphasize the plethora of phylogenetic methods and software packages that are currently available, and focus their introduction to trees on an attempt to help practitioners navigate their way through the forest. This is a very different pedagogic approach to phylogenetics.

This distinction does highlight one possible weakness of the book, in that molecular biologists, who form perhaps the biggest group of users of phylogenetic trees, may feel a bit uncomfortable with the focus on individuals. As Yang and Rannala (2012, p. 303) have observed:

Besides representing the relationships among species on the tree of life, phylogenies are used to describe relationships between paralogues in a gene family, histories of populations, the evolutionary and epidemiological dynamics of pathogens, the genealogical relationship of somatic cells during differentiation and cancer development and the evolution of language. More recently, molecular phylogenetics . . . is used: to classify metagenomic sequences; to identify genes, regulatory elements and noncoding RNAs in newly sequenced genomes; to interpret modern and ancient individual genomes; and to reconstruct ancestral genomes.

Of course the book cannot cover everything, but in it this widespread applicability of phylogenetics does take a back seat to an understanding of character evolution and phylogenetic relationships. To me, this is a strength of the book.

In my final analysis, I would say that this book is excellent but 10 years late. We needed a book on trees a decade ago, when a large number of general biologists started taking phylogenetics more seriously, which is also coincidentally about the time the cottage industry referred to above was started. Phylogenetics is now starting to move away from trees. Many botanists, for example, have found trees problematic as a phylogenetic model, due to the widespread hybridization that is assumed to occur among many plant species, and so have many microbiologists, due to the prevalence among bacteria of what we now call horizontal gene transfer. These people need to understand phylogenetic networks rather than phylogenetic trees, which is a much more complex task.

A tree is basically a set of interconnected chains, which is a suitable model for much of evolutionary history, but the rest of that history is more like a set of interconnected trees. So, Baum and Smith are trying to move people away from seeing evolution as a chain, and get them to see a set of interconnected chains, but we

really need to move on to a set of interconnected trees. The book of the future will be called: *Network Thinking: An Introduction to Phylogenetic Biology*.

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