

nothing to convince the reader that this is a better way to do things than the obvious alternatives. I am sure that biologists are prepared to be convinced one way or the other, but it will take some quantitative evidence to do so. Hopefully, this book will act as a catalyst, so that we will not have to wait too much longer to be convinced.

REFERENCES

- Bininda-Emonds, O. R. P. 2004. The evolution of supertrees. *Trends Ecol. Evol.* 19:315–322.
- de Queiroz, A., M. J. Donoghue, and J. Kim. 1995. Separate versus combined analysis of phylogenetic evidence. *Annu. Rev. Ecol. Syst.* 26:657–681.
- Gatesy, J., R. H. Baker, and C. Hayashi. 2004. Inconsistencies in arguments for the supertree approach: supermatrices versus supertrees of Crocodylia. *Syst. Biol.* 53:342–355.
- Semple, C., P. Daniel, W. Hordijk, R. D. M. Page, and M. Steel. 2004. Supertree algorithms for ancestral divergence dates and nested taxa. *Bioinformatics* 20:2355–2360.
- Wilkinson, M., J. A. Cotton, C. Creevey, O. Eulenstein, S. R. Harris, F.-J. Lapointe, C. Levasseur, J. O. McInerney, D. Pisani, and J. L. Thorley. 2005. The shape of supertrees to come: Tree shape related properties of fourteen supertree methods. *Syst. Biol.* 54:419–431.

David A. Morrison, Department of Parasitology (SWEPAR), National Veterinary Institute and Swedish University of Agricultural Sciences, 751 89 Uppsala, Sweden; E-mail: David.Morrison@bvf.slu.se

Syst. Biol. 55(3):532–533, 2006
Copyright © Society of Systematic Biologists
ISSN: 1063-5157 print / 1076-836X online
DOI: 10.1080/10635150600697515

Mathematics of Evolution and Phylogeny—Olivier Gascuel (editor). 2005. Oxford University Press, New York, New York. 416 pp. ISBN 0-19-856610-7. £45 (hardcover).

Over the past two decades our understanding of evolutionary pattern and process has advanced rapidly. In part this reflects the ever-increasing ease with which we generate molecular data; assembling even quite large molecular data sets is becoming a relatively straightforward process. Equally important, however, has been ongoing development of our analytical tools. The increasing power and sophistication of our analytical methods has allowed ever more complex questions to be addressed and has ultimately provided many important insights. Indeed, the importance of continuing to extend our analytical methods—and the mathematical and computational concepts on which they are based—cannot be understated. The ongoing refinement and development of approaches to evolutionary analysis is critical for building on our current level of understanding.

Until recently, the development of analytical tools for evolutionary biology was the domain of a surprisingly small contingent of mathematically minded biologists. However, over the past few years the number of people involved in this area of research has grown rapidly. In particular, the mathematical and computational challenges that evolutionary problems present have attracted many applied mathematicians and computer scientists into this area. The two “Mathematics of Evolution and Phylogeny” conferences held at the Institut Henri Poincaré in Paris, the first during June 2003 and the second in June 2005, illustrate this trend. Considered from a biological standpoint these meetings have featured arguably some of the most exciting areas

in contemporary evolutionary biology. For example, the 2005 conference included presentations addressing relaxed molecular clocks (E. Douzery), bacterial phylogenomics (V. Daubin), and reconstructing the ancestral vertebrate genome (H. Roest Crolius). However, as the conference name and presentation titles suggest, the focus is not on the latest empirical biological results but rather on the mathematical concepts and techniques that underlie the analysis of evolutionary data. Essentially, these meetings highlight the analytical approaches and tools used in evolutionary biology as potential research avenues in applied mathematics and computer science.

The recently published volume *Mathematics of Evolution and Phylogeny*, edited by Olivier Gascuel, is a collection of 14 papers based on the invited presentations from the first of these meetings. As could be expected, both the conference and volume focus on the mathematical and computational concepts underlying evolutionary analysis. The book begins with an informative introduction that provides both an overview of the central role that mathematical concepts play in evolutionary analysis and outlines the general structure of the book. Each of the chapters that follow is a self-contained and authoritative review; all of them provide a summary of the mathematical concepts and techniques that are in current use, some historical perspective, a brief discussion of the biological relevance or interpretation, and an outlook on future research. In addition, for those who wish to delve further, the comprehensive reference lists offer plenty of additional reading.

Whilst for the mathematically minded each chapter represents a thorough review, the extensive mathematical “chicken scratching” will be daunting for the not so

mathematically minded—more than just a passing understanding of mathematics is required in order to get the most out of this volume. Quite clearly *Mathematics of Evolution and Phylogeny* is not for the faint-hearted or mathematically unprepared, but this is perhaps not surprising given the title. If you progress very far into any of the chapters it will become fairly obvious that the target audience is mathematicians (or computer scientists) rather than biologists. For those with a more modest mathematical background, a “field trip” to the nearest mathematics department may be necessary in order to decipher some of the more technical points. That said, several of the chapters do incorporate empirical biological examples, and these help to make these contributions more accessible.

There is a great deal more mathematical theory behind evolutionary analysis than could ever be covered in a single volume. Indeed, *Mathematics of Evolution and Phylogeny* does not address close to the full diversity of concepts and techniques. However, even quickly flipping through the introduction or table of contents will make it obvious that in a little over 400 pages a lot of mathematical ground is covered. The first seven chapters focus on the use of DNA sequence data for phylogeny reconstruction (this topic is likely to be of greatest interest to many systematists). Of these, the first three discuss the minimum evolution (Desper and Gascuel), likelihood (Bryant et al.), and Bayesian (Yang) approaches to building phylogenies. Chapter 4 (Holmes) addresses the issue of statistical testing in phylogenetics, whereas the following two chapters consider aspects of evolutionary models—specifically, Meade and Pagel address mixed models and Hendy discusses Hadamard conjugation. The topic of the final chapter in this section is perhaps less familiar, as here Huber and Moulton describe split-based approaches to reconstructing phylogenetic networks. There is a similar breadth in the six chapters that are devoted to the analysis of genome organization data. Specifically, the first three focus on constructing duplication and rearrangement histories (Gascuel et al.; Sankoff; and Bergeron et al.), El-Mabrouk reviews methods that account for the occurrence of multigene families, and two further chapters (Moret et al.; Wang and Warnow) deal with phylogeny reconstruction from genome organization data. The exception to this general division of the topics is the final chapter, which considers an issue relevant to both sequence and genome organization data. Here Mossel and Steel take an analytical approach to the question: how much information about the underlying process can we expect from evolved characters?

The publication of *Mathematics of Evolution and Phylogeny* follows closely upon that of two other books addressing the mathematical basis of evolutionary analysis. These are Joe Felsenstein's *Inferring Phylogenies* (2003) and *Phylogenetics* by Charles Semple and Mike Steel (2003), both of which are excellent contributions

to the field. Rather than competing directly with these, *Mathematics of Evolution and Phylogeny* has its own niche. Primarily this volume stands apart because it includes a somewhat wider set of evolutionary topics. Whereas both *Inferring Phylogenies* and *Phylogenetics* focus exclusively on phylogeny reconstruction, *Mathematics of Evolution and Phylogeny* also discusses the evolution of genome structure and reconstructing ancestral genomes. The inclusion of these research areas may well make the volume of interest to a broader segment of the scientific community. However, despite its broader scope *Mathematics of Evolution and Phylogeny* could not be considered a general introductory or teaching text. In most cases the topics are covered in a level of detail that goes well beyond introductory, whether in the context of evolutionary biology, computational biology, or even applied mathematics. Instead, the volume is much more likely to be of use to postgraduate students and researchers, the in-depth discussions making *Mathematics of Evolution and Phylogeny* a key reference for those with mathematical or computational perspectives on evolution. Certainly, anyone wanting to contribute to the development of an area covered in this volume would be well advised to read the relevant chapters.

That *Mathematics of Evolution and Phylogeny* focuses on the mathematical aspects of evolutionary analysis will likely make it less appealing to many evolutionary or systematist biologists. However, the volume is an important contribution because it highlights the analysis of evolutionary problems as potential research avenues in applied mathematics. Rather than explaining the mathematical concepts to biologists, the value of *Mathematics of Evolution and Phylogeny* is in enticing mathematicians and computer scientists into this emerging area of applied research. Extending our understanding of evolution relies on continuing to expand our computational and analytical capacity, and it is clear that collaborations with mathematicians and computer scientists offer the most effective way to do this. It seems that increasingly it will be our colleagues in the mathematics or computer science department who will be leading the development of the concepts and tools we use for evolutionary analysis. Although evolutionary biology stands to gain a great deal from such collaborations, there is one small problem—I will need a crash course in advanced mathematics in order to understand what it all means.

REFERENCES

- Felsenstein, J. 2003. *Inferring phylogenies*. Sinauer Associates, Sunderland, Massachusetts.
- Semple, C., and M. Steel. 2003. *Phylogenetics*. Oxford University Press, New York, New York.
- Richard C. Winkworth, Departamento de Botânica, Universidade de São Paulo, Caixa Postal 11461, CEP 05422-970, São Paulo, SP, Brasil; E-mail: richard.winkworth@yale.edu