

BOOK REVIEW

A book like its cover

The Phylogenetic Handbook: A Practical Approach to DNA and Protein Phylogeny

Edited by M Salemi and A-M Vandamme.

Cambridge University Press, Cambridge, UK. 2003; 406 pp.
£40.00, hardback. ISBN 0-521-80390-X.

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Reviewed by MP Cummings

Molecular evolution and phylogenetics have close interdependencies and shared histories, not the least of which is that phylogenetics is now largely dominated by molecular data. These fields have been the focus of numerous books, particularly in the last decade (eg, Hillis *et al*, 1996; Li, 1997; Page and Holmes, 1998; Graur and Li, 2000; Nei and Kumar, 2000). Relatively recent books in phylogenetics include the magnum opus of Joseph Felsenstein (2004). Thus, a new entry into this field should substantially distinguish itself to provide *une raison d'être*. This book does differ in several fundamental characteristics from most other books in the field. First, it is an edited volume, with all the associated strengths and weaknesses. The strengths coming from the contributions of many experts result in the weaknesses of different voices and sometimes contradictory views. Second, the book provides explicit practical instruction in numerous programs used in phylogenetics. This latter feature proves to be the principal strength of this book. While the book by Hall (2004) also provides instruction on the use of programs, The Phylogenetic Handbook covers many more programs, and provides more depth into the coverage of theory. In addition to phylogenetics, this book has chapters covering multiple sequence alignment, detecting viral recombination, estimating population genetic parameters from molecular data, and other relevant topics.

Organizationally, all but the introductory chapter are partitioned into paired theory and practice sections, sometimes with different authors. While in concept this is an attractive approach, the execution comes up a bit short. This structure leads to some curious topical coverage and writing assignments, which may be the result of trying to accommodate different authors and their interests/expertise. For example, some chapters focus on important conceptual areas (eg, nucleotide substitution models, phylogenetic inference based on various methods, selecting models of evolution, analysis of coding sequences), and others are almost exclusively focused on a specific computer program (eg, SplitsTree, DAMBE, TREECON).

Chapter 1, Basic concepts of molecular evolution by Anne-Mieke Vandamme, one of the editors, attempts an impossible task: conveying the basics of molecular biology, molecular evolution, population genetics, and phylogenetics in a single concise chapter. The result is a

presentation so cursory as to be of little use. Those who do not already know the material covered would be served better by reading any one of several excellent texts covering much of the same material (eg, Li, 1997), and those who already have a fair understanding will find little benefit in reading the chapter.

Other chapters that provide some instruction on the use of a sizable set of software and software packages (ClustalW, ClustalX, PHYLIP, TREE-PUZZLE, PAUP*, TREECON, MODELTEST, MEGA2, SplitsTree, DAMBE, Simplot, and LAMARC) range from perfunctory to profound. An example of the latter is Chapter 7, Phylogeny inference based on parsimony and other methods using PAUP*, by David L Swofford and Jack Sullivan. The presentation of theory is clear and accessible to a wide range of readers, and well illustrated. The associated practice section is perhaps the best written detailed description of how to use PAUP* available and contains practical advice that will greatly improve the use of this powerful program.

A glaring omission is the lack of coverage of Bayesian inference of phylogeny, arguably the most important recent analytical development in phylogenetics. The current computational tool of choice in this area is MrBayes, which is in its third major release (Ronquist and Huelsenbeck, 2003), and it should have been covered here.

Little annoyances populate the book. For *example*, the book uses (poorly) the *tool* of *typesetting* particular *terms* in a different and *bold font*. However, these words and terms are often undefined. Through such typesetting, the reader is led to believe that these text elements are of particular importance, but apparently they are not of enough importance that a definition is consistently provided. As the book is ostensibly targeted at an audience of researchers less familiar with the phylogenetics terminology, a glossary would be useful and appropriate. Another inexcusable shortcoming is the lack of a unified reference list rather than a separate list for each chapter. One would have thought that someone at Cambridge University Press would have suggested this if for no other reason than to save on typesetting and page count. For example, the reference for PHYLIP (Felsenstein, 1993) is listed at the end of seven of the 15 chapters, and the classic references of Jukes and Cantor (1969) and Kimura (1980) are each listed at the end of six chapters, and these are not formatted consistently among chapters. Another production feature showing lack of concern for the reader is that color figures from all chapters are put together between chapters 12 and 13, rather than being integrated with the associated text.

The cover design, credited to Dennis M Arnold, is perhaps a fitting graphical metaphor for the book. The background image is an autoradiographic image of a 'manual' sequencing gel. Presumably, the majority of readers so new to the field to be most interested in this book would be more familiar with capillary electrophoresis and the now ubiquitous four-color chromatographic representations of DNA sequences. Further, there appear to be a number of lanes with missing data (ie, not all four bases are represented for some samples). So, like the

image on the cover, the book as a whole is a bit behind the times and missing a few things.

As someone who advises and instructs students, postdoctoral scholars, and colleagues in the theory and practice of phylogenetics, I ask myself a simple question, the answer to which sums up my impression of this book: Would I recommend it to those I am trying to educate? No for the book as a whole, but definitely yes for several chapters.

References

- Felsenstein J (1993). *PHYLIP. Phylogenetic Inference Package*. Version 3.5c. Department of Genetics, University of Washington.
- Felsenstein J (2004). *Inferring Phylogenies*. Sinauer Associates: Sunderland, MA, USA, pp 604. ISBN 0-87893-177-5.
- Graur D, Li W-H (2000). *Fundamentals of Molecular Evolution*. 2nd edn. Sinauer Associates: Sunderland, MA, USA, pp 443. ISBN 0-87893-266-6.
- Hall BG (2004). *Phylogenetic Trees Made Easy: A How-To Manual*. 2nd edn. Sinauer Associates: Sunderland, MA, USA, pp 238. ISBN 0-87893-312-3.
- Jukes T, Cantor CR (1969). Evolution of protein molecules. In: Munro HM (ed) *Mammalian Protein Metabolism*. Academic Press: New York, pp 21–132.
- Kimura M (1980). A simple method for estimating evolutionary rate of base substitutions through comparative studies of nucleotide sequences. *J Mol Evol* **16**: 111–120.
- Li W-H (1997). *Molecular Evolution*. Sinauer Associates: Sunderland, MA, USA, pp 487. ISBN 0-87893-463-4.
- Nei M, Kumar S (2000). *Molecular Evolution and Phylogenetics*. Oxford University Press: Oxford, pp 333. ISBN 0-19-513584-9.
- Page RDM, Holmes EC (1998). *Molecular Evolution: A Phylogenetic Approach*. Blackwell Science: Oxford, pp 346. ISBN 0-86542-889-1.
- Ronquist F, Huelsenbeck JP (2003). MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* **19**: 1572–1574.
- Hillis DM, Moritz C, Mable BK (eds) (1996). *Molecular Systematics*. 2nd edn. Sinauer Associates: Sunderland, MA, USA, pp 655. ISBN 0-87893-282-8.

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