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Frontiers of Biogeography

Title

book review: Getting to the root of phylogenetics

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Journal

Frontiers of Biogeography, 2(3)

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Publication Date

2010

DOI

10.21425/F5FBG12346

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news and update ISSN 1948-6596

book review

Getting to the root of phylogenetics

The Phylogenetic Handbook: A practical approach to phylogenetic analysis and hypothesis testing (2nd Ed.), ed. by Philippe Lemey, Marco Salemi & Anne-Mieke Vandamme Cambridge University Press, 2009, 722 pp. ISBN13: 9780521730716 http://www.cambridge.org/

The molecular genetics revolution revitalized historical biogeography (Riddle et al. 2008), allowing a greater understanding of phylogenetics at interand intraspecific levels, essential in the burgeoning science of 'phylogeography' (Avise 1987, 2009). Proponents of phylogenetics must master the theoretically and practically rich, rapidly changing facets of this field. As a diverse group of graduate students, with assorted backgrounds in taxonomy, genetics, conservation and evolutionary biology, ecology, genomics, and biogeography, we recently completed a class using the revised second edition of The Phylogenetic Handbook: A Practical Approach to Phylogenetic Analysis and Hypothesis Testing, a book we found to be a useful starting point for those inexperienced in the field of phylogenetics, such as ourselves.

This book is a good introductory text for those who hope to understand and practice the theories of phylogenetics, as each chapter has both a theoretical and a practical application section. The editors have assembled a number of prominent researchers in their respective disciplines within phylogenetics to pen different chapters, including the creators of many of the phylogenetic programs widely used today, such as MODELTEST with David Posada (Posada and Crandell 1998), PAUP* with David Swofford (Swofford 2002) and MRBAYES with Frederick Ronquist and John Huelsenbeck (Ronquist and Huelsenbeck 2003). We found this collection of authors to be reassuring, given our familiarity with their research and their ability to introduce and explain ideas, theories, and related software programs. However, it should also be stressed that the authors of this book make the assumption that the reader is well versed in the basics concerning mathematics, statistics, genetics, and advanced computer literacy.

The book begins with introductory topics in phylogenetics, spanning a range of topics from

collection and alignment of data through to phylogenetic reconstruction methods and hypothesis testing. Chapters are divided into two parts; a theoretical section, followed by a practical section which walks the reader through actual data within an example program. Most authors appeared to demonstrate an intimate knowledge of the material and instructions for the programs, easing readers into the actual execution of software. Separation of theory and practice was extremely helpful for us, though no practical application should be attempted without a complete understanding of the results. Essential ideas concerning tree topology, distance methods, maximum parsimony, maximum likelihood, and Bayesian approaches are all covered in detail, as are introductions into related topics such as coalescence and population genetic parameter estimation. Readers wishing to explore a more in-depth explanation of the algorithms implemented in most phylogenetic analyses should also look to Felsenstein (2004).

The use of different authors seemed to introduce biases and discrepancies between chapters. Authors naturally focused on their particular expertise, and, while providing unique learning opportunities, may not have explored additional, and possibly equally pertinent, ideas within the given topic. Understandably, the use of different authors also produces gradations in chapter quality, with the chapter on Bayesian theory being exceptionally well written and understandable in our opinion. However, the diversity of authors, while effective for individual chapters, makes it difficult at times to integrate overlapping methods and techniques. We found the need to often jump ahead in the book for explanations or revisit ideas from other authors to try to fully understand the intention of individual chapters. Additionally other excellent sources outside the "handbook" were often needed for further clarification and explanaISSN 1948-6596 news and update

Phylogenetics is a difficult and fluid field of study. Currently there appears to be no uniform way of performing a phylogenetic study or interpreting its results; consequently, we recognize that writing a handbook on this field might be exceptionally difficult. The editors and authors of this book have done a commendable job of laying down the basics on which to build. They provided not only theory, but also practical information essential to studies of this kind. Other texts tend to concentrate on either theory (Page and Holmes 1998; Felsenstein 2004) or practical applications (Hall 2004). While this handbook is not the only primer on phylogenetics, its strength lies in this dual focus, and up to date coverage of these ideas. In all, we recommend this book as a great phylogenetic resource, suitable for advanced undergraduate and/or graduate students or the reference library of any professional researcher.

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New editorial policy for book reviews

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