

BOOK REVIEW

Ex Cathedra Cladistics

Cladistics: A Practical Primer on CD-ROM

P Skelton, A Smith and N Monks

Cambridge University Press, Cambridge, UK; 2002. 80pp plus CD. £29.95, hardback ISBN 0-521-52341-9.

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Reviewed by VS Smith

There is barely a field of biology that remains untouched by the use of phylogenies. From linguistic analysis to the study of conservation and biodiversity, phylogenies are an integral tool for comparative studies in all branches of biology. It is therefore not surprising that teaching the basic elements of phylogeny reconstruction has become an essential part of most undergraduate biology courses, and for many students cladistics is their first introduction to this subject. Yet its strict logic and daunting technical vocabulary mean that for many the cladistic method is difficult to grasp, especially when taught from the rather dry accounts available in some evolution textbooks. This publication is the latest in a series of recent books attempting to bridge this gap. Combining an interactive CD-ROM and accompanying book, the authors provide an introductory account of the cladistic method that takes advantage of the electronic medium while assuming no prior knowledge of cladistics.

Forming part of the Open University Evolution course, Peter Skelton and Andrew Smith have devised an introductory course that is specifically designed for independent learning. A series of audio presentations, animated sequences and practical exercises take the user through the basics of cladistic phylogeny reconstruction. Complimentary text is provided in the accompanying booklet by Neil Monks. However, for most users the true strength of this product lies in the interactive CD, which can be used completely independent of the book.

The CD is divided into five core sections introducing the principles of homology and parsimony, through to tree reconstruction (covering weighting, rooting and consensus methods); and finally tackling measures of character fit and robustness (specifically consistency/retention indices, bootstrap and Bremer support values). Each section concludes with a series of questions and exercises designed to test the readers understanding of the issues and techniques introduced. The CD culminates in an extensive practical exercise during which the user is guided through the process of scoring a morphological data set with images and characters provided, and aligning a small molecular data set. Drawing upon skills gained throughout the course, the user is finally invited to analyse and interpret the resulting trees. Shorter practical exercises are present throughout the CD and provide valuable insight into the

process of carrying out molecular and morphological cladistic analyses with real data.

For the most part both the CD-ROM and book are clear and well presented and I am confident most students would learn the elements of cladistic analysis by working through the exercises. I particularly liked the trilobite example used to illustrate the problem of character state delimitation – an aspect of practical cladistic analysis inadequately treated even in the scientific literature. Long branch attraction is given a cursory mention, as is the problem of homoplasy in molecular data. Both morphological and molecular data are given balanced coverage throughout the text – something seldom achieved in similar introductory accounts of cladistics. The book and CD lack an index, but an electronic glossary is present on the CD-ROM defining key cladistic terms. It would have been nice if the photos and illustrations in the book could have been reproduced in colour as they are on the CD-ROM; however, this is of minor concern. Each section takes an estimated 1–1.5 h to complete, and with the text recommending that you set aside a whopping 5 h for the final exercise, it would take a dedicated student to complete the whole exercise in one go. However, the electronic format allows the user to navigate through each section as required.

My principal criticism of the book and CD concerns not so much its contents but rather its omissions. Systematics is a vibrant subject that embodies the very latest developments in molecular biology, comparative morphology and information technology that underpin all of biology. Cladistics plays an integral role in this endeavour, yet the text conveys nothing of the relevance of systematics to the reader or the excitement and enthusiasm that might attract people to this subject. In fact, much of the contents could have been directly lifted from my undergraduate lecture notes on this subject taken nearly 10 years ago. The result is that despite the electronic format, the contents feel slightly stale. This criticisms could equally be applied to many texts on systematics and the cladistic method. However, it is particularly germane here as the CD and book have been designed predominantly for use in independent study. The result is that I fear this publication will do little to endear new students to the subject even if it does impart plenty of knowledge on cladistics. A second key omission is the failure of the text to acknowledge the existence of alternative methods of phylogeny reconstruction. Maximum likelihood gets the briefest of mentions, but is instantly dismissed in the commentary on account that it 'cannot be applied to morphological data' – a statement rendered inaccurate by recent developments. While I would not expect a book on elementary cladistics to cover these methods in any depth, some recognition that alternative methods of phylogeny reconstruction are available would have been useful, even if it just took the form of a bibliography providing some further reading.

In short, if you are searching for an elementary text to recommend covering the basics of cladistic analysis, I would suggest you look no further. However, if you are seeking an account that provides a more rounded perspective of what practicing systematists actually do (and the pages of this or any other systematics journal are a testament to this), I would suggest you keep looking!

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