BOOK REVIEW

Cladistics: A Practical Primer on CD-ROM. Peter Skelton, Andrew Smith & Neale Monks. Cambridge University Press. 2002. 92pp. ISBN 0 521 52341 9. £29.95 (hardback).

Both as an MSc student at the Royal Botanic Garden Edinburgh and an undergraduate at Edinburgh University, I have been introduced to the theory and practice of cladistics. I have therefore written this review from the point of view of a student introduced to the subject relatively recently. This appears to be the target audience of the work.

Cladistics: A Practical Primer on CD-ROM is a great idea in many respects. The medium of CD-ROM is a good choice as it allows the reader to try out some of the procedures which are explained in the text. The format is quite similar to a TV documentary, with an easy to follow commentary accompanying graphic illustrations of the principles and practice of cladistics. As we watch, phylogenetic trees grow before our eyes, while they are explained in clear and simple terms. The narrative is interspersed with chances to apply what we have learnt. There are, for example, chances to try out creating unrooted trees, mapping character changes, measuring tree lengths, rooting unrooted trees, aligning simple DNA sequences, calculating consistency and retention indices, and working out bootstrap and jackknife values. All these concepts are clarified by having to work out examples for yourself, and it is in this that CD-ROM format is very helpful.

A large portion of the CD is devoted to an extensive practical exercise. This involves the construction of a morphological data matrix for some sea urchin species, based on a database of information about morphology and character choices. Another matrix is then constructed using molecular characters, which provides practice in aligning more complex sequences than those used as examples in the narrative part of the CD. These matrices can then be compared with the 'correct' matrices provided by the authors. Unfortunately, because a program such as PAUP cannot be included on the CD, it is not possible to construct trees from your own data matrices, only to look at pre-constructed trees based on the authors' matrices. So, while you can compare your own matrices with theirs, it is impossible to compare the trees which result from your own matrices with those of the authors. However, it is useful practical experience of character conceptualization, the coding of states and aligning DNA sequence data. If I had to criticize this section of the CD, I would suggest that there is perhaps a bit too much guidance through each morphological character – we are told how to codify each character and exactly what it is. However, especially for the novice, this could be very useful, and it didn't stop me from making the odd mistake in my matrices, highlighting the subjectivity of judgement which is unavoidable in coding morphological characters.

So, all in all, I was very impressed with this product, but there are a few criticisms which I would level at it. Firstly, the whole approach is zoological and there is no reference to phylogeny reconstruction in plants. This no doubt reflects the disciplines of the authors, but as a botanist I found it slightly off-putting. Because of this bias, there is no mention of the relative difficulty of using cladistics in botany, such as the relative paucity of suitable morphological characters at species level, and the high incidence of hybridization in the plant kingdom.

My second criticism is that the introduction congratulates cladists on being scientific and objective, while criticizing other methods of classification, decrying them as 'ad hoc' and 'eclectic'. Anyone who has read about cladistics should be aware that the methods require some subjective judgements and are therefore not entirely objective. There is no need for this attack as the 'cladist wars' of the 1970s and 1980s are long since over and sensible workers have realized that there is no need for conflict between phenetic and cladistic methods of classification. Both are valid and serve particular purposes. This willingness to try to rubbish the methods of the past reminds me of the tendency in systematics to regard any 'new' source of information as the 'be all and end all', often at the expense of continued study into the older sources of information. Chromosome numbers, isozyme data and the molecular revolution are all examples of this.

However, these are minor quibbles compared with the biggest problem, which is the definition and explanation of outgroup comparison, character polarity and tree rooting. Polarization of the tree is introduced in section 1.2, with the suggestion that the polarization of characters will give an idea of tree polarity. However, in general we do not polarize characters first and then infer the polarity of the tree, but root the tree using outgroups and then infer the polarity of the characters. This avoids the highly contentious issue of choosing primitive and derived states of characters before the analysis. The authors return to this in section 3, in which they again root their trees by judging the polarity of characters. The method mentioned for rooting the tree is the ontogenic criterion, the suggestion that derived character states will appear later in development than primitive ones. This may be a reasonable guide to primitive and derived states, but is rarely used to root phylogenies in botany. Outgroup comparison is another intimately related area which I felt was lacking and had been oversimplified to the point of being incorrect. This is a serious problem, as this technique is used to root nearly all published cladistic analyses. The authors choose an outgroup, with no indication of how it is chosen. They state that the outgroup is more distantly related to the ingroup than the ingroup members are to one another, but how do the authors know this? They have not done any cladistic analysis yet, and do not indicate how they have determined the degrees of relatedness between the ingroup species and outgroup. The authors also fail to point out the importance of including more than one outgroup. The use of just one outgroup cannot test the assumption that the ingroup is monophyletic. More than one outgroup should be included to ensure that this assumption is tested (Nixon & Carpenter, 1993).

Despite these criticisms, I feel that the CD-ROM is a sound introduction to the methods of cladistics. The format works very well for illustrating and giving examples of the techniques and calculations involved. The whole thing is beautifully presented, clearly stated and easy to follow. The problems of tree and character polarity and outgroup comparison are serious, but as a general introduction for the undergraduate, or the postgraduate with little knowledge of cladistics, it is highly recommended.

Reference

Nixon, K. C. & Carpenter, J. M. (1993). On Outgroups. *Cladistics* 9: 413–426.

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