

Preface

Inadequate theory permitted belief that systematics was well understood. Remarkable is the fact that despite inadequate theory, systematics worked as well as it did through the centuries of its modern (post-enlightenment) development. Yet what human endeavour has ever required perfect understanding for its profitable pursuit?

(Nelson 2011, p. 140)

Cladistics: A Guide to Biological Classification is the third edition of the cladistics primer first published under the auspices of the Systematics Association, a London-based organisation dedicated to the promotion and development of systematics and taxonomy (Nature 140, pp. 163–164, 1937). The first edition, *Cladistics: A Practical Course in Systematics*, based on a week-long workshop given at the Natural History Museum, London, was published over 25 years ago (Forey et al. 1992); the second edition, *Cladistics: The Theory and Practice of Parsimony Analysis*, with a heavily revised content, was published 22 years ago (Kitching et al. 1998). With over two decades having passed since the second edition, why, now, offer a new version?

The first edition covered a series of topics considered to encapsulate the subject matter of cladistics, such as it was then understood in the early 1990s. The idea was that the book functioned as a manual and would form a baseline for teaching the rudiments of cladistics to neophytes: character coding, character polarity, tree-building techniques, tree statistics, DNA analysis, fossils, biogeography and classification. It appeared to be a success.

The second edition was revised, modified and updated, with the chapters on DNA analysis, fossils, biogeography and classification being retired (simply because other books covered those topics in more detail, such as Hillis and Moritz 1990 and Hillis et al. 1996, for molecular systematics; Humphries and Parenti 1986 for biogeography; Schoch 1986 and Smith 1994, for palaeontology) and, in addition to the technique-based chapters (character coding, character polarity, tree-building techniques, tree statistics), a few (then) topical and specialised problems related to analytical methods were added: the effect of missing values, character

weighting, consensus trees, the 'simultaneous or partitioned analysis' of datasets discussion and three-item analysis. The second edition focused more on method than theory – although the way in which each new topic addressed theory was of some significance, as a close reading will detect growing differences among the contributors. In short, the second edition was primarily a discourse on what, with hindsight, might have been better called *Quantitative Cladistics* or *Quantitative Phyletics* (the former now used as a title for a teaching course on *Quantitative Cladistics and the use of TNT*, the latter after Kluge and Farris 1969, p. 1), a method associated directly with the workings of (in theory and practice) the Wagner parsimony algorithm and its implementation in various computer programs (of which *TNT*, 'Tree analysis using New Technology', is its most recent incarnation, Goloboff et al. 2008). It was as if the intervening years between the two versions of this book – 1992 to 1998 – forged a direct and (almost) absolute equation between cladistics and parsimony, as implemented by the Wagner algorithm, in spite of the fact that some of the contributors to the 2nd edition were becoming violently opposed to such an equation. Of significance, too, is that those intervening years saw the increase in and use of many statistically-based programs designed specifically to analyse the abundance of DNA sequence data that was becoming available. Those methods of data analysis now dominate the systematics landscape.

With this third edition, and the benefit of 20 odd years of reflection, we thought it appropriate to present a more holistic view of cladistics – in terms of its relationship to general taxonomic practice: that is, the discovery of taxa.

To articulate those aims we can do no better than re-state Gareth Nelson's 'Two Questions' concerning the original goals and tasks of cladistics:

Question 1: In the simplest terms of three organisms, species or taxa, what is the evidence that two are related more closely to each other than to the third? Never mind if they are known from fossil or living material, alone or in combination.

Question 2: If two of them are related more closely, what does this mean about the organisms, species or taxa: about their evolution, classification, even their nomenclature and usefulness and interest to humans? (Nelson 2004, p. 128)

If cladistics became associated with a particular viewpoint, rather than a discipline that focused on the generalities stated in these two questions, it is the fault of those who have promoted it as such – including, we are forced to say, the authors of the second edition of this book. Still, hopefully we all learn and move on. And in any case, we find the two questions above to still be of interest and their exploration still of some significance:

These are questions, not answers, because the spirit of cladistics is enquiry, not ideology, propaganda, sloganizing, or the husbandry of sacred cows and clams. At least, that is what the spirit was, once upon a time, when it achieved general relevance lasting to the present. (Nelson 2004, p. 128)

In this short book we hope to outline and re-state – some might say re-found ('to found or establish again') – the rudiments of cladistics, demonstrating its wide utility, and offer reasons why and how it is of value, especially for taxonomy, a subject often characterised as being devoid of any great scientific merit.

Along the way, we hope to pose a few questions of our own, in the spirit of enquiry that launched cladistics in the first place, mainly because '... you never know enough about anything, and if for a few months or years you should ever believe that you do, you are either past it or in for a surprise ... Yesterday's secure knowledge is tomorrow's laughing matter' (Patterson 2011).

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