



## Crusade? A Reply to Nelson

Martin Barrett; Michael J. Donoghue; Elliott Sober

*Systematic Biology*, Vol. 42, No. 2 (Jun., 1993), 216-217.

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be the tree for pooled data. If so, then Barrett et al. erroneously assume that the anomaly must be the consensus—as if tree 3 represents “total evidence” but trees 1 and 2, in combination, do not (propositions that Barrett et al. inexplicably accept as axioms).

Science progresses through discovery of error, especially when the source of error is mistaken theory. In this case, relevant theory, whether mistaken or not, is not evident. What theory dictates axioms biased against the windmills of consensus? If there is no theory, then other factors drive the crusade.

*Syst. Biol.* 42(2):216–217, 1993

## Crusade? A Reply to Nelson

MARTIN BARRETT,<sup>1</sup> MICHAEL J. DONOGHUE,<sup>2,3</sup> AND ELLIOTT SOBER<sup>1</sup>

<sup>1</sup>*Philosophy Department, University of Wisconsin,  
Madison, Wisconsin 53706, USA*

<sup>2</sup>*Department of Ecology and Evolutionary Biology, University of Arizona,  
Tucson, Arizona 85721, USA*

Nelson (1993) showed that three-taxon analysis (Nelson and Platnick, 1991) of our combined data set (Barrett et al., 1991) does not yield the parsimony tree (“tree 3,” (AC)(BD)) but instead gives trees that match those obtained in the separate analyses. According to Nelson (1993:215), “If relevant to the argument of Barrett et al., then these results of three-taxon analysis support the alternative interpretation: the anomaly is tree 3.”

Nelson’s observation is irrelevant to our argument. We demonstrated that a consensus tree could be positively at odds with a combined tree, and we therefore suggested that one check to see “whether the consensus tree is consistent with the best tree based on the pooled data” (p. 491). Nelson

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*Received 10 August 1992; accepted 29 December 1992*

demonstrated that the three-taxon method gives a different result, but we did not claim that the same result would be obtained using every method of analysis. Nelson’s conclusion would be relevant if he also showed that combined analyses using the three-taxon method never contradicted the consensus of separate analyses using that method, but he did not provide such an argument. In any event, the three-taxon method has not been clearly justified, and there are arguments against it (Harvey, 1993; Kluge, in prep.). Perhaps, to use Nelson’s words, the anomaly is three-taxon analysis. If this method is ever used to compare data sets, we think it would be wise to also try a combined analysis.

Are we crusading against consensus, as Nelson suggests? The aim of our paper was to caution against a tacit assumption that consensus trees are safe. Our hope was that more attention would be paid to this prob-

<sup>3</sup> Present address: Harvard University Herbaria, 22 Divinity Avenue, Cambridge, Massachusetts 02138, USA.

lem, perhaps leading to the development of new methods. In particular, we think it would be valuable to develop additional methods for quantifying the conflict between different subsets of characters in combined analyses (cf. Mickevich and Farris, 1981; Swofford, 1991). We noted in our paper that there are legitimate uses for consensus methods (we listed four uses on p. 491), and we suspect that such techniques may play an especially important role in connection with the interpretation of separate gene trees (de Queiroz, 1993). We had hoped that the blunt title of our paper would insure a careful reading, but this was evidently a tactical error on our part.

Finally, Nelson implies that we may have ulterior motives—that “other factors drive the crusade.” Such cryptic pronouncements are difficult to address, except by our honest assertion that we have no hidden agenda. In any case, Nelson’s guesses about our motives, like his three-taxon example, are irrelevant to the question of whether our claims are correct.

#### ACKNOWLEDGMENTS

We are grateful to Alan de Queiroz, Alan Harvey, and Arnold Kluge for making their manuscripts available to us and for helpful discussion of these issues.

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Received 16 November 1992; accepted 26 January 1993