

FORUM

MOVING TARGETS AND SHELL GAMES

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Nelson and Platnick (1991) presented the transformation of an original synapomorphy matrix into a matrix of three-taxon statements as a possible improvement to cladistic methodology. The following quotations from their initial paper, and relevant subsequent publications (Nelson, 1993; Platnick, 1993), leave no doubt as to the nature of their intention and the context in which their contribution was to be evaluated^a: (1) the question posed in the title of their 1991 paper (p. 351) is whether or not three-taxon statements provide “a more precise use of parsimony”; (2) each three-taxon statement resulting from a transformation “can be expressed as a synapomorphy” (p. 351), and “[i]f . . . characters are hypotheses of homology and synapomorphy, then they must be relational, and the units of those relations are three-taxon statements” (p. 362; see also Forey et al., 1992); (3) Farris’ (1988) Hennig86 software is used to analyze original and transformed matrices, “an all-zero [plesiomorphic] outgroup” is added in order to root the “cladograms” derived from both matrices, and the “most parsimonious” fit to data is judged in terms of “number of steps” and “consistency” and “retention” indices (p. 352); (4) the transformation is applied to “additive (ordered)” multistate characters (p. 358); (5) transformed data are discussed in terms of “homology” (p. 359) and “homoplasy” (p. 360); (6) “[T]he [three-taxon] approach does not score apparent reversals as synapomorphic. It does not follow, however, that the three-taxon approach cannot identify components supported only by apparent reversals” (p. 362; see also p. 363); (7) “[N]ot all of the three-taxon statements supported by a given character are logically independent”, and one might attempt to compensate “by reducing the weight accorded to each of the three-taxon statements supported by a particular character” [p. 363; see Farris (1983) for discussion of logical independence]. Nelson’s (1993: 261) subsequent paper reveals more as to the intention of Nelson and Platnick (1991): (8) “Clear at this point is that the two matrices [original and transformed] relate such that one is derivable from the other” (see also p. 262 concerning *recoding* transformed data to reflect “symplesiomorphy”). Likewise, Platnick’s (1993) subsequent paper provides additional documentation regarding Nelson and Platnick’s (1991) intention: (9) “[M]ost parsimonious cladograms are thus those that most efficiently describe the set of three-taxon statements” (p. 268), which I take to be a reference to the descriptive efficiency of Farris (1980; see p. 270); (10) “Any cladogram that accommodates a given three-taxon statement

^a Thus, in terms of Ward Wheeler’s (pers. comm.) metaphorical “fish-bowls”, there is only one sense, that of cladistics, in which to judge Nelson and Platnick’s (1991) contribution to phylogenetic inference.

requires no extra steps (i.e. no *ad hoc* hypotheses), and would always be considered better than any cladogram that cannot accommodate the three-taxon statement" (p. 269; see also p. 270); (11) "A cladogram can only explain the homology statement expressed in a three-taxon statement by common cause (ancestry) if that three-taxon statement can be accommodated [sic] at one of its nodes" (p. 271).

Several important cladistic concepts and practices are identified in these references, and these justify the bases for most of my previous (Kluge, 1993) and present criticisms of the three-taxon transformation. Although Nelson and Platnick (1991), Nelson (1993) and Platnick (1993) have not always consistently stated or employed those concepts and practices (see below), there can be no doubt that they intended three-taxon analysis to be an improvement to cladistics, not a competing or alternative form of phylogenetic inference. And presented as such, I will demonstrate that Nelson's (1993) and Platnick's (1993) responses to my review (Kluge, 1993) of their earlier paper (Nelson and Platnick, 1991) are a mixture of sophistry, inconsistency and misunderstanding. In this reply to Nelson (1993) and Platnick (1993), I focus mostly on those issues that are central to my previous conclusions that the three-taxon transformation negatively impacts the explanatory power of the original data. Ironically, while Nelson (p. 261) now denigrates my demand for justification (i.e. for a covering theory) of the three-taxon transformation in cladistics, as that "craved by a deductive mentality", I hasten to point out that he once employed that same demand in questioning non-Hennigian, "traditional or convenient", types of classification (Nelson, 1978: 105).

My major criticisms of the three-taxon transformation follow from the observed effect that operation has on explanatory power (Farris, 1983). Explanatory power served as the general basis for my previous evaluation because it is part of the most widely accepted covering theory (i.e. justification) for parsimony analysis in cladistics. Parsimony minimizes requirements for *ad hoc* hypotheses of homoplasy, and such best-fitting cladograms maximize explanatory power—synapomorphies interpretable as homologies. As Farris (1983: 18) stated, "[t]he explanatory power of a genealogy is consequently measured by the degree to which it can avoid postulating homoplasies". I claimed that many of the effects on explanatory power can be demonstrated simply by using a perfectly congruent set of characters and comparing the hypothesized sister group relationships and character histories derived from original and transformed data matrices (Kluge, 1993; see also below).

Nelson (1993) and Platnick (1993) attempt to blunt my criticisms with a variety of seemingly plausible arguments. For example, there is the elementary issue of what constitutes original data. Nelson (1993: 261; see also 1992) argues that we might as well "assume" that a transformed matrix is the original data set, and the original data set is the transformed matrix. In floating this possibility he clouds the target of one of my criticisms—that the three-taxon operation distorts and adds ambiguity to the *original* observations, as hypotheses of homology (Kluge, 1993: 255; my italics). As I demonstrated, the transformation certainly does have those effects on original data, unless of course one is prepared to assume, like Nelson, that the original data set is really the transformed matrix, and the transformed matrix is the original data set.

Nelson (1993) goes further in this regard (see also Platnick, 1993: 271). Although he (Nelson, 1993: 261) admits that "[e]mpirical data originate in observation", he raises the issue of how we come to know the generality of synapomorphies like

mammary glands. He suggests that knowledge of such a generality, as diagnostic of the taxon Mammalia, has resulted from formulating one or more three-taxon statements, e.g. A(B, C), A(B, D), A(C, E), where B–E constitute all or most of the entities we call mammals, and A stands for all non-mammals. In other words, the “original” matrix itself is a transformation of what we observe, just as the “transformed” matrix is a transformed version of the “original”. This argument is unconvincing for two reasons. Firstly, I simply followed Nelson and Platnick’s (1991) use of the terms *original* and *transformed*, and focused on the effect(s) the three-taxon operation has on a previously constructed matrix.

The second reason why Nelson’s argument is unconvincing is that it doesn’t take account of the fact that observations are made on organisms (any living being or its material structure)—observations are not made on taxa, the terminal taxa of three taxon statements or those of more inclusive groups. Observation alone does not lead to a taxon, like Mammalia. What is also required is a rule that allows a cladistic hypothesis of relationships to be reproduced exactly as a hierarchy of names, a monophyletic taxonomy (for other requirements see Frost and Kluge, 1995).

Similarly, Platnick (1993: 267) wants the reader to believe that the problem lies in my treating “a matrix of three-taxon statements as if it were an ordinary character matrix”. He asserts that “[i]t is *not* an ordinary character matrix; for every ‘character’, the entries for only three taxa are relevant (two 1 entries and one 0 entry). The remaining entries (all question marks) are neither indicators nor place holders for any conceivable ‘character’ state assignments, and cannot be optimized as if they were. Using a standard parsimony program to optimize them is simply a misuse of the program.” But, why shouldn’t the transformed matrix be evaluated as an ordinary character matrix? When Nelson and Platnick (1991) assess the three-taxon transformation, they evaluate their results in terms of consistency and retention indices, synapomorphy, homoplasy (including reversal), homology and clades. Nelson (1993: 261) even employs optimization in his attempt to validate the three-taxon transformation. Why can’t I entertain the same concepts and practices in my criticisms of the three-taxon transformation? If not, the transformation is removed from criticism and cannot therefore be considered scientific.

Again, Nelson (1993) and Platnick (1993) raise the issue of missing data. With respect to the three-taxon’s operation of changing 0 and 1 states into question marks, Nelson (1993: 262) asserts that “[n]o datum is missing”. Likewise, Platnick (1993: 267) claims that the question marks so created are “neither 0 or 1”. However, more generally this means that in Nelson and Platnick’s parsimony analyses the entire original matrix, including question marks denoting states 0 and/or 1, is considered data, but certain selected parts of the transformed matrix (*only* the question marks) are something other than a reference to data. Such a double standard cannot be defended. Further, Platnick’s (p. 267; see also Nelson, 1993: 261) raising the possibility that Farris’ (1988) parsimony optimization routine is *defective* when applied to a transformed matrix with its missing data is not on point. I am unaware of any one making such a claim when characters in an original matrix cannot be optimized unambiguously on a most parsimonious cladogram. Of course, Nelson and Platnick (1991) could avoid the controversy surrounding a parsimony analysis of question marks by employing some other grouping technique, such as character compatibility/clique analysis, but then the three-taxon operation could not be presented as a possible improvement to the use of parsimony in cladistics.

Platnick's (1993) current notion of evidence is particularly revealing for its inconsistency. He begins by stating that (p. 267–8), “[t]he three-taxon approach treats data as evidence for sister-group relationships, *not* in terms of maximizing the number of synapomorphies potentially interpreted as homologs, but rather in terms of maximizing the number of three-taxon statements potentially interpreted as indicators of monophyly” (my italics). However, he goes on to conclude (p. 269) that “[a]ny cladogram that accommodates a given three-taxon statement requires no extra steps (i.e. no *ad hoc* hypotheses)”, and (p. 271) “[a] cladogram can only explain *the homology statement expressed in a three-taxon statement* by common cause (ancestry) if that three-taxon statement can be accommodated [sic] at one of its nodes” (my italics). Nelson and Platnick cannot have it both ways. Whatever character matrix is finally analyzed cladistically with parsimony involves assessing the synapomorphy–homology relation as the basis for delimiting natural groups (see e.g. Nelson and Platnick, 1991). Substituting different or less well-known words, such as Platnick's (pp. 267–8) “false indicators of monophyly” for Farris' (1983) “*ad hoc* hypotheses of homoplasy” and “explanatory power” does not necessarily change the basic tenets of Hennigian cladistics which are at work. Those substitutions only introduce semantic confusion. If truly different concepts are involved, then Nelson and Platnick must describe them more fully and make a compelling argument for them.

The most parsimonious optimization of character states on a cladogram is an important consideration in cladistics because it determines the amount and quality of the evidence for sister-group relationships. Nelson's (1993: 262) statement that “Hennig86 (and PAUP) efficiently implements three-item analysis because tree length, if not optimization, is exact” suggests a basic misunderstanding of parsimony and its relationship to optimization and evidence. As Farris (1970: 92) pointed out long ago, the optimization of a character's states on a cladogram is “used to

Table 1

(a) Original data matrix

		Characters		
		1	2	3
Taxa	A	0	0	0
	B	1	0	0
	C	1	1	0
	D	1	1	1
	E	1	1	1

(b) Three-taxon statement matrix

		Characters		
		1 abcdef	2 abcdef	3 abc
Taxa	A	000000	000???	0??
	B	111???	???	000
	C	1??11?	11?11?	??0
	D	?1?1?1	1?11?1	111
	E	??1?11	?11?11	111

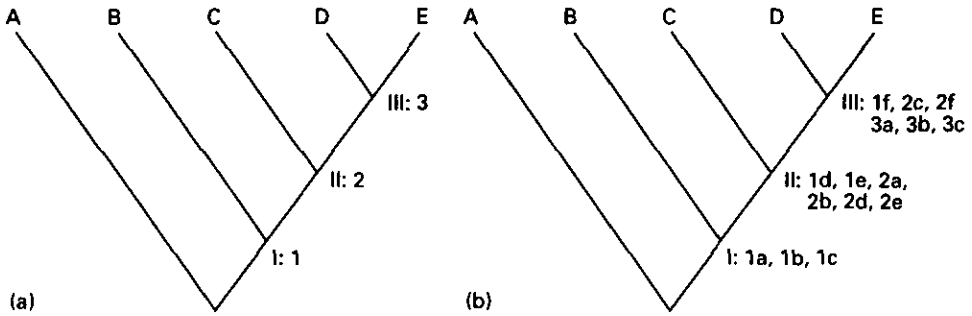


Fig. 1. The identical best-fitting cladograms for interconvertible original and three-taxon statement data matrices (Table 1a and 1b, respectively; after Kluge, 1993: 249). Comparable nodes are labelled with Roman numerals, I-III. (a) The unambiguous optimization provided by Hennig86 for the three binary characters (1-3) in the original data (Table 1a). (b) Nelson's (1993: 261-2) "Exact" optimization for the three-taxon statement data (Table 1b). Only statements 1a, 1b, 1c, 2d, 2e, and 3c can be unambiguously optimized with Hennig86, whereas statements 1d, 1e, 2a, and 2b are placed equally parsimoniously at nodes I or II, statements 1f, 2c, and 3a at nodes I, II, or III, and statements 2f and 3b at nodes II or III.

increase parsimony". Thus, optimization does affect tree length, as well as the amount of unambiguous evidence for clades.

In my review of Nelson and Platnick's 1991 paper, I was particularly critical of the three-taxon transformation because I documented that the operation adds ambiguity to the evidence where none existed before. Nelson's (1993: 261) response to my criticism concerning optimization reveals another fundamental problem with the three-taxon transformation. To begin with, as noted earlier, Nelson (1993: 261) states that "the two matrices [reproduced here as Table 1a, b] relate such that one is derivable from the other". That the two matrices are interconvertible, and contain the same information, is further documented by Nelson (1993: 262) in his claim that transformed data can be *recoded* to reflect "symplesiomorphy". Thus, when Nelson (1993: 262) concludes that "Hennig86 does not achieve *exact* optimization of three-item statements in all cases" he is contradicting himself. He even reiterates the contradiction in a tabular format when he shows how the Hennig86 and "Exact" optimizations differ (Fig. 1 summarizes those differences in a cladistic format). Indeed, if the two matrices (Table 1a, b) are interconvertible, and contain the same information, then their optimization on the most parsimonious cladograms cannot differ (compare, however, Fig. 1a and b).

Even though Nelson (1993) never says how to do "exact" optimization^b, the results in his table reveal the details of his contradiction. For example, those results indicate that state 1 of 1a is "exactly" optimized at the node (#I) for the group (BCDE), state 1 of 1d is "exactly" optimized at the node (#II) for the group (CDE), and state 1 of 1f is "exactly" optimized at the node (#III) for the group (DE). Now, given that the root always has state 0, character 1 in the original data matrix, that which has state 1 in every terminal except taxon A, diagnoses unambiguously only one clade, the group (BCDE), not the three nested groups, (B(C(DE))), that Nelson identifies with three-taxon statements (Fig. 1). Of course, this multiplication of information in the transformed matrix is bizarre, but only if the original and

^b Extrapolating from Nelson's (1993: 261-2) example, "Exact" optimization is achieved simply by choosing the least general character state distribution, among equally parsimonious alternatives. What an arbitrary basis for choosing has to do with exactness remains to be specified by Nelson.

transformed matrices are interconvertible. If three taxon statements are not synapomorphies, as Nelson (1992: 262) suggests elsewhere, then the conclusion may not be so troublesome, but then the results cannot be compared in terms of parsimony optimization. There are two choices here, but neither would seem to help the cause of Nelson and Platnick's (1991) three-taxon transformation.

Platnick (1993: 270) includes descriptive efficiency in his argument for three-taxon transformation. Farris (1980) argued that descriptive efficiency is maximized on that cladogram(s) with the smallest number of diagnostic entries, i.e. that which specifies the phylogenetic *information* in a given data set. Platnick applies Farris' idea of descriptive efficiency to different codings of the same information, as in the original and three-taxon statement data matrices. That seems a perfectly reasonable use of descriptive efficiency, but only if the information in the two matrices is the same. However, that being the case, the *descriptively most efficient* form of the data is the matrix with the smaller number of *diagnostic* entries, and that is the original, not the transformed, data matrix. The only way to avoid this conclusion is to claim that the data in the two matrices are not interconvertible, but then having taken that stance, Farris' idea of descriptive efficiency does not apply because it assumes the two matrices have the same information. Again, the three-taxon transformation of Nelson and Platnick (1991) is not helped by either choice.

In my review of the three-taxon operation (Kluge, 1993: 251), I pointed out that the "transformation distorts the original data as evidence for genealogical relationships because symplesiomorphies are no longer available to be tested with congruence for phylogenetic informativeness as evolutionary reversals". Platnick (1993: 268) demands an example, "[b]ecause reversals are conclusions from evidence presented by other characters, [and] it is not intuitively obvious that three-taxon matrices perform differently, in that regard, from standard ones." Thus, consider the original data matrix in Table 2, and the single best-fitting hypothesis in Fig. 2a, which shows nested monophyletic groups (I(J, K)) delimited solely on the basis of reversals in characters 1 and 2. The corresponding three-taxon statement matrix distorts the original data (the reversals are effectively lost in the transformation), as can be seen in Fig. 2b, where the relationships among taxa I-K are different and that taxon is rendered paraphyletic: (J, K(I(F, G, H))). A more subtle distortion is presented in

Table 2
Original data matrix

		Characters
		123456789
Taxa	X	000000000
	A	100000000
	B	110000000
	C	111000000
	D	111100000
	E	111110000
	F	111111111
	G	111111111
	H	111111111
	I	011111111
	J	001111111
K	001111111	

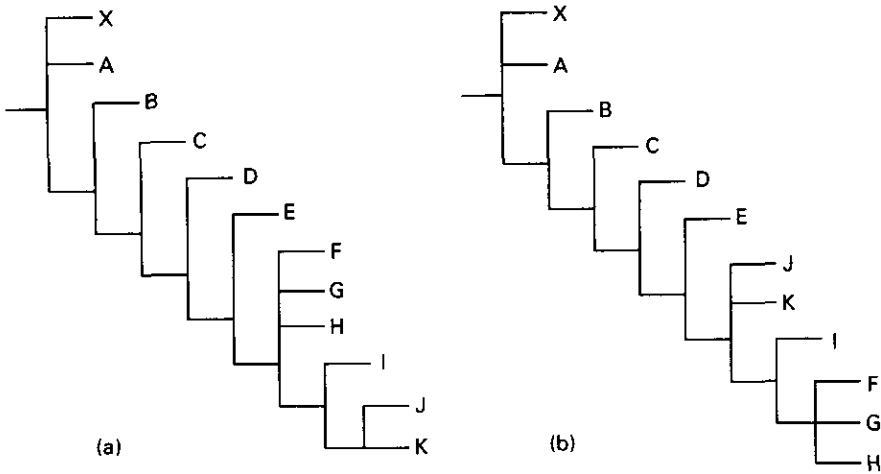


Fig. 2. Best-fitting cladograms derived from analyses of original (Table 2) and corresponding three-taxon transformed data matrices. (a) The single hypothesis ($C = 0.81$; $R = 0.94$) derived from the original matrix. (b) The strict consensus of nine equally parsimonious topologies ($C = 0.85$; $R = 0.83$) resulting from the analysis of the transformed data.

Table 3, with the corresponding single best-fitting cladogram shown in Fig. 3a. Notice, that G and F are highly derived sister taxa, with only the former taxon exhibiting reversals in characters 1 and 2. The two equally most parsimonious cladograms illustrated in Fig. 3b are derived from the corresponding three-taxon matrix. In either of those hypotheses, taxon G is far removed from the highly derived F.

Both Nelson (1993) and Platnick (1993) misunderstand character independence in cladistics. As reviewed by Farris (1983), independence is important in cladistics because choosing the best-fitting topology of sister-group relationships for a given character matrix involves minimizing the number of *ad hoc* hypotheses of homoplasy in those data. "It is thus important to ensure that the homoplasies combined in such totals are logically independent, since otherwise their number need not reflect required *ad hoc* hypotheses" (Farris, 1983; 19). That the *ad hoc* hypotheses of homoplasy are being discovered with character congruence means that the importance of character independence is to be understood in the context of taxic homology, not transformation homology.

Nelson's (1993) few comments emphasize non-independence in relation to trans-

Table 3
Original data matrix

		Characters
		123456
Taxa	X	000000
	A	100000
	B	110000
	C	111000
	D	111100
	E	111110
	F	111111
G	001111	

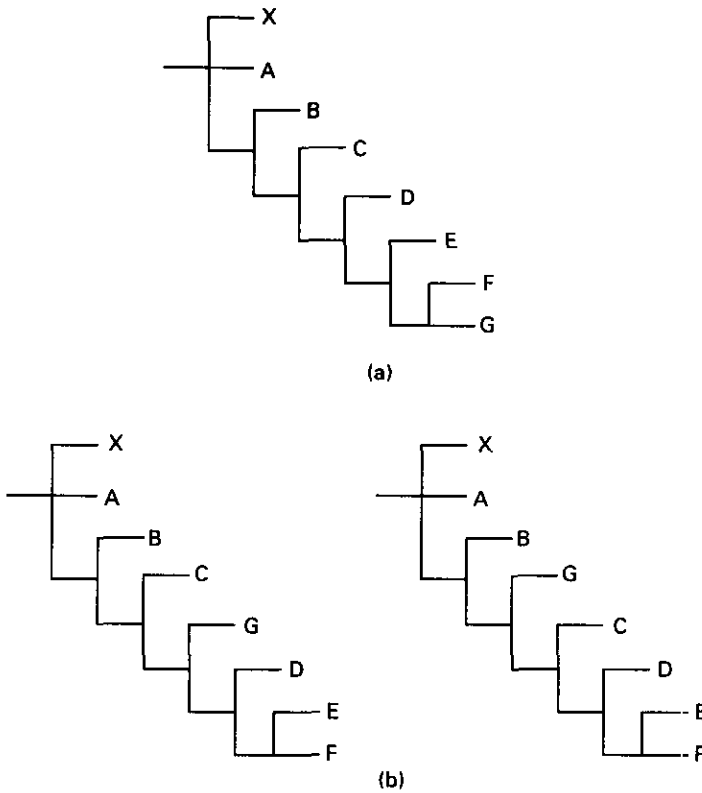


Fig. 3. Best-fitting cladograms derived from analyses of original (Table 3) and corresponding three-taxon transformed data matrices. (a) The single hypothesis ($C = 0.75$; $R = 0.81$) derived from the original matrix. (b) The two equally parsimonious topologies ($C = 0.79$; $R = 0.74$) resulting from the analysis of the transformed data.

formation homology, and are consequently beside the point. For example, he reasons (p. 262), with respect to an additive multistate character, that the "states are (assumed) non-independent", and *cannot* therefore be represented exactly by a series of binary characters. He does not consider the importance of character independence relative to taxic homology, except by asserting that the repetitions produced by the three-taxon transformation are significant, "[i]f independent". But, by his own admission elsewhere (Nelson and Ladiges, 1992), the repetitions produced by the transformation are not independent (see also Harvey, 1992; Kluge, 1993).

In order to expose Platnick's (1993: 269–271) misunderstanding of independence we need only consider his example of a single binary character: taxa A–I exhibit the plesiomorphic condition (0), and taxa J–O have the apomorphic state (1). For such a binary character arrayed over nine plesiomorphic and six apomorphic taxa, there is a total of 135 three-taxon statements: A(J, K), A(J, L), A(J, M), A(J, N), A(J, O), A(K, L), A(K, M), A(K, N), A(K, O), A(L, M), A(L, N), A(L, O), A(M, N), A(M, O), A(N, O); B(J, K), B(J, L), B(J, M), B(J, N), B(J, O), B(K, L), B(K, M), B(K, N), B(K, O), B(L, M), B(L, N), B(L, O), B(M, N), B(M, O), B(N, O); C(J, K), C(J, L), C(J, M), C(J, N), C(J, O), C(K, L), C(K, M), C(K, N), C(K, O), C(L, M), C(L, N), C(L, O), C(M, N), C(M, O), C(N, O); D(J, K), D(J, L), D(J, M), D(J, N), D(J, O), D(K, L), D(K, M), D(K, N), D(K, O), D(L, M), D(L, N), D(L, O), D(M, N),

Table 4
Number of accommodations on cladogram 1

A(J, K),	A(J, L),	...	A(N, O)	15
B(J, K),	B(J, L),	...	B(N, O)	15
C(J, K),	C(J, L),	...	C(N, O)	15
D(J, K),	D(J, L),	...	D(N, O)	10
E(J, K),	E(J, L),	...	E(N, O)	6
F(J, K),	F(J, L),	...	F(N, O)	3
G(J, K),	G(J, L),	...	G(N, O)	1
H(J, K),	H(J, L),	...	H(N, O)	0
I(J, K),	I(J, L),	...	I(N, O)	0
				65/135

Number of accommodations on cladogram 2

A(J, K),	A(J, L),	...	A(N, O)	6
B(J, K),	B(J, L),	...	B(N, O)	6
C(J, K),	C(J, L),	...	C(N, O)	6
D(J, K),	D(J, L),	...	D(N, O)	6
E(J, K),	E(J, L),	...	E(N, O)	6
F(J, K),	F(J, L),	...	F(N, O)	6
G(J, K),	G(J, L),	...	G(N, O)	6
H(J, K),	H(J, L),	...	H(N, O)	6
I(J, K),	I(J, L),	...	I(N, O)	6
				54/135

D(M, O), D(N, O); E(J, K), E(J, L), E(J, M), E(J, N), E(J, O), E(K, L), E(K, M), E(K, N), E(K, O), E(L, M), E(L, N), E(L, O), E(M, N), E(M, O), E(N, O); F(J, K), F(J, L), F(J, M), F(J, N), F(J, O), F(K, L), F(K, M), F(K, N), F(K, O), F(L, M), F(L, N), F(L, O), F(M, N), F(M, O), F(N, O); G(J, K), G(J, L), G(J, M), G(J, N), G(J, O), G(K, L), G(K, M), G(K, N), G(K, O), G(L, M), G(L, N), G(L, O), G(M, N), G(M, O), G(N, O); H(J, K), H(J, L), H(J, M), H(J, N), H(J, O), H(K, L), H(K, M), H(K, N), H(K, O), H(L, M), H(L, N), H(L, O), H(M, N), H(M, O), H(N, O); I(J, K), I(J, L), I(J, M), I(J, N), I(J, O), I(K, L), I(K, M), I(K, N), I(K, O), I(L, M), I(L, N), I(L, O), I(M, N), I(M, O), I(N, O). However, it is evident from this long list that there are only 15 different apomorphic relations, (J, K), (J, L) ... (N, O), each being repeated nine times, once for each of the plesiomorphic taxa, A-I (Table 4).

The biased effect of this non-independence in the 135 three-taxon statements can be easily demonstrated with two of Platnick's cladograms, a highly asymmetrical topology, his Cladogram 1, and a nearly perfectly symmetrical topology, his Cladogram 2 (Fig. 4). According to Norman Platnick (pers. comm.), the nine plesiomorphic and six apomorphic terminal taxa are distributed on those two topologies as shown in Fig. 4. Further according to Platnick (1993), state 1 is more *displaced* on Cladogram 1 than it is on Cladogram 2.

Platnick (1993) links three-taxon statements to displacement by way of a measure he calls *accommodation*. Platnick (p. 269) states that "[a]ny cladogram that accommodates a given three-taxon statement requires no extra steps (i.e. no *ad hoc* hypotheses)", and accommodated three-taxon statements are "those between any pair of taxa with 1 entries and any more basally situated taxon with a 0 entry". For example, according to Platnick, statement A(J, K) is accommodated by both Cladogram 1 and 2, statement A(J, M) is accommodated by Cladogram 1, but not Cladogram 2, and statement D(J, K) is accommodated by Cladogram 2 but

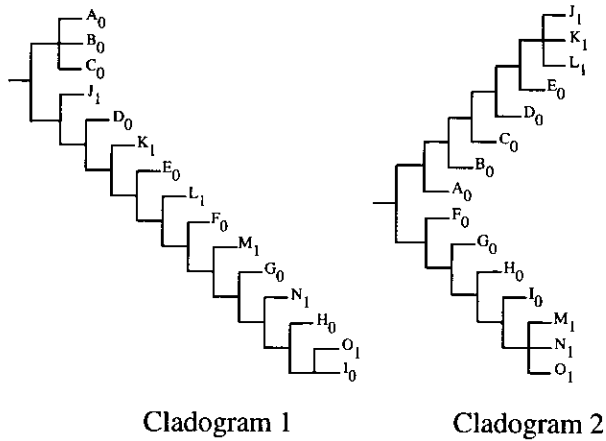


Fig. 4. Cladograms 1 and 2 from Platnick (1993: Fig. 1).

not Cladogram 1. Using his measure of accommodation, Platnick observes that Cladogram 1 accommodates 65 of the 135 possible three-taxon statements, whereas Cladogram 2 accommodates only 54.

Now for some revealing numbers. Platnick (1993) correctly notes that the *untransformed* binary character with nine plesiomorphic states and six apomorphic states has a much higher consistency index on Cladogram 2 ($c = 0.50$) than it does on Cladogram 1 ($c = 0.17$)^c. Thus, according to a parsimony analysis of untransformed data, Cladogram 2 exhibits much greater explanatory power. However, Platnick also notes that Cladogram 1 accommodates more three-taxon statements than does Cladogram 2, 65 and 54, respectively, and therefore it exhibits greater explanatory power ($C = 0.48$ versus $C = 0.40$). Here it might seem that we have an example of how, in the words of Nelson and Platnick, the precision of parsimony is improved by the three-taxon transformation. However, the larger number of accommodations exhibited by Cladogram 1 is *biased* by non-independent statements. It is a fact that there really are only 15 different apomorphic relations, (J, K), (J, L) . . . (N, O), each of which is replicated nine times, once for each of the plesiomorphic terminal taxa, A–I. The 65 accommodations that Platnick attributes to Cladogram 1 come from seven of the nine sets of redundant statements (Table 4). It is in fact Nelson and Platnick's (1991) way of eliminating symplesiomorphy that causes the logical non-independence, and consequently biases the accommodation numbers.

My concern for the non-independence of data created by the three-taxon transformation calls into question Platnick's preference for cladograms having greater "displacement". That the greater displacement exhibited by Cladogram 1 is a good thing only follows from Cladogram 1 accommodating more three taxon statements and being a more parsimonious explanation for those transformed data. But, as I have shown, the importance Platnick attaches to displacement is unconvincing because of the biased numbers he employs in his example. Thus, there is no basis in three-taxon transformation for preferring less parsimonious explanations of the original data.

In having been presented as a possible improvement to cladistics, the three-taxon

^c Character and ensemble consistency and retention indices, c and r , and C and R , respectively, follow the definitions of Farris (1989).

transformation cannot avoid being evaluated according to cladistic concepts and practices. Therefore, I see no reason to withdraw any of my previous criticisms (Kluge, 1993; 255) of the three-taxon transformation (Nelson and Platnick, 1991; see also Nelson and Platnick, 1981): (1) the transformation renders original data weaker than they are in fact—the level of character generality is ambiguous; (2) missing data are added where none existed before; (3) the phylogenetic informativeness of evolutionary reversals is discarded with the removal of symplesiomorphies; (4) the number of logically dependent and redundant characters increases; (5) homoplasy is added to the original data. Thus, I judge the three-taxon operation not to be an improvement to cladistics.

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