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Cladistics Is Useful for Reconstructing Archaeological Phylogenies: Palaeoindian Points from the Southeastern United States

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Cladistics, a method used to create a nested series of taxa based on homologous characters shared only by two or more taxa and their immediate common ancestor, offers a means of reconstructing artifact lineages that reflect heritable continuity as opposed to simple historical continuity. Although cladistically derived trees are only hypotheses about phylogeny, they are superior both to trees created through phenetics, which employs characters without regard as to whether they are analogous or homologous, and to trees created by using undifferentiated homologous characters. To date, cladistics is an unused approach to constructing archaeological phylogenies but one that holds considerable potential for resolving some of archaeology's historical problems. For example, it has long been noted that the southeastern United States exhibits the greatest diversity in fluted-point forms in North America—an observation that prompted Mason (1962) to propose that fluted points originated in the Southeast and then spread to other areas. However, because of a paucity of such points from well-dated contexts in the Southeast, it is difficult to ascertain chronological, let alone phylogenetic, relations among the various forms. Evolutionary trees derived from cladistical analysis are testable hypotheses about those phylogenetic relations.

Keywords: CLADISTICS, CULTURAL TRANSMISSION, DERIVED CHARACTERS, PHYLOGENETIC TREES.

Introduction

Archaeologists have used changes in artifact form—specifically, changes in character states of artifacts—to measure the passage of time. If evolved character states are ordered correctly, a historical sequence of forms is created, although independent evidence is needed to root the sequence—that is, to determine which end of the sequence is older. Ford's (1962) illustration of change in the form of ceramic vessels (Figure 1) is an excellent heuristic device in this respect because it clearly and concisely displays historical continuity (O'Brien & Lyman, 1998). One vessel form followed another, changing ever so slightly, and when one form is stacked on top of another in proper order, the forms create an historical sequence. But Ford intended his graph to show something beyond mere historical continuity. Although he was not explicit, he intended the graph to show heritable continuity between chronologically adjacent vessel forms; thus the sequence was a lineage of pottery forms. Ford was preceded by other prehistorians who, although they were interested primarily in chronological matters, created orderings that implied heritable continuity between sequent forms (O'Brien & Lyman, 1999, 2000*a*).

The notion that formal similarity of cultural phenomena can be used to indicate heritable continuity originated with the use of the comparative method in linguistic studies of the late 18th and early 19th centuries (Leaf, 1979; Platnick & Cameron, 1977). As Boas (1904: 518) observed, "Owing to the rapid change of language, the historical treatment of the linguistic problem had developed long before the historic aspect of the natural sciences was understood. The genetic relationship of languages was clearly recognized when the genetic relationship of species was hardly thought of. . . . No other manifestation of the mental life of man can be classified so minutely and definitely as language. In none are the genetic relations more clearly established." Boas was speaking metaphorically about the "genetic relationship of languages", but his point was solid: Linguistic similarity was the result of transmission and heritable continuity.

Culture historians of the mid-20th century regularly referred to general processes of cultural transmission, but they rarely were explicit about what was transmitted or why this might be important. For example, Willey (1953: 368) remarked that "theories of culture change and continuity are fundamental to [Americanist] archeological studies", but he did not

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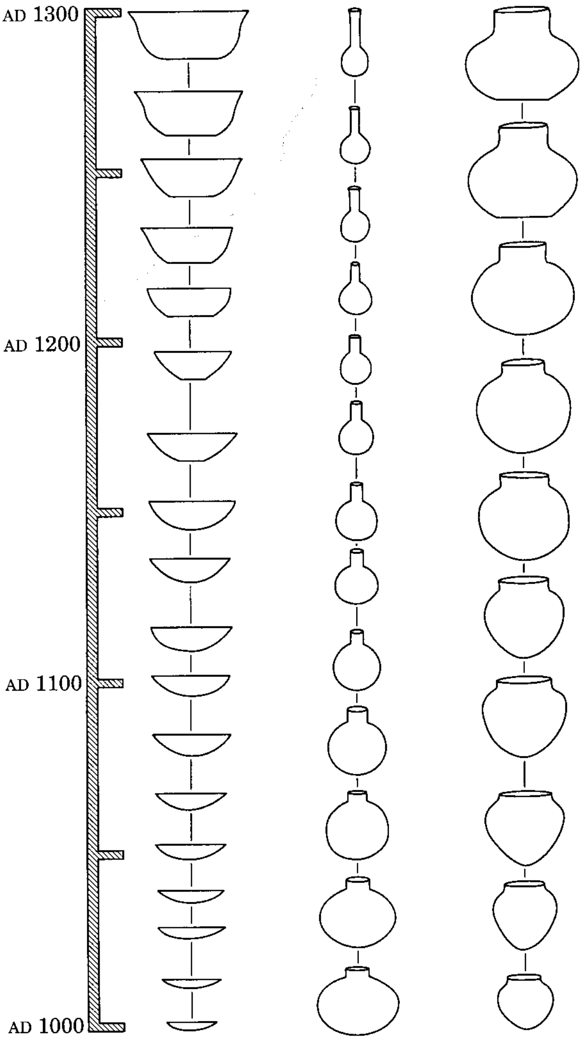


Figure 1. James A. Ford's conception of culture change as manifest in artifacts (after Ford, 1962). Note the consistent and gradual change in each of the three forms through time. Not only is the passage of time measured by the sequence of forms, but heritable continuity and transmission are implied, indicating that each line of vessels comprises a lineage.

elaborate on what those theories were, nor did he point out that the notion of continuity had to rest on heritability and transmission. Spaulding (1955: 14) provided a brief but revealing insight into the theories to which Willey was referring:

> If we view the ultimate task of archaeology as the development of the ability to explain the similarity or lack of similarity of any two [archaeological manifestations], the significance of [classifying those manifestations according to their positions in time and space and their formal resemblance] is easy to state. All [three—time, space, and form—] can be related to the proposition that culture change is systematic rather than capricious and to the auxiliary proposition that an important basis for the systematic behaviour of culture is its *continuous transmission through the agency of person to person contact.* (emphasis added)

Americanists seldom referenced Darwin's (1859) theory of descent with modification, although they believed at least implicitly that if formal similarity were taken to signify a historical relation between compared items, then heredity or transmission of some sort must be involved. Their belief was the result of using ethnologically documented mechanisms such as diffusion and enculturation to account for typological similarities in the archaeological record. Thus Willey's (1953: 363) statement that "typological similarity is an indicator of cultural relatedness (and this is surely axiomatic to archeology), [and thus] such relatedness carries with it implications of a common or similar history" was cause for little concern within the discipline. It should have caused considerable concern because the axiom falls prey to a caution raised by palaeobiologist George Gaylord Simpson (1961), using monozygotic twins as an example: They are twins not because they are similar, rather, they are similar *because* they are twins. This distinction was unclear in archaeology, and thus archaeologists relied on general artifact similarity to denote relatedness. Seriation offered a means of escaping this pitfall, but prehistorians overlooked the phylogenetic implications of their chronological orderings (O'Brien & Lyman, 2000*a*).

In systematic biology in the 1940s and 1950s, formal similarity was used to create evolutionary taxonomies (e.g., Dobzhansky, 1951; Mayr, 1942; Simpson, 1945) that were intended to reflect not only patterns of ancestry and descent but also the degree of divergence between and among taxa. Evolutionary taxonomy was based on the same axiom that underlay any approach to understanding evolutionary pathways: Similarity of phylogenetically related organisms is a result of replication through genetic transmission. During reproduction, organisms transmit genetic material, creating either an offspring that is an exact copy of the parent (asexual reproduction) or an offspring that has characteristics of both (sexual reproduction). Over time, because of transmission errors, mutation, and/or recombination, the organisms comprising a population (or species) change. These changes might not be detectable from one generation to the next, but after sufficient time we notice that the two ends of the lineage comprise dissimilar individuals whereas individuals adjacent to one another in the lineage are virtually identical. Despite close adherence to this axiom, evolutionary taxonomies were problematic because the two features of the evolutionary process that were being shown—pattern of descent and degree of divergence—did not always follow the same patterns and rates (e.g., Eldredge & Gould, 1972, 1977, 1997; Gould & Eldreidge, 1977, 1986, 1993). Thus it became difficult, if not impossible, to incorporate both the relative time of lineage splitting and the rate of change since the split into a consistent classification (Brown & Lomolino, 1998: 326). The end result was widespread subjectivity, with each systematist arguing for his or her own idiosyncratic taxonomy.

Overall similarity in terms of formal characters (traits) was used to group like with like in descending order of specificity, but overlooked was the notion that there were different kinds of formal similarity, each created by different processes. Biologists were not ignorant of the differences between homologous and analogous characters (nor were archaeologists, for that matter)—the former the result of genealogy and the latter of parallelism or convergence—and they correctly ignored analogous characters and focused only on homologous characters in their taxonomies. But they ignored the fact that there are different kinds of homologous characters and that it matters greatly how those different kinds of characters are handled during phylogenetic analysis. Another complication was the fact that despite the recognized distinction between homology and analogy, it often was difficult to label a specific character found in two or more taxa as a homologue or analogue without knowing the phylogenetic history of the taxa—the very thing the characters were being used to construct. Thus an alternative to evolutionary taxonomy made its appearance in the 1960s—numerical taxonomy, or phenetics (Mayr, 1981), which clusters objects or groups of objects on the basis of a large number of morphometric characters (Sokal & Sneath, 1963). The approach side-stepped the homology–analogy issue by incorporating any and all characters into analysis, but many evolutionary biologists ignored it for the simple reason that it overlooked phylogeny in favour of producing "natural" groups (e.g., Gilmour, 1937).

In the late 1940s German entomologist Willi Hennig devised a phylogenetic method that has come to dominate other approaches—an approach that he termed *phylogenetic systematics* (Hennig, 1950) but which in the years following publication of his treatise in English (Hennig, 1966) came to be known simply as *cladistics*. On the one hand, the method is identical in purpose to evolutionary taxonomy—the creation of phylogenetic trees that show evolutionary relationships between and among taxa. On the other hand, it differs from other methods of reconstructing evolutionary relationships in that it employs only a subset of homologous features—*shared derived characters* as opposed to *shared ancestral characters*—to create relationships between and among taxa. These are discussed in detail in the following section; here it is sufficient to state that shared derived characters are homologous traits held in common by two or more taxa and their most recent common ancestor but by no other taxa. In contrast, shared ancestral characters are homologous traits that, as the name implies, occur farther back in a lineage than in the most recent common ancestor.

Cladistics is a powerful tool for constructing phylogenetic histories of anything that evolves over time, including material remains found in the archaeological record (O'Brien & Lyman, 2000*b*). To date, its major use has been in the biological realm, but the basic approach is identical in logic and similar in method to tracing historical patterns of descent in languages (Platnick & Cameron, 1977; Ross, 1997). The logical basis for extending the use of cladistics into archaeology is the same as it is in biology: Artifacts are complex systems, comprising any number of parts that act in concert to produce a functional unit. The kinds of changes that occur over generations of, say, projectile-point manufacture are highly constrained in that new structures and functions usually arise through modification of existing structures and functions as opposed to arising de novo. Thus, "the history of these changes is recorded in the similarities and differences in the complex characteristics of related [objects]—in the extent to which the characteristics of their common ancestors have been modified by subsequent additions, losses, and transformations" (Brown & Lomolino, 1998: 328).

We anticipate objections to the applicability of cladistics to archaeological phenomena. Such objections might take several forms. First, it might be argued that artifacts do not breed, akin to Brew's (1946: 53) oft-quoted statement that "phylogenetic relationships do not exist between inanimate objects". Thus any attempt to use a method designed to reconstruct phylogeny is reductionism at its worst. Our response is that there certainly *are* phylogenetic relationships between inanimate objects; if it were otherwise, palaeontologists would be out of work. Our view (O'Brien & Lyman, 2000*a*) is that things found in the archaeological record—projectile points, ceramic pots, and the like—were once part of human phenotypes and were therefore shaped by the same evolutionary processes that shape somatic characters. This makes artifacts part and parcel of any discussion of human phylogeny. Tools do not breed, but tool makers *do* breed, and they *do* transmit information to other tool makers, irrespective of whether those other tool makers are lineal descendants. Cultural transmission is a different kind of transmission than what is produced intergenerationally by genes, but this is irrelevant as far as phylogeny is concerned. It also is irrelevant for reconstructing phylogenetic history except insofar as we suspect cultural phylogenies are sometimes more difficult to construct than are purely biological ones. Clarke (1978: 181) well understood the importance of transmission to maintaining heritable continuity among cultural items when he remarked that "it is the artefact maker who feeds back into the phenotypic constitution of the next generation of artefacts the modified characteristics of the preceding population of artefacts, and it is in this way that the artefact population has continuity in its trajectory and yet is continuously shifting its attribute format and distribution". Continuity is ensured by transmission, leading over time to *tool traditions*, or what we refer to as *tool lineages*. It seems naive, given what we know of the archaeological record, not to believe that tool forms are modelled on pre-existing tool forms. If so, then they carry inherited characters.

Second, it might be argued that although there are tool lineages, they are almost impossible to discover archaeologically because of the kind of process—cultural evolution—that produced them. The tempo of cultural evolution is much faster than that of biological evolution, as is the primary mode—reticulate for cultural evolution and branching for biological evolution. Thus it has been argued (Moore, 1994*a*, *b*; Terrell, Hunt & Gosden, 1997) that these factors, together with diffusion and its attendant processes, swamp all traces of phylogenetic history and reduce the cultural landscape to little more than a blur of hybrid forms. We, like Bellwood (1996), find it difficult not to agree that cultural differentiation *can* be reticulate; similarly, we do not view that as being particularly problematic to archaeological (or linguistic) analysis. Goodenough (1997: 178) makes an excellent point with respect to language: "Contact between Japan and the United States has resulted in considerable borrowing in language and culture by Japan and some reverse borrowing by the United States, but their languages and cultures retain their respectively distinct phylogenetic identities". Further, linguists do not flip a coin to determine whether two or more languages share a phylogenetic history. Innumerable case studies have provided the basis for deciding which linguistic characters might be derived characters—bound morphemes and vocabulary, for example—and which might be something else—syntax, for example (see Nichols, 1996). Thus Ross (1997: 183) can state, as a biologist would, that the comparative method used in linguistics "subgroups languages not on the basis of shared similarities but according to the distribution of shared innovations relative to a reconstructed protolanguage ancestral to the whole family" (emphasis added). This is nothing more than separating shared derived characters from ancestral characters and using the former to construct a phylogeny.

In the following section we describe the cladistic method, paying particular attention to the problem of distinguishing between homologous and analogous characters and, in the case of the former, distinguishing between derived and ancestral characters. In the subsequent section we present an example of how cladistics can assist in reconstructing phylogeny, here the phylogenetic history of Palaeoindian-period (*c.* 11,500–10,000 BP) projectile points from the southeastern United States. We stress that our discussion of cladistics is not intended to replace standard texts on the subject (for readable accounts see Brooks & McLennan, 1991; Kitching *et al.*, 1998; Ridley, 1996; Wiley, 1981; Wiley *et al.*, 1991); rather, we view it as a brief introduction to the logic behind, and key methodological elements of, cladistics. The basics of cladistics are simple enough, although there is a set of specific terms and concepts that goes along with them. To date, most archaeological discussions of cladistics (e.g., Moore, 1994*b*; Terrell, Hunt & Gosden, 1997) use the term indiscriminately to refer to any kind of branching phylogeny. Although such usage might be proper semantically—the Greek word *klados* means "branch"—archaeologists appear unaware (Foley [1987] and Harmon *et al.* [2000] are exceptions) that in the natural sciences cladistics refers to a very specific method of reconstructing phylogeny.

Cladistics and Reconstructing Phylogenetic History

We view the ultimate goal of cladistics as assisting in the reconstruction of the branching pattern of evolutionary descent—a view shared by most, but certainly not by all, biologists (Carpenter, 1987; Eldredge & Cracraft, 1980; Hull, 1979, 1984; Mayr, 1982). Regardless, it often is overlooked that cladistics in and of itself makes no claims about phylogeny. Logically it *cannot* make phylogenetic claims; rather, it produces only statements about similarity. This was not Hennig's original intent, nor is it the intent of most cladistically inclined biologists and palaeobiologists, but the fact remains that all a cladogram does is summarize a pattern of character distribution. It is then up to the analyst to place the distribution in correct historical sequence and then to explain the pattern. This is done through reference to Darwinian evolutionary theory (descent with modification), but this is a far cry from saying that descent with modification provides independent support *for* any kind of systematics, including cladistics. If we could get away with such epistemological sleight-of-hand, then we would be assured that descent "explains pattern similarity, modification explains pattern differences, and their combination can explain any pattern that might be observed" (Brower, 2000: 151). Such a notion is both metaphysical and unverifiable (Popper, 1974). The strength of cladistics is its non-reliance on evolutionary theory (or any other theory) as a necessary ontological basis (Brady, 1985; Lee & Doughty, 1997; Platnick, 1979, 1985; Rosen, 1982).

Figure 2(a) is a cladogram that classifies four taxa. It tells us that based on a certain character distribution, taxa C and D are more similar to one another than either is to any other taxon. It also says that taxa B, C, and D are more similar to one another than any of the three is to Taxon A. This information could easily be written as a Venn diagram or in parenthetical notation without changing any of the information. Darwinian evolutionism, however, tells us that taxa do not spontaneousaly appear but rather evolve from other taxa. Thus Figure 2(a) could be read as a historical statement that tells us that Taxon A is ancestral to taxa B–D and thus is older than its descendants.

We know that taxa A–D evolved from one or more ancestral taxa, although at this point we know little or nothing about those ancestors except that with respect

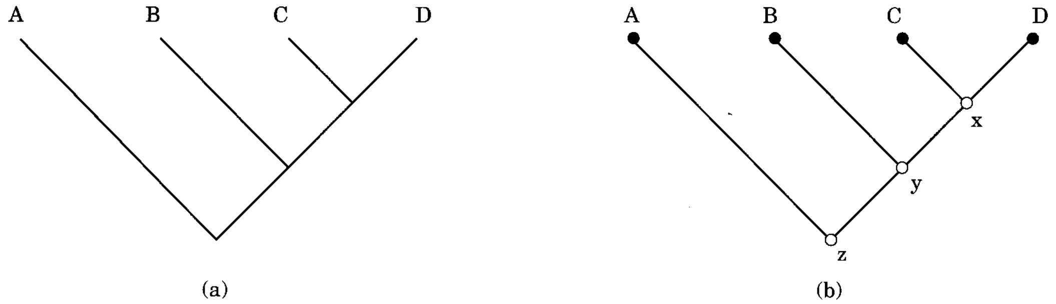


Figure 2. Two ways of illustrating formal relations of four taxa (A–D): (a) as a cladogram; (b) as a phylogenetic tree showing ancestral taxa x–z (open circles) and terminal taxa (filled circles).

to certain characteristics taxa C and D look more like their immediate common ancestor than they do the one that unites them with Taxon B. Likewise taxa B, C, and D look more like their common ancestor than they do the one that unites them with Taxon A. Convention is to place *nodes* at the points where branches meet and to refer to the nodes as ancestors that produced the *terminal taxa* (those at the branch tips) (Figure 2(b)). In our tree, taxa C+D, *together with* their hypothetical common ancestor (node x), form a *monophyletic group*, or *clade*. Taxa D+C+B, together with their common ancestor (node y), form another, more inclusive clade, and taxa D+C+B+A, together with their common ancestor (node z), form yet another, and the most inclusive, clade.

Distinguishing among kinds of characters

Day-to-day changes in the composition of a taxon, rendered as turnover in the individuals comprising its population(s), not only drives the evolution of that taxon but leaves traces—manifest as morphological variation—that allow us to reconstruct the evolutionary pathway of the taxon. Piecing together lineages, measuring rates of evolutionary change, and trying to understand the processes that create change are part and parcel of the worlds of biology and palaeobiology. At their core, the specific methods and techniques that have been devised to trace historical lineages revolve around identifying similarities and differences in *character states* of organisms. At any particular time all organisms in a species might have, for example, four digits, but in a suceeding generation some might have five. Such an appearance constitutes a change in the state, or condition, of the character "number of digits". The same problems, and methods of solving them, apply in archaeology.

The issue then becomes whether the characters under consideration are *analogous* or *homologous*. Analogues are functionally similar characters (or character states) that evolved separately in two or more lineages after those lineages diverged. Thus they are of no utility in reconstructing lineages. Homologues *are* useful for tracking heritable continuity because they are holdovers from a previous time when two lineages were a single lineage. Darwinian evolutionary theory provides the explanation for homology, but it does not tell us how to identify it. Although "similarity is the factor that compels us to *postulate* homology" (Cracraft, 1981: 25), simple similarity in form is not a particularly useful criterion *for* homology. The reason for this is clear: Similarity can result from convergence. Thus whereas similrity is factual, homology must remain an hypothesis (Patterson, 1988: 604). But if it is an hypothesis, then it is testable (e.g., Brady, 1985; McKitrick, 1994). Extensive treatment of how analogous characters are differentiated from homologous characters is beyond the scope of this paper, and we refer interested readers to Lyman (2001), who (1) compares the methods used by cladists and evolutionary taxonomists and (2) discusses parallel strategies in archaeology.

Phylogenetic trees constructed through cladistics use only a subset of all homologous characters; they are referred to as *derived characters*, or *apomorphies*. Figure 3 shows the evolution of a projectile-point lineage that begins with Ancestor A. For simplicity we are tracking only a single character, fluting, for which two character states are possible, fluted and unfluted. Over time, Ancestor A, which is unfluted, gives rise to two lines, one of which, like its ancestor, is unfluted and the other of which *is* fluted (Figure 3(a)). Thus the character state "fluted" in Taxon 2 is apomorphic, meaning it is derived from the *ancestral* character state, "unfluted". Ancestral characters or character states are termed *plesiomorphies*. In Figure 3(b), Ancestor B (old Taxon 2) gives rise to two new taxa, 3 and 4, each of which carries the derived character state, "fluted". At this point "fluted" becomes a *shared* derived character state, or *synapomorphy*, defined as a character or character state shared only by sister taxa and their immediate common ancestor. Characters in sister taxa that have been inherited from an ancestor more distant than the common ancestor are ancestral characters. In Figure 3(c), in which two descendent taxa have been added, fluting is now an ancestral character *relative* to taxa 5 and 6 because it is shared by three taxa and two ancestors. But relative to taxa 3, 5, and 6, fluting is a derived character state because it is shared by three taxa and their immediate common ancestor, B. Thus

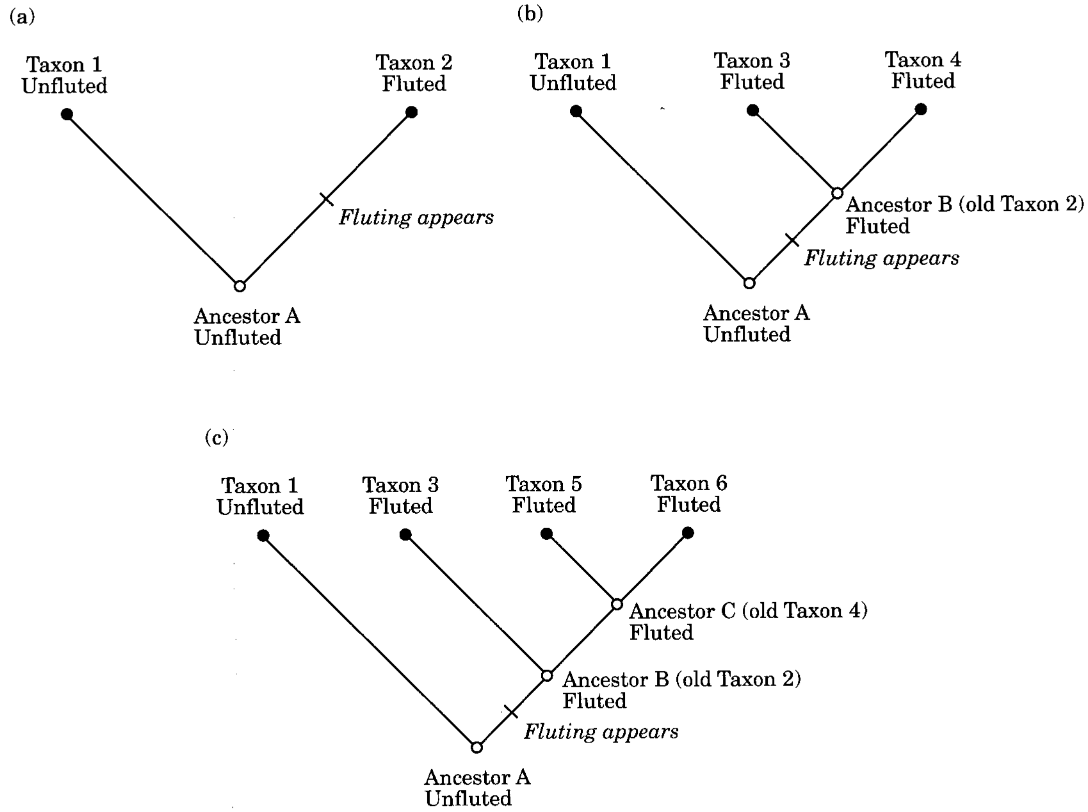
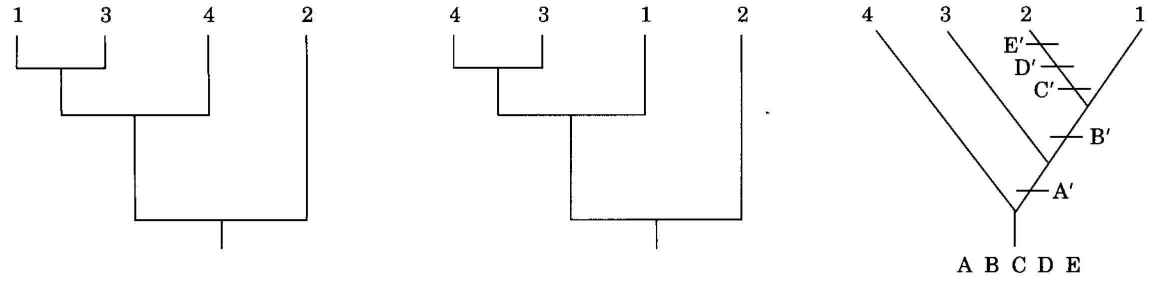


Figure 3. Phylogenetic trees showing the evolution of projectile-point taxa. In (a), fluting appears during the evolution of Taxon 2 out of its ancestral taxon. Its appearance in Taxon 2 is as an apomorphy. In (b), Taxon 2 has produced two taxa, 3 and 4, both of which contain fluted specimens. The appearance of fluting in those sister taxa and in their common ancestor makes it a synapomorphy. In (c), one of the taxa that appeared in the previous generation gives rise to two new taxa, 5 and 6, both of which contain fluted specimens. If we focus attention only on those two new taxa, fluting is now a plesiomorphy because it is shared by more taxa than just sister taxa 5 and 6 and their immediate common ancestor. But if we include Taxon 3 in our focus, fluting is a synapomorphy because, following the definition, it occurs only in sister taxa and in their immediate common ancestor.

depending on where in a lineage one begins, a trait can be apomorphic or plesiomorphic.

The use of shared derived characters to determine phylogenetic relations is founded in the notion of evolutionary descent with modification. Such characters "are nested. From the point when a feature first appears in phylogenetic history, it will be passed along in some guise (i.e., in the same or transformed version) to descendent taxa. [By] mapping the distribution of such attributes[,] monophyletic taxa—branches of the tree of life—are delineated, defined, and recognized" (Eldredge & Novacek, 1985: 67). Such taxa comprise "actual historical units" (Eldredge & Novacek, 1985: 66). The question is, how does one actually distinguish between ancestral and derived character states—termed *character polarity*—in order to plot the course of evolution relative to those taxa? The issue is complex, but one commonly used method is *outgroup* comparison, with an outgroup being defined as a closely related taxon that is known to be phylogenetically outside the clade being investigated. The character state in that outgroup, then, is likely to have been ancestral relative to the taxa under investigation. Ridley (1996: 476) makes an important point: "Outgroup comparison works on the assumption that evolution is parsimonious"—a reasonable assumption given that evolution is improbable to begin with. This means that when faced with the problem of character polarity, we choose the option that requires the fewest evolutionary events. For example, in Figure 3 it is more parsimonious to assume that fluting arose once and only once as opposed to having arisen twice in separate lineages.

A degree of circularity often is built into the cladistic technique of outgroup comparison because it presumes that we *know* a priori that the chosen outgroup is no more closely related to one group than it is to any other group under consideration. In other words, it assumes something about what it is we are trying to discover. This has resulted in observations such as Eldredge & Novacek's (1985: 68) that "cladistics is no panacea. It is hard to do a good piece of systematics research using cladistics—indeed, harder than ever before. The system is logically much more rigorous, requiring every available item of evidence". Available items of evidence now regularly used to lessen the circularity include (1)



(a) (b) (c)

Taxa	Character States				
1	A′	B′	C	D	E
2	A′	B′	C′	D′	E′
3	A′	B	C	D	E
4	A	B	C	D	E

(d)

	1	2	3	4
1	–	2	4	3
2		–	1	0
3			–	4
4				–

(e)

	1	2	3	4
1	–	2	1	0
2		–	1	0
3			–	0
4				–

(f)

Figure 4. Comparison of two phenograms (a and b) with a cladogram (c), based on hypothetical states of five characters in four taxa (d). Both phenograms can be constructed from the total character states shared by any pair of taxa (e). The cladogram is constructed from only the derived character states (marked by primes) shared by pairs of taxa (f). Changes in character state are marked in the cladogram. Note the differences between (a) and (b) compared with (c).

the *congruence criterion*—multiple characters suggesting the same phylogenetic tree (Rieppel, 1994); (2) an assumption of parsimony—that particular innovations will appear a minimum number of times (Sober, 1988); and (3) independent temporal data, such as that derived from superposition, to test indications of which character states are ancestral and which are derived (e.g., Donoghue *et al.*, 1989).

Stratocladistics is a relatively new approach that involves the use of temporal data, such as might be derived from superposition, to assist in the construction of phylogenetic trees (e.g., Benton & Hitchin, 1997; Benton, Hitchen & Wills, 1999; Fisher, 1991, 1992, 1994; Fox, Fisher & Leighton, 1999; Polly, 1997; Smith, 1994; Wills, 1999). Some cladists, however, argue that the temporal polarity of two apparently related characters—such as might be suggested by their order of appearance in a stratigraphic column—may be misleading as a result of the way in which the fossil record was formed or sampled (e.g., Stevens [1980] and references therein). Thus they argue that one should completely ignore the apparent temporal positions of characters and instead focus solely on the distribution of the characters in question across different taxa. We agree that assigning temporal polarity on the basis of superpositional information might lead to incorrect results, but we are not inclined to discard stratigraphic or other temporal information. What we would do is search for recurrent temporal patterns, our thinking being that such patterns support the initial assignment.

Features of cladistically derived trees

We highlight two important aspects of cladograms. First, although all phylogenetic trees are hypotheses, a cladistically derived tree should be a more realistic hypothesis than a tree produced using undifferentiated homologous characters (unless all the characters just happen to be derived). Figure 4 illustrates three possible historical patterns—two evolutionary trees (phenograms) constructed using undifferentiated homologous structures (Figure 4(a) and 4(b)) and one tree (a cladogram) using only derived characteristics (Figure 4(c))—for four taxa (1–4) and five characters (A–E). As shown in the matrix in Figure 4(d), for each taxon the five characters are in one of two character states, with derived character states designated by a prime sign and ancestral character states by lack of a prime sign. The matrix in Figure 4(e) shows the number of shared character states, regardless of whether they are ancestral or derived, between pairs of taxa. Which pattern best depicts phylogeny? Perhaps the tree in Figure 4(a) is optimal because it denotes a close relationship between taxa 1 and 3 which have four character states in common, but then again, it splits out Taxon 4 which has these states in common with Taxon 1 and four with Taxon 3. Maybe the tree in Figure 4(b) is better in that it minimizes the distance between taxa 4 and 3 and shows that Taxon 1 is closer to taxa 4 and 3 than any of them is to Taxon 2. Taxon 2 shares no character states with Taxon 4—thus we maximize the distance between them—one state with

Taxon 3—thus we place 3 closer to 2—and two states with Taxon 1—thus we minimize the distance between them.

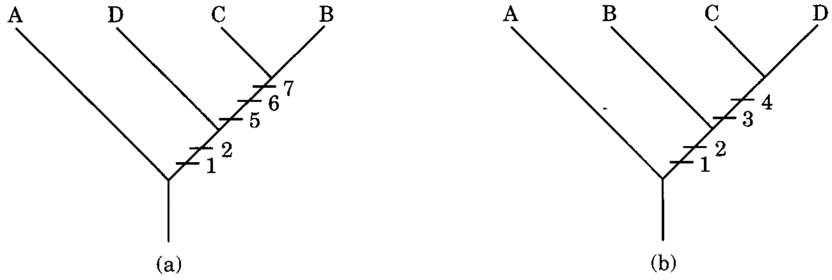
On the face of it, the tree in Figure 4(b) is far superior to the tree in Figure 4(a), a result that we probably would have obtained by plugging the data into most clustering programs. Clustering algorithms search all the data to find the most equitable solution in terms of minimum–maximum distances (similarity rendered as shared character states) between pairs. But does the tree in Figure 4(b) configure the historical evolutionary relationships among the four taxa correctly? Maybe, but we would bet against it because we made no attempt to discriminate between ancestral characters and derived characters. The tree in Figure 4(c)—the cladistically derived tree—illustrates the evolutionary history of the four taxa based solely on an analysis of shared derived character states, shown in Figure 4(f). Now taxa 1 and 3 share little in common, whereas before they were placed closer together simply because of the total number of character states they had in common. But three of them were ancestral states, not derived states. Analysis of shared derived character states alone indicates that Taxon 3 split off from the ancestral form that produced 1 and 2 at some point when Taxon 2 had not yet come into existence.

The second point to keep in mind with respect to cladistically derived trees is that although in the examples presented thus far all characters and character states evolved only once, such a neat package is rarely encountered in real-world situations. More likely a tree will contain multiple character states that show up in lines not related directly through one common ancestor. These are referred to as *homoplasies*. One kind of homoplasy results from character-state reversals—meaning, for example, that character state A changed to state A′ and then at some later point in the lineage reverted to state A. We view this kind of homoplasy more as a classification problem, meaning that rarely if ever will precisely the same character state reemerge after it disappears (Dollo's Law). More likely, the classification system (measurement) being used makes it *appear* as if the new character state is a homoplasy. Another kind of homoplasy results from parallelism or convergence—organisms, perhaps because of anatomical and/or environmental constraints (the first the result of common history, the second because of similar environments), independently evolve the same character state. All but the simplest cladograms contain homoplasies, and the task of the analyst is to reduce their influence on phylogenetic reconstruction—one of, if not *the*, most difficult problems in cladistic analysis.

Homoplasy leads to multiple solutions—usually thousands if not millions—to arranging taxa, and it is up to the analyst to sort through the solutions (there usually will be more than one optimal solution) and defend why one of them is chosen as the working phylogenetic hypothesis. Myriad procedures have been proposed for dealing with homoplasy, and our brief discussion is only a synopsis of general procedures. Borrowing an example from Brooks & McLennan (1991), suppose we have the data matrix shown in Figure 5, which shows the distribution of ancestral (labelled as 0) and derived (labelled as 1) character states for seven characters and three taxa (B, C, and D) plus an outgroup (A). The matrix shows us that (1) taxa B+C+D form a monophyletic group (based on characters 1 and 2), (2) taxa B+C form a monophyletic group (based on characters 5–7) (Figure 5(a)), and (3) taxa D+C form a monophyletic group (based on characters 3 and 4) (Figure 5(b)). Here we have a problem in that statements 2 and 3 cannot both be correct—either that or we have disproved the first principle of phylogenetic analysis, namely, that there is only one true phylogeny. We immediately suspect homoplasy is clouding the issue.

Character distributions can be portrayed in several ways: Either the states of characters 3 and 4 arose independently in taxa C and D (Figure 6(a)), or they arose in the common ancestor of B+C+D and were subsequently lost in Taxon B, meaning that they reverted to the ancestral states (Figure 6(b)). Examination of characters 5–7, which were left off the tree in Figure 5(b), produces a similar pattern of homoplasy: Either the states of characters 5–7 arose independently in taxa B and C (Figure 6(c)), or they arose in the common ancestor of B+C+D and subsequently reverted to the ancestral states in Taxon D (Figure 6(d)). How do we choose among the various options? One answer is to fall back on Hennig's principle that homology should always be assumed in the absence of contrary evidence. In other words, search for the tree that includes the greatest number of homologies and the fewest number of homoplasies. The trees in Figure 6(a) and 6(b), which share a common topology, contain seven derived character states each; the tree in Figure 6(a) also contains two instances of parallelism (or convergence), and the tree in Figure 6(b) contains two instances of trait reversal. The trees in Figure 6(c) and 6(d), which also share a common topology, contain seven derived character states each; the tree in Figure 6(c) also contains three instances of parallelism (or convergence), and the tree in Figure 6(d) contains three instances of trait reversal. Therefore we would choose the trees in Figure 6(a) and 6(b) over the trees in Figure 6(c) and 6(d). The trees in Figure 6(a) and 6(b) have a *length* of nine (the sum of derived character states plus homoplasies), and the trees in Figure 6(c) and 6(d) have a length of 10. Importantly, although the trees in Figure 6(a) and 6(b) are more parsimonious accounts of true phylogeny than the trees in 6(c) and 6(d) are, meaning they have shorter lengths, they are by no means surely correct. They are merely phylogenetic hypotheses.

The last topic we need to introduce before turning to a case example is perhaps the most important of all: the



	Characters and Character States						
	1	2	3	4	5	6	7
A (outgroup)	0	0	0	0	0	0	0
B	1	1	0	0	1	1	1
C	1	1	1	1	1	1	1
D	1	1	1	1	0	0	0

Figure 5. Two logically incompatible trees (a and b) for four taxa (A–D) and the character-state matrix used to generate the trees (0 = ancestral state, 1 = derived [apomorphic] state). Tree (a) places taxa B and C in a clade; tree (b) places taxa C and D in a clade. Together (a) and (b) violate Hennig's principle that there is only one correct phylogeny (adapted from Brooks & McLennan, 1991).

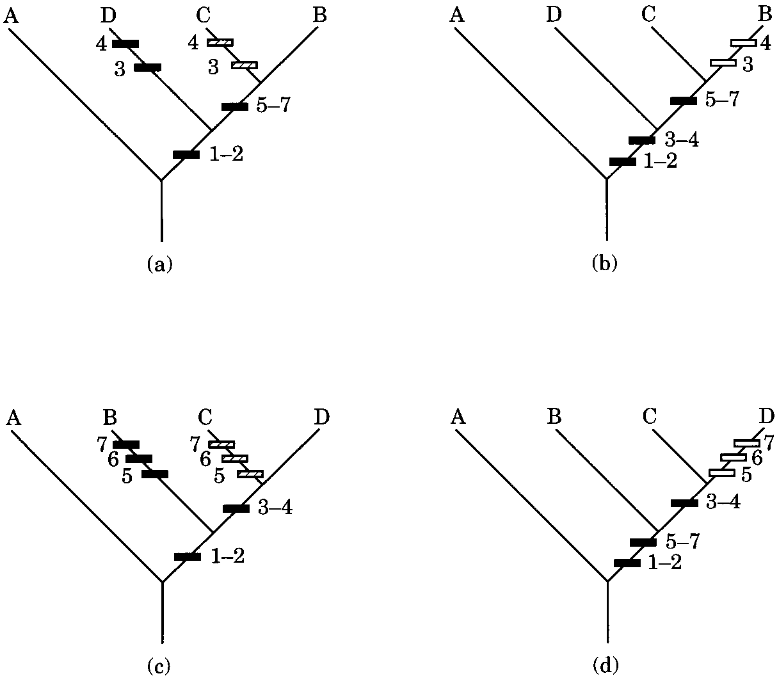


Figure 6. Alternative hypotheses for the relationships of taxa B–D (see Figure 5) that result from homoplasy. With respect to the states of characters 3 and 4, they could have arisen (a) independently in taxa C and D or (b) in the common ancestor of B+C+D but then reverted to the ancestral states in Taxon B. With respect to the states of characters 5–7, they could have arisen (c) independently in taxa B and C or (d) in the common ancestor of B+C+D but then reverted to the ancestral states in Taxon D (adapted from Brooks & McLennan, 1991). ■, apomorphic character state; ▨, parallel or convergent evolution; □, reversal to ancestral state.

means by which we judge the overall robustness of our cladistically derived trees. Calculations of robustness are easy to perform when only simple examples are involved, but in complex examples that contain numerous taxa and characters, computers are required. However, the basics are the same, irrespective of how they are carried out. A *consistency index*, which ranges from 0 (complete homoplasy) to 1·0 (no homoplasy), is calculated by dividing the number of characters in the data matrix by the number of characters on the tree. For example, the CI for trees in Figure 6(a) and 6(b) is 0·78 (7/9), and the CI for trees in Figure 6(c) and 6(d) is 0·70 (7/10) (see Figure 5 for the matrix). Even without calculating the CIs we know that the trees in Figure 6(c) and 6(d) will have a lower score than the trees in Figure 6(a) and 6(b) because of the greater number of homoplasies relative to apomorphies.

Palaeoindian Points in the Southeastern United States

The first comprehensive study of eastern United States Palaeoindian artifacts, dating *c.* 11,500–10,000 BP, was an article by Mason (1962), who, after surveying the distribution of fluted points in the East and adjacent portions of the Midwest, concluded that fluted points were not a western invention that had been diffused to eastern parts of the country, perhaps as Plains groups escaped the drying effects of the terminal Pleistocene. Rather, it was the other way around:

> the distributional and some of the typological evidence, as currently understood, would not seem to favour the proposed western origin for the development of Clovis points and the Llano complex. On the contrary, fluted points of every description except Folsom are far more numerous in the East, particularly in the southeastern United States, than they are in the Southwest or on the High Plains; and this area also has produced the greatest diversification in fluted point styles. On these grounds, then, it is defensible to suggest the southeastern United States, and not the West, as a possible "homeland" of the Clovis complex. (Mason, 1962: 234–235)

Mason's proposal subsequently was endorsed, either tentatively or wholeheartedly, by Bryan (1991), Meltzer (1988), Stanford (1991), and others (e.g., Griffin, 1977), and demonstrated empirically by Anderson (1990, 1991); Anderson & Faught, 1998, 2000; Anderson & Gillam, 2000; Faught, Anderson & Gisiger, 1994).

The Southeast is literally awash with fluted-point types that have been devised over the years to encompass the tremendous variation noted in what are termed Palaeoindian projectile points. One of these is the Cumberland point (Lewis, 1954), so named because of its occurrence in significant numbers in and around the Cumberland and Tennessee drainages of Tennessee (e.g., Breitburg & Broster, 1994), although it occurs across most of the eastern United States (Anderson & Faught, 2000). Cumberland points (Figure 7) are distinguished by their narrowness and greater thickness relative to Clovis points (Figure 7) and by the presence of recurved blade edges and flaring "ears" at the basal corners that are accentuated by incurving blade edges. They also exhibit fluting, usually made by removal of a single flake that on most specimens runs from the concave base almost to the tip—a feature analogous to the fluting on Folsom points. Other Palaeoindian projectile-point types in the Southeast *include* Suwannee (Bullen, 1968), Simpson (Bullen, 1968), and Hazel (Van Buren, 1974), all of which have indented bases and basal thinning, which often takes the form of fluting. Specimens of all these types share morphological characteristics with Clovis points and in our view fit into sister taxa with Clovis. The problem is, how do they relate to each other phylogenetically?

There are numerous proposed chronological sequences of projectile-point forms for the Southeast. Anderson, O'Steen & Sassaman (1996), for example, illustrate a hypothetical sequence that begins approximately 11,500 BP with Clovis points, proceeds to Cumberland, Suwannee, and Simpson forms, then to Beaver Lake and Quad forms, and then to Dalton forms at approximately 10,000 BP (Figure 7). The rooting of the Anderson, O'Steen & Sassaman sequence in Clovis points is traditional in North American archaeology (e.g., Morrow & Morrow, 1999), but that tradition is based entirely on radiocarbon dates and stratigraphic evidence from the Plains and Southwest. There is no a priori reason to believe that the rooting is correct for the Southeast, as Anderson, O'Steen & Sassaman (1996) point out. Stanford (1991), in fact, speculated that Simpson/Suwanee points are slightly older than Clovis points. Ignoring for a moment the rooting of the chronological sequence, there are several hints that other aspects of the sequence might be incorrect. One hint comes from closer examination of specimens placed in the Dalton type. Specimens assigned to this type exhibit such wide variation that a host of type names and subtype names have been used, such as Holland (Perino, 1971), Colbert (DeJarnette, Kurjack & Cambron, 1962), Greenbrier (Lewis & Kneberg, 1958), Meserve (Bell & Hall, 1953), and Hardaway-Dalton (Coe, 1964).

The dating of Dalton points has long been problematic because of the almost total absence of secure radiocarbon-dated contexts (Goodyear, 1982; O'Brien & Wood, 1998)—a problem that plagues the Southeast in general relative to all the projectile points discussed here. The overall shape, flaking characteristics, and presence of haft-area grinding—features that many Dalton points share to greater or lesser degrees with Palaeoindian points such as Clovis (concave and thinned base; ground base and blade edges in the haft area)—led archaeologists early on (e.g., Chapman, 1948; Mason, 1962; Wormington, 1957) to argue in favour of a "cultural continuity" between early Palaeoindian tool complexes and Dalton. If the points were technologically similar, so the

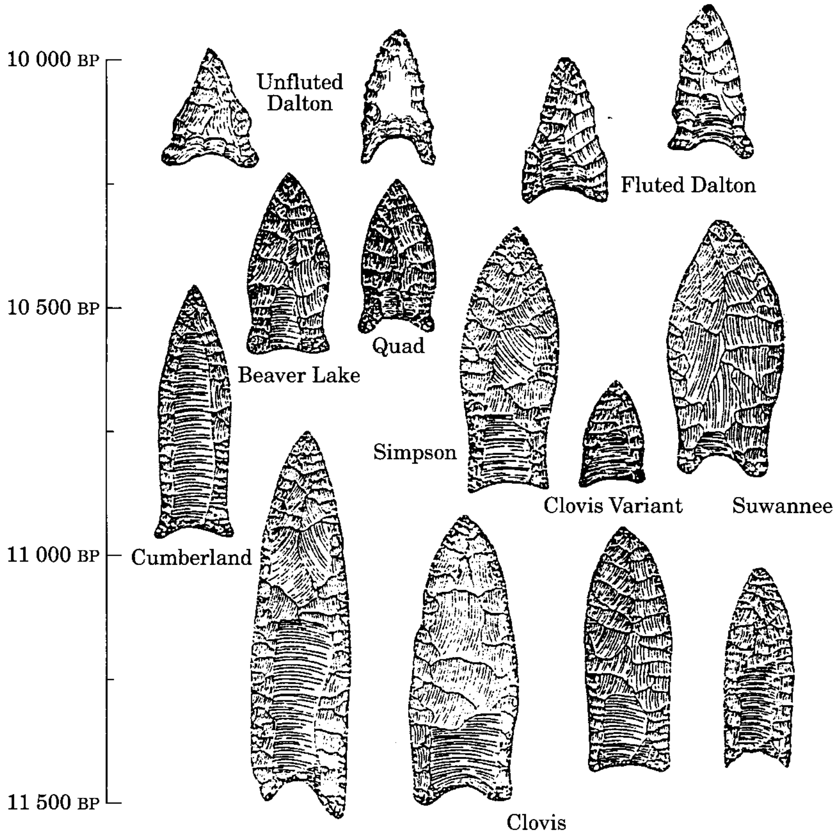


Figure 7. One possible historical sequence of Palaeoindian projectile-point types in the southeastern United States (after Anderson *et al.*, 1996).

reasoning went, then they should be fairly closely related temporally. This reasonable proposition received support from the fact that many of the other tools—wedges, gravers, end scrapers, and bone needles (Coe, 1964; DeJarnette, Kurjack & Cambron, 1962; Goodyear, 1974; Lewis & Kneberg, 1958; Morse, 1973)—found in Clovis and Dalton tool kits are similar.

Based on morphological criteria, it seems likely that Dalton points evolved directly out of Clovis points (Anderson, O'Steen & Sassaman, 1996; O'Brien & Wood, 1998)—a proposition supported by Bradley's (1997) examination of 146 complete Dalton specimens from the Sloan site in northeastern Arkansas (Morse, 1997). His conclusion that "the data currently point to an in situ technological development of Dalton points directly out of a Clovis technology" (Bradley, 1997: 57) is written in clear evolutionary language. Bradley is not speaking metaphorically when he says that Dalton points developed out of a Clovis technology, any more than we are speaking metaphorically when we say that one biological species developed out of another species or that the Pentium® chip developed out of the 486 processor. Lineages of projectile points or computer chips are the products of cultural rather than genetic transmission, but this does not make them less real than biological lineages. Bradley's language is the result of careful examination of technological variation as manifest in morphological characters—the features that provide the basis for a cladistical analysis of projectile points from the Southeast.

Analytical units

One of the numerous methodological issues in cladistics is the suitability of quantitative versus qualitative data and continuous versus discrete data. There is a tendency to favour qualitative and discrete data, but many so-called qualitative characters—for example, a *side-notched* projectile point—are in reality characters that have a quantitative base filtered through what Stevens (1991: 553) referred to as "reified semantic discontinuities of . . . terminology". The distinction between qualitative and quantitative refers more to "mode of expression rather than to intrinsic properties of the data" (Kitching *et al.*, 1998: 20). Another issue concerns the actual coding of data, with some cladists arguing for the use of multistate characters with linked states (e.g., thin and black; thick and white) and others opting for treating multistate characters as independent states (e.g., thin, black; thick, white). Our opinion is that cladistic analysis should represent independent hypotheses of relationship among taxa. Indeed, one of the strongest tests of

Table 1. System used to classify projectile points

Character Character state	Character Character state
I. Location of maximum blade width	V. Outer tang angle
1. Proximal quarter	1. 93°–115°
2. Secondmost proximal quarter	2. 88°–92°
3. Secondmost distal quarter	3. 81°–87°
4. Distal quarter	4. 66°–88°
II. Base shape	5. 51°–65°
1. Arc-shaped	6. <50°
2. Normal curve	VI. Tang-tip shape
3. Triangular	1. Pointed
4. Folsomoid	2. Round
III. Basal indentation ratio*	3. Blunt
1. No basal indentation	VII. Fluting
2. 0·90–0·99 (shallow)	1. Absent
3. 0·80–0·89 (deep)	2. Present
IV. Constriction ratio†	VIII. Length/width ratio
1. 1·00	1. 1·00–1·99
2. 0·90–0·99	2. 2·00–2·99
3. 0·80–0·89	3. 3·00–3·99
4. 0·70–0·79	4. 4·00–4·99
5. 0·60–0·69	5. 5·00–5·99
6. 0·50–0·59	6. ≥6·00

*The ratio between the medial length of a specimen and its total length; the smaller the ratio, the deeper the indentation.

†The ratio between the minimum blade width (proximal to the point of maximum blade width) and the maximum blade width as a measure of "waistedness"; the smaller the ratio, the higher the amount of constriction.

hypothesized relationships is congruence—two or more independent character states that map the same topology on a cladogram. Therefore, in the analysis presented below we treat characters as independent. We know that in reality some character states probably *are* linked, but this is an avenue for future analysis.

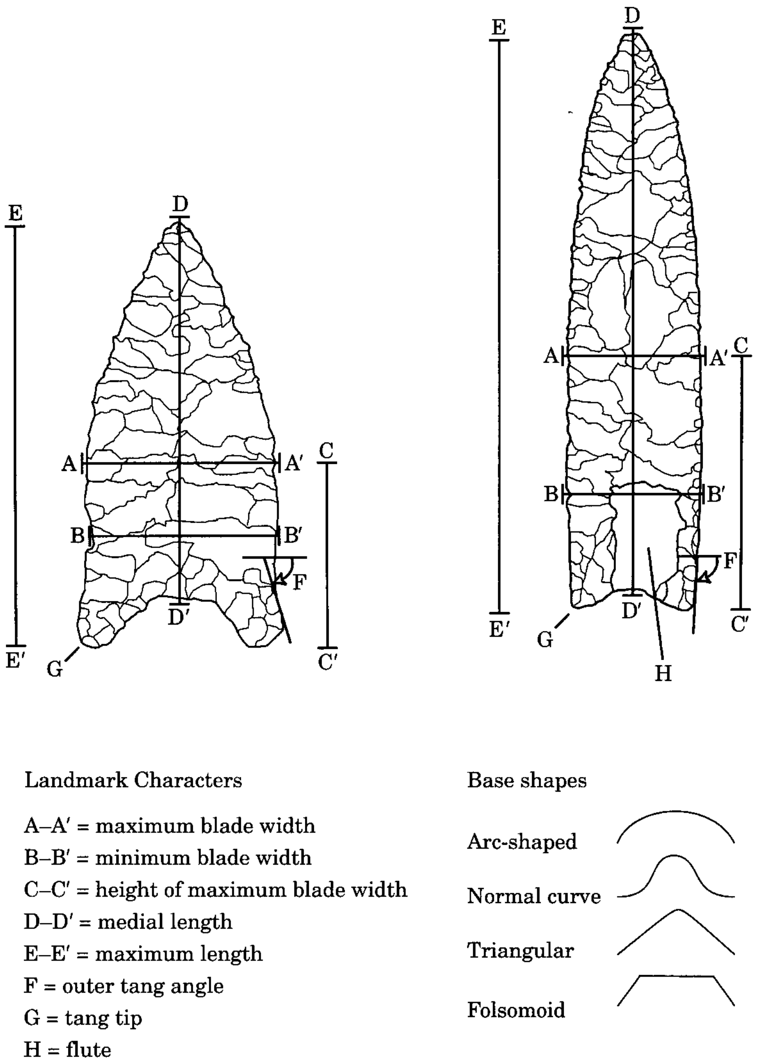
We used paradigmatic classification (Dunnell, 1971) to create our taxa, or classes. Each class comprises eight unweighted characters, each of which has a variable number of character states (Table 1). The characters are defined as follows; locations of the characters are shown in Figure 8:

I. Height of maximum blade width—the quarter section of a specimen in which the widest point of the blade occurs.
II. Overall base shape—qualitative assessment of the shape of the basal indentation.
III. Basal indentation ratio—the ratio between the medial length of a specimen and its maximum length; the smaller the ratio, the deeper the indentation.
IV. Constriction ratio—the ratio between the minimum blade width (proximal to the point of maximum blade width) and the maximum blade width; the smaller the ratio, the higher the amount of constriction.
V. Outer tang angle—the degree of tang expansion from the short axis of a specimen; the lower the angle, the greater the expansion.
VI. Tang-tip shape—the shape of the tip ends of tangs.
VII. Fluting—the removal of one or more large flakes (≥1 cm long) from the base of a specimen and parallel to its long axis; subsequent flake removal may obliterate earlier flake scars.
VIII. Length/width ratio—the maximum length of a specimen divided by its maximum width.

Our choice of characters was based on expectations as to which parts of a projectile point would change the most over time as a result of transmission and thus create a strong phylogenetic signal. A glance at Figure 7 indicates that considerable variation exists in the overall size and shape of Palaeoindian points, so we selected characters I, IV, and VIII to explore changes in size and shape. All three avoid potential bias that could be introduced by using direct measurements of length and width—bias created by some points having been resharpened. Figure 7 also indicates that the hafting element of Palaeoindian projectile points is a likely region in which to find other good candidates for use in phylogenetic analysis. Five characters—II, III, V, VI, and VII—were selected to monitor changes in such features as base shape, the shape of tang tips, and the angle formed by a tang relative to the long axis of a specimen.

As an alternative to creating classes, we could have used existing projectile-point types—Clovis, Dalton, Cumberland, and so on—and then attempted to abstract characters and character states from the specimens in each type. We have discussed the issue of classes versus types in considerable detail elsewhere (e.g., O'Brien & Lyman, 2000*a*, 2002) and cover only the major points here. First, there is a lack of redundancy among established projectile-point types in terms of the characters used in the definitions. One type might be defined by base shape and degree of shouldering whereas another type might be defined by base shape and angle of notching. One might argue that in biology species are nonredundant in terms of definition, especially in cases where morphological characters are used as sorting criteria, and yet they constitute the taxa often used in cladistics. We agree with this assessment, but the lack of redundancy in species definitions is no warrant for introducing the problem into archaeological systematics (O'Brien & Lyman, 2000*a*).

Second, artifact types in most cases are *extensionally* defined (Dunnell, 1986)—the definitions are derived by sorting through a pile of specimens, placing similar specimens together, and using average properties of the specimens in each pile as the basis of the definitions. When more specimens are introduced, type definitions must be reconfigured to account for the new variation. At some point the analyst may decide too much variation is being introduced and create another type. Types formed in such a manner are often fuzzy amalgams of character states—a problem realized over



Landmark Characters

A–A′ = maximum blade width
B–B′ = minimum blade width
C–C′ = height of maximum blade width
D–D′ = medial length
E–E′ = maximum length
F = outer tang angle
G = tang tip
H = flute

Figure 8. Locations of characters used in the analysis of projectile points (see Table 1 for character states). Character states for base shape are shown at the lower right.

a half century ago (Phillips, Ford & Griffin, 1951). The problem reduces to this: Extensionally derived units (types) conflate the taxon and the specimens in it. Some biologists (e.g., Jardine, 1969) have recognized this problem with respect to organisms and taxa. This is not to say that we see no role for traditional units such as named projectile-point types, because some of those traditional units are excellent at what they are supposed to do, such as tracking the passage of time. But even the most useful types are not multipurpose units. Neither are the classes discussed here. Rather, they are useful for *specific* analytical purposes. If this is true, then there can be no "discoverable" units in archaeology.

Third, the way in which classes are defined here offers a way around a problem that cladistics has faced since the days of Hennig. The term *transformation* is routinely used in cladistics—Hennig (1966), for example, spoke of "transformation series"—but rarely is consideration given to the fact that characters do not transform from one state to another. Rather, the frequency of a particular state of a given character changes within a population relative to the frequencies of other states of that character (Kitching *et al.*, 1998; O'Brien & Lyman, 2000*a*). Plotting such changes at the more inclusive scale of discrete object is the basis of frequency seriation and percentage stratigraphy (Lyman, Wolverton & O'Brien, 1998; O'Brien & Lyman, 1999, 2000*a*); at the less inclusive scale of individual character, classes offer an easy means of monitoring changes in character states (see below).

Methods and materials

Six hundred and twenty-one points from the Southeast were classified. We measured actual specimens if available or used published drawings or photographs if the requisite data could be obtained. For each specimen we

Table 2. Class definitions, abbreviations, and common type names of projectile-point classes

Class	Abbreviation	Common type names*
21225212	BQD	Beaver Lake–Quad–Dalton
21214322	CU	Cumberland–Unidentified
21214312	DAQS	Dalton–Arkabutla–Quad–Simpson
21224312	DCSuw	Dalton–Cumberland–Suwanee
21224212	DUCold	Dalton–Unidentified–Coldwater
21214222	DV	Dalton–Vandale
21223223	Kc	Clovis
31234322	KC	Clovis–Cumberland
21221122	Kdoon	Clovis–Doon
12212223	KDR	Clovis–Dalton–Redstone
21223322	Kk	Clovis
31222122	Krus	Clovis–Russellville
11212122	KUA	Clovis–Unidentified–Arkabutla
21212222	KUD	Clovis–Unidentified–Dalton
21235312	QC	Quad–Cumberland
11214312	QD	Quad–Dalton
21215312	QUD	Quad–Unidentified–Dalton

*Names taken directly from archaeological reports producing the sampled specimens.

listed (1) the state of each character in numerical order I through to VIII (producing a number string such as 12234236); (2) the type name for that specimen given in the literature; and (3) the state from which it was reported. The number string is the class definition of the specimen. A program that sorted on the number strings produced a list of specimens in each class. The 621 specimens fell into 491 classes, 86 of which contained multiple specimens. For the analysis reported here we used only those classes that contained a minimum of four specimens, the rationale being that although any class is as real analytically as any other class—even classes with no known members—we were interested more in repetitive behaviour and less in idiosyncratic behaviour. Secondarily, we reasoned that fewer classes would have been insufficient to reveal nuances of history and more classes would have made the first analytical pass too complex.

The analysed subset comprised 17 classes that together contained 83 projectile points. Class definitions are listed in Table 2 and illustrated in Figure 9; Table 3 lists the number of specimens per class by state (site-provenience information and literature references are available from the authors). Because it is much easier to use class abbreviations than it is to write out class definitions (the number strings), we use the abbreviations listed in Table 2 and shown under each example in Figure 9. As an important aside, note that the abbreviations are based on commonly used type names, which appear to the right of the abbreviations in Table 2. In each case the type names appearing in that column were taken directly from the literature in which the specimens were illustrated. For example, Class DAQS contains six specimens (Table 3), at least one of which was originally referred to as a Dalton point, at least one as an Arkabutla point, at least one as a Quad point, and at least one as a Simpson point. This ought to give us pause the next time we use traditional projectile-point types as analytical taxa.

A problem arose in choosing an outgroup. Recall that outgroups are used to determine character-state polarity—that is, to determine which character states are ancestral and which are derived. There are various rules for outgroup comparison, but the matter still reduces to identifying an *appropriate* outgroup. Ideally, given that the outgroup is used to identify ancestral character states, we would like that taxon to be ancestral to the ingroup taxa, but it often is impossible to identify such a taxon. In an earlier study (Darwent, O'Brien & Lyman, 2000) we used a Folsom point from the Lindenmeier site in Colorado as an outgroup, our thinking being that if Folsom was not a direct ancestor of the southeastern types, it was at least related to them. We later realized that we could be dealing with entirely unrelated traditions (lineages), and thus we dropped Folsom as an outgroup.

In strictly logical terms the outgroup taxon does not have to be ancestral to the ingroup taxa; it only has to carry enough ancestral character states so that state polarity can be determined. However, if we root our phylogenetic tree at the outgroup node, we are implying that the outgroup taxon *is* ancestral. Given the age of the taxa (point classes) with which we are dealing, it is difficult if not impossible to select an appropriate ancestral taxon from outside, so we selected one from inside the group and made it the outgroup. If Clovis points are ancestral to the sequence, then it would make sense to select them as the outgroup, but as shown in Table 2, there is not a single class of Clovis points. Rather, what various authors have termed Clovis points occur in eight separate classes. Of these, two, Kk and Kc, contain only points specified as Clovis points, so maybe they qualify as outgroup candidates. But what if Stanford (1991) is correct that what typically are referred to as Simpson points preceded Clovis points in the Southeast? By automatically choosing a class that contains only Clovis points, we are stacking the deck against deriving a correct phylogenetic ordering. There is, however, an objective means of selecting an outgroup—one that we have never seen reported in the biological literature.

We selected KDR (a class containing specimens originally identified as Clovis, Dalton, and Redstone) as an outgroup based on its consistent position in least-step occurrence seriations, where each "step" comprises a single change in a character from one state to another. To produce the seriation we used an algorithm that searched the classes continuously for the ordering that could be produced using the fewest number of steps (O'Brien *et al.*, n.d.). The ordering shown in Table 4 is one of 14 orderings requiring 28 steps, the lowest number of steps found (see below). KDR was at one end of each of the 14 orderings, with various classes appearing at the other end. As in any seriation, either end of the ordering could be early or

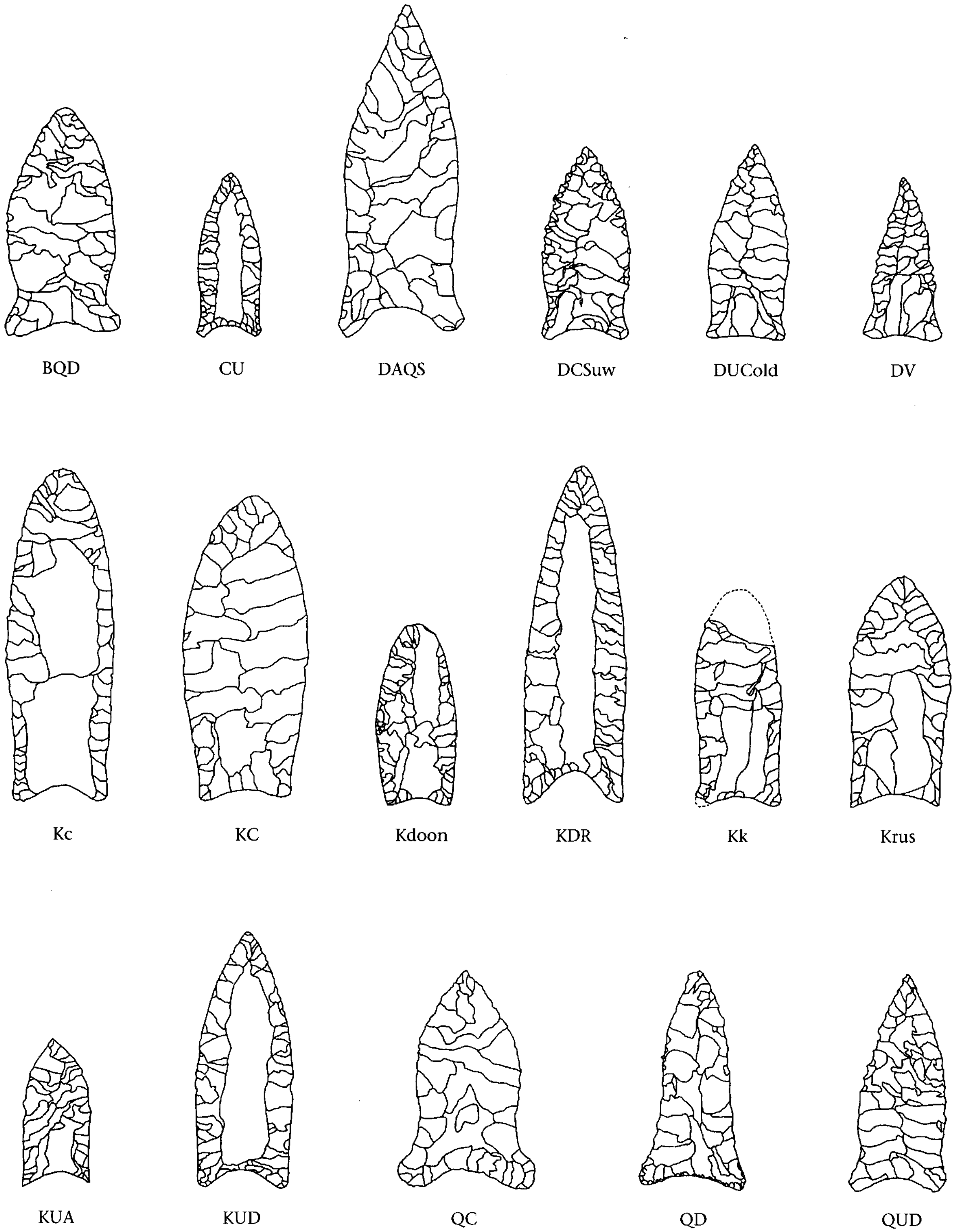


Figure 9. Illustrations of specimens in each of 17 classes used in the analysis; class abbreviations appear under each example (see Table 2 for class definitions).

Table 3. Frequencies of 17 projectile-point classes by state

	State											
Abbreviation	Ala.	Ark.	Fla.	Ga.	Ky.	Miss.	Mo.	N.C.	S.C.	Tenn.	Va.	Total
BQD	—	—	—	—	—	1	—	—	—	3	—	4
CU	2	—	—	—	—	—	—	1	—	1	—	4
DAQS	3	—	—	1	1	1	—	—	—	—	—	6
DCSuw	5	—	1	—	—	—	—	—	1	1	—	8
DUCold	4	—	—	—	—	1	—	—	—	1	—	6
DV	2	2	—	—	—	—	—	—	—	—	—	4
Kc	1	—	—	—	—	—	—	—	1	4	—	6
KC	—	—	—	—	—	—	2	—	—	2	—	4
Kdoon	1	2	—	—	—	—	2	—	—	2	—	7
KDR	1	—	—	—	—	—	2	—	—	1	—	4
Kk	1	—	—	1	—	—	—	1	—	1	—	4
Krus	—	1	—	—	1	—	—	—	—	2	—	4
KUA	1	—	—	—	—	—	—	—	—	—	3	4
KUD	2	—	—	—	—	—	1	—	—	—	2	5
QC	1	—	—	—	3	—	—	—	—	—	—	4
QD	3	—	—	—	1	—	—	—	—	—	—	4
QUD	3	—	—	—	—	1	—	—	—	1	—	5
Total	30	5	1	2	6	4	7	2	2	19	5	83

late; we view KDR as anchoring the early end of the ordering because of (a) the presence of what typically are referred to as Clovis and Redstone points in the class and (b) the fact that BQD often appeared at the opposite end of an ordering—a class that contains Beaver Lake and Quad points, two types that normally are considered (e.g., Driskell, 1996) to be later than Clovis and Redstone. Beginning with KDR as the oldest taxon and reading up the ordering in Table 4, each character-state change is circled. For example, there are four changes from KDR to Kc—in characters I, II, IV, and V—and two changes from Kc to Kk—in characters VI and VIII. Summing the character-state changes yields a total of 28. Thus we say that there are 28 steps in the 14 least-steps occurrence seriations.

Table 4. One of 14 occurrence-seriation orderings of the 17 classes

2	1	2	2	⑤	2	1	2	BQD
2	1	2	2	4	②	1	2	DUCold
2	1	2	②	4	3	1	2	DCSuw
②	1	2	1	4	3	1	2	DAQS
①	1	2	1	④	3	1	2	QD
2	1	2	①	5	3	1	2	QUD
②	1	2	3	⑤	3	①	2	QC
③	1	2	③	4	3	2	2	KC
2	1	2	1	4	③	2	2	CU
2	1	2	1	④	2	2	2	DV
②	1	2	1	2	②	2	2	KUD
①	1	2	①	2	1	2	2	KUA
③	1	2	2	②	1	2	2	Krus
2	1	2	2	①	①	2	2	Kdoon
2	1	2	2	3	③	2	②	Kk
②	①	2	②	③	2	2	3	Kc
1	2	2	1	2	2	2	3	KDR

Occurrence seriation of taxa, using character-state changes as the basis of the ordering, provides a logical and objective means of selecting an outgroup when no obvious choice presents itself. In practice, with a small number of taxa and relatively few characters, occurrence seriation will usually produce but a single ordering, and it will be similar or identical to the ordering of taxa produced by cladistical methods. Not only that, but the length of the phylogenetic tree will be equal to the least number of steps needed to produce the seriation. In Figure 10, for example, the best seriation of taxa A–E—best meaning the least number of steps used to create the seriation—is shown at the left. Seven steps, or character-state changes (each change is circled, similar to the changes shown in Table 4), are required (notice there are no character-state reversals). The cladogram at the right, with a length of seven, is the optimal solution to ordering the taxa using derived character states. Because there is no homoplasy, the consistency index (CI) is equal to 1·0. This example is a useful heuristic device, but it is only that. It typically is the case that many more taxa are involved, as are character-state reversals and other forms of homoplasy, all of which together greatly increase the number of optimal orderings, as with our 14 orderings of the 17 taxa. Occurrence seriation monitors change in character states, but it cannot account for all instances of complex homoplasy. Also, evolution is primarily a cladogenic (branching) process as opposed to an anagenic (linear) one; thus only in a textbook example could we expect a one-to-one correspondence between the number of steps in an occurrence seriation, which recognizes only anagenesis, and the length of a cladogram. Similarly, only in a perfect world could we expect to generate a cladogram that has a CI equal to 1·0.

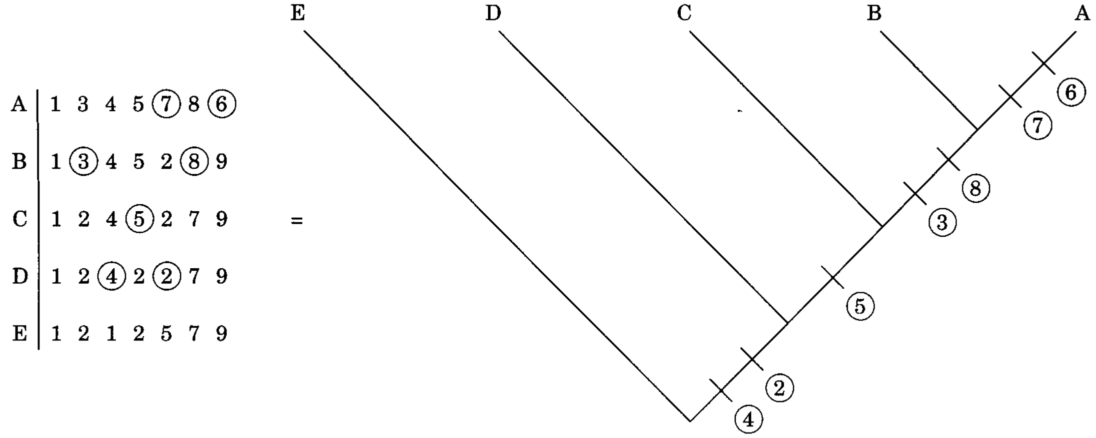


Figure 10. Diagram showing similarity in ordering of hypothetical taxa obtained by occurrence seriation (left) and cladistics (right) when few taxa and characters are involved. Seven steps, or character-state changes (each change is circled), are required to produce the best seriation. The cladogram, with a length of seven, is the optimal solution to ordering the taxa using apomorphic character states. There are no instances of homoplasy. Taxa A and B could switch places (by pivoting the clade at the A+B node) and not change the topology of the cladogram. That is why we say that there is similarity, not necessarily sameness, between the occurrence-seriation ordering and the cladistical ordering.

Results

The phylogenetic tree—and interestingly there was only one most parsimonious tree—generated for the 17 projectile-point classes is shown in Figure 11. We used Swofford's (1998) PAUP* (version 4) program to generate the tree, setting the program to construct it by the *branch-and-bound* method. This method quickly establishes a cladogram and then systematically removes from further consideration partial cladograms whose length exceeds the length of the initial cladogram, where "length" is measured as the number of changes in character states, or what we termed "steps" with respect to the occurrence seriation. When the program encounters a complete cladogram that is shorter than the initial one, it resets the upper bound and begins the process anew. The algorithm guarantees to find at least one most parsimonious (shortest) tree. The shortest tree we found, shown in Figure 11, has a length of 22 and a CI of 0·59—the latter much higher than we expected based on our review of cladistical analyses in biology and palaeobiology. The tree contains several *polytomies*, or points at which the program cannot make a simple dichotomous split. For example, there is a polytomy in the form of a trichotomous branching that produces KC, CU, and the clade comprising BQD+DUCold+DCSuw+DAQS+QC+QUD+QD. Cladistical analysis often assumes that diversification occurs only by a series of bifurcations, but this assumption is unnecessary and may obscure reality (Hoelzer & Meinick, 1994). In fact, cultural transmission *may* result more often in polytomies than in bifurcation. Alternatively, in reality there may be a bifurcation, but the phylogenetic signal is too weak for the program to resolve the pattern. Thus it treats it as a polytomy.

Character-state changes—there are 22 of them, hence the tree length of 22—are represented by the small boxes in Figure 11. Each box has two numbers associated with it: The Roman numeral refers to the character (Table 1), and the subscript number indicates the evolved state of that character (moving from left to right). Open boxes indicate single changes from one character state to another within the entire set of taxa. Shaded boxes indicate parallel changes—that is, a change in character from one particular state to another particular state occurs more than once within the entire set. For example, character IV changes to state 3 in both the line leading ultimately to QC and the line leading ultimately to KC. Finally, half-shaded boxes indicate characters that reverted to an ancestral state. For example, character VI began in KDR, the outgroup, as state 2; it later changed to state 3 and then changed back to state 2 in the line leading from KDR to the clade of BQD+DUCold.

The first characters in the outgroup (KDR, defined as 12212223) to change were (1) character II—base shape—which changed from state 2 (normal curve) to state 1 (arc-shaped), and (2) character VIII—length/width ratio—which changed from state 3 (3·00–3·99) to state 2 (2·00–2·99). This produced (1) an ancestor (11212222) that in turn produced KUA after an additional change in character VI from state 2 to state 1 and (2) an ancestor to all the other taxa. The latter ancestor underwent a change in character I—location of maximum blade width—from state 1 (proximal quarter) to state 2 (secondmost proximal quarter) and produced an ancestor (21212222) that in turn produced (1) KUD (with no modification), (2) the clade comprising Kk+Kc+Kdoon+Krus, and (3) the clade comprising all remaining taxa.

There are six instances of parallelism (characters I [character state 3], IV [character states 2 and 3], V [character state 5], and VI [character states 1 and 3]) and three instances of characters (I, VI, and VIII) reverting to an ancestral state. Parallelism might be expected if there are mechanical or technological

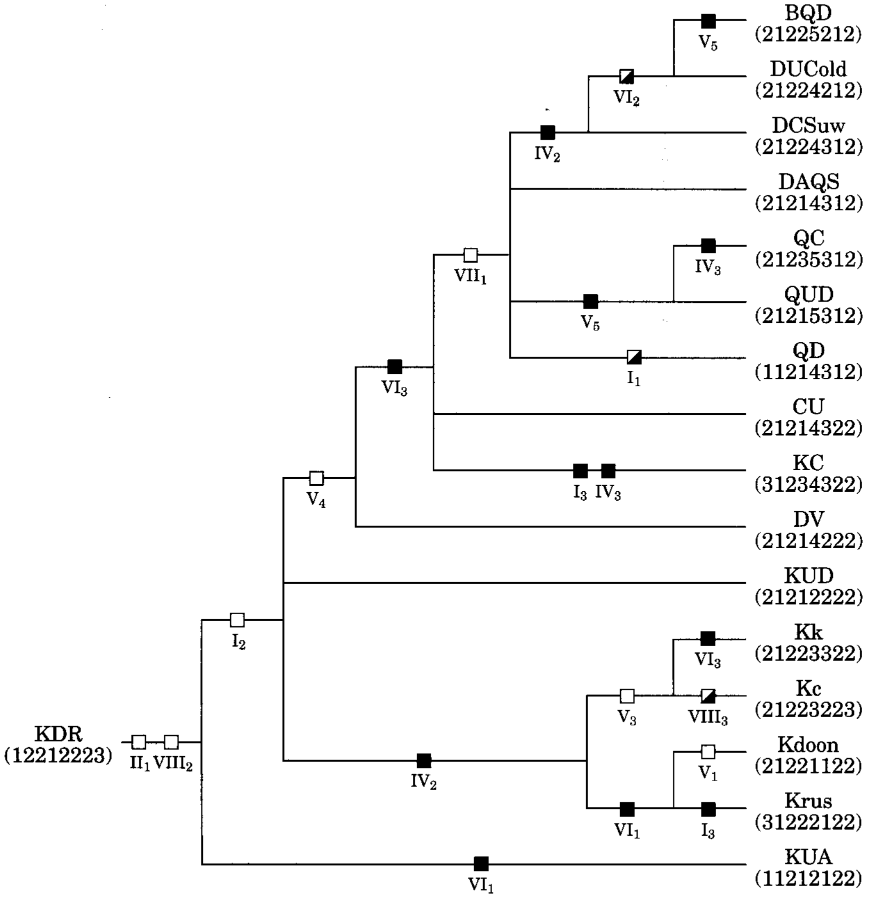


Figure 11. Phylogenetic tree (cladogram) of 17 projectile-point classes. The tree has a length of 22 and a consistency index of 0·59. For simplicity, KDR is shown as an ancestor as opposed to a terminal taxon. Changes in character state are denoted by boxes; Roman numerals denote characters, and subscript numbers denote character states. For example, the boxes at the far left indicate that Class KDR underwent changes in characters II (to state 1) and VIII (to state 2) to produce the ancestor of the other 16 classes.

constraints on how projectile points of several classes are produced. This issue requires the close scrutiny of lithic technologists. Instances of character-state reversals are rare in the organic world (if they occur at all); in that world, what appear to be reversals are artifacts of classification, especially with respect to measurement scale. With human-manufactured tools, there is nothing to prevent the recurrence of earlier states, given how cultural transmission works (e.g., Boyd & Richerson, 1985), although in some cases apparent reversals could be attributable to classification error or the character states chosen.

The most stable characters—excluding character II, which was found only in character-state 2—are characters II and VII, each of which underwent a single change, followed by character VIII, which changed twice. The most unstable characters are V and VI, each of which changed five times, followed closely by characters I and IV, each of which changed four times. These trends are predictable given the changes noted in the best-fit occurrence seriation shown in Table 4. Exactly what these trends mean in terms of the evolving weapon-delivery system in the Southeast is beyond the scope of this paper.

Discussion

Two things regarding the phylogenetic tree in Figure 11 require discussion. First, to underscore the difference between a cladogram and a phenogram, we produced Figure 12 using the same data used in Figure 11. We used an unweighted pair-group algorithm (Hintze, 1999) to construct the phenogram. Insofar as the phenogram might reflect descent with modification, it suggests a different evolutionary history than the cladogram. For example, at the dissimilarity level of 0·70 in the phenogram, there are three clusters. One cluster includes the same nine classes as the clade beginning with the change to state 3 of character VI: BQD, DUCold, DCSuw, CU, DAQS, QD, QC, QUD, and KC. The phenogram links these particular classes differently than the cladogram, however. For example, the phenogram links CU, DAQS, and QD whereas the cladogram links these three

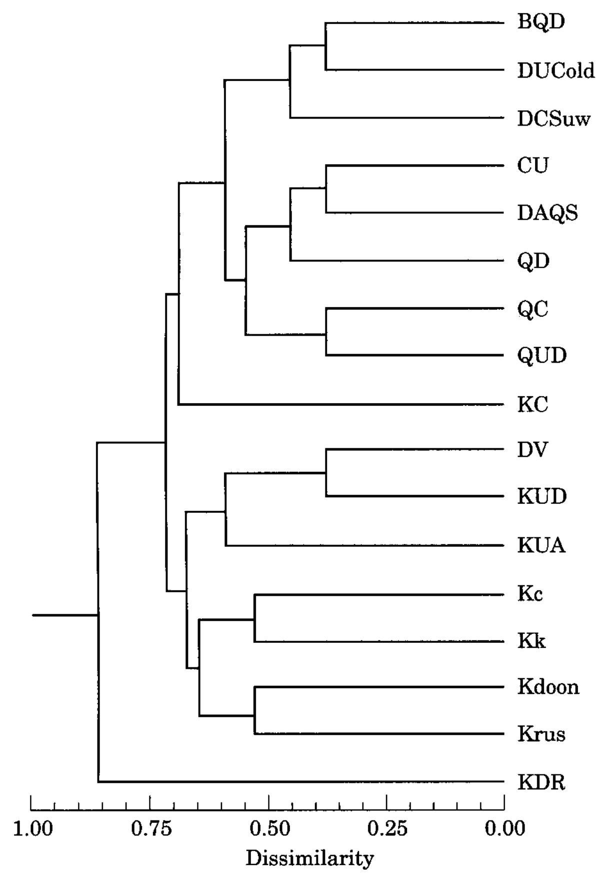


Figure 12. A phenogram of the 17 projectile-point classes obtained by means of a clustering algorithm (Hintze, 1999).

classes only through the clade that also contains the other six taxa. The second cluster in the phenogram links classes DV and KUD with classes KUA, Kc, Kk, Kdoon, and Krus, and although this cluster is similar to the clade of Kk, Kc, Kdoon, and Krus, in the cladogram DV is more closely related to the aforementioned clade of nine classes and KUA is set apart as a distinct clade after the first instance of branching. The third cluster in the phenogram comprises only class KDR, our outgroup in the cladogram.

General similarities between the cladogram and the phenogram were not unexpected and suggest that the traditional projectile-point types represented by our classes comprise pretty good historical types, or styles. That is, at a gross level the types capture the evolutionary history of this set of projectile points, probably because the types are defined primarily by homologous characters, at least some of which are derived character states. The point here is not that phenetics is incapable of producing phylogenetic relationships but that it is potentially invalid. Thus, as Ridley (1996) points out, when the issue is phylogeny, we have considerable reason to distrust distance statistics, which are based solely on phenetic similarity.

Table 5. Comparison of class orderings by occurrence seriation and cladistical methods

Cladistical method	Occurrence seriation
21225212 (BQD)	21225212 (BQD)
21224212 (DUCold)	21224212 (DUCold)
21224312 (DCSuw)	21224312 (DCSuw)
21214312 (DAQS)	21214312 (DAQS)
21235312 (QC)	11214312 (QD)
21215312 (QUD)	21215312 (QUD)
11214312 (QD)	21235312 (QC)
21214322 (CU)	31234322 (KC)
31234322 (KC)	21214322 (CU)
21214222 (DV)	21214222 (DV)
21212222 (KUD)	21212222 (KUD)
21223322 (Kk)	11212122 (KUA)
21223223 (Kc)	31222122 (Krus)
21221122 (Kdoon)	21221122 (Kdoon)
31222122 (Krus)	21223322 (Kk)
11212122 (KUA)	21223223 (Kc)
12212223 (KDR)	12212223 (KDR)

*Brackets denote groupings preserved in both the cladogram and the occurrence-seriation ordering.

Second, both the cladogram and the occurrence seriation (Table 4) are monitoring heritable continuity among the projectile points at the scale of their characters, which is in part why the two ordering algorithms provide rather similar orderings (Table 5). We refrain from comparing the two orderings statistically because the "order" of classes in the cladogram could be changed considerably without changing the topology of the cladogram. For example, in Figure 11 we could take the clade containing classes Kk+Kc+Kdoon+Krus and rotate it at the ancestral node and it would be the same clade. Although the ordering of the taxa would be reversed, the phylogenetic relationships would be identical.

Conclusion

Virtually since the birth of archaeology as a distinct discipline, a primary goal has been to write the histories of cultural lineages. That goal found expression in the Americas in what came to be known as the culture-history paradigm (Lyman, O'Brien & Dunnell, 1997). Within that paradigm, evolutionary descent with modification, although more implicit than explicit, underpinned the chronometers developed by culture historians to mark the passage of time (Lyman, Wolverton & O'Brien, 1998; O'Brien & Lyman, 1999). It is for precisely this reason that various archaeological chronometers are similar to palaeobiological ones (Lyman, 2001; Lyman & O'Brien, 2000*a*; O'Brien & Lyman, 1999, 2000*a*). By making the underpinning ontology explicit, archaeologists can use various palaeobiological methods for writing and explaining the evolutionary history of cultural lineages (e.g., Lyman & O'Brien, 2000*b*; O'Brien & Lyman, 2000*a*).

In this paper we have described one such method—cladistics—and have used it to help gain a preliminary understanding of the evolutionary history of early projectile-point lineages in the southeastern United States. Like seriation, cladistics seeks to arrange phenomena in time, but it goes beyond seriation in the important sense of hypothesizing particular phylogenetic relations between phenomena. As we have argued here, seriation—particularly occurrence seriation—provides an important addition to cladistics. We see cladistics, and the phylogenies it produces, not as end products but as solid starting points from which to begin to answer some of archaeology's historical, and therefore evolutionary, questions.

We emphasize that cladistics is not a biological method that depends on genetic continuity as a basis for reconstructing phylogeny. It depends on *transmission*, regardless of the kind of transmission. The use of cladistics in archaeology recognizes both cultural *and* biological (genetic) transmission, both of which play a role in the evolution of tool lineages. Archaeological materials were at one time parts of human phenotypes in the same way that shells, teeth, and fossilized bones were parts of phenotypes. Whether a tooth represents one or multiple genes—replicators—is as yet unknown, but this does not hinder the efforts of palaeobiologists to determine and explain the evolutionary histories of the organisms whose phenotypic hard parts they study. Artifacts are not replicators; they are what gets replicated. Cultural traits conceived as ideas held in the mind of individuals are the replicators that are transmitted; social learning is both the transmission mechanism and the source of variation that results from transmission errors and recombination. If there is phenotypic change, and if over time enough variation is generated, cladistical analysis might indeed be able to detect the phylogenetic signal. If so, we should be able to create a phylogenetic ordering that has testable implications. This apparently was what Clarke (1978: 262) had in mind when he stated that

> The taxonomic assessment of affinity between entities will suggest the limited number of possible transformation trajectories which might link the network of particular entities in passing time. Great care must then be taken to avoid the danger of interpreting affinity relationships simply as descent relationships—a condition further complicated by the peculiar nature of branch convergence and fusion found in cultural phylogeny. This problem can only be controlled by providing an adequate chronological frame and by postulating multiple alternative hypotheses of development to link the established degree of affinity between sets of entities under investigation.

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References

Anderson, D. G. (1990). The Paleoindian colonization of eastern North America: A view from the southeastern United States. In (K. B. Tankersley & B. L. Isaac, Eds) *Early Paleoindian Economies of Eastern North America*. Greenwich, CT: JAI Press, pp. 163–216.

Anderson, D. G. (1991). Examining prehistoric settlement distribution in eastern North America. *Archaeology of Eastern North America* **19,** 1–22.

Anderson, D. G. & Faught, M. K. (1998). The distribution of fluted Paleoindian projectile points: Update 1998. *Archaeology of Eastern North America* **26,** 163–187.

Anderson, D. G. & Faught, M. K. (2000). Palaeoindian artefact distributions: Evidence and implications. *Antiquity* **74,** 507–513.

Anderson, D. G. & Gillam, J. C. (2000). Paleoindian colonization of the Americas: Implications from an examination of physiography, demography, and artifact distribution. *American Antiquity* **65,** 43–66.

Anderson, D. G., O'Steen, L. D. & Sassaman, K. E. (1996). Chronological considerations. In (D. G. Anderson, & K. E. Sassaman, Eds) *The Paleoindian and Early Archaic Southeast*. Tuscaloosa: University of Alabama Press, pp. 3–15.

Bell, R. E. & Hall, R. S. (1953). Selected projectile point types of the United States. *Oklahoma Anthropological Society, Bulletin* **1,** 1–16.

Bellwood, P. (1996). Phylogeny vs reticulation in prehistory. *Antiquity* **70,** 881–890.

Benton, M. J. & Hitchin, R. (1997). Congruence between phylogenetic and stratigraphic data on the history of life. *Proceedings of the Royal Society of London: Biological Sciences* **264B,** 885–890.

Benton, M. J., Hitchen, R. & Wills, M. A. (1999). Assessing congruence between cladistic and stratigraphic data. *Systematic Biology* **48,** 581–596.

Boas, F. (1904). The history of anthropology. *Science* **20,** 513–524.

Boyd, R. & Richerson, P. J. (1985). *Culture and the Evolutionary Process*. Chicago: University of Chicago Press.

Bradley, B. A. (1997). Sloan site biface and projectile point technology. In (D. F. Morse, Ed.) *Sloan: A Paleoindian Dalton Cemetery in Arkansas*. Washington, DC: Smithsonian Institution Press, pp. 53–57.

Brady, R. H. (1985). On the independence of systematics. *Cladistics* **1,** 113–126.

Breitburg, E. & Broster, J. (1994). Paleoindian site, lithic, and mastodon distributions in Tennessee. *Current Research in the Pleistocene* **11,** 9–11.

Brew, J. O. (1946). Archaeology of Alkali Ridge, Southeastern Utah. *Peabody Museum of American Archaeology and Ethnology, Papers* **21.**

Brooks, D. R. & McLennan, D. A. (1991). *Phylogeny, Ecology, and Behavior: A Research Program in Comparative Biology*. Chicago: University of Chicago Press.

Brower, A. V. Z. (2000). Evolution is not a necessary assumption of cladistics. *Cladistics* **16,** 143–154.

Brown, J. H. & Lomolino, M. V. (1998). *Biogeography* (2nd edn.). Sunderland, MA: Sinauer.

Bryan, A. L. (1991). The fluted-point tradition in the Americas—One of several adaptations to late Pleistocene American environments. In (R. Bonnichsen & K. L. Turnmire, Eds) *Clovis: Origins and Adaptations*. Corvallis, OR: Center for the Study of the First Americans, pp. 15–33.

Bullen, R. P. (1968). *A Guide to the Identification of Florida Projectile Points*. Gainesville: Florida State Museum.

Carpenter, J. (1987). Cladistics of cladists. *Cladistics* **3,** 363–375.

Chapman, C. H. (1948). A preliminary survey of Missouri archaeology (part IV): Ancient cultures and sequence. *The Missouri Archaeologist* **10,** 133–164.

Clarke, D. L. (1978). *Analytical Archaeology* (2nd ed.). New York: Columbia University Press.

Coe, J. L. (1964). The Formative Cultures of the Carolina Piedmont. *American Philosophical Society, Transactions* **54**(5).

Cracraft, J. (1981). The use of functional and adaptive criteria in phylogenetic systematics. *American Zoologist* **21,** 21–36.

Darwent, J., O'Brien, M. J. & Lyman, R. L. (2000). Southeastern fluted-point lineages. Paper presented at the 65th Annual Meeting of the Society for American Archaeology, Philadelphia.

Darwin, C. (1859). *On the Origin of Species by Means of Natural Selection, or, The Preservation of Favoured Races in the Struggle for Life*. London: Murray.

DeJarnette, D. L., Kurjack, E. B. & Cambron, J. W. (1962). Stanfield–Worley Bluff Shelter excavations. *Journal of Alabama Archaeology* **8**(1–2).

Dobzhansky, T. (1951). Mendelian populations and their evolution. In (L. C. Dunn, Ed.) *Genetics in the 20th Century*. New York: Macmillan, pp. 573–589.

Donoghue, M. J., Doyle, J. A., Gauthier, J., Kluge, A. G. & Rowe, T. (1989). The importance of fossils in phylogeny reconstruction. *Annual Review of Ecology and Systematics* **20,** 431–460.

Driskell, B. N. (1996). Stratified late Pleistocene and early Holocene deposits at Dust Cave, northwestern Alabama. In (D. G. Anderson & K. E. Sassaman, Eds) *The Paleoindian and Early Archaic Southeast*. Tuscaloosa: University of Alabama Press, pp. 315–330.

Dunnell, R. C. (1971). *Systematics in Prehistory*. New York: Free Press.

Dunnell, R. C. (1986). Methodological issues in Americanist artifact classification. *Advances in Archaeological Method and Theory* **9,** 149–207.

Eldredge, N. & Cracraft, J. (1980). *Phylogenetic Patterns and the Evolutionary Process*. New York: Columbia University Press.

Eldredge, N. & Gould, S. J. (1972). Punctuated equilibria: An alternative to phyletic gradualism. In (T. J. M. Schopf, Ed.) *Models in Paleobiology*. San Francisco: Freeman, Cooper, pp. 82–115.

Eldredge, N. & Gould, S. J. (1977). Evolutionary models and biostratigraphic strategies. In (E. G. Kauffman & J. E. Hazel, Eds) *Concepts and Methods of Biostratigraphy*. Stroudsburg, PA: Dowden, Hutchinson & Ross, pp. 25–40.

Eldredge, N. & Gould, S. J. (1997). On punctuated equilibria. *Science* **276,** 338–339.

Eldredge, N. & Novacek, M. J. (1985). Systematics and paleobiology. *Paleobiology* **11,** 65–74.

Faught, M. K., Anderson, D. G. & Gisiger, A. (1994). North American Paleoindian database: An update. *Current Research in the Pleistocene* **11,** 32–35.

Fisher, D. C. (1991). Phylogenetic analysis and its application in evolutionary paleobiology. In (N. L. Gilinsky & P. W. Signor, Eds) *Analytical Paleobiology*. The Paleontological Society, Short Courses in Paleobiology No. 4, pp. 103–122.

Fisher, D. C. (1992). Stratigraphic parsimony. In (W. P. Maddison & D. R. Maddison, Eds) *MacClade: Analysis of Phylogeny and Character Evolution* (version 3). Sunderland, MA: Sinauer, pp. 124–129.

Fisher, D. C. (1994). Stratocladistics: Morphological and temporal patterns and their relation to phylogenetic process. In (L. Grande & O. Rieppel, Eds) *Interpreting the Hierarchy of Nature*. San Diego: Academic Press, pp. 133–171.

Foley, R. (1987). Hominid species and stone-tool assemblages: How are they related? *Antiquity* **61,** 380–392.

Ford, J. A. (1962). A Quantitative Method for Deriving Cultural Chronology. *Pan American Union, Technical Bulletin* No. 1.

Fox, D. L., Fisher, D. C. & Leighton, L. R. (1999). Reconstructing phylogeny with and without temporal data. *Science* **284,** 1816–1819.

Gilmour, J. S. L. (1937). A taxonomic problem. *Nature* **139,** 1040–1042.

Goodenough, W. H. (1997). Comment on "The dimensions of social life in the Pacific: Human diversity and the myth of the primitive isolate" by Terrell, J. E., Hunt, T. L. & Gosden, C.. *Current Anthropology* **38,** 177–178.

Goodyear, A. C. (1974). The Brand Site: A Techno-Functional Study of a Dalton Site in Northeast Arkansas. *Arkansas Archaeological Survey, Research Series* No. 7.

Goodyear, A. C. (1982). The chronological position of the Dalton horizon in the southeastern United States. *American Antiquity* **47,** 382–395.

Gould, S. J. & Eldredge, N. (1977). Punctuated equilibria: The tempo and mode of evolution reconsidered. *Paleobiology* **3,** 115–151.

Gould, S. J. & Eldredge, N. (1986). Punctuated equilibrium at the third stage. *Systematic Zoology* **35,** 143–148.

Gould, S. J. & Eldredge, N. (1993). Punctuated equilibrium comes of age. *Nature* **366,** 223–227.

Griffin, J. B. (1977). A commentary on early man studies in the northeast. *New York Academy of Sciences, Annals* **288,** 3–15.

Harmon, M. J., Leonard, R. D., VanPool, C. S. & VanPool, T. L. (2000). Cultural transmission: Shared intellectual traditions in ceramics of the prehistoric American Southwest and northern Mexico. Paper presented at the 65 Annual Meeting of the Society for American Archaeology, Philadelphia.

Hennig, W. (1950). *Grundzüge einer Theorie der phylogenetischen Systematik*. Berlin: Deutscher Zentralverlag.

Hennig, W. (1966). *Phylogenetic Systematics*. Urbana: University of Illinois Press.

Hintze, J. L. (1999). *NCSS 2000 Statistical System for Windows*. Kaysville, UT: Number Cruncher Statistical Systems.

Hoelzer, G. A. & Meinick, D. J. (1994). Patterns of speciation and limits to phylogenetic resolution. *Trends in Ecology and Evolution* **9,** 104–107.

Hull, D. (1979). The limits of cladism. *Systematic Zoology* **28,** 416–440.

Hull, D. (1984). Cladistic theory: Hypotheses that blur and grow. In (T. Duncan & T. F. Stuessy, Eds) *Cladistics: Perspectives on the Reconstruction of Evolutionary History*. New York: Columbia University Press, pp. 5–23.

Jardine, N. (1969). A logical basis for biological classification. *Systematic Zoology* **18,** 37–52.

Kitching, I. J., Forey, P. L., Humphries, C. J. & Williams, D. M. (1998). *Cladistics: The Theory and Practice of Parsimony Analysis*. Oxford: Oxford University Press.

Leaf, M. L. (1979). *Man, Mind, and Science: A History of Anthropology*. New York: Columbia University Press.

Lee, M. S. Y. & Doughty, P. (1997). The relationship between evolutionary theory and phylogenetic analysis. *Biological Reviews* **72,** 471–495.

Lewis, T. M. N. (1954). The Cumberland point. *Oklahoma Anthropological Society, Bulletin* **2,** 7–8.

Lewis, T. M. N. & Kneberg, M. (1958). The Nuckolls site. *Tennessee Archaeologist* **14,** 60–79.

Lyman, R. L. (2001). Culture historical and biological approaches to identifying homologous traits. In (T. Hurt & G. Rakita, Eds) *Style and Function: Conceptual Issues in Evolutionary Archaeology*. Westport, CT: Bergin & Garvey, pp. 69–89.

Lyman, R. L. & O'Brien, M. J. (2000*a*). Chronometers and units in early archaeology and paleontology. *American Antiquity* **65,** 691–707.

Lyman, R. L. & O'Brien, M. J. (2000*b*). Measuring and explaining change in artifact variation with clade-diversity diagrams. *Journal of Anthropological Archaeology* **19,** 39–74.

Lyman, R. L., O'Brien, M. J. & Dunnell, R. C. (1997). *The Rise and Fall of Culture History*. New York: Plenum.

Lyman, R. L., Wolverton, S. & O'Brien, M. J. (1998). Seriation, superposition, and interdigitation: A history of Americanist graphic depictions of culture change. *American Antiquity* **63,** 239–261.

Mason, R. J. (1962). The Paleo-Indian tradition in eastern North America. *Current Anthropology* **3,** 227–346.

Mayr, E. (1942). *Systematics and the Origin of Species*. New York: Columbia University Press.

Mayr, E. (1981). Biological classification: Toward a synthesis of opposing methodologies. *Science* **214,** 510–516.

Mayr, E. (1982). *The Growth of Biological Thought: Diversity, Evolution, and Inheritance*. Cambridge, MA: Harvard University Press.

McKitrick, M. C. (1994). On homology and the ontological relationship of parts. *Systematic Biology* **43,** 1–10.

Meltzer, D. J. (1988). Late Pleistocene human adaptations in eastern North America. *Journal of World Prehistory* **2,** 1–52.

Moore, J. H. (1994*a*). Ethnogenetic theories of human evolution. *Research and Exploration* **10,** 10–23.

Moore, J. A. (1994*b*). Putting anthropology back together again: The ethnogenetic critique of cladistic theory. *American Anthropologist* **96,** 925–948.

Morse, D. F. (1973). Dalton culture in northeast Arkansas. *The Florida Anthropologist* **26,** 23–38.

Morse, D. F. (1997). *Sloan: A Paleoindian Dalton Cemetery in Arkansas*. Washington, DC: Smithsonian Institution Press.

Morrow, J. E. & Morrow, T. A. (1999). Geographic variation in fluted projectile points: A hemispheric perspective. *American Antiquity* **64,** 215–230.

Nichols, J. (1996). The comparative method as heuristic. In (M. Durie & M. Ross, Eds) *The Comparative Method Reviewed: Regularity and Irregularity in Language Change*. New York: Oxford University Press, pp. 39–71.

O'Brien, M. J. & Lyman, R. L. (1998). *James A. Ford and the Growth of Americanist Archaeology*. Columbia: University of Missouri Press.

O'Brien, M. J. & Lyman, R. L. (1999). *Seriation, Stratigraphy, and Index Fossils: The Backbone of Archaeological Dating*. New York: Kluwer Academic/Plenum.

O'Brien, M. J. & Lyman, R. L. (2000*a*). *Applying Evolutionary Archaeology: A Systematic Approach*. New York: Kluwer Academic/Plenum.

O'Brien, M. J. & Lyman, R. L. (2000*b*). Meeting theoretical and methodological challenges to the future of evolutionary archaeology. *Review of Archaeology* **20,** 14–22.

O'Brien, M. J. & Lyman, R. L. (2002). The epistemological nature of archaeological units. *Anthropological Theory* (in press).

O'Brien, M. J., Lyman, R. L., Saab, Y., Saab, E., Darwent, J. & Glover, D. (n.d.). Two issues in archaeological phylogenetics; Taxon construction and outgroup selection. *Cladistics* (in press).

O'Brien, M. J. & Wood, W. R. (1998). *The Prehistory of Missouri*. Columbia: University of Missouri Press.

Patterson, C. (1988). Homology in classical and molecular biology. *Molecular Biology and Evolution* **5,** 603–625.

Perino, G. (1971). Guide to the Identification of Certain American Indian Projectile Points. *Oklahoma Anthropological Society, Special Bulletin* **4**.

Phillips, P., Ford, J. A. & Griffin, J. B. (1951). Archaeological Survey in the Lower Mississippi Alluvial Valley, 1940–1947. *Peabody Museum of American Archaeology and Ethnology, Papers* **25**.

Platnick, N. I. (1979). Philosophy and the transformation of cladistics. *Systematic Zoology* **28,** 537–546.

Platnick, N. I. (1985). Philosophy and the transformation of cladistics revisited. *Cladistics* **1,** 87–94.

Platnick, N. I. & Cameron, D. (1977). Cladistic methods in textual, linguistic, and phylogenetic analysis. *Systematic Zoology* **26,** 380–385.

Polly, P. D. (1997). Ancestry and Species Definition in Paleontology: A Stratocladistic Analysis of Paleocene–Eocene Viverravidae (Mammalia, Carnivora) from Wyoming. *University of Michigan, Museum of Paleontology, Contributions* **30**.

Popper, K. R. (1974). Darwinism as a metaphysical research programme. In (P. A. Schillp, Ed.) *The Philosophy of Karl Popper*. La Salle, IL: Open Court, pp. 133–143.

Ridley, M. (1996). *Evolution* (2nd ed.). Cambridge, MA: Blackwell.

Rieppel, O. (1994). Homology, topology, and typology: The history of modern debates. In (B. K. Hall, Ed.) *Homology: The Hierarchical Basis of Comparative Biology*. San Diego: Academic Press, pp. 63–100.

Rosen, D. E. (1982). Do current theories of evolution satisfy the basic requirements of explanation? *Systematic Biology* **31,** 76–85.

Ross, M. (1997). Comment on "The dimensions of social life in the Pacific: Human diversity and the myth of the primitive isolate" by Terrell, J. E., Hunt, T. L. & Gosden, C.. *Current Anthropology* **38,** 182–184.

Simpson, G. G. (1945). The principles of classification and a classification of mammals. *American Museum of Natural History, Bulletin* **85,** 1–350.

Simpson, G. G. (1961). *Principles of Animal Taxonomy*. New York: Columbia University Press.

Smith, A. B. (1994). *Systematics and the Fossil Record: Documenting Evolutionary Patterns*. London: Blackwell.

Sober, E. (1988). *Reconstructing the Past: Parsimony, Evolution, and Inference*. Cambridge, MA: MIT Press.

Sokal, R. R. & Sneath, P. H. A. (1963). *Principles of Numerical Taxonomy*. San Francisco: Freeman.

Spaulding, A. C. (1955). Prehistoric cultural development in the eastern United States. In (B. J. Meggers & C. Evans, Eds) *New Interpretations of Aboriginal American Culture History*. Washington, DC: Anthropological Society of Washington, pp. 12–27.

Stanford, D. (1991). Clovis origins and adaptations: An introductory perspective. In (R. Bonnichsen & K. L. Turnmire, Eds) *Clovis: Origins and Adaptations*. Corvallis, OR: Center for the Study of the First Americans, pp. 1–13.

Stevens, P. F. (1980). Evolutionary polarity of character states. *Annual Review of Ecology and Systematics* **11,** 333–358.

Stevens, P. F. (1991). Character states, morphological variation, and phylogenetic analysis: A review. *Systematic Botany* **16,** 553–583.

Swofford, D. (1998). *PAUP*: Phylogenetic Analysis Using Parsimony (*and Other Methods)* (version 4). Sunderland, MA: Sinauer.

Terrell, J. E., Hunt, T. L. & Gosden, C. (1997). The dimensions of social life in the Pacific: Human diversity and the myth of the primitive isolate. *Current Anthropology* **38,** 155–195.

Van Buren, G. E. (1974). *Arrowheads and Projectile Points*. Garden Grove, CA: Arrowhead.

Wiley, E. O. (1981). *Phylogenetics: The Theory and Practice of Phylogenetic Systematics*. New York: Wiley.

Wiley, E. O., Siegel-Causey, J., Brooks, D. R. & Funk, V. A. (1991). *The Compleat Cladist: A Primer of Phylogenetic Procedures*. Lawrence: University of Kansas, Museum of Natural History.

Willey, G. R. (1953). Archaeological theories and interpretation: New World. In (A. L. Kroeber, Ed.) *Anthropology Today*. Chicago: University of Chicago Press, pp. 361–385.

Wills, M. A. (1999). Congruence between phylogeny and stratigraphy: Randomization tests and gap excess ratio. *Systematic Biology* **48,** 559–580.

Wormington, H. M. (1957). *Ancient Man in North America* (4th ed.). Denver: Denver Museum of Natural History, Popular Series No. 4.