Cladistics & Archaeological Phylogeny

by Michael J. O'Brien

Archaeologists have long used changes in artifact form—specifically, changes in character states of artifacts—to measure the passage of time. If the changes in character states are ordered correctly, a historical sequence of forms is created, although independent evidence is needed to root the sequence chronologically. However, historical continuity—X is older than Y, which is older than Z—is different than heritable continuity—X produced Y, which in turn produced Z (Figure 1). 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; Nichols 1996; Platnick and Cameron 1977; Ross 1997). As Franz Boas (1904:518) observed almost a century ago, “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 lan-

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Historical Continuity

Heritable Continuity

\[ \begin{align*}
\text{Z} \\
\text{Y} \\
\text{X}
\end{align*} \]

\[ \begin{align*}
\text{Z} \\
\text{Y} \\
\text{X}
\end{align*} \]

\[ \text{Time} \]

**Figure 1.** The difference between historical continuity (left) and heritable continuity (right). The former signifies only a sequence; the latter signifies a lineage (genetic and/or cultural).

guage. 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 cultural transmission and heritable continuity (Figure 2).

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 in some cases to reflect not only patterns of ancestry and descent but also degrees 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. Phylogeny involves a reconstruction of evolutionary patterns and relationships (what is related to what and how). Overall similarity in terms of formal characters (traits) was used to group like with like in descending order of specificity,
but overlooked in the process was the notion that there were different kinds of formal similarity, each created by different processes. It wasn’t that biologists (or for that matter archaeologists) were ignorant of the differences between homologous and analogous characters—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.

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. The method is identical in purpose to evolutionary taxonomy—the creation of phylogenetic trees that show evolutionary relationships between and among taxa—but it differs in that it employs only a subset of homologous features to create relationships between and among taxa.

Cladistics is a powerful tool for constructing hypotheses concerning phylogenetic histories of anything that evolves over time, including material remains found in the archaeological record (O’Brien and Lyman 1999, 2000a,
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 tool manufacture are highly constrained, meaning that new structures and functions almost always 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 and Lomolino 1998:328). To date, most archaeological discussions of cladistics (e.g., Moore 1994a; Terrell et al. 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"—most archaeologists appear unaware (Collard and Shennan [2001], Foley [1987], and Harmon et al. [2000] are exceptions) that in the natural sciences cladistics refers to a very specific method of reconstructing phylogeny.

**The Cladistics Method**

The initial product produced in cladistics is a cladogram, which is nothing more than a statement of relationship. The cladogram shown here (Figure 3) tells us that based on a certain character (trait) 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. Despite the fact that a cladogram summarizes only similarity, our interests are in phylogeny. We know that taxa A through D did not appear miraculously out of nothing; rather, they evolved from one or more ancestral taxa. At this point we know little or nothing about those ancestors except for the implication, derived from our cladogram, that with respect 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 4). 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 ancestors (nodes x and y), form another, more inclusive clade, and taxa D + C + B + A, together with their common ancestors (nodes x, y, and z), form yet another, and the most inclusive, clade.

Cladistically built trees, like evolutionary trees in general, are constructed using only homologous characters, but the former use only a subset of those characters, termed derived characters, or apomorphies. When these derived characters are shared between taxa related by a common ancestor, such as C and D (Figure 5), they are referred to as synapomorphies. Characters shared by sister taxa and that have been inherited from an ancestor more distant than the most recent one—here the most recent ancestor is the one that produced taxa C and D (Figure 6)—are termed synaplesiomorphies, or ancestral (primitive) characters. Characters that show up in lines not related directly through one common ancestor are referred to as homoplasies (Figure 7). One kind of
Figure 4. A rooted cladogram (phylogenetic tree) consisting of four terminal taxa (A–D) and hypothesized ancestors (x–z).

Synapomorphy (Derived)

Figure 5. A cladogram showing the initial appearance of a character and its continued appearance in descendant taxa. This is a synapomorphic (shared derived) character.


**Symplesiomorphy (Ancestral)**

Figure 6. A cladogram showing the initial appearance of a character and its continued appearance in descendant taxa. Here the character is symplesiomorphic (shared ancestral). Note that at one time—when the character appeared in Taxon B and in the line that eventually evolved into taxa C and D—it was synapomorphic.

**Homoplaspy**

Figure 7. A cladogram showing the parallel and unrelated appearance of a character in two distantly related taxa. Such a character is referred to as a homoplasy.
homoplasmy results from character-state reversals—meaning that a character changes from character-state 1 to character-state 2 and at some point in a lineage reverts to state 1 (Figure 8). I view this kind of homoplaspy more as an analytical problem, meaning that rarely if ever will precisely the same character state reemerge after it disappears. More likely, the measurement scale being used makes it appear as if the new character state is a homoplasy. Another kind of homoplaspy (Figure 8) results from parallelism or convergence. All but the simplest cladograms contain homoplasy, and the task of the analyst is to reduce its influence on phylogenetic reconstruction. There are numerous techniques for measuring the robustness (goodness of fit) of the arrangement of taxa, but none of them can be expected to produce more than a locally optimal solution(s). Thus it is imperative to emphasize that any phylogenetic tree is merely a hypothesis concerning genealogical relationships among the taxa under investigation.

Two Kinds of Homoplasy

- Character-state reversal

\[
0 \rightarrow 1 \rightarrow 0
\]

- Convergence

\[
\text{Taxon A} \quad \text{Taxon B}
\]

\[
\text{Convergence on common solution}
\]

Figure 8. Two kinds of homoplasy: (top) character-state reversal, (bottom) convergence.
An Example

In one of the few archaeological uses of cladistics of which I am aware, my colleagues and I examined 17 classes of projectile points (83 specimens) from the southeastern United States (Figure 9) that date roughly 11,500–10,000 radiocarbon years before the present (O’Brien et al. 2001). Instead of using established projectile-point types, we used classes created around eight morphological characters. This assured that each class contained members that were identical in terms of the characters employed. Space does not permit me to discuss the analysis in detail, but shown in Figure 10 is the phylogenetic tree generated. Surprisingly, the program (PAUP* [version 4] [Swofford 1998]) generated but a singletree. I say “surprisingly” because it is not uncommon for hundreds or even thousands of trees to be generated by computer programs designed for cladistic analysis. The tree’s consistency index, or measure of robustness, is 0.5909, which is much higher than we expected and is an indication that although homoplasious characters are present, there is still a strong phylogenetic signal created by the arrangement of apomorphic characters. I emphasize that the tree is a hypothesis of relationship among projectile-point classes; future analysis will allow us to refine the sequence.

Discussion

Objections to the applicability of cladistics to archaeological phenomena might take several forms, three of which are of interest here because they provide a vehicle for exploring several key issues. First, it might be argued that artifacts do not breed—akin to J. O. Brew’s (1946:53) oft-quoted statement in Americanist archaeology that “phylogenetic relationships do not exist between inanimate objects.” True, tools do not breed, but neither do the teeth and bones studied by paleobiologists. Such an argument misses the point: Tool makers do breed, and they transmit information to other tool makers, irrespective of whether those other tool makers are genetic descendants. Artifact taxa are replicated with greater or lesser fidelity of replication as a result of cultural transmission; therefore, tool makers are cultural descendants. In fact, cultural trans-
Figure 10. Phylogenetic tree (cladogram) of 17 projectile-point classes from the southeastern United States. The tree has a length of 22, a consistency index of 0.5909, and a retention index of 0.7000 (from O'Brien et al. 2001).
mission creates what archaeologists have long referred to as *traditions* (e.g., Phillips and Willey 1953; Willey 1945), defined as “(primarily) temporal continuity represented by persistent configurations in single technologies or other systems of related forms” (Willey and Phillips 1958:37). We prefer the term artifact *lineages* to artifact traditions, but both terms reflect transmission, persistence via replication, and heritable continuity. It seems naive, given what we know of the archaeological record, not to believe that tool forms are modeled on preexisting forms.

Second, it has been argued (Dewar 1995; Moore 1994a, 1994b; Terrell et al. 1997) that although there might be tool lineages, they are almost impossible to discover archaeologically because of the kind of process—cultural evolution—that produced them. Under this view, cultural evolution is seen as a vastly different kind of process than biological evolution, with a faster tempo and often a different pattern—reticulation, where the lines cross each other to form a network rather than straight branches—both of which act to swamp all traces of phylogenetic history and thus reduce the cultural landscape to little more than a blur of interrelated, particularly hybrid, forms. This is the difference that A. L. Kroeber (1948) illustrated in his two trees (Figure 11): the biological tree on the left and the cultural tree on the right. I agree that cultural evolution probably is, in most respects, faster than biological evolution and that cultural evolution might on occasion involve reticulation, but I do not view these aspects as being theoretically problematic. My reasoning is simple and comprises two points. First, biological evolution often involves reticulation (Arnold 1997; Doolittle 1999; Endler 1998), especially in the plant kingdom, but this has not precluded phylogenetic analysis. Second, paleobiologists who examine the phylogenetic history of fossils (e.g., Fisher 1994; Smith 1994) must *assume* that the units of analysis—sets of morphometrically similar fossils—termed species (or more inclusive taxa) in fact comprise species (Eldredge and Novacek 1985) and thus do not interbreed. Genetic transmission, in other words, is assumed to occur *only* within a lineage of some taxonomic scale—species, genera, families, and so on. Phylogenetic analysis of artifact lineages requires the same assumption—that cultural transmission is primarily within either a lineage or a series of closely related lineages rather than between dis-
tantly related lineages. In neither paleobiology nor archaeology can it be *demonstrated* that such is in fact the case, yet the assumption seems to raise few eyebrows in the former.

Since late in the 19th century, anthropologists and archaeologists have grappled with the fact that cultural evolution can sometimes be reticulate (references in Lyman 2001). Two small groups of archaeologists met in the 1950s to deal with precisely this issue (Lathrap 1956; Thompson 1958). The criteria they used to distinguish between (1) intralineage change, the source of which was internal to the lineage, and (2) interlineage change, the source of which was external to the lineage, were the ones that had been discussed over the preceding 60-plus years. Key among these was the order of magnitude evident in the change: The greater the magnitude, the more probable the source of change was external to the cultural lineage under scrutiny. This same criterion is used today by archaeologists attempting to separate instances of "phylogenesis," or internal change, from "ethnogenesis," or change caused by external stimulus. Rarely is "magnitude" quantified, with most investigators (e.g., Dewar 1995; Kirch and Green 1987; Moore 1994a, 1994b) relying instead on qualitative assessments such as how strongly one tradition resembles
a previously unrelated one. This line of reasoning, of course, is circular: How does one know that the two traditions are unrelated? Of more immediate interest here, however, is the fact that in modern parlance “ethnogenesis” is equated with hybridization—the production of a new tradition out of two older ones (Figure 12). In this view, only two processes are possible: divergence (phylogenesis) and convergence (ethnogenesis).

I view cultural “hybridization” as a red herring that deflects attention from what really goes on most of the time in cultural traditions. Individual characters or character states can originate inside a tool lineage, just as they can originate outside a lineage and, through transmission, be grafted onto preexisting forms within that lineage (Figure 13). But why should this be equated with hybridization? The answer is, it shouldn’t, given the marked difference in scale. That a single individual of a species occasionally breeds with an individual of another, closely related species, yet otherwise the two species interbreed internally, does not destroy the phylogenetic signal of either. The addition of those extramural characters or states might interfere with the phylogenetic signal we are trying to detect, but this is simply an analytical hurdle, not a reason to abandon cladistics. Linguistic anthropologist Ward Goodenough

![Phylogenesis and Ethnogenesis Diagram](image)

**Figure 12.** Two possible processes behind culture change: (left) phylogenesis, where a culture divides into two or more cultures, and (right) ethnogenesis, or hybridization of cultures. These dichotomous views overlook the real nature of much culture change, in which pieces are borrowed or lost continually.
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Character derived internally

A  B  C  D

Character derived externally

A  B  C  D

Figure 13. Individual characters or character states can originate inside a lineage (left), just as they can originate outside a lineage and, through transmission, be grafted onto preexisting forms within that lineage (right).

(1997:178) made 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.” In other words, borrowing has not created a “hybrid” culture or language (Bellwood 1996).

The third objection that might be raised against the use of cladistics in archaeology is the same one that has been raised in biology with respect to intraspecific applications of phylogenetic methods: Are we even dealing with a nested hierarchy to begin with (Figure 3)? In other words, are the terminals in question themselves related hierarchically (Brower 1999; Brower et al.1996; Davis and Nixon 1992; Goldstein and DeSalle 2000)? I argue that indeed we are dealing with nested hierarchies, irrespective of whether characters or character states are “borrowed” from outside a lineage. Cultural phenomena reside in a series of nested hierarchies that comprise traditions, or lineages, at
ever more-inclusive scales and that are held together by cultural as well as genetic transmission. I agree that in practice the lines between nested hierarchies and reticulating (not hybridizing) networks are sometimes blurred, just as I agree that without a boundary around the reticulating networks there can be no nested hierarchy and hence no monophyly (Goldstein and DeSalle 2000). Such boundaries are fuzzy at best, and often difficult to delimit, but they are by no means beyond our power to determine archaeologically, as several studies have indicated (e.g., Bettinger and Eerkens 1997, 1999; Lipo 2001; Lipo et al. 1997; O’Brian and Lyman 1999, 2000a; O’Brien et al. 2000; Pfeffer 2001; Vaughan 2001).

**Conclusion**

Cladistics is not a method that depends on genetic continuity as a basis for reconstructing phylogeny. It depends solely on heritable continuity, irrespective of the *mode* of transmission. Proper use of cladistics in archaeology recognizes both biological (genetic) and cultural transmission, both of which play a role in the evolution of such things as tool lineages. Materials found in the archaeological record were once parts of human phenotypes in the same way that teeth, fossilized bones, and shells were parts of other phenotypes. Regardless of whether we know that a shell represents one or multiple genes (replicators), our efforts to determine and explain the evolutionary history of the organism behind the shell is not severely hampered. Artifacts are not replicators; rather, 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 overtime enough variation is generated, cladistics might indeed be able to detect the phylogenetic signal. If so, we can create phylogenetic orderings that have testable implications.
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