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sponse to changing circumstances, materials, and traditions." It is in figuring out those circumstances, materials, and traditions where evolutionary studies become exciting.

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We thank Enrico Coen of the John Innes Centre, Norwich, United Kingdom, for bringing Bashford Dean's work to light and for his subsequent correspondence with us. We also thank Stuart Pyhrr and Donald LaRocca, both of the Metropolitan Museum of Art, New York, for providing copies of Dean's drawings of artifact phylogenies; and Mary French of the University of Missouri for her assistance in obtaining the drawings. Mark Collard and Stephen Shennan provided helpful comments on an earlier draft.

## 6

### The Resolution of Cultural Phylogenies Using Graphs

*Carl P. Lipo*

Evolutionary archaeologists (e.g., Dunnell 1982; Hunt et al. 2001; O'Brien and Lyman 2000a) commonly repeat biologist Richard Lewontin's (1974: 8) comment that "we cannot go out and describe the world in any old way we please and then sit back and demand that an explanatory and predictive theory be built on that description." This is not a trivial adage: theoretically and empirically robust explanations require that phenomena be described using variables embedded within a coherent theoretical framework. In the case of explanations that invoke Darwinian evolution as a process, two kinds of descriptions are critical: measures of performance differences and measures of relatedness.

Relatedness is an everyday way of talking about similarity that results from shared inheritance. Inherited similarity is considered to be the result of two entities sharing characteristics as a result of sharing a common ancestor. However, having a common ancestor is not the only possible explanation for why two entities share a feature. They could have developed it independently, converging on a common solution to a common problem. Likewise, it is possible that two entities are similar because one is the ancestor of the other.

This is as true for objects in the archaeological record as it is for organisms: similarity can potentially be a product of both kinds of ancestry. This means that archaeological explanations require two kinds of descriptions. First, the things we study must be arranged chronologically. Second, we must evaluate the degree to which similarities among observations have independent origins or are related through inheritance. Determining historical relatedness specifies if and how entities descended from one another. Together these lines of evidence form the foundation of explanations that take the form "descent with modification," the defining concept in evolution (O'Hara 1988).

Archaeologists are adept at determining chronology and inheritance and have been doing this since the early twentieth century (e.g., Kroeber 1916a, 1916b; Phillips et al. 1951; Sayles 1937; Spier 1917). Archaeologists routinely place items of material culture into so-called "time-space" charts that depict spatial, chronological, and historical relationships among artifact classes (Lyman et al. 1997; O'Brien and Lyman 1998, 2000; Spaulding 1955; Willey 1953). These charts form the core of our empirical knowledge of the archaeological record.

Figure 6.1 is one such chart. It shows Dunnell's (pers. comm. 2003) unpublished reconstruction of the evolution of eastern North American projectile

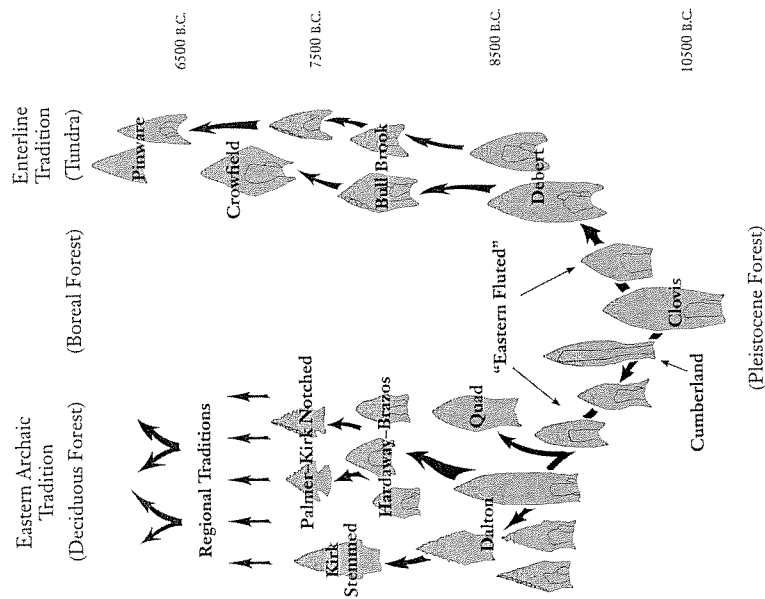
points. It adds a spatial component to change through time that maps how projectile points diverge into two spatially and environmentally distinct traditions. What is clear from this and similar figures (e.g., those in chapters 1 and 5, this volume) is that we have the means of studying evolution within existing archaeological practices. In combining elements of time and relatedness to track the descent with modification of artifacts, these diagrams provide us with the products needed to generate evolutionary explanations.

It is tempting to think that the presence of these time-space charts preadapts archaeology to make use of evolutionary explanations in accounts of the past. However, despite the potential match between these products and the demands of evolutionary theory, archaeology continues to fall short of becoming an evolutionary science (Dunnell 1989). This failure is the result of a number of factors. First, the discipline has relied on common-sense-based descriptions of the archaeological record that are incompatible with measures of evolutionary relatedness (Dunnell 1982). For example, if we want to study historical relationships, it is necessary to build classifications that focus on the measurement of homologous similarity. Second, archaeology sorely lacks statistically defensible and quantifiable measures of relatedness. Although they form the basis of culture histories and take the form needed for evolutionary studies, time-space charts have relatively little statistical warrant. The creation of such charts is done primarily on the basis of intuition and arguments of authority rather than on repeatable measurements and quantitative evaluation (O'Brien and Lyman 2000a). This does not make the inheritance claims of culture historians wrong, just relatively limited in their usefulness.

Fortunately, these deficiencies can be overcome. By generating variables from theory, we can build descriptions of the archaeological record that are explicable within evolutionary frameworks (e.g., Lipo 2001). The potential of this approach has been powerfully demonstrated by Greenlee (2002) in an evolutionary account of prehistoric subsistence variability in eastern North America. Significant strides have also been made in adopting, developing, and modifying quantitative methods for studying patterns of cultural inheritance (e.g., Bettinger and Eerkens 1997, 1999; Lipo 2001; Lipo et al. 1997; Neiman 1995; O'Brien and Lyman 2003a; O'Brien et al. 2001, 2002; Shennan 2000; Shennan and Wilkinson 2001). Of these developments, two areas are of particular interest: seriation (e.g., Dunnell 1981; Graves and Cachola-Abad 1996; Lipo 2001; Lipo et al. 1997; O'Brien and Lyman 1998; Teltser 1995) and cladistics (e.g., Collard and Shennan 2000; Jordan and Shennan 2003; O'Brien and Lyman 2003a; O'Brien et al. 2001, 2002; Tehrani and Collard 2002).

Cladistics is a powerful means of building hypotheses about inheritance that is well established in biology and paleontology (Eldredge and Cracraft 1980; Felsenstein 2004; Hennig 1950, 1966; Nelson and Platnick 1981; Wiley

Figure 6.1  
Hypothetical Evolutionary Relationships among Types of  
Projectile Points from Eastern North America



(R. C. Dunnell, pers. comm. 2003.)

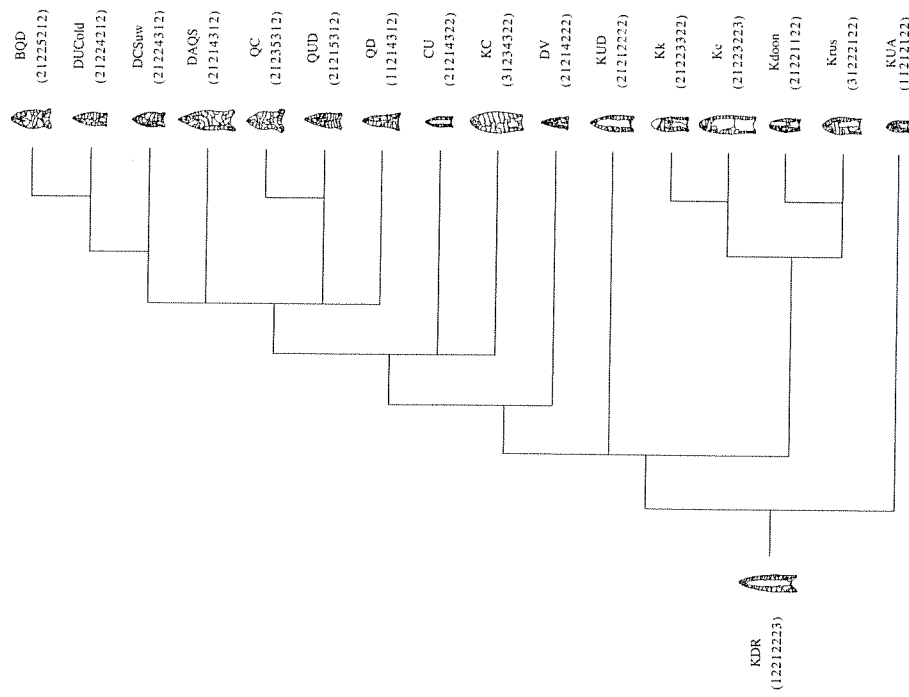
1981). Although initially created for the study of organisms, cladistics depends only on mapping the results of transmission of information among entities and is potentially applicable to any inheritance system (O'Brien and Lyman 2003a; O'Brien et al. 2001). Cladistic analyses of biological, genetic, and linguistic inheritance are conducted primarily by determining ancestral relationships among contemporaneous samples. Linguists, for example, reconstruct ancestry based on descriptions of languages taken at a specific point in time (e.g., Campbell 1999; Gray and Atkinson 2003; Gray and Jordan 2000; Jordan 1999; McMahon and McMahon 1995; Ringe et al. 2002). In the same way, geneticists make inferences based on samples of DNA taken from modern populations (e.g., Cavalli-Sforza 2000; Cavalli-Sforza and Feldman 2003; Underhill 2003). In many cladistic analyses, the ends of a phylogenetic tree—referred to as “terminal,” or “sister,” taxa—are contemporaneous samples, and nodes in the tree represent reconstructed ancestors that presumably existed in the past. Importantly, the nodes often are then shown as sister taxa, even though in a strict sense they may not be (see below).

Contemporaneity among taxa is rarely the case when we deal with objects in the archaeological record because characters (attributes) used to describe artifacts are chronologically variable. This means that it is highly unlikely that terminal taxa in an archaeological cladistic analysis are contemporaneous. The same is true in paleontology. It is important to point out that the presence of chronologically variable taxa does not violate assumptions of cladistics; the method still resolves relative degrees of relatedness. But we need to be aware of how cladistics may overestimate the amount of branching that may have taken place.

The problem gets more complicated with real data. Take for example, the tree produced by O'Brien et al. (2001) for early projectile points from the southeastern United States (figure 6.2). O'Brien and colleagues built this tree using seventeen taxa defined by the states of eight characters. Is distance in figure 6.2 a function of relatedness or simply of chronological position? Given that relatedness and chronology need not be linearly related, the order of branching between clades (an ancestor and all of its descendants) is problematic.

The problems that cladistics faces in handling non-contemporaneous taxa are widely recognized, but thus far there have been no easy solutions. Stratocladistics is one attempt by paleontologists to address this issue. Fisher 1991, 1992, 1994; Forey 1992; Heyning et al. 1999) use stratigraphic data to evaluate hypotheses about phylogenetic trees. Despite its promise, however, the method is limited. Stratocladistics is a manual technique, and there is no agreement as to which solution should be given the stronger weight—stratigraphic order or cladistic analysis (Fisher et al. 2000; Fox et al. 1999; Heyning et al. 1999; Smith 2000). Is there an alternative?

Figure 6.2  
The Cultural Phylogeny of Paleoindian-Period Projectile Points from the Southeastern United States



(From O'Brien et al. 2001.)

### Mapping Cultural Phylogenies Using Graphs: A Complementary Method

In recognition of the limitations inherent in cladistics, a number of new approaches have been developed to model patterns of relatedness. These methods include the use of networks (e.g., Bryant and Moulton 2002; Huson 1998)

and graphs (e.g., Baroni 2003, 2004) and are particularly robust when evolutionary processes such as recombination and hybridization may have been present in a dataset (Bryant and Moulton 2002). In the remainder of this chapter I describe one such method based on graph theory that can serve alongside cladistics. This method makes use of a simple set of assumptions for mapping transmission and is capable of detecting constraints, measurement problems, and processes that impact patterns of homologous similarity.

The key component of any method for studying relatedness is the careful construction of units for describing the empirical record. Here, I am interested in constructing descriptions in which the dimensions (characters) used to construct classes (taxa) are independent and measure neutral variation. Dimensional independence is critical; mechanically linked change between characters is likely a function of architectural and technological constraints and not of transmission. Thus, we need to exclude allometric effects (e.g., West et al. 1997), the “spandrels” of Gould and Lewontin (1979), and the design constraints of Conway Morris (2003). This requires developing general awareness of “evolutionary kinematics” (Fontana 2003; Stadler et al. 2001) when we build classifications and descriptions (see also chapter 2, this volume).

The use of stylistic descriptions—those that measure neutral variation only—is also a key component of the method. Stylistic descriptions make use of culturally transmitted, alternative traits that have no significant differences in fitness values and thus are said to be neutral with respect to selection (Dunnell 1978; Lipo and Madsen 2000; Neiman 1995). This feature of the descriptions helps ensure we are studying similarity derived from inheritance and not similarity resulting from convergence. If we measure variation using taxa built with these style-related criteria, cultural-transmission theory states that traits will change as a result of one of three distinct processes: social learning (transmission), individual innovation (mutation), and sampling error (chance).

Consider an artifact that is described by three characters (A, B, C), each of which has three character states (1, 2, 3). Taxon definitions take the form of a sequence of numbers where each digit represents a state of a separate character. In this example, taxa take the form of number strings such as 321 or 322. If we identify instances of taxa 321 and 322, for example, we can hypothesize that the difference in the third character was caused by innovation, cultural transmission, and/or chance. Using the principle of parsimony, we can order our descriptions using the smallest number of possible changes to form hypotheses about change (Felsenstein 2004).

The minimum number of character states that must change to convert one taxon to another is known as the “Hamming distance” (Hamming 1980). This method is akin to O’Brien et al.’s (2002) “occurrence method” for studying the distribution of character-state changes with a set of ordered taxa (see also chapter 5, this volume). The method works because we have specified that

changes occur only because of transmission factors; the resulting order must be explicable in those terms. In this way, the patterns we generate can be inferred to reflect transmission in time and/or space. For example, if innovation and vertical transmission are the primary processes that structure patterns of character states, we can expect patterns of change to be linear. In this scenario, variation will reflect the passage of time. Additional factors will alter this simple pattern. As a result of the effects of innovation rate in a population that has limited horizontal transmission, we would expect that taxon definitions will diverge within the population.

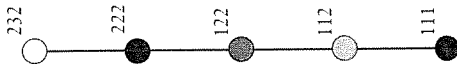
### *Graph Representation*

Patterns of stylistic descriptions ordered by the principle of parsimony can be represented visually in the form of an undirected graph. Graphs are a simple means of representing data structures when they are nonlinear and nonhierarchical (e.g., Flament 1963; Harary 1969; Wasserman and Faust 1994). Graphs are used frequently in computer science to solve problems such as finding the shortest airplane route between two cities. They are also used to begin to aid in the interpretation of trees (e.g., Morris, Asnake, and Yen 2003) and to visualize timelines of interaction (e.g., Morris et al. 2003). Visually, the graphs consist of a collection of nodes and edges, with the latter connecting the former.

We can create a graph representation of our data by connecting taxa that differ in only a single character. For example, Taxon 112 differs from Taxon 122 in only a single character. This allows us to map the order of changes between taxa and thus generate hypotheses about the processes responsible for change. In the case where innovation and vertical transmission are primary factors, a linear pattern is expected in which taxa are linked to only two neighbors (figure 6.3), each differing by character states in but a single character. The order generated is a hypothesized chronological order.

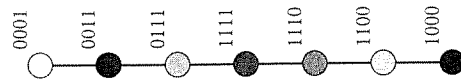
In fact, if we build taxa that allow only two states per character, absence/presence, the resulting graph (figure 6.4) takes the form of what we commonly recognize as an “occurrence seriation” (Lyman et al. 1998). This means that the construction of graphs using comparisons of taxa to generate connectedness is a general version of a method for mapping change that includes occurrence seriation as a special case when the character states are binary. In this respect, the graph method for arranging descriptions has the same constraints as occurrence seriation. For example, we need additional, external information in order to tell the top from the bottom. The theoretical rationale for linking the graph method with occurrence seriation comes from the inference that linear orders are primarily a result of mutation. Thus, orders are predominantly chronological. However, in its general form this can be true if we use traits that are binary or can take multiple states.

Figure 6.3  
A Graph Linking Taxa (Nodes) Together into an Order



The taxa are defined by three characters (e.g., Taxon 111) and are linked by lines to other taxa that differ only in a single character.

Figure 6.4  
Linear Graph of Taxa Ordered Using Binary Character States



This results in what is commonly recognized as "occurrence seriation."

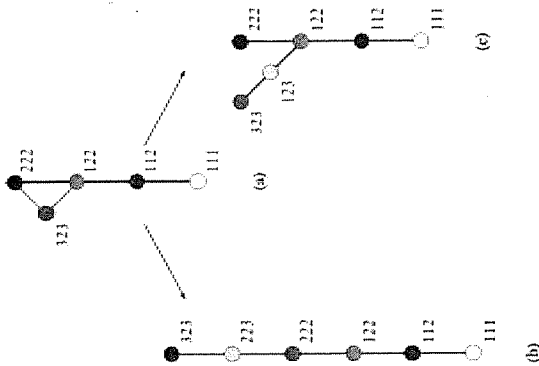
The pattern we generate depends on the number of differences in dimensions that are used to determine nodes. Ordered taxa will differ in an increasingly large number of characters depending on the taxa that are compared. For example, Taxon 122 differs from Taxon 323 in two characters. Based on the assumptions of the model—that change in character states occurs only by mutation, cultural transmission, or chance—the method is most robust in explaining changes in only a single character. Concurrent multiple character changes mechanically create links to more than one taxon. With multiple character changes, no single order is possible, and without external information explanatory ambiguity can occur. The graph method allows one to identify the location in the taxon definition (the number string) that is causing multiple trees and thus where the results are ambiguous.

Explanations are simplest when descriptions that are being compared have a Hamming distance of one (e.g., 112 to 122). Of course, the minimum Hamming distance between pairs of descriptions will often differ by values greater than one. Larger Hamming distances (e.g., 113 to 122) can be potentially explained as (1) the distribution of taxa within the classification space; (2) a sampling problem that results in the absence of instances of intermediate forms available for measurement; or (3) an indication of linked characters. For example, taxa in figure 6.5a that differ in only one character are linked by thick lines. Taxa with differences in two characters are connected by thin lines. In this example Taxon 323 is equally different in two characters from taxa 222 and 122. This pattern potentially indicates that there might be missing intermediate taxa that could be placed between one of the two pairs of taxa (e.g., taxa 223 or 123 as shown in figures 6.5b and 6.5c). Locating instances of one of these would help us resolve whether 323 should be modeled as in figure 6.5b or as in figure 6.5c.

Graphs produced with nodes linked by minimum Hamming distances that are greater than one can produce useful results, but there will often be multiple solutions, given that the results are no longer deterministic. There also might be cases in which no intermediate ancestors exist, as traits have changed synchronously in multiple dimensions. This can indicate that characters are technically linked. For example, in the case of projectile points, a character such as "basal stem angle" could be mechanically constrained by certain forms of notching. In this case, forms of notching may always result in changes in basal stem angle, and changes in the characters will be synchronous. Resolving this problem requires a reexamination of the classification and modification of the characters so that they are not technologically and/or functionally linked (chapter 7 and 12, this volume).

Unlike with occurrence seriation, linear patterns are not required. Indeed, this is one of the strengths of using the graph method for mapping relatedness: There are no constraints so long as the assumptions of the method are met. If, for example, we find an instance of Taxon 123 to help resolve the ambiguity in

**Figure 6.5**  
**Graphs of Taxa Defined by Three Characters, Showing the Potential Ambiguity that Arises When Taxa Simultaneously Show Differences in More than One Character**



The thick lines indicate differences between taxa in only a single character, and the thin lines indicate two character differences between taxa. In (a) the placement of Taxon 323 is ambiguous, whereas in (b) and (c) intermediate taxa help resolve the placement.

figure 6.5, we can definitively generate a graph that links each taxon with single character differences. In this case, Taxon 123 falls between taxa 122 and 323. When placed into the graph (figure 6.6), the resulting pattern is one of divergence.

Similarly, using the graph method we can also track convergence if it is present within a set of descriptions (figure 6.7), even in cases that also include divergence. From an inheritance perspective, patterns of convergence can be generated when traits are shared across lineages through horizontal transmission. In addition, we can map reticulate patterns that are present when there is a significant amount of horizontal transmission (figure 6.8). In cases where traits are exchanged in a way that is unconstrained, a dense network will appear, in which taxa are linked to many others in nonlinear patterns.

In figure 6.8, for example, taxa are shown linked by single differences in characters. If we had external information in order to orient the figure so that the bottom of the graph is early and the top is late, we could imagine that traits are being shared across a population in a way that is not strictly vertical. This kind of inheritance creates a bushy appearance that is characteristic of reticulate evolution and potentially a factor in cultural transmission (e.g., Kroeber 1948; Lyman 2001).

Given its flexibility, the use of graphs has significant potential for analyzing historical relatedness in phenomena that vary simultaneously in time, space, and inheritance. The strength of the method comes from the fact that graphs represent patterns of inheritance as determined by the assumptions of the method. Like determining the root of a cladogram or the orientation of an occurrence seriation, shape and orientation of the graph must be determined by external information. Using stratigraphic or absolute dates, for example, we can orient the graph chronologically. We can also evaluate hypotheses about spatial variation by assigning relative positions to nodes based on geographic locations. We can also add new data by moving and stretching the graph, and we can move nodes around by using ordinal- or ratio-scale data (e.g., dates and absolute positions).

#### Application to Archaeological Data: Projectile Points from the Southeastern United States

A reexamination of the data used by O'Brien et al. (2001, 2002) in their cladistic analysis of projectile points from the southeastern United States provides an example of how the graph method can analyze patterns of inheritance. The data in the original phylogenetic analysis consist of metric and morphological measurements made by combining eight characters, each consisting of two to six possible states (table 6.1). Using this classification system and measurements from eighty-three projectile points, O'Brien and colleagues identified seventeen unique taxa (table 6.2). For example, 21223223 is a pro-

**Figure 6.6**  
**Taxa Linked Together by Differences in Single Characters Showing a Divergent History**

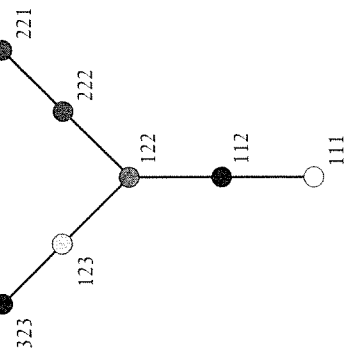


Figure 6.7  
Taxa Linked Together by Differences in Single Characters  
Showing Convergent History

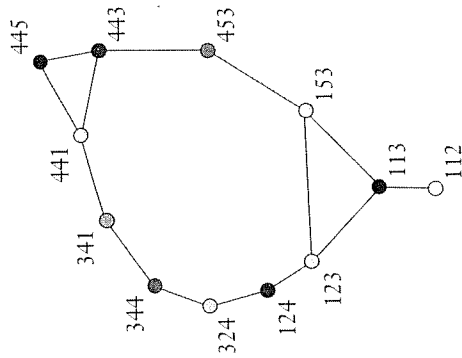
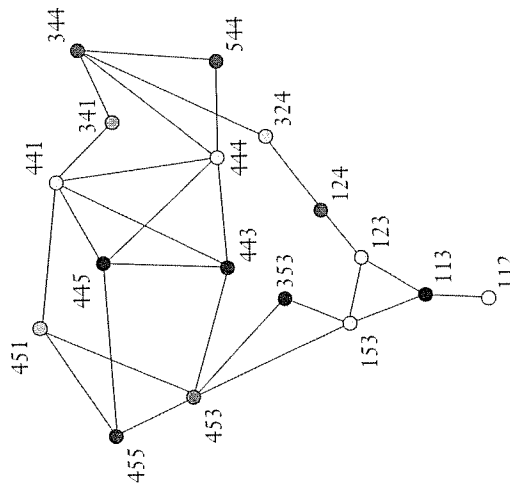


Figure 6.8  
Taxa Linked Together by Differences in Single Characters Showing an  
“Entangled Bank” that Can Be Produced by a Combination of  
Divergence and Horizontal Transmission



jectile-point taxon (abbreviated as Kc) that consists of a combination of states of eight characters and is commonly identified as “Clovis.”

To build the graph, I first calculated the Hamming distance between each pair of taxa and placed them in a matrix. I then used NetDraw<sup>1</sup>, a network-visualization program, to plot the taxa as nodes in a network and the edges as the distance between taxa. The key advantage of NetDraw is that it allows one to plot and visualize a network with different parameters of “connectedness,” or in this case character-distance parameters. The algorithm used to generate the graphs places nodes in locations that are scaled by the number of differences in characters for each pair of descriptions.

Using this procedure, I generated a graph that consisted of the linkages between taxa with the fewest differences in characters. The results are shown in

Table 6.1  
System Used by O’Brien et al. (2001) to Classify Projectile Points

Character <i>Character state</i>	Character <i>Character state</i>
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°–80°
	5. 51°–65°
	6. <50°
II. Base shape	VI. Tang-tip shape
1. Arc-shaped	1. Pointed
2. Normal curve	2. Round
3. Triangular	3. Blunt
4. Folsomoid	
III. Basal indentation ratio	VII. Fluting
1. No basal indentation	1. Absent
2. 0.90–0.99 (shallow)	2. Present
3. 0.80–0.89 (deep)	
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

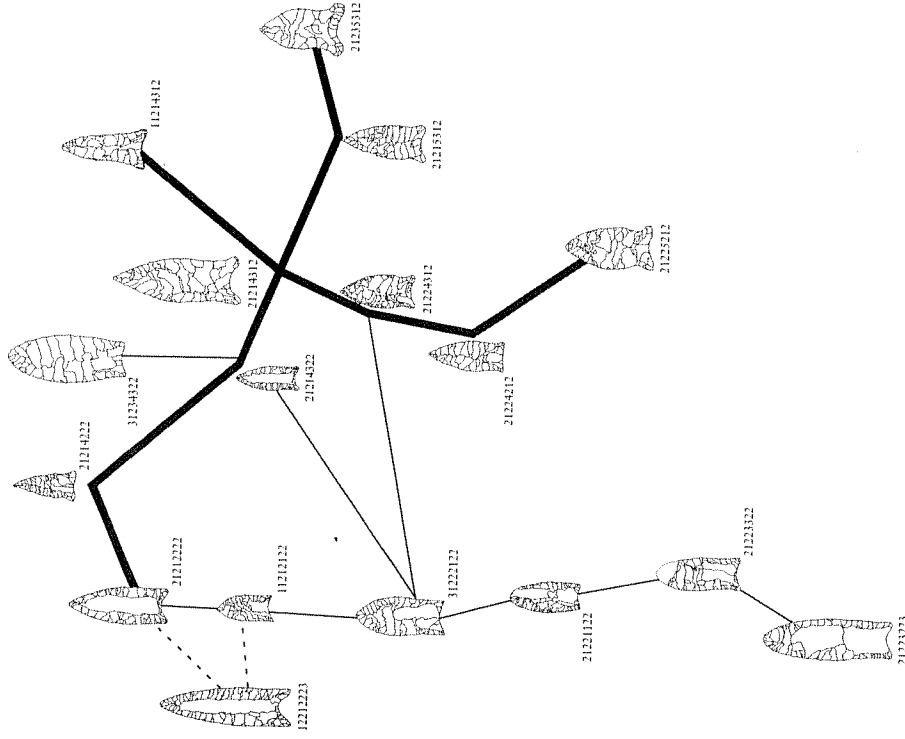
**Table 6.2**  
**Taxon Definitions, Abbreviations, and Common Type Names of Projectile-Point Taxa Used by O'Brien et al. (2001)**

Taxon	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

Figure 6.9. Not all of the taxa differ by only a single character. Six taxa differ from other taxa by two characters, and one taxon (12212223) differs by three characters. For the most part, the descriptions can be ordered into a branched pattern, where ten of the taxa can be linked with single steps. The remainder of the taxa are connected in a nearly linear pattern, with two exceptions. An ambiguity exists with Taxon 31222122, as it differs in two dimensions from four different taxa. It is possible that additional intermediate examples will resolve this problem. In addition, because Taxon 12212223 differs in three dimensions from two other taxa, its relationship is unclear.

It is necessary to determine the degree to which the graph results might have been determined by chance. It is possible to obtain patterns of connected nodes in random assignment of character states, especially when the size of the classification is small. The smaller the classification, the more likely chance will play a role in generating descriptions that differ by only a single character. The classification constructed by O'Brien and colleagues is reasonably large, consisting of 62,208 combinations of character states. With only seventeen taxa, the likelihood of the classification space constraining the descriptions is extremely small. This suggests that chance likely played a minor role in pro-

**Figure 6.9**  
**Graph Produced by Linking Taxa to Their Most Similar Neighbors**



Bold lines represent differences in taxa of only a single character (single steps), and thin dotted lines show differences in taxa of two characters. The dotted lines reflect differences of three characters. The multiple lines that connect Taxon 31222122 to other taxa reflect ambiguity caused by equivalent differences between multiple taxa. Additional information or intermediate specimens will potentially resolve which connection represents the evolutionary pathway. (Taxa from O'Brien et al. 2002.)



ters VI and VII, outer tang angle and tang-tip shape (table 6.1). This suggests that the two characters are not fully independent or may be linked with another character such as base shape. Further research into the structure of the projectile-point classification is required to resolve the potential impact of this dependency.

Second, although chronology explains much of the structure of the graph, spatial variation may also play a role. The points described by the classification are located across eleven southeastern states. Although preliminary examinations (O'Brien and Lyman 2003a) do not indicate strong spatial patterning, it is reasonable to expect that at least some of the variation in taxa is a function of distance. Lack of spatial variation might be explained by the rate of cultural transmission relative to innovation and a suppression of regional variants, perhaps for functional or technological reasons, resulting in spatial autocorrelation.

Third, further work is required to refine the chronological assignments of the projectile-point taxa. Rather than typological cross dating, we need direct dating information for as many representatives of each taxon as possible in order to build robust empirical estimates of the temporal distributions. Luminescence dating of catastrophically heated chert-tool manufacturing debris offers one promising avenue for generating direct chronological information on individual specimens (Wilhelmsen and Miles 2005).

Fourth, there are no empirical "packages" of information in cultural transmission, meaning that projectile points may not form a single unit of transmission. As Bettinger and Eerkens (1999) have pointed out, the set of instructions that produce what we know as projectile points may be the result of a variety of attributes and attribute sets, each with its own historical trajectory (see also chapter 11, this volume). Consequently, the patterns measured here can be considered to reflect only the history of one portion of the information required to produce projectile points—in specific, only the history of basal shape and fluting. Determining the scale of the transmission package is an empirical question that requires examining the history of multiple trait groups. Some trait groups may coincide, which implies either that the traits came as packages or that they came from consistent sources along consistent pathways, even if it happened over some period of time as opposed to all at once.

### Conclusions

Developing methods for studying the archaeological record in a way that is founded in evolutionary theory is a critical task. As long as variation was measured in terms of discrete objects, culture historians had a reasonable but intuitive way for generating hypotheses about chronology, spatial pattern, and relatedness (Lyman 2001; Lyman et al. 1997). Although roughly capturing the broad features of culture history, time-space diagrams produced by

culture historians had little theoretical foundation. More-recent attempts at producing tools for studying inheritance move us in the right direction, but the interpretation of results can be problematic in archaeological cases where observations vary simultaneously in terms of time, space, and relatedness.

The graph method described here provides a means of building and testing cultural phylogenies that is complementary to methods such as cladistics. The strength of the method is that it can be used to generate hypotheses about relatedness, spatial variation, and chronological relationships of artifacts based on homologous similarity. It is an excellent tool for examining evolutionary dynamics.

### Note

1. NetDraw is a shareware program available as part of the UCINET social network analysis package (Borgatti et al. 2002). This analysis used version NetDraw 1.0, which can be downloaded at <http://www.analytictech.com>.

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As contributors to [*Mapping Our Ancestors*] make perfectly clear, the application of evolutionary theory to cultural change cannot be done without reference to biological evolution. Cultural transmission is different from genetic transmission and requires different principles, which cannot be borrowed but must be developed by anthropologists, and linguists. Among the differences between genetic and cultural transmission are the presence of horizontal inheritance, the greater propensity for neutral variation, and the greater probability of recombination (or hybridization), and a more gradual rate of change. While much work remains to be done, the book is a great stride in identifying the various ways that cultural change might be resolved. The various chapters are just abstract theorizing but practical attempts to grapple with the issues. After reading this book, how an evolutionary theory of culture becomes clearer." —James K. Feathers, Department of Anthropology, University of Washington

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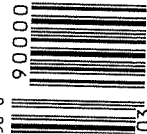
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