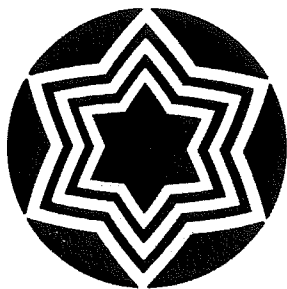# AMERIND STUDIES IN ANTHROPOLOGY

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CROW-OMAHA

NEW LIGHT ON A CLASSIC PROBLEM OF KINSHIP ANALYSIS

THOMAS R. TRAUTMANN AND
PETER M. WHITELEY, EDITORS

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alternative transformation trajectories: Dravidian → Iroquois and Iro-quois → Crow-Omaha in North America (the Trautmann-Barnes hy-pothesis), and Dravidian → asymmetric-prescriptive in South Asia (see also chapter 2, and Kryukov 1998). In North America, the loosening of a two-line exchange system (with a shift from Type A to Type B cross-ness) seems a precondition for the emergence of Crow-Omaha/semi-complex alliance, but the Hopi case shows that some "prescriptive" ex-change persists in Crow-Omaha formations.

Pueblo social structures emerge as more similar to each other than is generally allowed, as exemplars of "a closed, regular alliance structure of a specific type" (Tjon Sie Fat 1998a:262). Marriage prohibitions for key descent lines fade out beyond a close range of cognatic kin, and more distant relatives of supposedly prohibited classes make a preferred category of spouses. In the Hopi case, one's father and his clan-set re-main, as it were, affines, a condition marked by the skewed crossness terms. These terms also express affinity as a renewable value in the evi-dent marriage preferences they connote. Crow skewing appears as the key articulating principle of Hopi social structure, proceeding from the conjuncture of matrilineal descent with patrilateral alliance. I find no evidence of an alternative unskewed system for Hopi (as Kronenfeld [e.g., chapter 8] argues for other Crow-Omaha cases), nor, therefore, that Crow skewing is an optative overlay. Hopi Crow nomenclature and semi-complex alliance reflect the co-presence of restricted and gen-eralized exchange principles. On this combination may rest the princi-pal structural advantage of Crow-Omaha systems: the simultaneous maintenance and flexible enhancement, under certain conditions of circumscription and adaptation, of alliance networks, those engines of emergent polity.

Phylogenetic Analysis of Sociocultural Data

Identifying Transformation Vectors for Kinship Systems

Ward C. Wheeler, Peter M. Whiteley, and Theodore Powers

The use of trees as metaphor to describe the historical kinship of crea-tures has a long history in biology. Today, we tend to look to the "I think" illustration of Darwin (1859) and the explicit phylogenetic tree of Haeckel (1866) as origins, but implicit tree thinking extends back at least an additional 2,000 years to natural philosophers such as Theo-phrastus (Nelson and Platnick 1981). The basic idea of the tree repre-sentation is to both model the evolutionary process of diversification from root to tip and represent sets of related taxa as branches of the tree. The narrative was that some ur-creature or overall common ances-tor was at the root of the tree, which grew and subsequently split into branches and sub-branches as time progressed. Any one time would be a horizontal slice through the tree, with current time at the tips and cur-rent taxa the leaves. The goal of systematic biology is to reconstruct the entirety of the tree when only given the leaves.[1]

When we abstract this notion, trees are a form of graph with two sorts of components: vertices and edges (figure 6.1). Vertices are points connected to each other by edges. In the biological tree metaphor, edges are branches that connect splitting points (crotches) to other splitting points or leaves. A tree must not have any "cycles" or paths from vertex to vertex via edges that return to their starting point. For analytical convenience, we usually treat trees as dichotomous, where each vertex is connected to a single other vertex if it is a leaf, or three others if it is not a leaf. If the tree is "directed," a root is present, which is a special vertex along an existing edge that connects to two other vertices. Less ab-stractly, the leaves are observed entities, whereas internal (i.e., nonleaf) vertices are hypothetical ancestral taxa.[2]
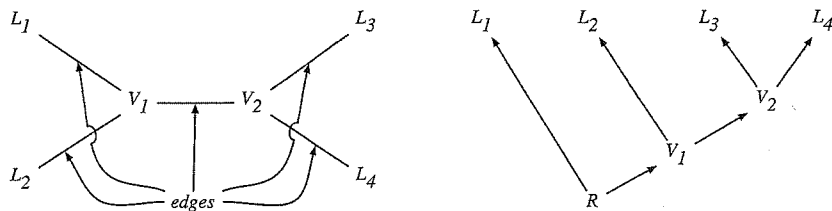
Figure 6.1 Trees, undirected and directed. Left, an undirected tree with leaf vertices $L_1 \ldots L_4$, internal vertices V_1 and V_2, and edges labeled. Right, a directed (rooted) representation of the left tree with root R along edge $L_1 V_1$.

One of the strengths of such a tree representation is that we can infer the sequence of events (at least from edge to edge) that have occurred among the observed taxa and localize them on the tree. Such changes would occur between ancestor and descendent vertices on a directed (rooted) tree. Those entities that descended from a common ancestor share unique features that are evidence both of their relationship and of the transformations that occurred in the past. Transformations along adjacent edges form a chain of events describing the history of diversification in the features of the taxa.

There are an enormous number of trees, more than particles in the known universe, for relatively small sets of taxa (table 6.1).[3] So many, in fact, that identifying the "best" one is impossible to guarantee for non-

Table 6.1 Number of binary trees for n taxa

n	Unrooted	Rooted
3	1	3
4	3	15
5	15	105
10	2,027,025	34,459,425
20	8.20×10^{21}	3.03×10^{23}
50	2.84×10^{74}	2.75×10^{76}
100	1.70×10^{182}	3.35×10^{184}

trivial problems,[4] and we are forced to rely on heuristic computational techniques when analyzing real data.

The challenge and promise of phylogenetic tree analysis of sociocultural data is to identify trees that best represent the historical branching patterns among cultures and/or their component elements; then, based on this tree, identify those elements that are shared due to common history and those due to multiple origin or exchange; and finally determine whether there are general, even directional, patterns of cultural transformation between human behavioral systems. The value of this approach to human societies and their histories, so far realized only in limited fashion, was predicted by Lévi-Strauss almost three decades ago:

> It is striking that this new systematics of living or extinct species, called cladistics, may be interpreted, alternatively and sometimes simultaneously, as a method for determining a temporal order of succession among more or less related species, *or* as a classification indifferent to the search for [parent] stocks. In the latter case, the formulation of rigorous procedures for defining groups, establishing a hierarchical order among them, and their embedded and inclusive relationships, may offer heuristic value not only in biology but in every field of study where we observe relationships comparable to homologies. (1983:1227, our translation)

Trees as Explanations

Trees are explanations of data in that they present scenarios of change that require the smallest amount of "extra" change over the minimum possible given observed variation (Farris 1982). The amount of extra change can be measured in a variety of ways, such as parsimony steps, likelihood units, or posterior probability (see later discussion), but in each case a "best" tree description represents the ensemble minimum over all the data. It may be that the favored tree is not minimal for any of the observed features individually (table 6.2, figure 6.2) but is optimal for their combination.

A rooted tree offers historical explanation in that some aspects of features temporally precede others. In this sense, they are "primitive" with respect to the "derived" condition. Given the nonminimal changes in nearly all features (i.e., homoplasy), taxa are mosaics of primitive and

Table 6.2 Binary data of nineteen characters for twenty taxa

Taxon	Characters																		
t0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
t1	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
t2	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0
t3	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
t4	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
t5	1	1	1	1	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0
t6	1	1	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0
t7	1	1	1	1	1	1	1	0	0	0	0	0	1	0	0	0	0	0	0
t8	1	1	1	1	1	1	1	1	0	0	0	1	0	0	0	0	0	0	0
t9	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
t10	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0
t11	1	1	1	1	1	1	1	1	0	1	1	0	0	0	0	0	0	0	0
t12	1	1	1	1	1	1	1	0	1	1	1	1	0	0	0	0	0	0	0
t13	1	1	1	1	1	1	0	1	1	1	1	1	1	0	0	0	0	0	0
t14	1	1	1	1	1	0	1	1	1	1	1	1	1	1	0	0	0	0	0
t15	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0	0	0	0	0
t16	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0
t17	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0
t18	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
t19	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

derived aspects. Mammals, for instance, possess external hair, which is derived with respect to other vertebrates, yet they are also characterized by the primitive feature of lungs (with respect to the swim bladder of teleost fishes).

Historical explanation is "vertical" in that transformations occur between ancestors and descendants. Those features that do not fit this mode of change require secondary (ad hoc) explanation as either convergence or perhaps nonvertical transmission. Convergence refers to the
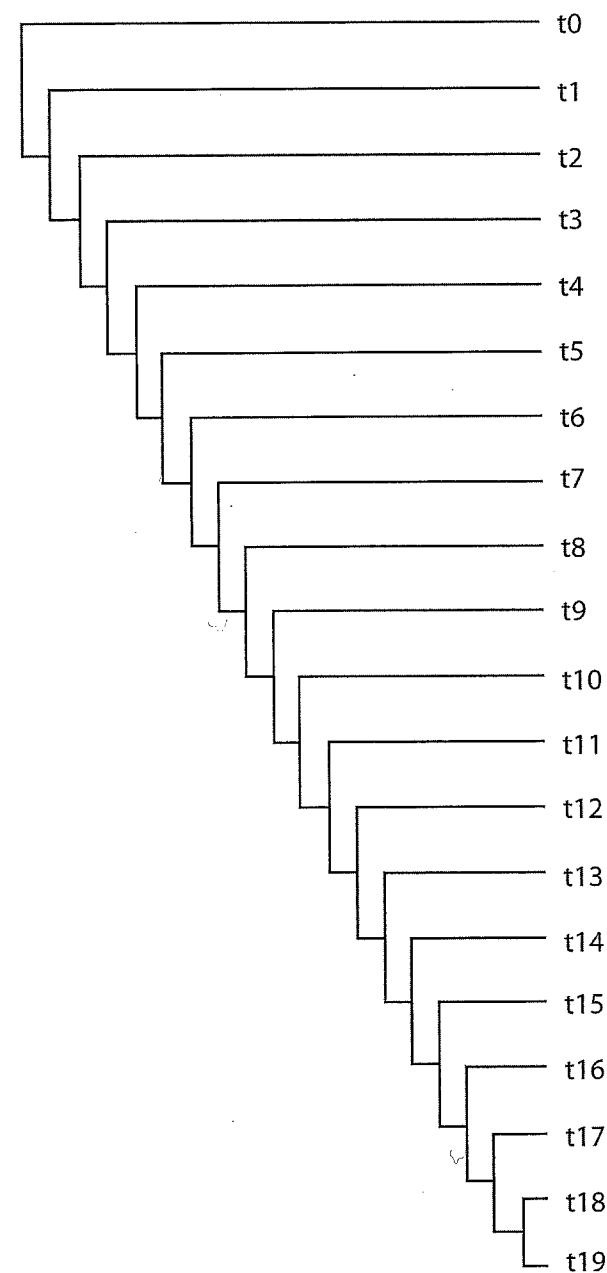
Figure 6.2 Tree for the data of table 6.2. Assuming the minimum number of character changes, two for each of the nineteen characters for a length of thirty-eight steps.

nonunique acquisition of derived features, such as wings in bats, ptero-saurs, and some dinosaurs (birds). The identity of these features does not necessarily indicate errors in any way but signifies actual multiple origins, which then continue to change in a vertical fashion. A second explanation of homoplasy is "horizontal" inheritance. In this non–tree-like form of transformation, descendants may have multiple ances-tors resulting in a phylogenetic network. For trees to be a reasonable explanatory framework, vertical change should be more prevalent than horizontal change. For most biological variation, this is clearly true and has been shown to be the case as well for a variety of human cultural features (Collard et al. 2006).

Networks and Multiple Explanations

A network is a tree with edges added to signify multiple ancestry for some vertices (figure 6.3). To avoid cycles, networks must be directed, hence rooted. Given that there are many extra edges that can be added to a tree to form a network,[5] the number of networks is considerably
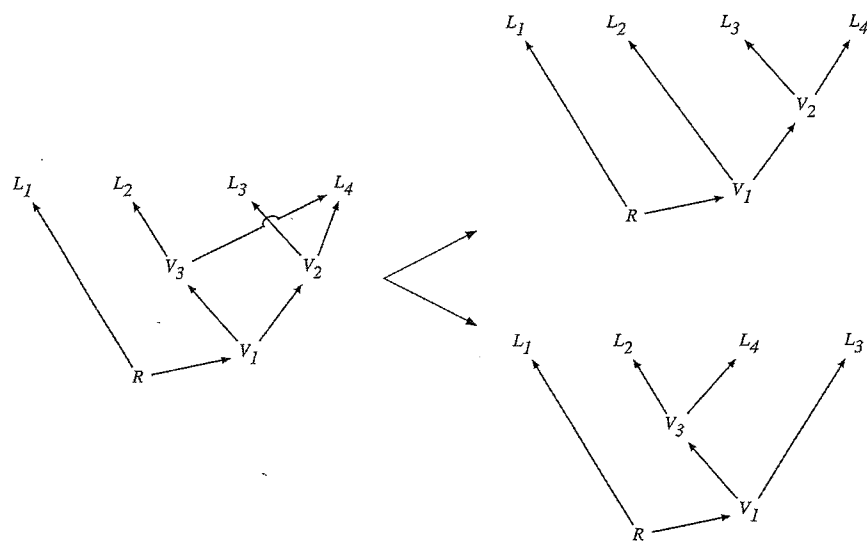

Figure 6.3 A network of four taxa (as in figure 6.1). Shows a network edge ($V_3 \rightarrow L_4$) on the left and the two trees derivable from alternate resolution of the ancestors of L_4.

larger than that of trees. Networks are usually treated as sets of largely similar trees (e.g., Jin et al. 2006; Nakhleh et al. 2005) based on alter-nate resolution of ancestral edges (choosing each in turn to generate an alternate tree). This allows for networks to be employed as multiple tree explanations, each tree yielding alternate explanations of homoplastic data. The network-derived trees can then be ordered based on optimal-ity (see later discussion), offering quantitative levels of explanatory power. Such a ranking of explanations allows the assessment of the rela-tive importance of alternate historical scenarios. For many aspects of human behavior, networks have demonstrated explanatory value (e.g., Borgerhoff-Mulder et al. 2006; Hage and Harary 1998; Hamberger et al. 2009; White and Johansen 2005).

Hypothesis Testing, Optimality Criteria, and Models

A tree (or network) is a hypothesis of the phylogenetic relationships of a set of taxa. This includes not only the groups described by the tree (subtrees or "clades"), but the transformations required by the tree as well. Each tree implies an optimal set of transformations (which need not be unique), allowing the calculation of a numerical value that lets the hypotheses be compared. The search for the best or optimal hy-pothesis consists of evaluating candidate trees in pairwise fashion, in each case retaining the tree with better optimality value. As long as the optimality value is transitive (if a > b and b > c, then a > c), such a search guarantees the optimal result (or results, if multiple equally op-timal trees are identified). In practice, there are usually such a large number of trees that only a heuristic subset is actually considered.

Of the diversity of possible optimality criteria, three are in common empirical use. They are the simplicity-based parsimony and the statisti-cal approaches of likelihood and posterior probability (Bayesian). These methods differ in whether they employ stochastic models of change and how they incorporate such models (Farris 1982; Felsenstein 1973; Ran-nala and Yang 1996). All these methods are optimality based; they sim-ply differ in the entity being optimized.

Regarding sociocultural data, parsimony has been used by Rexová et al. (2003) for Indo-European languages and by Tehrani and Collard (2009) in their study of Iranian weaving practices.[6] Bayesian statistical

approaches have used both likelihood (e.g., Fortunato et al. 2006; Holden and Mace 2005) and posterior probability (e.g., Fortunato et al. 2006; Fortunato and Mace 2009; Holden et al. 2005; Pagel 2009; Pagel and Meade 2005). Yet problems result from models of biological processes lacking clear analogues for human sociocultural data. For example, Fortunato et al. (2006) employ the HKY model (Hasegawa et al. 1985) to construct their likelihood tree based on human speech variation. The HKY model is based on specific molecular structural and empirical properties of nucleic acid sequence data (transitions, transversions, and stationary frequency of nucleotide types). These aspects are without obvious correspondence in sociocultural practices.

In posterior probability approaches, specific problems occur owing to the need for priors that affect the calculations. There are two flavors of Bayesian analysis in current use that are quite different in approach. In the first, the hypothesis that maximizes the product of its prior probability and its integrated likelihood is referred to as the maximum a posteriori tree or MAP (Rannala and Yang 1996), which is the optimal tree based on posterior probability. In the second, a tree is constructed from subtrees with greater than 50 percent posterior probability (Larget and Simon 1999; called "clade-posteriors" by Wheeler and Pickett 2008), irrespective of the trees within which they are nested. This is returned as the Bayesian tree. There are many problems with this second approach, foremost that this sort of tree does not attempt to optimize anything in particular, and hence cannot participate in hypothesis testing as defined here. Furthermore, this flavor of tree may conflict with the MAP tree (Wheeler and Pickett 2008). For clade-posterior analyses, see, for example, Fortunato et al. (2006), Fortunato and Mace (2009), Pagel and Meade (2005), and Pagel et al. (2007).

No-Common-Mechanism and the Unity of Methods

Each of the three phylogenetic methods discussed here has strengths and weaknesses, mainly centering around the lack, or specific assumptions of, a stochastic model of character change. Much blood has been spilled on this battlefield. There are, however, analytical circumstances in which these three methods converge, or at least intersect. In these situations, parsimony and likelihood estimators converge, and MAP

results can, too, with appropriate priors. The situation of greatest interest here concerns the stochastic model. Usually, a single time parameter is applied to all characters through the stochastic model. This time parameter (μt) is the product of the time between tree splitting events, t, and the rate of change, μ. In essence, all characters share the same overall rate (even if modified by gamma classes). This may or may not be appropriate for nucleic acid sequences (there is even argument there), but it seems inappropriately restrictive for sociocultural features. Is it reasonable to assume that aspects of language, textiles, ceramics, and marriage practices evolve at the same rate?

A generalization of the Neyman (1971) r-state model (r signifying the number of states for each character) that relaxes this condition, allowing each feature to have a unique time parameter over each edge of a tree, has been described by Tuffley and Steel (1997) and Steel and Penny (2005). This no-common-mechanism (NCM) model allows each feature to change such that the overall tree likelihood (lik_T) is maximized with all state-to-state transformations equally likely. This likelihood occurs precisely on the most parsimonious tree when each feature is weighted by the negative logarithm of its states (r_i states and l_i parsimony changes in character i on tree T):

$$lik_T = \prod_i^{characters} r_i^{-(l_i+1)}$$

Not only are the best likelihood and parsimony trees identical, but the ordering of each tree from best to worst is preserved. If the priors are set to be suitably uninformative, the MAP solution will be this same tree. NCM offers a robust, agnostic transformation model, with unique time parameter flexibility. For these reasons and the confluence of methods, NCM appears to be uniquely well suited to sociocultural phylogenetics.

Example Analyses

Kinship Systems

Sixteen kinship systems were chosen as an initial data set (data were drawn from literature sources): eight Crow (Hopi, Hano, Zuni, Cherokee, Tlingit, Sirionó, Trukese, and Senufo Fodonon), three Omaha

(Fox, Menominee, and Omaha), two Iroquois (Seneca and North-Central Ojibwa), one Dravidian (Northern Ojibwa), one Hawaiian (Southern Paiute), and one Eskimo (Taos). Eighty-five features of each culture were scored, including aspects of kin nomenclature, social organization, marriage patterns, linguistic features, demography, economy, and polity (see http://anthro.amnh.org/CrowOmaha6). Sample societies were chosen with various associations in mind: (1) to represent contrasting culture areas (Southwest Pueblos, Southeast, Northwest Coast); (2), culture types in regional clades with contrasting languages (Pueblos, with Crow systems, but three unrelated languages); (3) culture types within regions with contrasting kinship systems (Pueblos with Crow versus Eskimo type); (4) language groups (Uto-Aztekan among proximate Crow and non-Crow systems on the Southwest–Great Basin divide; Central Algonquian societies reflecting adjacent Dravidian, Iroquois, and Omaha systems); (5) some deliberate Crow outliers from outside North America (Trukese, Sirionó, and Senufo Fodonon).

Most coded variables were binary, marked as either present or absent. Features include diagnostic kin term equations, descent emphasis, type of kin groups, other associative groups, marriage rules, residence; language relationships, ritual emphases; population size and density, settlement pattern, community distribution, house form, economic type, domesticated species dependencies, and production emphases; and polity, including general levels of sociocultural integration. As well as features identified by prior analysts of Crow-Omaha systems, these features were inductively developed from a partial rereading of the ethnographic record. Some variables were drawn from the *Ethnographic Atlas* (Murdock 1967, 1970; see also Gray 1999), and were informed by some in the Standard Cross-Cultural Sample (Murdock and White 1970; Standard Cross Cultural Sample 2006; Fischer, n.d.). Specific variables chosen and grouped mostly reflect our own designations.

Figure 6.4 is derived from an analysis using POY4 (Varón et al. 2008, 2010) adapted to sociocultural data. It includes both tree and network hypotheses. The underlying tree (straight, solid black lines) represents a strict majority consensus tree (unrooted) for the sixteen kinship systems. This depicts an analysis (100 Wagner builds + TBR branch-swapping) resulting in 8 equally optimal (parsimonious) trees at length 244; strict consensus (total agreement among all 8) is shown
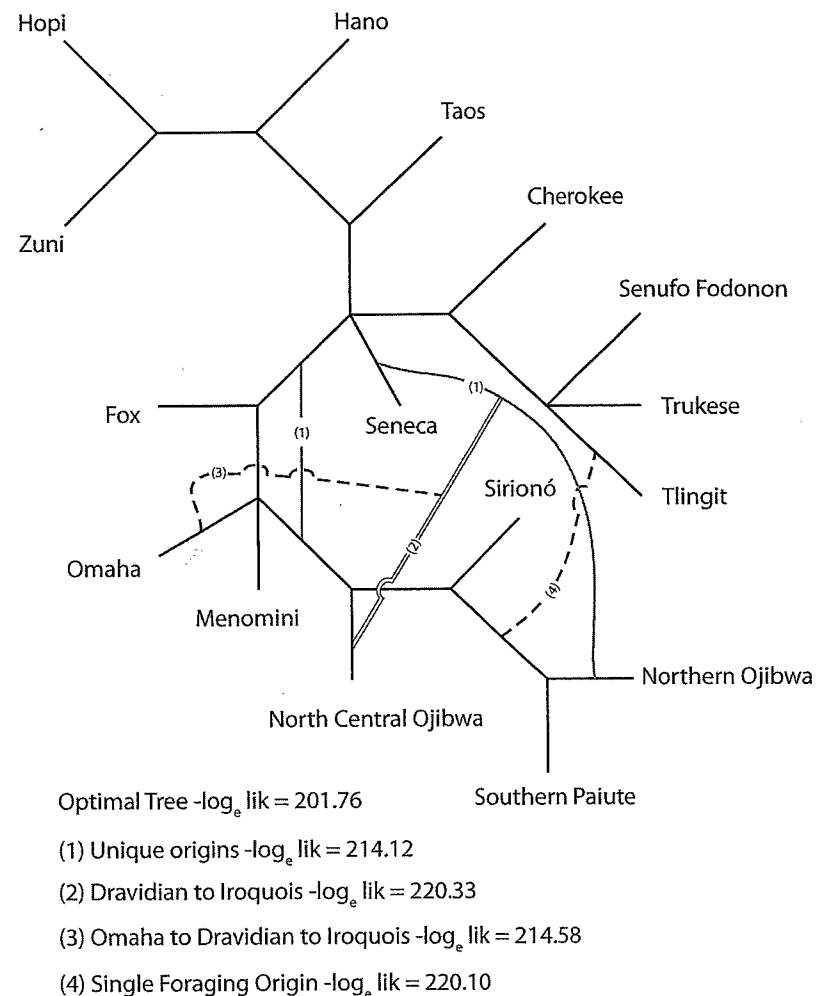
Optimal Tree -log$_e$ lik = 201.76

(1) Unique origins -log$_e$ lik = 214.12

(2) Dravidian to Iroquois -log$_e$ lik = 220.33

(3) Omaha to Dravidian to Iroquois -log$_e$ lik = 214.58

(4) Single Foraging Origin -log$_e$ lik = 220.10

Figure 6.4 Tree/network for sixteen social systems (thirteen North American, three outliers). Most likely scenario of cultural relationships (straight, solid black lines) at log –lik 201.76. Alternate modes of transfer based on hypotheses in text: (1) log –lik 214.12; (2) log –lik 220.33; (3) log –lik 214.58; (4) log –lik 220.10.

unrooted. A ten-minute timed search resulted in the same consensus after 1,549 hits at the shortest length.

Propinquities are suggestive of correlations: for example, among Puebloan Crow systems (Hopi, Hano, Zuni) and among Omaha systems (Fox, Omaha, and Menominee)—in both cases, transecting linguistic boundaries. The leaf cluster of Sirionó (Crow), Southern Paiute (Hawaiian), and Northern Ojibwa (Dravidian) reflects similar economic adaptations (foraging) and low population densities. The Senufo Fodonon-Cherokee-Tlingit-Trukese (all Crow) proximity suggests the influence of social complexity (i.e., all are chiefdoms). The leaf clusters thus promote the identification and testing of hypotheses concerning linguistic, cultural, demographic, and other correlations.

If we examine alternate scenarios, four hypotheses (depicted on figure 6.4 with dashed, gray, or parallel reticular lines, respectively) merit immediate examination: (1) all kinship systems have a unique origin; (2) Iroquois systems are uniquely derived from Dravidian; (3) Iroquois are derived from Omaha and then from Dravidian; and (4) the kinship systems of foraging-based societies (here Tlingit, Northern Ojibwa, and Southern Paiute) share a single origin. We can (using NCM) assign likelihoods to these hypotheses and their overall contribution to an ensemble network hypothesis. The best hypothesis (straight, solid black lines of figure 6.4) contains over 99 percent of the overall likelihood.

Analysis of Characters from the *Ethnographic Atlas*

The revised *Ethnographic Atlas* (Gray 1999) represents cumulative additions to the comparative societal database begun by G. P. Murdock in the 1930s and published in abbreviated form in the 1960s (Murdock 1967). It has been the target of both blame and praise ever since its publication (e.g., Callan 2008), and some of its variables remain in question, but it remains the most comprehensive coded database of human social systems available. While acknowledging its shortcomings, we believe the data are adequate to disclose broad patterns of the type shown in the present demonstration (for the features and their codings see http://anthro.amnh.org/CrowOmaha6).

In treating cultures as taxa and their behavioral aspects as characters, we have limited ourselves to those aspects of societies that are intrinsic. By this, we mean features of the cultures themselves as opposed to their

environments. Environmental mean rainfall or temperature are external to cultures, and hence are not included as phylogenetic data. Responses to such conditions, through technology or custom, would be included because they are determined by the cultures themselves.

Our two subsets of data, "Algonquian systems" and "Eastern North American systems," are both selected from the revised *Ethnographic Atlas* (EA). Ninety sociocultural features from the EA total (115: see Gray 1999) were selected for analysis (EA variables 1–88, 90, and 94).[7] Extrinsic features (climate, environment, region) were excluded, as well as inconsistent column entries, and those based on EA name and date identifiers. Given that the analysis includes high ratios of cultures (30, 55) to variant features (90), complete resolution of resultant trees is not expected.

Analytical Methods

For all analyses, the program POY version 4.1.2 was used (Varón et al. 2008, 2010). In all cases, the searches were accomplished by six parallel executions of the "search (max time:0:2:0)" command for two hours, three times for a net processor time of thirty-six hours on an eight-core Mac Pro (3.2 Ghz). This procedure employs a mixture of random addition sequences + TBR, tree fusing, and ratcheting. The set of optimal trees was selected, and strict consensus cladograms were produced.

In the parsimony analyses, all characters were treated as unordered and equally weighted. The likelihood searches were performed with a Jukes-Cantor model (Jukes and Cantor 1969) under NCM (Steel and Penny 2005; Tuffley and Steel 1997). Characters were weighted as the natural logarithm of the number of states.

Algonquian Systems

This subset comprises all those representatives (thirty) in the *Ethnographic Atlas* of the Algonquian language family encompassing environments from the Plains, Woodlands, and Subarctic and showing variant kinship terminologies. The goal here is to compare social system distributions within a single ethnolinguistic clade. The resultant trees (figures 6.5, 6.6) rooted (arbitrarily) on Naskapi suggest clusters correlative to variant aspects of economy, polity, kinship, and social organization.
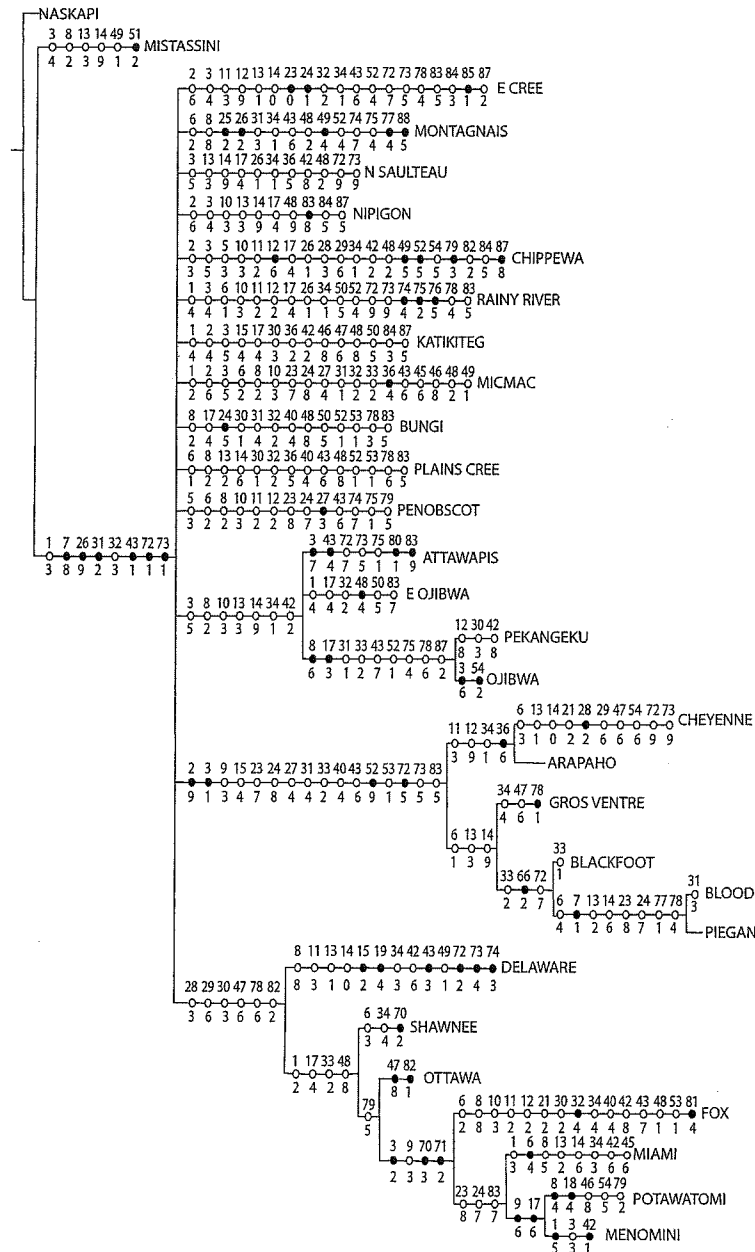
Figure 6.5 Tree for social systems of the Algonquian language family (Parsimony). Analysis of thirty lineages and ninety characters under parsimony. Five equally parsimonious trees were found at length 362. This strict consensus is arbitrarily rooted on Naskapi. This cladogram and those in Figures 6.6–6.8 are visualized with CLADOS (Nixon 1993).
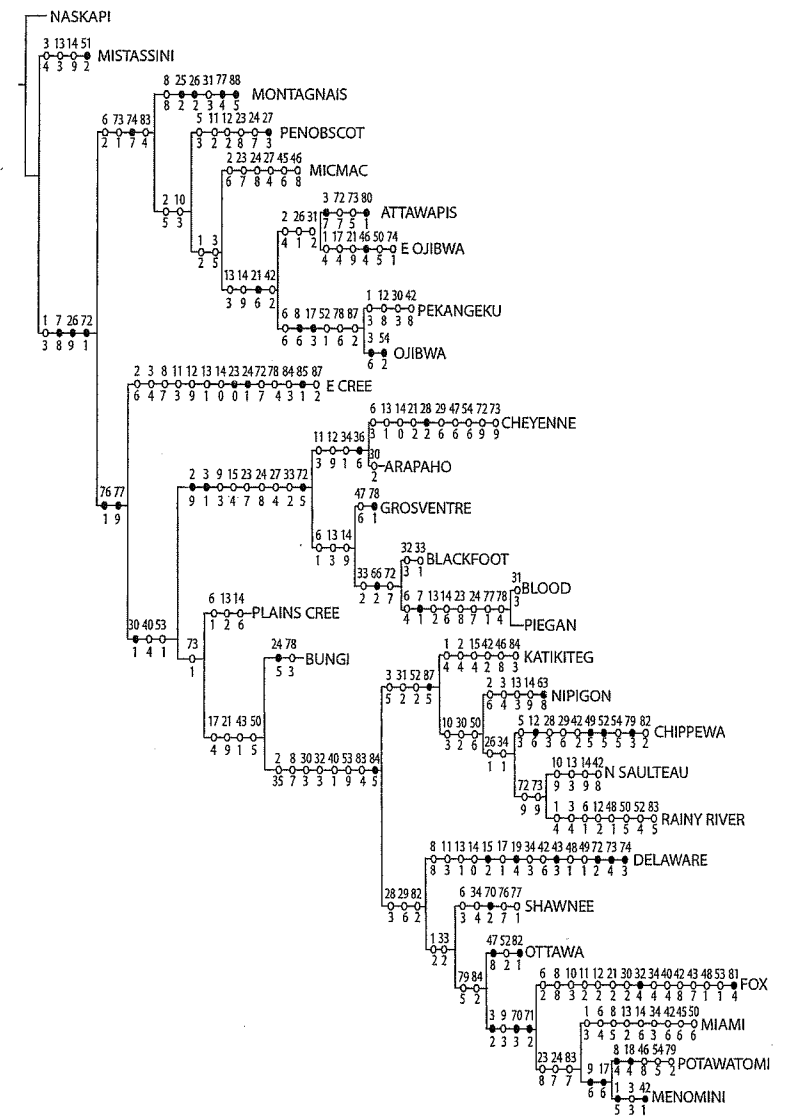
Figure 6.6 Tree for social systems of the Algonquian language family (No-Common-Mechanism). Analysis of thirty lineages and ninety characters under likelihood –NCM. A single tree was found at cost –log lik 772.127. Tree is arbitrarily rooted on Naskapi.

Figures 6.5 and 6.6 offer a condensed description of features producing branching patterns under parsimony and NCM, respectively. EA character numbers are shown above the edges and character states (the EA coded entry for a particular society) below. Only unambiguous character changes are shown—thus, optimizations on polytomous clades represent the most conservative set of changes for each clade. Each character-state pair embraces an open or solid circle, representing changes that occur in more than one place on the tree (open) or only once (solid). In figure 6.5 there is no weighting of changes, with the assumption (implausible) that all changes occur at a similar rate (e.g., hunting dependency [v. 2], postmarital residence [v. 10–14], and games [v. 35]). In contrast, NCM allows differential weighting for changes, resulting in a more resolved tree. Note, for example, in figure 6.6, the Montagnais-Ojibwa clade, whose primary node forms partly on patrilineal inheritance of land (v. 74, state 7). The comparable grouping in figure 6.5 (Eastern Cree to Penobscot) is far less resolved. Where patterns are similar on both trees (e.g., the Cheyenne-Piegan clade), clades gain in robustness, resulting from different methodologies. In most instances, kinship and marriage characters (notably, v. 17–27, 43) are not obviously major causes of branching patterns, although, to take one example, v. 27 state 4 (Generational cousin-terms) is one among several branching causes for the Cheyenne–Piegan clade in both figures. However, branching and clusters, especially under NCM, are often highly indicative for societies with similar kinship structures, notably Crow and Omaha—suggesting these do indeed correlate with economic, political, and other sociocultural features that cause branching at specific nodes (see later discussion).

In figure 6.6, branches generally follow a north–south trajectory from top to bottom, with a westward Plains grouping in the center of the tree. Northern foraging "bands" branch into more sedentary, more complexly structured agricultural "tribes," with the western cluster representing an equestrian, nomadic, bison-hunting adaptation. The main branch of systems with Generational cousin terms correlates neatly with this High Plains adaptation—Cheyenne, Arapaho, Gros Ventre, Blackfoot, Blood, Piegan—thus corroborating the inference of Eggan (1937a) that Prairie societies moving onto the High Plains after acquiring horses adopted the more "flexible" social systems associated with Generational

terminologies. Only two other cases here have Generational cousin terms: Micmac and Delaware, both originally along the northeastern seaboard. Delaware's propinquity to Shawnee on the tree may well reflect historical change: in the eighteenth century (the "ethnographic present" for the EA Delaware entry) Delawares moved west to Ohio nearby the Shawnee. Penobscot, adjacent to Micmac, represents the only Algonquian case with Eskimo cousin-terms (v. 27, state 3), probably reflecting assimilation to colonial society (EA ethnographic present: 1900).

Societies with Omaha cousin-terms (v. 27, state 6)—Shawnee, Fox, Miami, Potawatomi, Menominee—all cluster tightly on the tree, corresponding with southernmost Algonquian presence in the Eastern Woodlands and greater agricultural adaptation. The only intervener here is Ottawa (Iroquois cousin-terms). EA ethnographic present for Ottawa is 1650, but this is retrojected: in the eighteenth century, Ottawa were proximate geographically to Potawatomi and Fox but had migrated earlier from the Ottawa River, their terminology thus perhaps reflecting closer proximity to a Sub-Arctic adaptation and geographical proximity to Huron and Iroquois.

All remaining societies have Iroquois cousin terms (v. 27, state 5; Mistassini and Eastern Cree are EA unknown [state 0] in this regard). Figure 6.6's subtrees, again more definitive, cluster in two clades: (1) Naskapi through Ojibwa, and (2) Plains Cree through Rainy River. Societies with both Iroquois cousin-terms and preferential symmetrical cross-cousin marriage (v. 25, state 1) are found *only* in the Sub-Arctic (identifiable within the EA's "Arctic America" class): Naskapi, Eastern Ojibwa, Attawapis, Chippewa, Rainy River, and Northern Saulteau. Following Trautmann and Barnes (1998), we hypothesize that all these in fact had kinship systems with Type A (Dravidian, rather than Iroquois) crossness. Moreover, even though Mistassini cousin-terms are marked unknown, preferential cross-cousin marriage (v. 25, state 1) together with geographical proximity to Iroquois systems with the same marriage type predict Type A terminology. Systems where cross-cousin marriage was permitted (v. 23, state 1) but not preferred (v. 25, state 15) cluster in two groups: (1) Ojibwa and Pekangeku, and (2) Plains Cree, Bungi, Katikiteg, and Nipigon, where again subtrees are better resolved under NCM. All live within the same area along the Sub-Arctic/Plains

border, and their closest Plains neighbors all have (Dakota-) Iroquois kin terminologies, with no cross-cousin marriage. This would corroborate the Trautmann-Barnes hypothesis: that is, that greater opening out of affinal ties from Sub-Arctic to Woodlands, north to south, progressively transforms cross-cousin marriage from prescription (where cross-cousin terms = same-generation affines)—or at least preference—to possibility, and finally to proscription (where cross-cousin ≠ affine).

Systems of Eastern North America

This subset represents all fifty-five EA representatives of the major language families from the Plains eastward throughout the Woodlands and eastern Sub-Arctic: thirty Algonquian (as before), five Muskhogean (Choctaw, Creek, Seminole, Timucua, Natchez), twelve Siouan (Crow, Hidatsa, Mandan, Winnebago, Omaha, Ponca, Oto, Iowa, Santee, Teton, Assiniboine, Catawba), five Caddoan (Caddo, Pawnee, Arikara, Wichita, Hasinai), and three Iroquoian (Cherokee, Huron, Iroquois).[8] Included are the classical Crow and Omaha cases first described by Morgan (1871) and all their linguistic relatives throughout these three (Murdockian) culture areas. The aim is to see what light may be shed on kin terminology distributions across major linguistic boundaries. Again, nonintrinsic variables—notably including the language group identifiers themselves (v. 98, 99)—were excluded.

The major pattern of Algonquian distribution (figures 6.7, 6.8) remains similar to figures 6.5 and 6.6, with a few shifts, and some interesting intrusions. Some of the latter are evident under both parsimony (figure 6.7) and NCM (figure 6.8), others are noticeably clearer under NCM. In figure 6.8, all cases with Omaha cousin-terms (Winnebago through Iowa) group in a tight subtree (transecting the Algonquian-Siouan language boundary and the Plain-Woodlands culture area boundary), with only Ottawa (Type B terminology) intruding by the Winnebago edge. Moreover, with only Penobscot (oddly) intervening, Plains Omaha systems group adjacent to Plains Crow societies (Arikara through Pawnee), which all group tightly, except for the Crow proper. Moreover, the Plains Crow clade branches proximately into Southeastern Crow systems. Except for Delaware (the non-Crow Algonquian intruder), figure 6.8 shows a more discrete clade of Southeastern Crow societies (with Cherokee and Choctaw edges) than figure 6.7, where

Huron and Iroquois (Iroquoian speakers with Type B terminology) intrude into the subtree edged by Timucua and Creek. Moreover, in figure 6.7, Natchez, Hasinai, and Caddo—all geographically near the Southeast-Plains boundary—appear remote from this Southeastern Crow cluster, with no ostensible reason to look for associations. In figure 6.8, however, both their independent subtree clustering and their propinquity to the Southeast Crow subtree are striking. None of the three is EA Crow (v. 27, state 1), yet the broader ethnographic record indicates that Caddo (and implicitly Hasinai, a subgroup) formerly had Crow terms (Rogers and Sabo 2004:625). Although Natchez cousin-terms are unknown, Urban (1994:179), who does not infer Crow terms, suggests Natchez and Muskhogean proper (Choctaw et al.) social structures are "transformations of one another."

Crow proper is the stark outlier among Crow systems, intruding among Plains Algonquians—Gros Ventre, Blackfoot, Cheyenne, Arapaho, Blood, and Piegan—all with Generational (Cheyenne) terminology, but all are immediate geographic neighbors to the Crow. Eggan (1937a) suggested the Crow—recent arrivals on the High Plains from the Missouri River in the early nineteenth century, and the only High Plains society recorded with Crow kin terminology—were in a process of transition toward Generational terminology at the time of American annexation. The hypothesis represented by the subtree (Gros Ventre through Piegan) would favor Eggan's prediction, that is, if we assume Crow society's adaptive and reproductive conditions were most similar to its immediate neighbors on the tree.

In short, the tree propinquity under likelihood NCM of most Omaha and Crow systems (by Murdock's cousin-term classification, at least)—both to each other, and within each type—across major language families and culture area boundaries is quite striking. A hypothesis represented by this clustering should target similarities of social structural, economic, and political forms, including alliance mechanisms, among near neighbors of the Prairie Plains and Woodlands.

Discussion

As Popper (1959) enduringly demonstrated, a methodological procedure is valuable insofar as it operates to disclose meaningful patterns
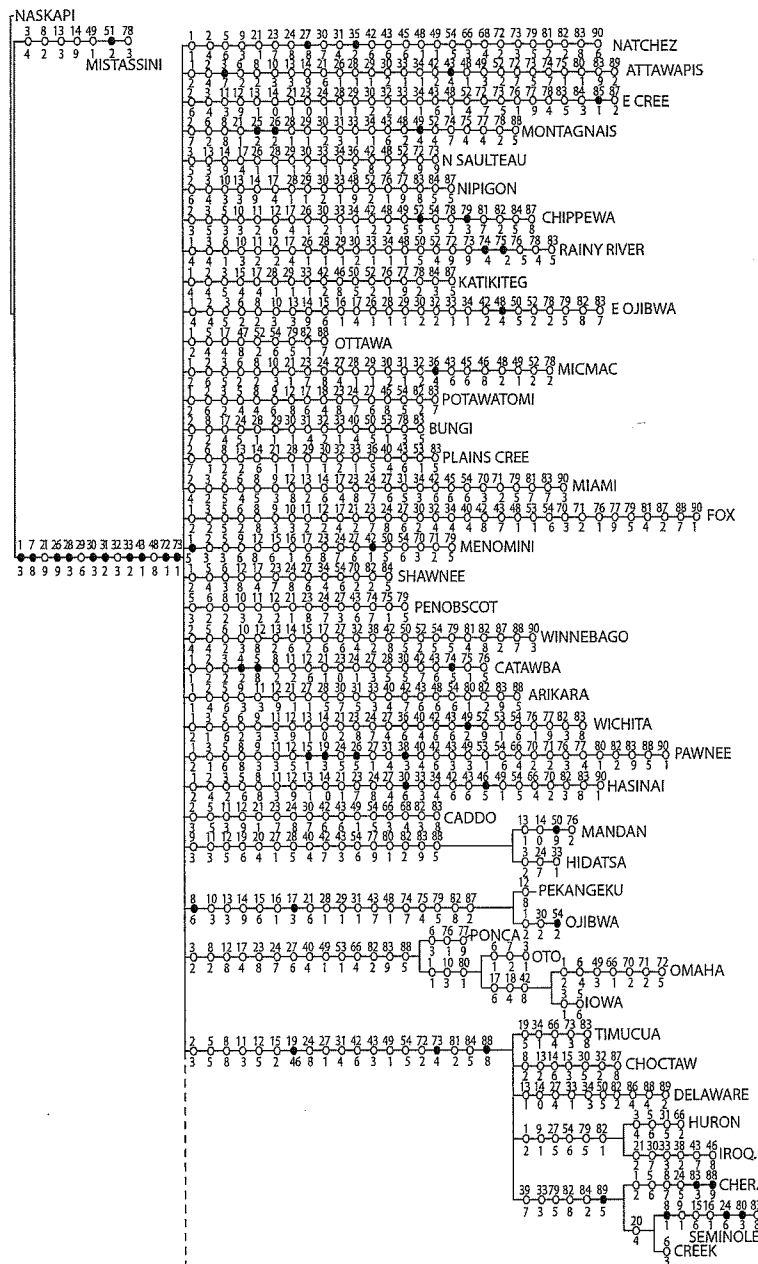
Figure 6.7 Continued

Figure 6.7 Tree for social systems of eastern North America (Parsimony). Analysis of fifty-five lineages and ninety characters under Parsimony. Seven equally parsimonious trees were found at length 667. Tree is arbitrarily rooted on Naskapi.

among empirical phenomena, patterns from which testable hypotheses may be generated to explain the phenomena with maximum parsimony and adequacy. Application of phylogenetic models to sociocultural data is in its infancy and has encountered some substantive obstacles (e.g., Borgerhoff-Mulder 2001). Overcoming these is no simple issue. We believe that existing approaches that depend on restricted applications of parsimony, likelihood, and posterior probability, do not provide effective solutions, primarily because they borrow biological models that are inadequate for the explanation of sociocultural phenomena. In contrast, NCM approaches, which permit testing of multiple scenarios, offer more promising possibilities. We hope to have shown here that tree analysis with POY4 can provide a powerful and salient method for discovering patterns in social system distributions that (1) are susceptible to the generation of meaningful testable hypotheses, and (2) speak directly to existing hypotheses about the emergence and spread of kinship systems. In particular, the clusters of Omaha systems in the Woodlands and Plains generated from the EA data seem ripe for testing against the McConvell and Alpher (2002) model of ethnolinguistic expansionism near language family boundaries and against the hypothesis that Crow-Omaha systems disperse marriage alliances (e.g., Héritier 1981; Lévi-Strauss 1966; McKinley 1971b; Trautmann and Barnes 1998), associated with broader extension of sociopolitical alliances. Alliance structures in Crow-Omaha systems are in turn evidently correlated with forms of economic adaptation and, although we have excluded these from direct analysis, with patterns of ecological and/or
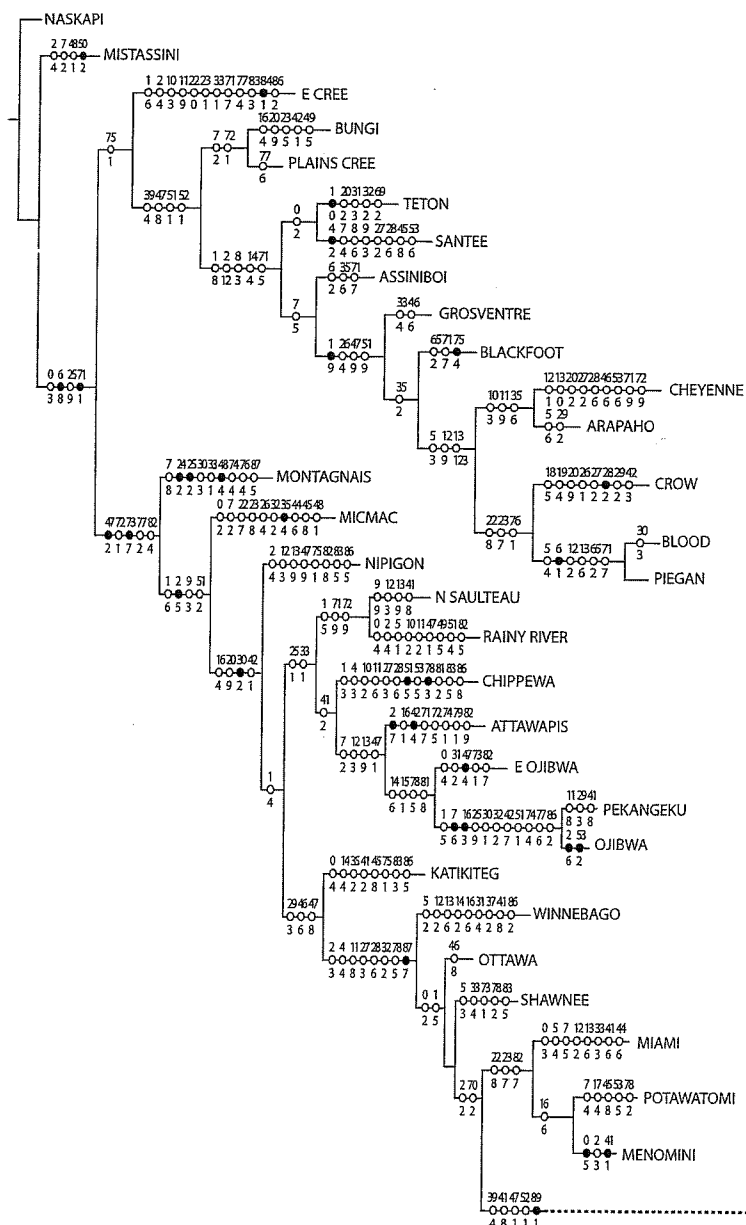
Figure 6.8 Tree for social systems of eastern North America (No-Common-Mechanism). Analysis of fifty-five lineages and ninety characters under likelihood –NCM. A single tree was found at cost –log lik 1268.686. Tree is arbitrarily rooted on Naskapi.
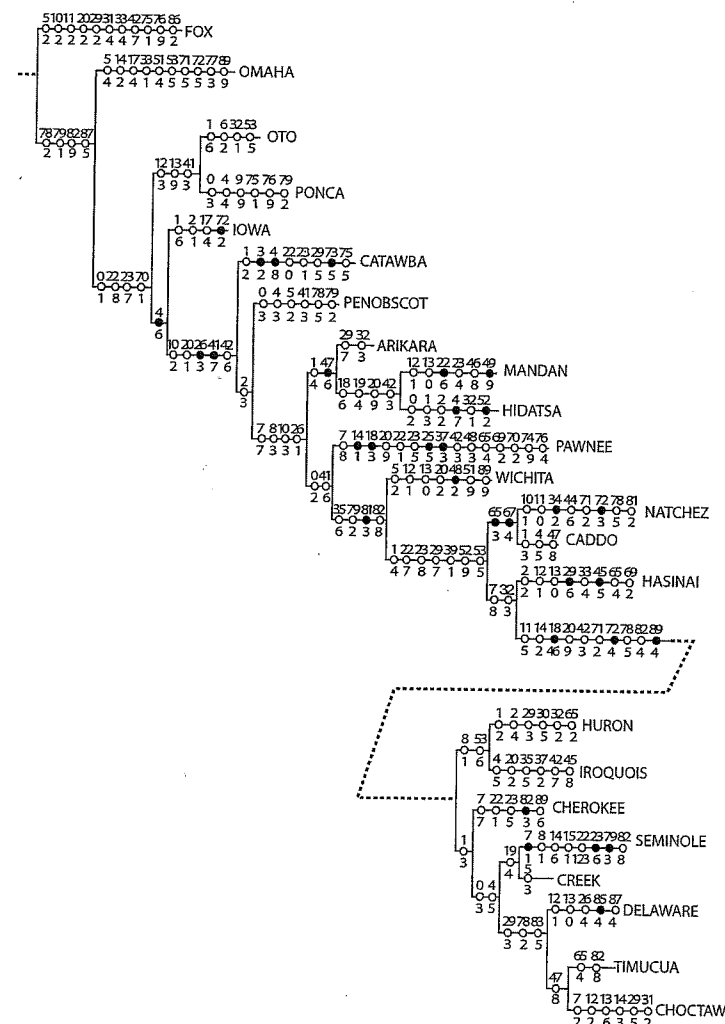
Figure 6.8 Continued

sociodemographic circumscription (after Carneiro 1970). Exceptions clearly require explanation, but hypotheses focusing on particular forms of historical influence (e.g., for Crow, Delaware, Micmac), of the type most prominently associated in North American ethnology with Eggan (1937a, 1937b, 1950), should be investigated.