

Are Cultural Phylogenies Possible?

Robert Boyd

Monique Bogerhoff-Mulder

William H. Durham

and

Peter J. Richerson

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Introduction

Biology and the social sciences share an interest in phylogeny. Biologists know that living species are descended from past species, and use the pattern of similarities among living species to reconstruct the history of phylogenetic branching. Social scientists know that the beliefs, values, practices, and artifacts that characterize contemporary societies are descended from past societies, and some social science disciplines, linguistics and cross cultural anthropology for example, have made use of observed similarities to reconstruct cultural histories. Darwin appreciated that his theory of descent with modification had many similarities of pattern and process to the already well developed field of historical linguistics. In many other areas of social science, however, phylogenetic reconstruction has not played a central role.

Phylogenetic reconstruction plays three important roles in biology. First, it provides the basis for the classification. Entities descended from a common ancestor will share novel, or derived characters inherited from that ancestor, and therefore, it is possible to group them into hierarchically organized series of groups---species, genus, family, order, and so on in the biological case.

Second, knowledge of phylogeny often allows inferences about history. The knowledge that humans are more closely related to chimpanzees and gorillas than to orangutans provides evidence that the human lineage arose in Africa. Phylogenetic reconstructions based on the characters of extant species or cultures often allow us to reconstruct the history in the absence of a historical, archaeological, or fossil record. In practice, the history of many biological and cultural groups is so poorly known that only by combining phylogenetic and historical or archaeological information can be reliable reconstructions be obtained.

Finally, entities descended from a common ancestor will share features that may constrain the pathways that more recent evolution has followed. For example, selection for terrestrial locomotion may lead to quadrupedal locomotion in a small monkey that runs along the tops of branches, but lead to bipedal locomotion in a large arboreal ape that swings below branches (Foley, 1987). The latter pattern allows the hand to specialize on manipulative tasks, and on many accounts is why the ape but not the monkey lineage eventually was able to produce a cultural species.

The importance of descent is the crux of some of the deepest controversies of all historical sciences. Some social scientists and biologists (e.g. Hallpike, 1986, Sahlins, 1976, Boyd and Richerson, 1992) argue that history strongly constrains adaptation, and as a result to strictly limit adaptive interpretations of current behavior. As Francis Galton taught both biologists and social scientist in the 19th Century, the study of adaptation or function requires that patterns of descent be known in order to control for the effects of common ancestry. Our inability to always provide appropriate roles for history and

function is a chronic source of controversy (Shennan discusses the example of Archaeology in this volume).

If the analogy is real, an interdisciplinary exchange of concepts and tools could pay great dividends. In particular, social scientists may be particularly interested in the near-revolutionary developments in systematics (Ridley, 1986) and comparative methods (Harvey and Pagel, 1991) developed by evolutionary biologists in the last two decades.

The purpose of this chapter is to examine the role of descent in culture evolution theory. We believe that the critical question is whether human cultures, or parts of them, are isolated from one another to the same degree as biological entities like species and genes. Cultures are frequently characterized by sharp in-group-outgroup boundaries (Levine and Campbell, 1972) that may function to limit the flow of ideas from one population to another (Boyd and Richerson, 1987). However there are also many examples of the diffusion of cultural traits across such boundaries (Rogers, 1983). Are the isolating processes sufficiently strong to provide at least a core of important cultural traits that are sufficiently protected from diffusion that phylogenetic analysis is possible? If so, concepts and methods from biological systematics can be used to reconstruct the history of cultures. If not, human cultures are more like subspecies or local populations linked by gene flow than like reproductively isolated species. In this case, it may be useful to make separate phylogenies for each subunit of culture that is substantially protected from diffusion, in much the way that modern molecular procedures are used to reconstruct the phylogeny of subgenomic units, especially individual genes. It may also be that there are no cultural units with sufficient coherence, and therefore, that phylogenetic methods are useless.

We begin by reviewing the notions of descent used in evolutionary biology. Biologists have been making use of the concept of descent ever since Darwin, and they have developed a sophisticated appreciation for the concept and its problems that may be helpful in the human case. The complexity and diversity of biological systems of inheritance is wondrous to those of us brought up on the simple mendelism of 20 years ago (Jablonka, chapter _). While it is likely that the process of cultural descent with modification is very different from the analogous process in organic evolution, we believe that much can be learned from biologists' century of hard work. We then consider data from the social sciences which indicate the extent to which cultures form bounded wholes, analogous to species. Finally, we consider how the descent concepts, partly borrowed from biology, might be used to tackle important questions in the social sciences.

II. Descent in Organic Evolution

In biology two different entities exhibit the clear patterns of descent with modification. The most familiar example is the species. The collection of individuals who make up a species during any generation are descended, perhaps slightly modified, from the

collection of individuals who made up the species during the previous generation. When a new species is formed, it is by the splitting of an existing population. Then each of the daughter species is descended from the single ancestral species that gave rise to them.

Much the same holds for genes one by one. Since genes result from the copying of DNA, every gene is descended from the gene which provided its template. Modified genes arise from existing genes by mutation, recombination, and gene conversion at a given locus. A genetic locus can give rise to another locus by duplicating itself on the chromosome after which the daughter locus begins independent evolution. The relationships among genes is not simply the relationships among the species that carry them (although this is often the case). We can keep track of the relationship of genes *within* a single species, for example various forms of hemoglobin within human populations. It is also possible to speak of relationships among genes that are inconsistent with relationships among species. For example, genes for globin molecules in vertebrates and certain plants seem to share a more recent common ancestor than the genes in vertebrates and arthropods, as surprising as this seems at first blush (Jeffereys et al, 1983).

Descent relationships are often represented using branching diagrams like that shown in figure (1). The diagram conveys the idea that both *B* and *C* are descended from an ancestor *A*. (Systematists use similar branching diagrams called cladograms to represent patterns of similarity without reference to time, or ancestor-descendant relationships, statistical clustering algorithms tree-like dendograms without any pretense to representing ancestor-descendent relationships. Tree diagrams are used here to represent phylogeny.) The same diagram is used to represent the relationship between very different kinds of things. For biologists *A*, *B*, and *C* may represent species or genes. Social scientists use similar diagrams to express the relationship among languages, or other aspects of culture, often with the explicit intention of representing a phylogeny. What, if anything, does the descent of genes and species, have in common? Can these commonalities provide some help in analyzing the descent of cultures, languages, and technologies.

A. The descent of genes

To try to answer this question, let us begin with the simpler case, the descent relationship among genes. If we ignore for a moment the possibility of recombination, every gene is a copy of another gene. And, of course, that gene was the copy of yet another gene and so on. Thus, if we pick any two genes, *B* and *C*, we can, in principle, trace back through a series of copies until we find a gene, *A*, that served as a template for both. We say that genes *B* and *C* are descended from *A*. If mutations have occurred, *B* or *C* may be different from *A* and each other. As long as mutations are rare and the gene includes enough bases, then genes that share more derived mutations are more likely to be related. Taxonomists use this fact to reconstruct the branching pattern among genes sampled from living species. Notice that there is nothing in the discussion which specifies that *A*, *B*, and *C* have to belong to the same (or different species). The same argument would hold whether

B and *C* are genes found within a single species, or among distantly related species, say humans and bean plants.

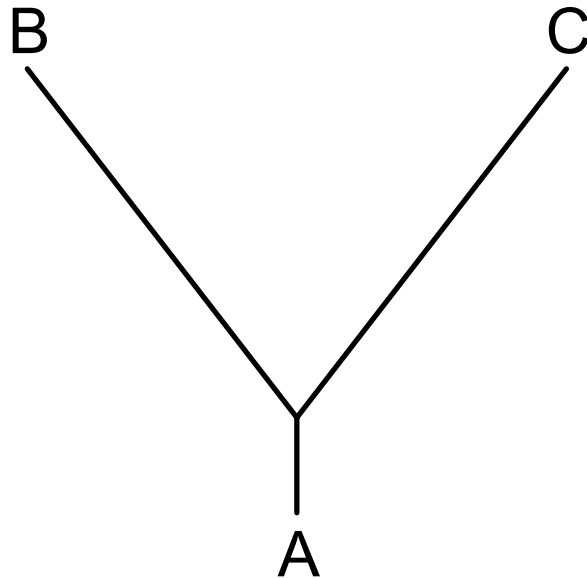


Figure 1: A hypothetical phylogeny in which species *B* and *C* are descended from species *A*.

B. Units with reticulated phylogenies

Recombination, the shuffling chromosomes of the genes along a chromosome and the sequence within a gene, complicates matters because it leads to what cladists call reticulated phylogenies. Figure (2) shows the lineages of three genes. Recombination has occurred within the gene three times. After each recombination event, each of the daughter genes is a copy of part of each of the two parents. The daughter genes are no longer descended from the parental genes in the same way that they were in the absence of recombination. They are no longer almost exact copies of the parents, rather they are partial copies of both parents. Further recombination events create yet more complicated patterns of relationship. After some time, every copy of the gene will be related to a large number of other genes in some complicated way than utterly obscures descent. Recombination within a gene is rare, but recombination within chromosomes between different genes is quite common. Deep phylogenies can be reconstructed for genes, but only very shallow ones for chromosomes.

Gene flow (migration) between sub-populations of a species has a similar effect. Any given local group will have acquired genes from many different local groups in the past. Even if most subpopulations are created by the subdivision of a single parental population, a relatively small rate of individual level migration between subpopulations will carry genes evolved in one daughter subpopulation to its sisters, and fairly shortly descent at the subpopulation level will be impossible to detect. Thus, there is a large range of genetic units ranging in size from roughly small chromosome segments to the subspecies for which phylogenetic analysis is usually impossible.

Some large gene collections, such as mitochondrial genomes, are protected from recombination because they are transmitted asexually. Mitochondrial phylogenies of some depth can be constructed, although they illustrate another process that eliminates phylogenetic information in the long run. Mitochondria are subject to high mutation rates. In a matter of a few million years, most descendant pair of mitochondrial genes will have independently mutated more than once, and the traces of descent will be lost. Very conservative genes like the cytochromes have very slow rates of evolution and can be used to reconstruct phylogenetic relationships reaching back to near the origin of life, but these are exceptional. More typically, deep phylogenetic reconstructions based on less faithful structures are quite controversial even when we can be almost certain that recombination and migration have not confused the picture.

C. The descent of species

Species and higher taxa are the classic focus of phylogenetic analysis in biology. Linnean systematists formalized the common observation that the organic world comes in readily observable clusters. Species and higher taxa seem to be separated by distinctive gaps that do not occur within species or among many other natural objects. Darwin's theory of descent with modification gave a theoretical underpinning to the trees of relationships that Linnaeus had enshrined in hierarchical classification system, though Darwin himself had little to say about the species isolating mechanisms that enforce the gaps between species. His followers have made up this deficiency; the issue of speciation is a major topic in modern evolutionary biology.

In the basic picture constructed by the architects of the mid-century neo-Darwinian Synthesis like Ernst Mayr, species are created when a barrier to gene flow evolves to isolate two sets of populations. Once isolated, the evolution of the two new species is independent, and slowly changes accumulate due to natural selection, genetic drift, mutation, and so forth. There may be some evolutionary differentiation within a population due to selection or drift, but interbreeding among populations unites a species, while absolute speciating barriers definitively separate them from other species. Over the long run species become different enough to be classified as new genera, families, orders and on up Linnaeus' hierarchy. In the classic picture, complete isolation and the slow accumulation of differences allow the reconstruction of relationships of descent by splitting over very great time depths.

The basic picture provides a clear causal explanation for the temporal and spatial coherence of species. Advocates of the *biological species concept* hold that only when this picture applies do we have species properly speaking. However, there are several lines of evidence which suggest that the absence of gene flow is neither necessary nor sufficient for the existence of coherent species in the sense of lumpy entities that show clear evidence of descent. Species can maintain their coherence without gene flow within the species, and species boundaries may be maintained despite gene flow between species.

Some species have maintained species typical phenotypes, including the ability to form fertile hybrids despite long periods without any gene flow. For example, sycamores in Europe and North America have diverged little despite the fact that these two populations have been genetically isolated from one another for at least 30 million years (Stebbins, 1950). There are also many examples (Levinton, 1987) of cryptic "sibling" species that are long isolated, but have evolved no detectable morphological differences. Some taxonomists claim that it is no more difficult to detect species in asexual organisms than it is in sexual organisms (e.g. Mishler and Brandon 1987), despite the fact that there is no gene flow to unite such populations.

Some species persist in spite of substantial gene flow (Barton and Hewitt, 1989). A hybrid zone can exist between what seem to be good species, and often a few genes have clearly leaked across the boundary from one species to another. It would seem as if such species must either be formerly geographically isolated subspecies that will hybridize away or incipient species that will eventually evolve an isolating barrier but in fact active hybrid zones between rather distinctive species sometimes persist for very long periods of time. Selection can apparently maintain the coherence of species both without any help from gene flow and in the face of substantial amounts of it.

Things are not always so neat. In bacteria, genes are frequently transmitted horizontally among lineages (Eberhardt, 1991, provides an excellent review). Bacterial DNA exists in two distinct forms: Most of the DNA is contained in a large chromosome, but about one percent is contained in small loops of DNA called plasmids. The two forms of DNA are transmitted differently. For the most part, the chromosomal DNA is transmitted vertically. When bacteria divide, the chromosomal DNA is duplicated and each daughter cell contains a copy. In contrast, plasmid DNA is transmitted horizontally from one bacteria to another during conjugation. Moreover, bacteria that are classified as belonging to different genera or families according to their chromosomal DNA, readily conjugate and exchange plasmid DNA. As a result, genes carried on plasmids may jump from one lineage to another quite distant one. It is not certain that two types of DNA are completely separate; sometimes plasmid DNA may be incorporated into the chromosome, although if this occurs it is probably very rare (Eberhardt, 1991). In the case of bacteria, there are really two sets of phylogenies, one for the chromosomal DNA

and one for the mitochondrial. Relationships between these phylogenies break down rapidly because of the horizontal transmission of plasmids across chromosomal lineages.

The opposite situation occurs with the lineages of hosts and parasites and predators in many animals and plants. For example, ectoparasites like lice and fleas are often isolated with their hosts, so that host and parasite phylogenies are very similar despite there being no transfer between host and parasite genomes.

III. The common properties of genes and species

Genes and species are units at quite different levels of organization. For them, but not units between them on the scale of organization, deep phylogenies can usually be constructed. The reason is a pair of similarities. First, both units are replicated with great fidelity, and evolve slowly due to ongoing evolution. Second, when daughter genes and species change these changes are not very effectively shared with sister lineages by mixing or any other form of communication. For systems with high rates of change, even mitochondrial genomes, deeper descent is obscured because recently evolved differences completely obliterate the ancient similarities that are necessary to detect descent. In the case of units like chromosomes and local populations with high rates of mixing, descent is generally untraceable because descent derived differences are erased as rapidly as they arise.

Note that having genealogy is not enough by itself to generate much descent. There is a hierarchy of genealogical entities in biology: genes, chromosomes, individuals, populations, species, and communities. These are genealogical entities because they are all descendants of other entities at the same level. In the face of rapid mixing or rapid evolution (or both) genealogy alone can't preserve detectable patterns of descent. At least not for long. Note that patterns of descent are a matter of time scale. If we are interested in relationships only over a few splittings of daughter entities, these may be detectable in the face of considerable mixing and high rates of evolution. If we want to know relationships traceable many splits ago, the criteria are more demanding.

IV. Reconstructing Cultural Phylogenies

Can we apply these ideas from biology to the analysis of human culture? As we saw in the previous two chapters, Darwinian models of cultural evolution hold that culture is information that is transmitted from individual to individual by imitation, teaching, and other forms of social learning. Various processes cause the pool of cultural variants that characterize a population to change through time.

This view of culture and cultural evolution implies the existence of a hierarchy of genealogical entities analogous to the genealogical hierarchy of organic evolution. We do not know what is the smallest unit of cultural inheritance, because we do not know, in detail, how culture is stored in brains (Chapter 9). Nevertheless, scholars proposed

histories of quite small elements: particular words, particular innovations, elements of folk stories, and components of ritual practice. Such small elements are linked together in larger culturally transmitted entities: systems of morphology, myth, technology, and religion. Such medium-scale units are collected together into "sub-cultures" and "cultures" that characterize human groups of different scales: kin group, village, ethnic group, nation, and so forth. Cultural subunits sometimes crosscut one another in complex ways, as when religion or occupation crosscuts ethnicity (much like bacterial chromosomes and plasmids).

A. Four hypotheses

Reconstructing cultural phylogenies will be possible to the extent that there are genealogical entities that have sufficient coherence relative to the amount of mixing and independent evolution among entities to create recognizable history. There is a continuum of possible views about what units in the hierarchy of cultural descent that satisfy these desiderata. It is useful to identify four regions along this continuum.

1. Cultures as species

Cultures are isolated from one another and/or are tightly integrated. They contain within them powerful sources of isolation (ethnocentric discrimination against strangers) or coherence (such as organizing systems of thought that act as biases against ideas one by one rather than strangers as whole individuals). Both mechanisms could cause cultures to act as single entities or "individuals" in the course of cultural evolution (see, e.g., Marks and Staski 1988). By one mechanism or another, there is little cross-cultural borrowing of any significance. New cultures are formed completely by the fissioning of populations and subsequent divergence. In this case, whole cultures are analogous to species or to mitochondrial genomes. Biological methods of systematics can be applied almost intact, and deep cultural phylogenies will be relatively easy to infer for at least the bulk of a people's culture.

2. Cultures with hierarchically integrated systems.

While cross-cultural borrowing may be frequent for many peripheral components, a conservative "core tradition" in each culture is rarely affected by diffusion from other groups. New core traditions mainly arise by the fissioning of populations and subsequent divergence of daughter cultures. Isolation and integration protect the core from the effects of diffusion, though peripheral elements are much more heavily subject to cross-cultural borrowing. In this case, core traditions are analogous to the bacterial chromosome and the peripheral components to plasmids. Biological methods of systematics can be modified to deal with cross-cultural borrowing. Reasonably deep core-cultural phylogenies can still be inferred, but this requires disentangling the effects of borrowing by distinguishing core and peripheral elements, and especially by methods to identify elements "introgressed" into the core.

3. Cultures as assemblages of many coherent units.

Cultures could be quite ephemeral assemblages of small units, but the small units may have limited mixing and slow evolution. Culture may have no "species" but it might have "genes," "plasmids," and "mitochondria." Different domains may have different patterns of inheritance, and different evolutionary histories. The components may be fairly large, plasmid or mitochondrion like, such as language, or small, solitary memes, such as the idea of using a magnetized needle to point north. Any given culture is an assemblage of many such units acquired from diverse sources. Methods of phylogeny can be applied independently to each domain. The essential problem is to determine the boundaries of the domains and establish that they are stable in time and space.

4. Cultures as collections of ephemeral entities

There are no observable units of culture which are sufficiently coherent for phylogeny reconstruction to be useful. Observable aspects of culture could be the result of units that are beneath the resolution of current methods to observe. The forms of Acheulean handaxes are so similar that they cannot be used to infer anything about descent among their makers. Perhaps there were really many traditional ways of reaching this apparently uniform end result, and if we knew the details we could reconstruct cultural phylogenies of hand ax making. Or there may be observable differences, but if they are the product of many recombining elements that cannot be observed, there is no information that would allow us to construct a phylogeny of the bits. Alternatively, if cultural evolution is sufficiently rapid, behavior may reflect such recent history that all phylogeny is lost. The "jukebox" culture of Chapter 7 in which cultures are rapidly modeled and remodeled to serve current adaptive purposes would have this effect due to functional convergence rapidly destroying any trace of history.

There are two issues at stake. First, what should we use descent to mean? Proponents of the view that whole cultures are like species reserve descent for describing cultural replication of complex coherent groups by the mechanism of group fission or budding, while those who believe that only components of culture, at best, cohere would use descent describe ancestor-descendant relationships resulting from any pattern of cultural preserving the footprints of its history. We shall try to be clear in our own usages, but this is a merely terminological issue we devote no further space to it. Second, what is the world like? This is a much more interesting question, to which we devote the rest of the chapter. At one end of the continuum, all of the elements that make up a culture cohere and resist recombination. Cultures as a whole are analogous to species. At the other end, the observed elements of culture are the result of memes diffused or invented on a time scale too short for phylogenetic reconstruction. What is culture really like?

B. Mechanisms

There are several general mechanisms that might cause longevity and coherence in cultural units so that descent can be determined.

1. Longevity of historical traces

As in the case of genes, the phylogenetic process of cultural transmission provides some level of historical continuity. As with genes, the deepest phylogenies will be possible when culture changes slowly, and is not subject to functional convergence. Slow evolution will occur when people either cannot or have no reason to invent new forms. Surprisingly simple bits of culture are often apparently too obscure to reinvent, and all known modern exemplars derive from a single invention. Needham (1988) has given many plausible examples of Chinese technology that subsequently diffused to the rest of Eurasia, for example the magnetic compass. Nonetheless, in the long run, functional convergence seems to be the rule for technology. A long tradition in the social sciences, including the classic cultural ecology of Julian Steward (1955) to modern evolutionary anthropology trade upon the reality of substantial convergent evolution in human cultures. As in the biological case, the best elements for historical analysis are those that are functionally arbitrary and symbolic. Language and other symbolically meaningful but non-functional variation are often used as indices of descent, much as functionally neutral flower form is used in plant systematics. Flowers are a plant's way of communicating with pollinators, so the analogy with language is real.

In the next subsection we describe some mechanisms that may prevent mixing between coherent elements. Similar mechanisms may act to slow the rate of evolution if internal innovations if innovations or innovators are perceived as strange, either because of a poor internal fit or because they arouse suspicions of heresy or deviance on the part of innovators.

2. Processes that give rise to coherence

What general processes could give cultural elements an enduring coherence, leaving aside the size of cohering units and their relation to one another? In the symbolic and interpretive anthropology literature the "glue" has been attributed to the "meaning" that inheres in culture. Meaningful cultural information provides a convincing and compelling Weltanschauung for its bearers. Meaningful components help to organize and make sense of other parts of the cultural system and natural world. They also legitimize and justify the system in the minds of its bearers. For this reason, meaningful components have variously been called "root paradigms" (Turner 1977), "ultimate sacred postulates" (Rappaport 1979), "core principles" (Hallpike 1986:ch. 6), and the like. Critically important to a peoples' understanding of the world and their place within it, they often have special, even sacred, status. The notion of meaning is often linked to the idea of cultural holism. There is no logical reason for this limitation, and the idea may apply to cores or much smaller units. Subcultural units as small as the individual social scientific

disciplines, street gangs, and clans often appear to have well-articulated systems of meaning.

The special status of meaningful elements could provide coherence in several ways. First, the internal logic of a coherent block of culture may discriminate against intrusive elements. Diffused elements may be known to individuals, but the mismatch of meanings between whole cultures or sub-cultures entails that "foreign" values and ideas will be misunderstood, disliked, and neglected. The mismatch may be between literally foreign elements, but also between domains within a single culture, for example gender marked identities or even sets of subsistence skills. See Chap 10 for details of mechanisms.

Second, meaningful culture often involves markers of group identity that are especially salient to the definition of in-group and out-group. Contexts where coherent units of meaning-rich culture are available for acquisition from foreigners are likely to involve marked ritual observances or ceremony that mobilize ethnocentric sentiments more thoroughly than mundane contacts like trade, in which symbolically less marked elements may diffuse readily. Ethnocentrism can provide an effective isolating barrier to diffusion of cultural elements in theory and apparently in practice (Boyd and Richerson, 1987) at the whole-culture level. Class, caste, gender, occupation and even hobby groups are symbolically marked within some societies. Within the bounded group however large it may be, intermarriage, diffusion, and other mixing processes create cultural uniformity within the bounded groups and sharp differences between them. In the terms of Chapter 10, this is a form of indirect bias.

Third, to the extent that what coheres in culture is a symbolic system of organizing meanings rather than being the meanings themselves, it is quite protected from ordinary adaptive evolutionary pressures. In language at least, the symbol system is so rich and flexible that quite novel new meanings can be coded with the existing system; only linguistically trivial changes in lexicon were needed to adapt modern languages to the industrial revolution.

Finally, elements may cohere because certain combinations are adaptive and favored by natural selection or derivative adaptive decision-making rules. Adaptive forces may simply discriminate so strongly against recombinants that coherence is maintained despite massive mixing, as seems to be the case a certain hybrid boundaries in the biological case (Barton and Hewitt, 1989). A related sort of selective "glue" could come from the multiplicity of evolutionarily stable strategies (ESS) that seem to exist in social systems (see discussion in Chapter 9). Perhaps the stability of coherent features comes from the failure of new or foreign social practice to fit into actual arrangements, rather than from inconsistencies at the cognitive/affective or meaning level. The symbolic or ideological level may follow the social rather than dictate it.

Rushforth and Chisholm (1991) give a possible example in their discussion of Athapaskan "structures of communicative social interaction." According to these

investigators, a core "framework of meaning and moral responsibility" has persisted among Bearlake Athapaskan of northern Canada with "extraordinarily little change" across many generations and hundreds of years (p. 64). Moreover, remarkably similar beliefs and values---urging industriousness, generosity, autonomy, and restraint---have been documented among more than thirty other Athapaskan-speaking peoples across three geographically discontinuous clusters in Canada and Alaska, the Pacific Northwest, and the American Southwest.

A deeply rooted family of social norms such as these might directly underpin social institutions. The norms that underpin social interactions are good candidates to be maintained as a coherent block because they are part of a local ESS. In game theory at least, is easy to imagine a locally stable ESS for complex social institutions that is impossible to change at the margin by either diffusion or within-lineage change because small movements away from current practice are disadvantageous.

Would the multiple ESS explanation account for the remarkable cultural persistence of Athapaskan norms? Focusing on the Bearlake version, Rushforth and Chisholm suggest that "The Bearlake interpretive scheme has persisted because of the historically stable composition of the [social interaction] strategies it informs" (p. 119). They argue that Bearlakers pursue goals in daily life that are defined and valued by their interpretive framework of beliefs and values. The interactions that follow generate regular rewards or "payoffs" that encourage individuals to convey certain intentions to others. But the actions that convey these intentions are precisely those defined by the framework; in short, the framework persists as "an unintended consequence of the strategic behavior of individuals operating in their own interests" (p. 121).

Sometimes coherent traditions are "acquired" by imposition by an invading, dominant culture, or assimilation to an attractive one. Even in this case, little admixture from the competing coherent structure of the adopting culture need result from its transfer from one biological population to another, as in the imposition of a common Greco-Roman urban civilization on a host of "barbarian" peoples in Ancient Europe and Western Asia. Note that individual people can move readily without disturbing the integrity of the coherent elements, as the assimilation of many immigrant peoples to at least aspects of Anglo-American culture over the last two centuries testifies. Nevertheless, replication by transfer to a new biological population is arguably normally accompanied by much mixing of old and new, and the fission of one population into two daughters probably conserves coherence more effectively. Similarly, high rates of immigration need not necessarily result in high rates of erosion of coherence, but cultural diffusion does seem likely to stimulated by immigration in typical cases.

C. Evidence

1. The descent of cultures as wholes

Commentators such as Marks and Staski (1988) sometimes imply that they defend this position. According to McNeill (1986:43ff) historians such as Toynbee imply a position as extreme as this end of our continuum, although without any specific defense. His own magisterial *Rise of the West* was written to demonstrate how it was not possible to write a world history without acknowledging the exchange of ideas between major culture areas, much less within them. Holistic arguments, ultimately deriving from Wittgensteinian philosophy, once had great appeal in history and many branches of the social sciences, and echoes remain. For example, in linguistics, Saussure (1959) is often cited as a proponent of extreme systemicity in language, and even today some linguists espouse this view (Wardhaugh, 1992). The limitations of such arguments have long been recognized by philosophers, and more recently by social scientists, as Mitchell/Weingart describe in Chapter 8. As we will argue below, there is such overwhelming evidence for substantial diffusion and for rapid evolution in many components of culture that we believe it unlikely that any tenable empirical defense of a completely holistic cultures-as-species position can be offered.

2. The descent of core traditions.

The hierarchical hypothesis of large-scale cultural coherence rooted in a core tradition is a point along the continuum warrants closer examination. Like alternatives 1 and 3, it assumes that culture is an ideational system--that is, that it consists of widely shared ideas, values, and beliefs that shape behavior in local human populations (the named Cultures of anthropologists). In this model, cultures are viewed as hierarchically integrated systems, each with its own internal gradient of coherence. At one extreme in the gradient are the "core" components of a culture—those ideational phenomena that constitute its basic conceptual and interpretive framework, and influence many aspects of social life. At the other are peripheral elements that change rapidly and (or) are widely shared by diffusion. On this hypothesis, the processes of coherence generate one main, central core coherent unit. But this central unit does not equally organize all elements of culture. There may be many other smaller elements that are only lightly or not at all influenced by the core.

a. Core vs. periphery

Whether the core gets its coherence from meaning, from protection from diffusion, from structured social interaction, or from all these sources, the key assertion of this model is that core components exhibit a remarkable resilience in the course of cultural history. The core "sticks together" as a cohesive bundle even through repeated episodes of culture birth, giving rise to a set of descendant branches that then share the same "tradition." As Vansina (1990) argues based on his case study (see next section), such traditions are

based upon "the fundamental continuity of a concrete set of basic cognitive patterns and concepts... [The] continuity concerns basic choices which, once made, are never again put into question... These fundamental acquisitions then act as a touchstone for proposed innovations, whether from within or without. The tradition accepts, rejects, or molds borrowings to fit. It transforms even its dominant institutions while leaving its principles unquestioned." (p. 258)

Despite these numerous sources of cohesion, the hierarchical hypothesis holds that many "peripheral" components exist that are only loosely tied to the core framework. These diffuse freely and readily, as in the well-studied case of technical innovations (Rogers, 1983). Peripheral components may include ideational elements that make sense on their own and can be socially transmitted without a lot of supplementary cultural information. Such components are assumed to play little or no organizational role within the broader ideational system, and they must be relatively easy to learn. Such components are expected to be highly "contagious," rather like Dawkins's viruses of the mind (Dawkins 1993). New forms will be adopted quickly, simply, and smoothly, particularly if there is some perceived functional advantage and low cost. In this instance change is quick and easy: different components come and go as independent interchangeable parts. They are likely to spread horizontally, between cultures, whether those cultures are related historically by branching or not. For this reason, their phylogenies will have the vine-like appearance mentioned above. Kroeber (1948: ch. 12) gives a long list of well known examples---days of the week, tobacco, printing, paper, gunpowder, etc. Unlike the descent of wholes hypothesis, the hierarchical hypothesis recognizes that cores are not as completely isolated as good biological species. Kroeber's "tree of culture" (1948) implied that cultural descent is like a rain forest canopy tree--one whose crown is a tangle of branches (related by birth) and vines (related by diffusion). For some substantial period of time, one can easily distinguish what grows as branches from what grows as vines, with more care, even in a very thick, old tangle. Eventually, however, over the course of thousands of years, vines will proliferate and come to obscure the branches. At the same time, processes of coherence will integrate elements with separate histories. Old vines will coalesce to form a solid trunk, much like the strangler fig that starts out as a viny parasite of a tree but gradually forms a solid trunk about its host, which then dies.

The hierarchical model also acknowledges the rapidity of cultural evolution, compared with the biological case. The evidence of a history of common descent will gradually disappear in independent lineages. Barth (1987) gives a detailed account of the rapid evolution of the core tradition of the Mountain Ok of New Guinea due to a mutation-like process. The case is probably unusual because the core traditions are transmitted in rare secret rituals that create high "mutation" rates via forgetting, but, even in the absence of diffusion, evidence of common ancestry in sister cultures will degrade on the millennial time scale (compared to 100s of millions of years in the case of sister species of mammals). We know from the massive convergence of agricultural technology and state level social institutions in the pre Colombian New and Old Worlds that cultural evolution can produce spectacular adaptive change on the time scale of a few thousand years. We can be almost certain that Old-New World similarities were independently derived

convergences, but only because we have the evidence of hundreds of cultures on both branches to help distinguish the vines. Notoriously, careless historians that ignore the massively redundant evidence have no trouble "finding" false descent relationships between Old and New World cultures (e.g. Heyerdhal, 1950).

b. The practice of constructing core-cultural phylogenies

The hierarchical hypothesis is supported to the extent that it can be shown that a large complex of core traits has a common pattern of descent. The core traditions in question must be related through a sequence of population fissionings (allowing for the odd core transfer). The existence of only one deep element, such as language, cannot alone be used to infer the existence of full core of shared traditions among cultures related by language only. Because language phylogenies can be traced to considerable depth using conservative aspects of vocabulary and phonology language trees are the usual starting point for attempting to trace out the descent patterns of larger core units. Related traditions can then be used as a basis for reconstructing a fuller culture history, including the "proto-tradition" out of which they evolved (see Aberle 1984, 1987). Sometimes genetic relatedness of the populations involved provides supplementary evidence, given that full core replication by processes other than fission of a parent culture is unusual. If, on the other hand, diffusion and rapid evolution swamped all traces of relationship by birth, anthropology could not speak of branches, only vines, and hypothesis 3 would be supported.

The work of Rushforth and Chisholm on Athapaskan similarities illustrates the method. Linguistic evidence indicates that Athapaskans are part of a second wave of Native Americans that arrive from Asia some few thousand years after the migration that contributed most known precolumbian populations. At contact, the Athapaskan language family was spoken by peoples in quite isolated clusters in Canada, California, and the Southwest (the Southwestern group includes the famous Apache and Navaho). According to their analysis, the evidence suggests that a core of meaning related to social behavior coheres with language and that all are all "cognate," that is, related historically by culture birth (p. 71). First, the authors imply that the pertinent beliefs and values in Athapaskan populations are distinct from those of the surrounding populations belonging to other language groups (although it is also true that the differences are not thoroughly documented in their presentation). Second, similarity by diffusion can be ruled out because of the highly discontinuous geographical clustering of the carrier populations (see their Fig. 1). Third, independent origins are highly improbable (p. 78), even if each cluster of populations is taken as a whole. Rushforth and Chisholm conclude that the pertinent beliefs and values are all "genetically" related, having "originated in and developed from a common, ancestral cultural tradition that existed among Proto-Athapaskan or, perhaps, even among [the ancestral] NaDene peoples" (p. 71). As they put it, "simplicity strongly argues" that "this cultural framework originated once, early in Proto-Athapaskan or NaDene history and has persisted (perhaps with some modifications) in different groups after migrations separated them from contact with each

other" (p. 78). The work of Indoeuropeanists to reconstruct the descent of societies speaking this family of languages is the most ambitious attempt yet made to reconstruct a pattern of descent for a core. According to Indoeuropeanists like Dumezil and Gimbutas, the Indo-Europeans are the bearers of a core tradition consisting of language elements, myths, and a distinctive tripartite pattern of social organization that had its origin in a particular culture of steppe horse nomads. Gimbutas' reconstructed "Kurgans" lived about 6,500 years ago between the Black Sea and the Caspian. Gimbutas' Kurgan proposal is widely respected, but also widely criticized; a reconstruction of such breadth and depth tests the margins of the hierarchical hypothesis (Mallory, 1989).

Shared core traditions have been proposed for peoples in a number of different regions of the world, each with time horizons dating back at least a few thousand years. Recently reviewed in Durham (1992), these include the oft-cited case of cultural similarity among Polynesian Islanders (see especially Kirch 1986, Kirch and Greene 1987; see critical review in Terrell 1986), the Athapaskan (Rushforth and Chisholm 1991) and Indo-European traditions mentioned earlier (e.g., Gamkrelidze and Ivanov 1990; Hallpike 1986:ch. 6; but see Mallory 1989), Mayans (Vogt 1964), Tibetans (Durham 1991:ch 2), and Tupi-speakers among native South Americans (Durham and Nassif 1991). Although one could always argue that the Polynesian case is exceptional because of the inherent isolation of its populations, plausible examples of enduring shared traditions among cultures related by birth have now been proposed for a diverse array of continental populations as well. Vansina's recent comprehensive study (1990) of political tradition in equatorial Africa. Through a controlled comparison of some 200 distinct societies in the basin of the Zaire river and its tributaries, Vansina concludes that these "widely differing societies arose out of [a] single ancestral tradition" (p. 191) by way of 3000 to 4000 years of historical transformations. As reconstructed by Vansina, the original ancestral tradition came into the region with the immigration of western Bantu speaking farmers. They brought with them a single distinctive pattern of social organization based upon fragile temporary alliances into House [capital H in original], village, and district, and a common ideology and world view to go with it (see 1990:95-99). From this common baseline, Vansina argues, through successive splits, migrations, and expansions (pp. 49-57), "widely differing societies arose out of the single ancestral tradition by major transformations" (p. 191). The variation included, for example, two kinds of segmentary lineage societies, four kinds of associations, and five kinds of chiefdoms or kingdoms. All the while, "the principles and fundamental options inherited [at birth] from the ancestral tradition remained a gyroscope in the voyage through time: they determined what was perceivable and imaginable as change" (p. 195).

Vansina makes it very clear that outside influences--"the new habitants, the autochthons [indigenous hunter-gatherers in the region], the non-Bantu, the eastern Bantu farmers with their different legacies--each influenced the development of this ancestral tradition differently from place to place" (p. 69). Yet as he repeatedly shows, change "was not mainly induced by outside influences... In all these cases [for example, in the inner Zaire basin] a chain of reactions fed continuous internal innovations. Outside innovations were

accepted only insofar as they made sense in terms of existing structures." Even in regions where external influences played a relatively heavy role, the internal sovereignty of distinct polities meant that "internal dynamics always remain determining" (p. 192). And even with the establishment of Atlantic trade after 1480 and the attendant challenges of slave raiding and more, "the tradition was not defeated. It adapted. It invented new structures... [N]o foreign ideals or basic concepts were accepted and not even much of a dent was made in the aspirations of individuals." Inherited at birth in each equatorial society, the tradition lived on for hundreds of years more, only to be destroyed by European conquest between 1880 and 1920.

c. Why core homology matters

Vansina's study illustrates a key proposition of the hierarchical model. Even in continental areas with high contact between peoples one can still trace "the historical course of a single tradition" (1990:261). But there is a second important implication as well: reconstructing the histories of peoples without written records requires that one distinguish between homologies (that is, similarities produced by culture birth), analogies (similarities produced by convergence or parallel change), and synologies (similarities produced by diffusion or borrowing). The reason, as Vansina notes, is that the reconstruction of past cultures requires that one "seeks out homologies first" (p. 261). Only by identifying genuine cultural homologies can one establish the nature of the initial ideational system that was later transformed by historical processes. To the extent that model #2 proves valid, it offers a useful tool that societies with no written records can use to gain access to their own histories.

3. *The descent of small cultural components.*

On this hypothesis, there is no central core culture which deserves special attention in phylogenetic analysis. Rather there are multiple "cores" as well as sometimes quite small units whose descent can be usefully traced. To characterize a narrow region on the continuum of possible hypotheses, we suppose that even the biggest deeply coherent blocks of culture are fairly small.

a. Definition

The components are collections of memes that are transmitted as units with little recombination and slow change, and therefore, their phylogenies can be reliably reconstructed to some depth. (As for the hierarchical hypothesis, how much recombination and change is tolerable depends on the time scale---deeper phylogenies require more coherent units and slower rates of evolution). Under this hypothesis, different components diffuse and recombine at a rapid rate compared to the rates of elements within components so that core-like complexes of components will have shallower phylogenies than their smaller constituent components.

The processes which provide "glue" for the hierarchical core hypothesis also explain the coherence within these smaller units. The amendments needed are only quantitative. If the scope of integration provided by internal processes is limited, and if ethnocentric barriers to diffusion are weak or shifting in kinds of components protected, recombination between large blocks of memes will be high, although the same processes may protect many small sets of coherent memes. In practice, the units have to be large enough to have significant internal complexity, or their actual document history has to be good. Otherwise the amount of information available for descent reconstruction is very limited. Thus, before the advent of modern molecular techniques, the functionally similar genes in various bacteria had a pattern of descent, but the traces of history needed to reconstruct the pattern were absent. When genes can be sequenced, a vastly greater array of data is available by reading the DNA strand directly. Strings of functionally irrelevant, highly improbable similarities and differences in the strands can now be used to construct phylogenies where classical biologists despaired.

Is there any theoretical reason to expect smaller rather than larger coherent units in the cultural case? The fact that different cultural variants can be acquired from different people during different parts of the life cycle makes genealogical processes less effective at maintaining coherence than the analogous processes in the case of genetic evolution. We all have many cultural parents, with the attendant potential for independent samples of culture from many sources. At the same time, mixing could be less effective within small units because one can learn some things from one person or a small group of closely related mentors, and other things from a quite different set of mentors. This may lead to small, but coherent, subcultures within a larger culture complex. For example, the culture of science is fairly coherent, and coexists within the same society as the culture of rock-climbers, but people from each of these partial cultures may share the partial culture of the English language. (Of course, to some extent science, rock climbing, and English are international institutions, and provide avenues of communication between the cultures that play host to them.) On this argument, maintaining cultural coherence over large units faces a considerable mechanical obstacle due to the hyper-recombinatorial nature of the cultural transmission system.

If one focuses on one special unit, such as those few features of language that do cohere over long time scales, one may indeed find a few correlated units of other types that persist in having a pattern of descent in common with the language features, merely as a matter of chance. From one attempt at deep reconstruction to another, different pseudo-core elements will be discovered.

The linguistic characters used by historical linguists (basic lexicon, phonological rules) provide a good example of what is meant by a cultural component. Linguists can reconstruct a phylogeny for basic lexicon and phonological rules that tells us the pattern of relationships among variants of this character. So, for example, we know that the basic lexicon and phonological rules that characterize English and German share a more recent ancestor than either does with French. In other words, we believe that we can trace the

sizable complex of memes that underlay English basic lexicon and phonology back through a series of ancestor descendant pairs to a point where the same people speak a language that has phonological rules and basic lexicon that are also the ancestor of German.

b. Examples of coherence of small units and recombination among them

A clear example of how sets of memes exhibit considerable coherence when borrowed between groups can be seen in the adoption of the age organization principle by Bantu peoples in Central and Eastern Africa (LeVine and Sangree 1962). Age sets are an institution in which children (boys and girls into different sets) born within a few years of one another are simultaneously initiated into a group of near same aged adolescents. After initiation, a given age set is a corporate organization that is formally charged with a series of roles in succession (warrior, married man, elder, etc.) with formal graduation from role to role of the whole set.

The Tiriki (an offshoot of the Abaluhya Bantu), for example, currently have an age organization almost identical to that of their Nilotic neighbors, the Terik, while remaining distinctively Abaluhya in language and culture. This situation arose as a result of intense political turmoil in the mid eighteenth century, when the Terik offered asylum to refugee segments of Abaluhya lineages, on condition that their men folk would become incorporated into the Terik warrior groups. At this time the Tiriki warriors not only accepted the full set of initiation rituals for their sons (circumcision and seclusion), but they also adopted the 7 named age set system; in addition the grades of warrior, retired warrior, judicial elder and ritual elder emerged as the principle corporate units of political significance at the local level, and the Nilotic ideology of bravery and prowess in battle became predominant. Indeed there is some evidence that the Tiriki became a distinct group within the Abaluhya as a result of their adoption of Terik customs, as is indeed suggested by their name. Interestingly, the practice of female circumcision was viewed with disfavor by the Tiriki, such that they never adopted this trait. In short, this example shows how a number of cultural elements can be borrowed as a package, although not indiscriminately so, and the packages are often smallish.

Linguistics also provides many good examples. Important components of the language spoken by a group of people often have a different evolutionary history than do the basic lexicon and phonology of the same language. A substantial fraction of the words in the English lexicon share more recent common ancestors with words in French than with German. This is also true of English syntax, SVO like French, not SOV like most Germanic languages. It is even true of aspects of English phonology, for example, English speakers distinguish veal and feel, apparently as a result of the influence of Norman loan words. Thus we can identify coherent cultural entities, words, syntactical and phonological rules that are longer lived than larger complex we call the English language and whose ancestry can be traced back through independent series of ancestor-descendant relationships. Thomason and Kaufman (1988) provide numerous other

examples, including the Ma'a language spoken in northern Tanzania which, despite classification as a Nilotic language, has a basic lexicon related to Cushitic languages and a grammar related to Bantu languages. (We return to the problems that this example raises for the practice of linguistic classification below.) Less formal data suggest that important social-organizational rules and values are often decoupled rather rapidly from descent as reckoned using basic lexicon and phonology. In Central and East Africa for example, cyclical and linear age sets, alternating generation classes, genital mutilation of males and females, warrior organizations and many other associated practices are common among people whose basic lexicons are categorized as Nilotic, Cushitic, and Bantu. While it was once thought that these customs were essentially of Cushitic origin, it is now clear from Ehret's (1971) linguistic analyses and voluminous ethnographic sources that different customs associated the recruitment, function and ritual validity of age organizations have been repeatedly borrowed between protolinguistic units over the last 5000 years, reflecting periods of proximity, expansion, and dependence. The resulting situation is one of a thorough intertwining of social-organization and language. In some cases the distribution of cultural traits appears to represent functional convergences, as in the case of the Tiriki (above) who adopted age sets and male circumcision in response to the turbulent militaristic conditions of the times. In other cases, there is evidence of a decoupling of apparently non-functional details. Thus the Bantu Gusii conduct male and female genital mutilation but have never apparently organized their men into age sets (LeVine and Sangree 1962), and the Datoga dropped the 5-8 cycling ageset system of their proto southern Nilotic ancestors for non-cycling generation classes (Ehret 1971). The Bantu Kuria provide a particularly revealing example of this complexity (Tobisson 19xx): men belong to age-sets almost indistinguishable in name from those of the Southern Nilotes but are recruited on entirely different principles (father's set membership rather than circumcision cohort). The Kuria do, however, have an important military units; these are based on circumcision, but are organized quite differently from those of the Nilotes, and are quite unrelated to the age-set system that among the Kuria bears Nilotic names. The inescapable conclusion that can be drawn from these complex observations is that the phylogeny of language and other cultural characters are often distinct.

Religious practices provide many further examples: the spread of the Sun Dance on the Great Plains, the spread of Islam from Western to Central and Eastern Asia and Northern Africa, millenarian movements in Melanesia, and so on. Ethnographic details are sometimes available for such borrowings, and the motives involved do not seem to be such as to enforce much coherence. For example, Sierra Leonean Creoles adopted Freemasonry beginning in the late 1940s. The reason seems to have been that exclusive occupation of elite political roles had long served Creoles with an integrative community symbolic system. When Creoles lost power to the large majority of tribal peoples without a slave background, this symbol system was lost. Freemasonry happened to be an available substitute and quickly become very important (Cohen, 1974). Of course, national and imperial powers sometimes maintain symbolic unit over wide areas for impressive periods of time. Hapsburg success in defending Catholicism and expelling

Protestantism and Islam from their dominions during the life of the Austro-Hungarian Empire is a famous example. However, the need to exercise a large measure of raw force to succeed in such an enterprise is perhaps testimony to the long-run weakness of large-scale coherence.

There may also be rather well-bounded subcultures within a language group (as defined by basic lexicon) as for example in the Indian caste system or the class, occupational, and religious subunits of many other state-level agricultural societies. Here some memes are confined to some subset of the group---the castes, the guild, and so on. These subgroups may be marked by boundaries that are rather impervious to the flow of at least some kinds of memes. This phenomena reaches its extreme in contemporary societies like the US, where a diverse array of specialized subcultures of many types exists (American writer Tom Wolfe's books are eloquent descriptions of some of these).

These subgroups may be far more enduring than the "cultures" to which they bear somewhat temporary allegiance. East Africanists, for example, often question the attribution of any time depth to the ethnic units currently residing in the area. This is not simply a consequence of European colonialist policy. Thus Waller (1986) paints a picture for the 19th century and earlier of ephemeral political associations of clans with different linguistic and cultural backgrounds, linked through diverse patterns of intermarriage, trade, expansion and dependency. These flexible and highly inclusive concepts of group identity are seen as an adaptation to heterogeneous and somewhat unpredictable environmental conditions, circumstances by no means unique to East Africa. Bruce Knauft (1985) tells a similar story about the Gebusi and their neighbors, the Bedamini, in the Fly River area of PNG. According to this picture there would be frequent recombination of memes due to temporary association of people who exchange memes while in contact.

c. Comparison of core and small units hypotheses

Whether such examples are more representative than those given by supporters of the core hypothesis is an important, unanswered question. Very little anthropological work is capable of answering the question. There are a few studies, but they are indecisive. Jorgensen's (1967; 1980) studies of the Salish and larger scale analysis of the Indians of Western North America is the kind comprehensive cultural analysis might do the job. However, his methods are based on measures of overall similarity and difference and are not proper analyses of descent. Biological systematists argue that the only evidence for membership in a given branch of a descent tree is given by characters which are shared by that branch alone, not more ancient or more recent similarities, much less similarities acquired by convergence.

Even in the case of language, "wave" models of linguistic evolution have long contended with "genetic" analyses based upon strict criteria of descent (Renfrew, 1987; Mallory, 1989; Jorgensen, 1980). Many features of Indo-European languages seem easier to

account for if we assume that the whole family was in contact throughout most of its history, and that innovative features tended to diffuse from multiple centers to neighboring languages. Tree-like models of relationship can certainly be constructed for data that are substantially influenced by wave-like processes, for example with clustering algorithms. Just because a tree diagram explains much of the variation in a set of data does not guarantee that the descent hypothesis itself is correct. It would be quite interesting to see the modern "cladistic" methods of biological systematists formally applied to such cultural descent problems. At least part of the solution to the debate between proponents of hierarchical core and small units hypotheses turns on the application of sharper methodological tools, and biologists have something to offer.

d. The descent of memes.

The boundary of the small units hypothesis toward the small end of the continuum is not very well defined. It is also possible that, aside from core vocabulary and phonology, there are few multi-meme cultural units that are well protected from diffusion. It could be that each of the cultural things we observe is affected by many memes, that these memes readily diffuse from one socially or linguistically defined group to another, and that memes that affect different cultural components readily recombine. For example, a religious system might be affected by many different memes: beliefs about causation, beliefs about the role of men and women, beliefs about disease and so on. This system could diffuse from one group to another, and then some of the memes could recombine with other aspects of the culture. Beliefs about the roles of men and women that came with the new religious system might then recombine with pre-existing beliefs about subsistence practices generating new, observable subsistence variants. If we could actually measure the memes that characterize different human groups, then this case would be much like the previous one, except we would reconstruct the phylogenies of memes much instead of whole cultural components.

4. Descent analysis impossible or uninteresting

There are several situations under which descent analysis as regards culture is impossible.

If we observe phenotype, not the mental representations that are stored and transmitted, then we cannot directly measure memes. The fact that many memes affect any given observable cultural attribute will make it very difficult to trace the path of recombining memes, and, reconstructing phylogenies is likely to be impossible. If the actual units to which descent might apply are as small or smaller than our practically observable units, descent will be impossible to trace simply because there is not enough information available to separate common descent from other hypotheses, such as independent origins. A quantitative character subject to blending inheritance is an extreme example.

In some cases, methodological improvements may increase resolution. Comparative ethnographic data with age sets scored as present/absent or as a quantitative variable on political importance would not contain enough detail to reconstruct much history in East Africa. A richer data set offers more possibilities as we saw.

The existence of coherent cultures will depend on the rate of diffusion and independent evolution. If the rate of diffusion between cultures for most characters is high, then there will be no cultural unit larger than some very small atomistic unit to track the descent of. Between the time that a newly formed group buds off its parent, and the time it creates buds itself many new traits will have entered the group from the outside. If the rate of evolution is high the trace of history also vanishes. High rates of random evolution, especially on simple characters with few observable states, will eventually result in so many random "hits" that descendent characters will have occupied all states fairly recently. Similar simple artistic motifs are found in many cultures, perhaps because artists frequently rediscover and abandon them. Functional convergence presents similar problems. Around the world, tropical horticulturalists often live in small-scale societies that are murderously hostile to their neighbors. This commonalty is presumably a byproduct of the population densities and level of political organization supportable in wet tropical climates, not due to common ancestry.

Even when descent analysis is possible, it may be uninteresting. The few components that resist diffusion, basic lexicon and so on, will be descended from the grandparental group (defined in terms of basic lexicon), but most components will not be descendants of components in the that same grandparental group. Put another way, a culture is nothing more than its most elementary components. Each component may well be traceable back to a grandparental society. But if we consider a neighboring society, they may share particular grandparents for particular traits at random. Phylogenetic analysis could still be conducted on an element-by-element case, and this might be of interest or utility for some special cases. However, one important use phylogeny is make manageable the overwhelming complexity of populations and cultures. With no coherence, the analysis of descent can promise nothing in this regard.

D. Partial phylogenies and the study of adaptation

Good phylogenies are crucial for the proper study of adaptation using the comparative method. Comparative studies attempt to determine the function of various attributes by looking for predicted correlations among societies. For example, Thornhill (1991) hypothesized that inbreeding avoidance rules function to preserve capital in powerful families. To test this hypothesis, she collected data on inbreeding rules and social stratification, predicting (accurately) that the degree of elaboration of rules would positively correlate with degree of social stratification. Similar studies utilizing correlations among species are widely used in comparative biology. A key problem in such comparative studies is determining the extent to which different societies (or species) are independent data points. In comparative biology, only independently

derived associations are counted as separate data points. So, for example, if an innovation arises and then the lineage speciates, preserving the innovation in both daughter species, the daughter species should be counted as a single data point. Thus the first step in the proper exercise of the comparative method is phylogenetic reconstruction (Harvey and Pagel 1991). In cross-cultural anthropology this problem is referred to as Galton's problem, and scholars working in this discipline attempt to select their samples so as to include only unrelated cultures or correct for diffusion using statistical methods (Burton and White 1987).

Adaptations acquired by diffusion from other groups are related by descent to the adaptations in those groups. If one analogizes with the practice in biology, such adaptations would not be counted as independent cases because the adaptation in the borrowing group is *not* an innovation. However, to the extent that diffusion represents the (adaptive) goal driven choices of individuals in the borrowing group (or some other adaptation-producing process), the borrowed adaptation *is* an adaptation. If it had not been an adaptation, it would not have been adopted. This problem is particularly acute given that the rate of diffusion of new cultural adaptations through biased transmission is likely to be much higher than the rate of innovation. If this is so, most groups will adapt by borrowing, and it is unreasonably conservative to disregard these cases.

The relationship between the Sun dance and the buffalo hunting ecology of great plains peoples illustrates this difficulty. A summer ceremonial called the sun dance characterized all the great plains buffalo hunting peoples. One might hypothesize that such a ceremony is related to the fission-fusion social organization that characterized the buffalo hunting ecology of the great plains peoples. But does one count this as one case, or several? It is likely that this ceremony originated with the Crow and diffused to other tribes, so the various versions of the ceremony are not independent inventions. On the other hand, each group did adopt the ceremony, perhaps because it served the hypothesized need. Moreover, it could be that in the absence of diffusion each group would have independently developed a summer ceremonial but did not because the rate of adaptation by diffusion is faster than independent invention (Oliver, 1962).

On a longer temporal and spatial scale, the problem is also well illustrated by basic technical innovations like agriculture or iron-working. The number of independent inventions of these techniques was few indeed, many fewer than the number of language-based descent groups that have subsequently adopted them. It seems absurd to say that we cannot really decide if iron-working is adaptive or not because all examples of iron-working technology are derived from a single common ancestor in Asia Minor about 3,400 years ago. And, regardless of our answer of how many cases of iron-working to count for purposes of estimating its adaptive value, it seems clear that language-based descent groups are largely irrelevant to solving this problem. We say "largely irrelevant" because it does seem to be the case that an association of an important adaptive innovation with a linguistic unit does sometimes last long enough to carry the language great distances, as with iron-working and the Bantu expansion in Africa in the last

millennium BC and the first millennium AD (Ehret 1982), the use of abundant but low-quality plant resources and the spread of Numic languages in the American Great Basin (Bettinger and Baumhoff, 1982), and the domestication of the horse and invention of wheeled transport and the spread of Indo-European (Mallory, 1989). Note that such associations tend to persist only for a millennium or so even though the expansion of the innovating group is tending to preserve the association. Rather soon, relative to depth that we can reconstruct linguistic phylogenies, the association is erased by diffusion.

V. Conclusion

It seems to us that, as regards most meme complexes, specific cultures are more like local populations within a species than like species. The whole human species is united by complex flows ideas from one culture to another. This has always been so, although the geographical isolation of the New World, Australia, and a few other areas from each other and Eurasia may have substantially isolated large blocks of cultures on multi-millennial time scales. On smaller time and space scales, other mechanisms of isolation and coherence do generate some patterns of descent that are traceable for a few millennia.

The use of descent analysis for cultural units has a long but controversial history. Many authors claim a degree of success reconstructing the history of descent of fairly large cultural units fairly far into the past. The most interesting outstanding question is the size and time scale of coherent units of culture. Do single cores in an interrelated complex have real histories that reach back 5 millennia or more? There seems to be no doubt that many small units have descent relationships that can be reliably inferred for this depth, but the upper size/time limit is not well defined by current methods. There is an ill-explored neutral analogy worth further work here. The cladistic revolution in systematic biology has sharpened concepts and built new tools for phylogenetic analysis. Might they be used, in spite of the problem of high diffusion rates between cultures compared to species to help advance the resolution of genetic versus wave explanations of culture history?

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