

## Afterword

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Efforts to build a science of human variation have a long history. Although a synthesis has yet to be reached, there is growing appreciation among social scientists that a Darwinian evolutionary perspective on variation can provide fruitful avenues of research. The key point of departure for incorporating Darwinian evolution within the social sciences is recognizing that evolution is a theory about history. Evolutionary explanations are historical because they concern themselves with how and why things change over time. Two points are worth making in this regard. First, evolutionary explanations explore “any net directional change or cumulative change in the characteristics of organisms and populations over many generations” (Endler 1986: 5). In this sense, the focus of evolutionary studies is on tracking change through time. Second, and related, evolutionary explanations rest on our ability to reconstruct genealogy. The key question here is: are two things similar because they are related phylogenetically, or are they similar as a result of other processes such as convergence and borrowing?

Interest in phylogeny has long been part of the research agenda for the social sciences. It is largely because of this interest that anthropologists have developed robust accounts of cultural, behavioral, biological, and linguistic histories for much of the world. These “culture histories” link modern, historical, and prehistoric populations through time and across space and are evolutionary accounts in the sense that they are narratives about relatedness. Indeed, the process of defining a culture-historical tradition consists of isolating a group of things that are linked in ancestor-descendent relations. Thus, evolutionary thinking fits comfortably with the kinds of analyses that anthropologists have routinely done for the better part of a century. The chapters in this book reflect the wide range of subject matter that can be studied phylogeneti-

cally, including projectile points, pottery designs, pottery composition, marriage patterns, puberty rituals, basketry, languages, and genes. These phenomena represent the broad spectrum of human variation and underscore the basic principle that phylogenetic methods are applicable to anything that is structured by a system of inheritance.

Several lessons stem from the study of this array of data classes. A key recognition is that the patterns derived through phylogenetic analyses often reflect unique histories of inheritance that depend at least in part on the characters of interest. Characters can be independently transmitted through a population and may not form coherent sets; each has its own history that may or may not be correlated with other characters in the population. In some cases, characters reveal strong branching patterns consistent with vertical transmission as the primary mode of inheritance. In these instances, variation among characters is produced by divergence caused by isolation of portions of a population from each other. In other examples, distributions of characters are consistent with blending, which occurs when inheritance is predominantly horizontal and patterns of relatedness are geographically structured so that similarity is correlated with spatial distance. Of course, horizontal inheritance can also produce tree structures, but they are orthogonal to the trees produced by vertical transmission—for example, a feature that spreads from one group to another, undergoes an innovation, and then spreads to another group. This means that each case needs to be evaluated independently.

In general, this observation of the nature of cultural transmission reflects our appreciation of the subtleties of phylogenetic approaches, and it underscores the fact that phylogenetics is clearly not the end point of analyses but rather an integrated and iterative part of the explanation of cultural phenomena. Methodological advances such as the ones represented in the chapters of this volume have resulted from improved and expanded models of transmission as well as from the development of statistical methods for evaluating the fit of data to the predictions of the models.

The chapters highlight a number of conceptual distinctions. One of the more substantial issues concerns the appropriate units of analyses: populations versus specific artifacts and/or characters. Some authors argue that groups of individuals can be analyzed as coherent units because groups share characters despite having somewhat permeable boundaries. Other contributors are critical of attempts to use cultures or societies as units, and suggest that populations cannot be treated simply as analogues for species. The resolution of this issue will depend on whether one can make a case for evaluating relatedness in sets of characters or populations exhibiting those characters. The latter situation is likely to characterize the study of ethnographic populations, whereas the former characterizes archaeological cases.

Another area in which authors' perspectives vary is the degree of confidence in identifying the factors that produce the variation we study. For some,

it is not clear that our methods, whether adopted from biology or built from scratch, are fully in alignment with our theoretical understanding of cultural transmission and the processes by which humans inherit cultural, behavioral, and linguistic information. Indeed, several contributors express concern over whether the methods are racing ahead of the theory that we use to explain the results of phylogenetic analyses. On the one hand, we have good reason to be cautious. The allure of statistical techniques and their success in the natural sciences is all too often used as an excuse to adopt and implement new numerical methods within the social sciences. On the other hand, we should recognize the iterative nature of theory construction and method implementation. As we build an evolutionary approach to the study of human diversity, we can expect a degree of interplay between theory and empirical evaluation as we try different approaches and determine the degree to which they produce falsifiable hypotheses.

With respect to method, the chapters demonstrate that there is no single approach that necessarily addresses all phylogenetic issues. At least two kinds of approaches are represented. Many of the authors adopt the view that human diversity can be explored productively using methods originally devised to study biological evolution. This view centers on the notion that cladogenetic models can be applied to the study of human diversity. Deviations from this model are detectable using a variety of statistical means. Other authors suggest alternative avenues of inquiry that have their roots in the social sciences. Both approaches appear to be fruitful.

The diversity in approaches used in phylogenetic analyses has other implications. There is, for example, no single procedure for studying relatedness. The examples in the volume vary from the use of compositional analysis to map patterns of relatedness among artifacts to the use of biological phylogenetic software such as PAUP\* and MacClade. In addition, graphical representations of relatedness can take the form of relatively familiar tree-like representations as well as network topologies.

To some degree, the differences reflected in phylogenetic approaches suggest the overall immaturity of our efforts, as social scientists explore the rich assortment of statistics and methods already existing within biology. These resources provide us with countless opportunities to experiment and investigate their application within anthropological, linguistic, and archaeological data sets. The adoption of methods from the biological sciences is unlikely to be abated; perusal of the phylogenetics literature suggests that ongoing innovations will fuel years of adaptations in the social sciences. Of particular interest to anthropologists will likely be new means of statistically inferring and evaluating trees under different types of assumptions (e.g., Felsenstein 2004), methods for studying biological phenomena such as reticulation among bacteria (e.g., Makarenkov 2001; Woese 2000), and new methods for dealing with temporal issues such as those found in the paleontological record (e.g., Huelsenbeck and Rannala 1997, 2000).

### Where Should We Go Next?

Our first step is to recognize that phylogenetic theory is not as far along in anthropology as is our ability to evaluate variation statistically. In general, we need more information on how traits are transmitted within and between populations and a more sophisticated understanding of how population configurations influence patterns of relatedness. We need, for example, better means of estimating the effects of varying rates of interaction, methods for determining the impact of structured spatial distributions of individuals, and models for assessing the role of interpersonal rules for transmission. In addition to increasing our understanding of empirical processes, we also need a more refined grasp of measurement issues such as sampling effects and the construction of units for studying transmission. Simulations likely will be an important component of this kind of research as a means to assess the effects of our assumptions on the results of our analyses. We also need to determine how varying the properties of transmission and changing our measurement procedures influence the patterns we detect with cladistics and other phylogenetic techniques.

In summary, this volume is only a starting point, a place from which further theory, models, methods, and techniques can be constructed. The work reported here represents the frontier of phylogenetic applications within the social sciences and shows that by gaining an understanding of the abilities and limitations of existing phylogenetic methods, new statistics and models will emerge that more closely match the empirical nature of anthropological and archaeological phenomena. This is the kind of focused development that will be needed to move the phylogenetic study of cultural phenomena from the adaptation of biological techniques into a fully formed integrated field of research. We believe phylogenetic methods are ultimately a key development within the social sciences, as they offer a quantitative means of explaining human diversity. There is still much to accomplish, but it promises to be exciting work.

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