It would be rash to generalize too far from limited results such as these, at least until we have a much broader set of comparable studies based either on linguistic signal (as here), or (more indirectly) on cladistic studies of cultural traits themselves, such as projectile points (O'Brien and Lyman 2004, also chapters 11 and 12, this volume), pottery (Collard and Shennan 2000, also chapters 13 and 14, this volume), carpets (Tehrani and Collard 2002), or baskets (Jordan and Shennan 2003, also chapter 4, this volume). Here, we end by emphasizing two points. First, patterns of interaction among cultural, genetic, and linguistic evolution are likely to depend on the scale of the study. Second, simple phylogenetic methods such as those used here have the potential to lend rigor to cultural continuity models used in interpretations of prehistory (Huffman 1984; Schmidt 1978) and, as this study shows, can produce somewhat unexpected results.

Lastly, as regards the rashness of generalization, we should stress that very different processes responsible for cultural diversity characterize different parts of the world. Thus the well-attested demic expansions across Polynesia (Gray and Jordan 2000), central Africa (Holden 2002), and Eurasia (Renfrew 1992) may be very specific to particular zones (Nettle and Harriss 2003), perhaps ultimately because of geographic considerations (Diamond 1997). Here, we have tried to present a simple tool for examining one component of this complex story at a very local scale.

Acknowledgments

4

Branching versus Blending in Macroscale Cultural Evolution: A Comparative Study

Mark Collard, Stephen J. Shennan, and Jamshid J. Tehrani

The processes responsible for producing similarities and differences among cultures have been the focus of much debate in recent years, as has the corollary issue of linking cultural data with the patterns recorded by linguists and biologists working with human populations (e.g., Ammerman and Cavalli-Sforza 1984; Bateman et al. 1990; Bellwood 1996b, 2001; Bellwood and Renfrew 2003; Boyd and Richerson 1985; Boyd et al. 1997; Brace and Hinton 1981; Cavalli-Sforza and Cavalli-Sforza 1995; Cavalli-Sforza and Feldman 1981; Collard and Shennan 2000; Durham 1990, 1991, 1992; Goodenough 1999; Guglielmino et al. 1995; Henrich 2001; Hewlett et al. 2002; Hurles et al. 2003; Jordan and Shennan 2003; Kirch and Green 1987, 2001; Laland et al. 1995; Lumsden and Wilson 1981; Mesoudi et al. 2004; Moore 1994a, 1994b, 2001; O'Brien 1996; O'Brien and Lyman 2000a; Renfrew 1987, 1992, 2000b, 2001; Romney 1957; Shennan 1991, 2000, 2001, 2002; Smith 2001; Tehrani and Collard 2002; Terrell 1987, 1988; Terrell et al. 1997, 2001; Vogt 1964; Whaley 2001; Zvelebil 1995). To date, this debate has concentrated on two competing hypotheses, which have been termed the "branching" hypothesis (also known as the "genetic," "demic diffusion," and "phylogenesis" hypothesis) and the "blending" hypothesis (also known as the "cultural diffusion" and "ethnogenesis" hypothesis) (Bellwood 1996a; Collard and Shennan 2000; Guglielmino et al. 1995; Hewlett et al. 2002; Kirch and Green 1987; Moore 1994a, 1994b, 2001; Romney 1957; Tehrani and Collard 2002; Vogt 1964).

According to the branching hypothesis, similarities and differences among cultures are the result of a combination of predominantly within-group information transmission and population fissioning. The strong version of the hypothesis suggests that "transmission isolating mechanisms" (TRIMS) (Durham

1992) impede the transmission of cultural elements among contemporaneous communities. TRIMS are akin to the barriers to hybridization that separate species and include language differences, ethnocentrism, and intercommunity violence (Durham 1992). The branching hypothesis predicts that similarities and differences among cultures can be best represented by the type of tree diagram that is used in biology to depict the relationships among species. The hypothesis also predicts that there will be a close association between cultural variation and linguistic, morphological, and genetic patterning (e.g., Ammerman and Cavalli-Sforza 1984; Bellwood 1995, 1996b, 2001; Cavalli-Sforza and Cavalli-Sforza 1995; Cavalli-Sforza et al. 1988, 1994; Chikhi et al. 1998, 2002; Diamond and Bellwood 2003; Kirch and Green 1987, 2001; Renfrew 1987, 1992, 2000b, 2001; Sokal et al. 1989, 1991).

In contrast, supporters of the blending hypothesis (e.g., Dewar 1995; Moore 1994a, 1994b, 2001; Terrell 1987, 1988, 2001; Terrell et al. 1997, 2001) believe that it is unrealistic "to think that history is patterned like the nodes and branches of a comparative, phylogenetic, or cladistic tree" (Terrell et al. 1997: 184). They argue instead that human biological, linguistic, and cultural evolution are best characterized as "a constant flow of people, and hence their genes, language, and culture, across the fuzzy boundaries of tribes and nations, spreading within a region such as the Plains or the Southeast within a few generations, and across the continent in a few more" (Moore 2001: 51). That is, according to the blending hypothesis the patterns of similarity and difference among cultural assemblages are a consequence primarily of individuals in different groups copying each other's practices, exchanging ideas and objects, and marrying one another. The blending hypothesis predicts that similarities and differences among cultures can best be represented by a maximally connected network, or reticulated graph (Terrell 2001). It also predicts that there will be a close relationship between cultural patterns and the frequency and intensity of contact among populations, the usual proxy of which is geographic propinquity.

Recently it has been asserted that blending has been the major process in the ethnohistorical period and is likely to have always been more significant than branching in cultural macroevolution (e.g., Dewar 1995; Moore 1994a, 1994b, 2001; Terrell 1987, 1988, 2001; Terrell et al. 1997, 2001). In our view, this claim is problematic. Most contributions to the branching/blending debate have focused on macroscale cultural evolution in specific regions of the world often over relatively short spans of time (e.g., carpets made by Turkmen tribes between the eighteenth and twentieth centuries) rather than dealing with this form of cultural evolution as a general phenomenon (Borgerhoff Mulder 2001; Collard and Shennan 2000; Dewar 1995; Guglielmino et al. 1995; Hewlett et al. 2002; Jordan and Shennan 2003; Kirch and Green 1987; Moore and Romney 1994, 1996; Roberts et al. 1995; Tehrani and Collard 2002; Terrell et al. 1997, 2001; Welsch 1996; Welsch et al. 1992). A few papers

addressed the debate's key issues in universal terms (e.g., Moore, 1994a, 2001; Terrell 1987, 1988, 2001), but the evidence discussed in these is anecdotal. As such, we contend it is currently unclear whether cultural evolution is dominated by blending or by branching.

Here we discuss a study that goes some way toward rectifying this situation. In the study we assessed how treelike cultural datasets are compared to biological datasets. Essentially, we fitted the biologists' tree model to a group of cultural datasets and to a group of biological datasets that have been used to construct the relationships of species and higher-level taxa. We then compared the average fit between the cultural datasets and the model with the average fit between the biological datasets and the model. Given that the biological datasets can be assumed to have been structured by speciation—a branching process—our assumption was that if the blending hypothesis is correct and macroscale cultural evolution is dominated by blending processes, the fit between the tree model and the cultural datasets should be significantly worse than the fit between the tree model and the biological datasets. Conversely, if the blending hypothesis is incorrect and cultural macroevolution is dominated by branching processes, the fit between the model and the cultural datasets should be no worse than the fit between the model and the biological datasets.

Materials and Methods

Our first step was to obtain biological and cultural datasets suitable for phylogenetic analysis. Acquiring the biological datasets was straightforward, as they are readily available in the literature, and many of them can be downloaded from on-line databases such as TreeBASE (Sanderson et al. 1994). Accordingly, we assembled a set of twenty-one biological datasets. We selected only datasets that have been used to reconstruct the relationships of species and higher-level taxa, assuming that the taxa have been structured by the branching process of speciation. Datasets pertaining to simple organisms (e.g., viruses, bacteria) and subspecies of complex organisms were avoided on the grounds that they may have been affected by blending processes (Mesoudi et al. 2004). An effort was made to include a broad range of taxa and characters. Thus, the biological datasets included DNA data for lizards, lagomorphs, and carnivores; morphological data for fossil hominids, seals, and ungulates; and behavioral data for bees, seabirds, and primates.

Currently, cultural datasets suitable for phylogenetic analysis are much less easy to come by than their biological counterparts. We had three datasets in our possession from previous work we had conducted on this topic (Collard and Shennan 2000; Jordan and Shennan 2002; Tehrani and Collard 2002). To these we were able to add three datasets from the literature (Jorgenson 1969; O'Brien et al. 2001; Welsch et al. 1992). In addition, Katerina Rexová of Charles University, Czech Republic, kindly provided us with data from her recent analysis of the relationships among Indo-European languages (Rexová

et al. 2002). This gave us a total of seven cultural datasets with which to work. Details of the biological and cultural datasets are provided in table 4.1.

Thereafter, we used PAUP* (Swofford 1998) to evaluate how well the most parsimonious tree explains the distribution of similarities and differences within

Table 4.1
Datasets Used in Analyses

Dataset	Source
Australasian teal mtDNA	Kennedy and Spencer (2000) [a, b]
Corbiculate bee behavior	Noll (2002)
Pelecaniforme bird behavior	Kennedy et al. (1996)
Anoles lizard morphology	Guyer and Savage (1986) [a]
Primate behavior	DiFiore and Rendall (1994)
Strepsirhine morphology	Yoder (1994)
Hominid morphology	Lieberman et al. (1996)
Platyrrhine morphology	Horowitz et al. (1998) [c]
Ungulate morphology	O'Leary and Geisler (1999) [a, d]
Phalacrocoracid bird mtDNA	Kennedy et al. (2000) [e]
Phocid seal morphology	Bininda-Edwards and Russell (1996) [a]
Hawaiian fruitfly mtDNA	Baker and DeSalle (1997) [a, f]
Hominoid craniodental morphology	Collard and Wood (2000) [g]
Carnivore mtDNA	Wayne et al. (1997) [a]
Mammal mtDNA (with emphasis on Malagasy primates)	Yang and Yoder (2003) [h]
Carnivore mtDNA (with emphasis on Malagasy taxa)	Yoder et al. (2003) [h]
Mammal mtDNA	Yoder and Yang (2000) [h]
Insectivore mtDNA	Stanhope et al. (1998) [a, i]
Lagomorph mtDNA	Halanych and Robinson (1999) [j]
Hominoid soft-tissue morphology	Gibbs et al. (2002)
Anolis lizard mtDNA	Jackman et al. (1999) [a, k]
Indo-European lexical items	Rexová et al. (2002) [l]
Neolithic pottery	Collard and Shennan (2000)
California Indian basketry	Jordan and Shennan (2003)
North American projectile points	O'Brien et al. (2001)
Salish cultural practices	Jorgensen (1969)
New Guinea material culture	Welsch et al. (1992)
Turkmen weaving designs	Tehrani and Collard (2002)

a Downloaded from TreeBASE.
b Data for ATPase 6, ATPase 8, and 12S genes.
c Craniodental data.
d Data from runs 5 and 6.
e Data for 12S, ATPase 6, and ATPase 8 genes; provided by Martyn Kennedy, Department of Zoology, University of Otago, New Zealand.
f Data from "all genes" analysis.
g Qualitative dataset.
h Downloaded from the Web site of Anne Yoder, Yale University.
i Data for 12S-16S genes.
j Data for 12S gene.
k Data for ND2 gene and tRNA.
l Provided by Katerina Rexová of Charles University, Czech Republic.

each dataset. In all the analyses, the characters were treated as unordered, and the most parsimonious tree was identified by means of the heuristic-search routine. The goodness-of-fit measure we used was Farris's (1989a, 1989b) "retention index" (RI). Equivalent to Archie's (1989) "homoplasy excess ratio maximum index" (Farris 1989b, 1991), the RI is a measure of the number of homoplastic changes (see chapter 1, this volume) a phylogenetic tree requires that are independent of its length. The RI is a useful goodness-of-fit measure when comparing diverse datasets because it is unaffected by either the number of taxa or the number of characters. The RIs for the twenty-one biological datasets and the seven cultural datasets are presented in table 4.2. Also shown in table 4.2 are RIs associated with most parsimonious phylogenetic trees derived from two cultural datasets that we were unable to include in our PAUP* analyses (Gray and Jordan 2000; Holden 2002). The RI for the Austronesian language dataset was kindly provided by Russell Gray of the University of Auckland. The RI for the Bantu dataset was obtained from the results section of Holden (2002).

In the next stage of the study, we compared the RIs of the twenty-one biological datasets with the RIs of the nine cultural datasets with a view to determining whether or not they are significantly different. This was accomplished with the Wilcoxon rank-sum test, which was implemented in the manner described by Swinscow (1977). The Wilcoxon rank-sum test employs the same statistic and yields the same results as the Mann-Whitney U-test (Sokal and Rohlf 1995).

Results

The RIs associated with the most parsimonious trees derived from the biological and cultural datasets (table 4.2) suggest that the fit between the tree model and the cultural datasets is little different from the fit between the model and the biological datasets. Not only are the averages similar, but the ranges are comparable. The mean, minimum, and maximum biological RIs are 0.60, 0.35, and 0.94, respectively. The corresponding figures for the cultural RIs are 0.60, 0.17, and 0.93. Thus, descriptive statistics do not support the hypothesis that blending is more important than branching in macroscale cultural evolution. On average, the cultural datasets appear to be no more reticulate than the biological datasets.

The results of the Wilcoxon rank-sum test are in line with the descriptive statistics. The sum of the ranks for the biological RIs is 321, and the sum of the ranks for the cultural RIs is 118. Since the 5-percent-level critical point of a nine versus twenty-one cases test is 95 (Swinscow 1977), and this is less than the sum of the ranks for the smaller set of RIs, the biological and cultural RIs are not significantly different according to the Wilcoxon rank-sum test. Thus, once again, the hypothesis that blending is more important than branching in cultural macroevolution is not supported.

Table 4.2
Goodness-of-Fit Values Associated with Most-Parsimonious Phylogenetic Trees Derived from 21 Biological and Nine Cultural Datasets

Datatset	RI [a]
Australasian teal mtDNA	0.94
Corbiculate bee behavior	0.94
Pelecaniforme bird behavior	0.84
Anoles lizard morphology	0.78
Primate behavior	0.73
Strepsirhine primate morphology	0.72
Hominid morphology	0.71
Platyrrhine morphology	0.70
Ungulate morphology	0.69
Phalacrocoracid bird mtDNA	0.65
Phocid seal morphology	0.60
Hawaiian fruitfly mtDNA	0.50
Hominoid craniodental morphology	0.49
Carnivore mtDNA	0.48
Mammal mtDNA (with emphasis on Malagasy primates)	0.47
Carnivore mtDNA (with emphasis on Malagasy taxa)	0.47
Mammal mtDNA	0.44
Insectivore mtDNA	0.44
Lagomorph mtDNA	0.39
Hominoid soft-tissue morphology	0.38
Anolis lizard mtDNA	0.35
Indo-European lexical items	0.93
Neolithic pottery	0.72
California Indian basketry	0.71
North American projectile points	0.70
Salish cultural practices	0.63
Bantu lexical items	0.59
New Guinea material culture	0.52
Turkmen weaving designs	0.44
Austronesian lexical items	0.17

[a] RI = retention index: a maximum RI of 1 indicates that the tree requires no homoplastic change, and the level of homoplasy increases as the index approaches 0.

Discussion

The failure of our analyses to support the claim that blending has always been the dominant macroscale cultural evolutionary process is in line with

region-specific quantitative studies that have been published to date (Borgerhoff Mulder 2001; Collard and Shennan 2000; Guglielmino et al. 1995; Hewlett et al. 2002; Jordan and Shennan 2003; Moore and Romney 1994, 1996; Roberts et al. 1995; Tehrani and Collard 2002). Several of these studies have focused on cultural variation among villages on the northern coast of New Guinea, using geographic distance and linguistic affinity as proxies for blending and branching, respectively. Using regression and correspondence analysis of presence/absence data, Welsch et al. (1992; see also Welsch 1996) found that similarities and differences among sets of material culture from the villages were strongly associated with geographic propinquity and unrelated to the linguistic relations of the villages. In contrast, correspondence and hierarchical log-linear analyses of frequency data carried out by Moore and colleagues (Moore and Romney 1994; Roberts et al. 1995) indicated that geography and language have equally strong effects on the variation in material culture among the villages. Moore and Romney (1996) obtained the same result in a reanalysis of Welsch et al.'s presence/absence data using correspondence analysis, thereby accounting for one potential explanation for the difference in findings, namely the use of different data sets. Recent work by Shennan and Collard (2005) confirms Moore and Romney's assessment that a combination of both branching and blending was operating in this case.

Three quantitative studies (Borgerhoff Mulder 2001; Guglielmino et al. 1995; Hewlett et al. 2002) have examined cultural macroevolution in African societies. The study by Guglielmino et al. (1995) explored the roles of branching, blending, and local adaptation in the evolution of forty-seven cultural traits among 277 African societies. The traits were divided into six categories ("family and kinship," "economy," "social stratification," "labor division by sex," "house," and "various other"), and then correlation and clustering analyses were undertaken to determine which of three models best explained the distribution of the traits in each category: demic diffusion, environmental adaptation, or cultural diffusion. Guglielmino et al. found that the "family and kinship" traits were best explained by the demic-diffusion model, whereas the "labor division by sex" and "various other" traits were best explained by the cultural-diffusion model. The distributions of the traits in the other three categories were found to be affected by demic diffusion, environmental adaptation, and cultural diffusion.

Hewlett et al. (2000) investigated the processes responsible for the distribution of 109 cultural attributes among thirty-six African ethnic groups. Using measures of genetic, linguistic, and cultural distance, together with an index of geographic clustering, they tested the same explanatory models as Guglielmino et al. (1995)—demic diffusion, environmental adaptation, and cultural diffusion. They found that 32 percent of the cultural attributes could not be linked with an explanatory model and that the distributions of another

27 percent of the cultural attributes were compatible with two of the models. Of the remaining cultural attributes, 18 percent were compatible with demic diffusion, 11 percent were compatible with cultural diffusion, and just 4 percent were compatible with local invention.

Borgerhoff Mulder (2001) examined correlations among cultural traits associated with kinship and marriage patterns in thirty-five East African societies. She found that when phylogenetic relationships were taken into account, the data supported roughly half the number of statistically significant correlations returned by analyses of phylogenetically uncorrected data. These results failed to support Borgerhoff Mulder's preferred hypothesis, which is that adaptation to local environments plus diffusion between neighboring populations erase any phylogenetic signature. Were that the case, the correlations between different traits in the phylogenetically controlled analysis would have returned similar results to a conventional statistical analysis of the raw data. This was not the case. However, Borgerhoff Mulder's results also do not lend unqualified support to the branching hypothesis either, in that a high proportion of correlations remained unaffected by phylogenetic correction. In these cases, the trace of descent is obscured either by a relatively fast rate of cultural evolution and adaptation or by the mixing and merging of cultural groups that has been reported in ethnographic and historical sources on East African societies. Thus, the three African studies provide evidence for the operation of both branching and blending processes (see chapter 3, this volume).

Four other quantitative contributions to the branching/blending debate have been published—those by Chakraborty et al. (1976), Collard and Shennan (2000), Jordan and Shennan (2002), and Tehrani and Collard (2002). The study by Chakraborty et al. used regression analysis to examine the relationships among genetic variability, geographic distance, degree of Caucasoid admixture, and cultural and linguistic dissimilarity in seven Chilean Indian populations. The analyses returned significant correlations between geographic distance and genetic distance, geographic distance and cultural dissimilarity, and genetic distance and cultural dissimilarity. Linguistic dissimilarity and degree of Caucasoid admixture were not significantly correlated with the other variables or with each other. Thus, Chakraborty et al.'s analyses supported the blending hypothesis.

Collard and Shennan (2000) used cladistics to examine the evolution of assemblages of pottery from Neolithic sites in the Merzbach Valley, Germany. Their first set of analyses focused on assemblages from four settlements that have evidence for occupation throughout the whole of the ten-phase period. They conjectured that if the branching hypothesis is correct, analyses of the assemblages should divide them into the same groups in consecutive phases. On the other hand, if the blending hypothesis is accurate, the analyses should separate the settlements into different groups in consecutive phases. The re-

were not wholly compatible with either hypothesis. Rather, they indicated that branching and blending both were involved in the generation of the pottery assemblages.

Collard and Shennan's second set of analyses focused on three instances in which a new pottery assemblage appears. They reasoned that if the branching hypothesis is correct, then the newly founded assemblages should have a single parent assemblage in the preceding phase. Conversely, if the blending hypothesis is accurate, then the newly founded assemblages should have multiple parents in the preceding phase. This set of analyses supported the branching hypothesis rather than the blending hypothesis. Overall, therefore, Collard and Shennan's analyses of the Merzbach Valley early Neolithic pottery supported the branching hypothesis more strongly than the blending hypothesis.

Tehrani and Collard's (2002) study examined decorated textiles produced by Turkmen groups between the eighteenth and twentieth centuries. Two sets of cladistic analyses were carried out. The first focused on the period before the Turkmen were incorporated into the Russian Empire. These analyses indicated that in the pre-colonial period the evolution of Turkmen textile designs was dominated by branching. A randomization procedure (the permutation tail probability test) suggested that the data contained a phylogenetic signal, and parsimony analysis indicated that the data fit the tree model associated with cultural branching reasonably well. The fit between the model and data was not perfect, indicating that blending played a role in the evolution of Turkmen culture. However, goodness-of-fit statistics and a second randomization procedure (bootstrapping) suggested that blending was markedly less important than branching. According to the goodness-of-fit statistics, about 70 percent of the similarities among the assemblages were homologous, and approximately 30 percent were homoplastic. This is compatible with borrowing being responsible for a third of interassemblage resemblances.

Tehrani and Collard's second set of analyses dealt with the weavings produced while the Turkmen were ruled by the Russians. These analyses suggested that the changes experienced by the Turkmen after their incorporation into the Russian Empire led to a greater role for blending in Turkmen cultural evolution. Branching remained the dominant cultural evolutionary process, but the importance of blending increased. The goodness-of-fit statistics indicated that roughly 60 percent of the interassemblage resemblances are homologous, and roughly 40 percent are homoplastic. This is consistent with more intertribal borrowing of designs and motifs. Tehrani and Collard concluded that the two sets of analyses supported the branching hypothesis more strongly than the blending hypothesis.

Contrasting findings were obtained by Jordan and Shennan (2003), who used cladistics to examine variation in California Indian basketry in relation to linguistic affinity and geographic proximity. Jordan and Shennan carried out three sets of cladistic analyses. In the first, they used the permutation tail

probability test to determine whether or not their basketry datasets (coiled baskets, twined baskets, all baskets) contain a phylogenetic signal. Analysis suggested that a significant phylogenetic signal was present in all three datasets. In the second set of analyses, Jordan and Shennan used a goodness-of-fit statistic (the consistency index) to assess the fit between the datasets and the bifurcating-tree model. Analysis suggested that the phylogenetic signal detected by the permutation tail probability test was weak. The fit between the datasets and the bifurcating-tree model was weak in all three analyses. In the third set of analyses, Jordan and Shennan used a statistical test developed by Kishino and Hasegawa (1989) to assess the fit between the datasets and trees reflecting linguistic relationships, geographic distance, ecological similarity, and adjacency (presence of shared borders). This test enabled them to distinguish between two different potential sources of homoplasy—independent invention and blending.

In the analysis of the complete sample of baskets, the fit between the dataset and the adjacency tree was considerably better than the fit between the dataset and the other trees. This suggested that blending had a larger impact on the distribution of similarities and differences among the basketry assemblages than branching or adaptation to local environments. In the analysis of only coiled baskets, blending was also found to play a more significant role than branching or adaptation to local environments. The analysis of the twined baskets contrasted with the preceding analyses in that the language tree fitted the dataset better than the other trees. This suggested that branching was more important in generating the twined baskets than blending or adaptation to local environments. Jordan and Shennan concluded on the basis of these results, and results of a range of multivariate analyses, that the variation observed among Californian Indian baskets is best explained by blending rather than branching, or rather that linguistic affiliation has not provided a strong canalizing force on the distribution of basketry attributes, which appears to be mainly determined by geographical proximity and therefore, presumably, frequency of interaction.

Overall, the suggestion that blending has always been a more important cultural macroevolutionary process than branching is not supported by the region-specific quantitative studies that have been published to date. Blending seems to have been the dominant process in the evolution of the Chilean and Californian datasets, but branching was at least as important as blending in generating the other datasets.

Conclusions

The results of the comparative study described here do not support the recent claim that blending, or ethnogenetic, processes such as trade and exchange have always been more important in macroscale cultural evolution than the branching, or phylogenetic, process of within-group information trans-

mission plus population fissioning. Collectively, the cultural datasets in our sample do not differ significantly from the biological datasets in terms of how treelike they are. The claim that blending has always been more important than branching in cultural macroevolution is also not supported by the region-specific quantitative assessments of cultural evolution that have been published to date. Blending processes clearly structure some datasets, but branching processes are equally clearly responsible for structuring other datasets. It appears, therefore, that branching cannot be discounted as a macroscale cultural evolutionary process. This in turn suggests that rather than deciding how cultural macroevolution has proceeded a priori (e.g., Moore 1994a, 1994b; Terrell 1988, 2001; Terrell et al. 1997, 2001), researchers need to ascertain which model or combination of models is relevant in a particular case and why.