



Culture, space, and metapopulation: a simulation-based study for evaluating signals of blending and branching[☆]



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ABSTRACT

This paper explores the robustness of phylogenetic methods for detecting variations in branching and blending signals in the archaeological record. Both processes can generate a spatial structure whereby cultural similarity between different sites decays with increasing spatial distance. By generating a series of artificial records through the controlled and parameterised environment of an agent-based simulation, we: a) illustrate the weakness and the strength of different analytical techniques (empirical distogram, Mantel test, Retention Index, and δ -score); b) determine whether they are capable of assessing how spatial isolation determines cultural diversity; and c) establish whether they can detect variations in the nature of horizontal transmission over time. Results suggest that variables other than the spatial range of interaction (e.g. the frequency of fission events, population dynamics, and rates of cultural innovation) have different effects on the output of some phylogenetic analyses.

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1. Introduction

The spatial patterning of culture (*sensu* Childe, 1929) can be explained by three interrelated processes. Two communities might share a number of cultural traits due to: 1) a parallel and convergent adaptation to similar selective pressures; 2) common ancestry and inheritance (*branching*); and 3) horizontal transmission by means of inter-group interaction (*blending*) (Mace and Pagel, 1994; Borgerhoff Mulder et al., 2006; Collard et al., 2006; Mace and Jordan, 2011; for the earliest accounts of this problem: Boas 1896, Kroeber, 1948). These processes are all characterized by a deep relationship with space (Freckleton and Jetz, 2009; Premo and Scholnick, 2011): the positive autocorrelation of most climatic and environmental variables ensures that two communities in close distance are likely to share similar environment and selective pressures; offspring settlements emerging from fission events are often located in spatial proximity; and inter-group interaction and possible exchange of information are shaped by a distance decay. Albeit the exact scale and nature of the spatial structuring may differ between these processes, the general assumption is that,

other things being equal, the cultural similarity between two communities will decay as a function of their physical inter-distance.

Consequently, samples cannot be regarded as truly independent, as different communities might share similarities due to common ancestry and interaction, affecting in turn the inference of cultural processes (Loftin, 1972; Mace and Pagel, 1994). Moreover, analysing the spatial distribution of cultural traits is often not sufficient to discern which, among the three processes listed above, determined the observed pattern.

Yet this spatial structure plays a pivotal role in many disciplines and its implications in archaeology are paramount (e.g. Lipo et al., 1997; Shennan and Bentley, 2008; Premo and Scholnick, 2011). If we ignore instances of adaptive convergent evolution and focus exclusively on neutral traits (Dunnell, 1978), the cultural similarity between two communities is the result of *branching* and *blending*.¹ Several authors have supported one or the other as the dominant force in cultural evolution, with their argument based on both empirical and theoretical grounds (see Collard et al., 2006 for a review).

Part of this discussion was also fomented by a methodological debate on whether some of the analytical techniques developed in

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¹ The convergent evolution of neutral traits is *possible* but their likelihood is heavily biased by the granularity of our classification system, and their occurrence can be regarded as negligible in most cases (O'Brien and Lyman, 2003: 154).

evolutionary biology are applicable for cultural data or not (see Borgerhoff Mulder, 2001; Collard et al., 2006; Eerkens and Lipo, 2007; Gray et al., 2007; Currie et al., 2010; Nunn et al., 2010). The reconstruction of phylogenetic trees (O'Brien et al., 2001; O'Brien and Lyman, 2003) offers a good example of this. One of its core assumptions relies on the notion that most of the shared traits are a result of common ancestry rather than the consequence of horizontal transmission between groups. If the dominant process is the latter, hypothesised trees will not be able to accurately represent the population history. Recent studies are thus increasingly coupling the reconstruction of phylogenetic trees with network-based analysis (see e.g. Coward et al., 2008; Cochrane and Lipo, 2010), an alternative set of techniques where blending is represented as a reticulated graph (see Heggarty et al., 2010 for a review). Yet, despite methodological discussions over a decade, inferring cultural interaction and blending processes from the study of material culture is still a complex task that often requires the support of external data (e.g. language trees, as in Tehrani et al., 2010) or an excellent prior knowledge of historical events (e.g. Beheim and Bell, 2011), both unavailable in most archaeological contexts.

This paper contributes to this methodological debate by investigating whether the rich body of tools borrowed from biological sciences is sufficiently robust for archaeological inferences on the evolutionary history of a human population. We approach this problem by developing a “methodological” simulation (Lake, 2010:15), whereby we first generate a series of artificial archaeological records with known and parameterised evolutionary processes and, subsequently, determine whether specific methods are capable of identifying and distinguishing these. This is an increasingly common solution for evaluating the efficiency of a variety of analytical tools in archaeology (e.g. Eerkens et al., 2005; Surovell and Brantingham, 2007; Rubio-Campillo et al., 2011).

The paper is structured as follows. Section 2 reviews some of the methods used to evaluate branching, blending, and patterns of spatial variation in culture; Section 3 introduces the simulation model and its scientific rationale, as well as the proposed experiment design; Section 4 illustrates our results; Section 5 discusses their broader implications in archaeology; and Section 6 presents our conclusions.

2. Branching and blending in space

Consider a matrix **C** with rows representing communities located at different spatial coordinates, columns representing specific cultural traits, and cell values indicating their presence/absence (or frequency). The character matrix **C** can be converted into a cultural distance matrix **H** based on the dissimilarity **h** between different communities, so that communities that share a similar distribution of traits (i.e. have the same traits) can be regarded as “closer”. The actual computation of **h** can vary according to the type of data and the underlying assumptions on the nature of the traits. For example, presence/absence data are usually measured using either *Hamming* or *Jaccard* distances. The former considers the presence and absence as character states, so that shared absence is treated in the same way as shared presence. Jaccard distance considers instead only the co-presence of traits, ignoring the number of shared absences. Both measures have been extensively used for archaeological analysis; for example Cochrane and Lipo (2010) examined the cultural evolution of Lapita pottery using Hamming distance, while Shennan and Bentley (2008) studied the decorative traits of LBK pottery using Jaccard distance.

As discussed in Section 1, both branching and blending events are expected to generate a pattern where cultural similarity decays as a function of spatial distance. We can visually assess this

by plotting, for each pair of sites, their spatial inter-distance against the dissimilarity **h**. The statistical significance of the correlation between the two variables cannot be computed by standard techniques, as distance values are not independent between observations (e.g. shifting a site location in space will change the entire distance matrix), hence a permutation based statistical test known as the Mantel test (Mantel, 1967) is commonly adopted. This has been used to assess patterns of cultural discontinuities over space for a variety of purposes, from the empirical support of a “great-ape culture” (Van Schaik et al., 2003) to the assessment of the cultural geography of European folktale tradition (Ross et al., 2013). Archaeological applications include the analysis of stylistic differences in basketry (Jordan and Shennan, 2003) and pottery (Hart, 2012), as well as diversity in farming practice (Zhang et al., 2010) and variation in biological traits inferred from dental metrics (Scherer, 2007). Although the exact interpretation of the mantel test varies between these case studies, they substantially agree on interpreting the presence of positive correlation as a proxy of cultural interaction (Jordan and Shennan, 2003; Hart, 2012).

The Mantel test provides a valuable tool for testing the correlation between space and cultural dissimilarity, but does not offer direct insights on whether the primary generative process behind the observed pattern is branching or blending. One way to approach this problem is to assume a branching process, generate the best bifurcating tree model from the empirical data, and examine its goodness of fit. This will require the choice of an algorithm to search among all possible trees using some selection criterion (e.g. parsimony, maximum likelihood, etc.; see O'Brien and Lyman, 2003, Coward et al., 2008; etc.) and a measure of goodness of fit which takes into account the frequency of patterns that are not explained by branching (e.g. parallel evolution, reversion, blending, etc.). The most commonly adopted statistic for the latter is the Retention Index (RI), equivalent to the ratio $(g - s)/(g - m)$, where g is the maximum number of character changes required on a tree where all taxa are equally related, m is the total character states changes expected given by the character matrix **C**, and s is the actual number of state changes on the proposed tree (Farris, 1989-a, 1989-b). RI ranges between 1 (a perfect branching tree) and 0 (complete *homoplasy*, i.e. character states are present in unrelated branches of the proposed tree).

RI, however, does not provide a direct evaluation of the branching–blending hypothesis, as no threshold measure can be used to make a definitive statement on whether a given set of empirical data provides robust evidence of each process. Thus, archaeological interpretations of RI have often relied on Collard et al.'s (2006) meta-analysis. The study, based on the statistical comparison of 42 samples from biological and cultural data (21 for each group), showed that branching can be a dominant force in cultural evolution, with biological RIs ranging between 0.35 and 0.94, and cultural RIs between 0.42 and 0.78. Values lower than this range are rarely reported in the archaeological literature and hence few works have explored their implications. Cochrane and Lipo's (2010) obtained fairly low RI values (0.35 and 0.49) for their study of Lapita pottery, and they explain their result as evidence of a blending process with the additional support of network analysis. Coward et al.'s (2008) study on the spread of plant economy in Neolithic Europe also returned a low fit (0.46), which they explain as a possible effect of reticulation processes after initial spreading and branching events (supported by detailed analysis of individual clades in relation to the geographic distribution).

An alternative approach to RI, based on a direct assessment of the cultural distance matrix rather than the reconstruction of hypothetical trees, is offered by Holland et al.'s δ -score (2002). The

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