Introduction

Evolutionary approaches to cultural and linguistic diversity

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Evolutionary approaches to cultural change are increasingly influential, and many scientists believe that a 'grand synthesis' is now in sight. The papers in this Theme Issue, which derives from a symposium held by the AHRC Centre for the Evolution of Cultural Diversity (University College London) in December 2008, focus on how the phylogenetic tree-building and network-based techniques used to estimate descent relationships in biology can be adapted to reconstruct cultural histories, where some degree of inter-societal diffusion will almost inevitably be superimposed on any deeper signal of a historical branching process. The disciplines represented include the three most purely 'cultural' fields from the four-field model of anthropology (cultural anthropology, archaeology and linguistic anthropology). In this short introduction, some context is provided from the history of anthropology, and key issues raised by the papers are highlighted.

Keywords: evolution; cultural change; phylogenetics

1. INTRODUCTION: CULTURAL TRANSMISSION AND EVOLUTION

Evolutionary approaches to cultural change are increasingly influential, and many scientists believe that a 'grand synthesis' is now in sight (e.g. Mesoudi, Whiten & Laland 2006). At the 'microevolutionary' scale, modern theories of cultural evolution recognize that cultural traditions and innovations are socially transmitted person-to-person between and within generations (respectively, by vertical or oblique and by horizontal transmission routes; Cavalli-Sforza & Feldman 1981), with learners applying generalized rules of thumb in choosing when to engage in independent trial-and-error learning, and in selecting whose example to copy when this is the preferred strategy (transmission biases; Boyd & Richerson 1985). Preservation of a historical signal within the cultural traditions carried by populations depends on traits being consistently selected and replicated, often with some degree of modification, ensuring that they survive from one generation to the next.

Cultural 'macroevolution' refers to the historical processes that explain cultural similarities and differences between human populations arising from such

repeated copying with modification (Mulder *et al.* 2006). Mesoudi *et al.* (2006), who propose a multi-disciplinary framework for the Darwinian analysis of cultural dynamics, draw an explicit parallel between evolutionary archaeology, cultural anthropology and comparative anthropology (among the cultural sciences), and the macroevolutionary disciplines in biology (respectively, palaeobiology, biogeography and systematics). Historical linguistics should certainly be added to the list of cultural disciplines with a macroevolutionary focus.

This special issue, which derives from a symposium held by the AHRC Centre for the Evolution of Cultural Diversity (University College London) in December 2008, focuses on the latest developments in this rapidly expanding field. The main focus is on how the phylogenetic tree-building and network-based techniques used to estimate descent relationships in biology can be adapted to reconstruct cultural histories, where some degree of inter-societal diffusion will almost inevitably be superimposed on any deeper signal of a historical branching process. The disciplines represented include the three most purely 'cultural' fields from the four-field model of anthropology (cultural anthropology, archaeology and linguistic anthropology). Integration with the fourth field, physical or biological anthropology, is being actively pursued elsewhere (e.g. Bellwood & Renfrew 2002), but would have required a separate issue in its own right.

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One contribution of 14 to a Theme Issue 'Cultural and linguistic diversity: evolutionary approaches'.

It is well known that Darwin saw similarities between the evolution of species and the evolution of languages (van Wyhe 2005), and that the use of genealogical approaches in nineteenth century historical linguistics (e.g. Schleicher 1863) paralleled their use in zoology. As Sereno (1991) points out, languages share with biological organisms the properties of heritability (transmission to offspring); mutation; deme-based structuring of transmission pathways and allopatric (e.g. geographical) and sympatric (e.g. sociolinguistic) divergence mechanisms. Recent phylogenetic and statistical approaches have explored this analogy further, focusing both on applying novel phylogenetic techniques and on explaining empirical heterogeneity in evolutionary rates for different linguistic traits (e.g. Pagel 2009). Descent-with-modification has also been a precept informing studies of manuscript traditions in the genealogical or stemmatological approach since the nineteenth century (Robins 2007), with recent studies applying formal phylogenetic methods (e.g. Barbrook *et al.* 1998) and modelling the survivorship of variants in terms of an underlying birth–death process (Weitzman 1987; Cisne 2005).

Similar approaches to the evolution of stylistic attributes of material culture can also be traced to the late nineteenth century, such as Evans' attempt to reconstruct the descent histories of variants of design of British Iron Age coins (descendants of copying chains originating ultimately with Macedonian exemplars). Reviewing the development of his own thinking on this matter, Evans (1890) noted that it was a prerequisite for cultural descent with variation '1st, that the successive issues or generations of coins should resemble each other sufficiently to pass as current together; but 2nd, that, art being imperfect, there must have been more or less important variations and modifications in the successive dies that were engraved' (p. 422). He also argued that (other things being equal) there should be a tendency for designs to evolve under unconscious selection for symmetry, and for ease of execution. Much recent experimental work on cultural transmission chains builds on these kinds of early insights and conjectures (e.g. Smith *et al.* 2008).

The transmission histories of functional aspects of traditional technologies, and of social structure (kinship systems and political organization), have been less often analysed from a phylogenetic perspective, because it is usually assumed that such cultural attributes come under stronger selective pressure (and are therefore more prone to horizontal diffusion and to adaptive convergence). However, such assumptions need to be tested, the *locus classicus* being Galton's comment in 1889 on a paper by Tylor purporting to show adaptive convergence (and an evolutionary societal trajectory) based on empirical correlations, in a sample of 350 cultures, between type of kinship system (descent and marriage rules) and other measures of cultural complexity (Galton 1889; Tylor 1889). Galton commented that these cultures could not be assumed to be statistically independent of one another, and that the case for convergent evolution could not be made until commonalities had been

controlled for that are simply owing to common historical descent or to cultural borrowing. Galton's problem is a problem for testing hypotheses of the adaptive cultural evolution of social systems under selection (e.g. Mace & Pagel 1994), but the flipside is that there may be an underlying conservatism in the transmission of social institutional attributes that could enable historical inferences to be made about cultural ancestry (e.g. Jones 2008). The implication is that societies with shared cultural histories may also inherit common social structural features, and this has been supported empirically by Guglielmino *et al.* (1995).

Such aspects of anthropology's disciplinary history have shaped the content and structure of this special issue.

2. UNITS AND MODELS OF CULTURAL TRANSMISSION

A number of contributors to this issue address general principles of cultural transmission and macroevolutionary dynamics. Most contributors assume the validity of their units of analysis, whether linguistic vocabulary items or material cultural design traits. However, O'Brien *et al.* (2010) focus explicitly on this matter, examining cultural units of transmission that have some material correlate in the archaeological record in order to reconstruct the evolution of traditions in prehistory. They focus on the hierarchical organization of the underlying ideational units into 'design recipes', and their pattern of transmission. Although they have in mind the transmission of recipes for production of artefact designs sampled from a larger design space, their analysis also has implications for the transmission of language-encoded traits (e.g. semantic networks, sociolinguistic conventions). They discuss the circumstances in which cultural traits should be expected to be transferred in a piecemeal fashion, and in which they might be more likely to be transmitted as a coherent package.

Historical reconstruction of cultural descent histories presents all the familiar limitations of inverse problems (cf. Boyd & Richerson 2008). In assessing the fit between a model and a set of data, forward approaches to modelling use the known dynamics of the empirical system to predict outcomes for a given parameter constellation. In inverse problems, the outcomes are known to some degree, but the dynamics of the empirical system and the parameter constellation are unknown and must be estimated by 'reverse engineering'. Typically in such situations, difficulties arise where parameter values cannot be reliably estimated from observable data, and where it can be shown that alternative models and alternative parameter constellations would yield the same observed outcomes (e.g. Steele *et al.* 2010). Simulation provides one solution, by enabling forward modelling of a simplified version of the historical system.

Focusing on cultural applications of cladistic methods to estimate historical descent relationships, Nunn *et al.* (2010) use simulations to explore the effects of rates of inter-societal diffusion and of innovation on the coherence and reliability of statistical indices of a phylogenetic branching signal (cf. Collard *et al.* 2006).

They suggest that a high value for one such index (the Retention Index; Farris 1989; Naylor & Kraus 1995) may be a reliable indicator that such rates were low and had limited influence on observed inter-societal cultural diversity. However, a low value for the Retention Index can have several causes and is therefore not a sufficient indicator of high inter-societal diffusion rates. Currie *et al.* (2010) use Nunn *et al.*'s simulation methodology to explore the robustness of inferences about adaptive convergence in sociocultural evolution, since horizontal transmission between societies only exacerbates 'Galton's problem' for historical interpretation. They find that such inferences are less robust in the presence of either high rates of piecemeal stochastic diffusion of individual traits between societies, or coupled stochastic transfers of the two traits whose correlation is being examined by comparative analysis. Estimating the tempo and mode of inter-societal diffusion therefore becomes crucial for any comparative cross-cultural analysis, if its statistical methodology requires that adaptive convergence be assumed to have been superimposed on a strictly tree-like population history.

Focusing on the more fundamental question of what factors affect rates of inter-societal cultural transfer, Boyd & Richerson (2010) suggest that cultural group selection provides one boundary-enforcing mechanism that may give rise to a coherent cultural phylogenetic signal. They outline the conditions for intergroup selection on cultural traditions using the Price equation (Price 1970), suggesting that social transmission biases can 'fix' one of a number of alternative solutions within a group when there are multiple cultural equilibria (e.g. local optima in artefact design space or in a space of possible social structures and social rules), with sorting mechanisms such as competitive group extinction, imitative intergroup copying and selective migration then favouring the group that has converged on a globally optimal solution. Kandler *et al.* (2010) illustrate such sorting processes using modified Lotka–Volterra competition equations to model language shift, suggesting that this can be seen as a form of selective cultural sorting based on contrasts in the underlying social and economic opportunities afforded by membership of competing linguistic communities. They address the conditions required for preservation of two parallel sets of traditions within a group (in this case, bilingualism and the preservation of the heritage encoded in the usages of an endangered language) by stabilizing multiple, sociolinguistically discrete domains of use.

In the absence of such selective forces, cultural traditions may diverge though drift-like processes affecting individual traits in a piecemeal way. Nerbonne (2010) examines the effects of geographical proximity on dialect similarity in the absence of strong large-scale social boundaries, showing through simulation that a process analogous to isolation-by-distance in genetics can lead to regularities in the sublinear relationships observed between dialect distance and geographical distance. His work emphasizes the importance of spatially localized social interaction biases for the evolution of cultural diversity in such traits.

3. CULTURAL MACROEVOLUTION AS AN INVERSE PROBLEM

Phylogenies (trees) typically describe ancestor–descendant relations between species—can they also be used to describe variation between cultures within the same human species? Do models for describing variation across species work well when looking at human cultural diversification (cf. Mace *et al.* 2005; Lipo *et al.* 2006)? Some of the clearest parallels lie between patterns of genetic and linguistic evolution. As with genes, languages are passed between generations and are modified; with enough time linguistic communities may eventually diverge, generating branching trees of historical relatedness. In historical linguistics, cognate occurrence is used to model common ancestry; results are affected by the choice of data, with the core lexicon or basic vocabulary evolving more slowly and consequently giving a stronger phylogenetic signal. There is an inevitable conformist bias reinforcing fidelity of transmission, in that language usage must be co-ordinated and errors corrected if intelligibility is to be maintained. However, even in historical linguistics it is increasingly clear that cases vary in the importance of the signals of branching processes and of areal diffusion. Heggarty *et al.* (2010) explore the value of phylogenetic network methods to characterize linguistic relationships at larger time and space scales, where the underlying processes discussed by Nerbonne may have been active. They show that such methods are preferable to methods that force a tree topology onto lexical data, and can bring to light distinct aspects of language history including both large-scale branching episodes, and small-scale local diffusion. They also caution that segregation of local interactions on linguistic grounds (for example, associated with rules defining group membership) can complicate the interpretation of branching signals in such datasets. Bowern (2010) explores similar issues in the context of Australian linguistic prehistory and the expansion of the Pama-Nyungan languages. Using NeighborNet (Huson & Bryant 2006) and a fractionation of lexical items into more and less borrowable semantic classes (based on the prior assumption that, for example, body part terms diffuse less readily, while words for local plants, animals and locally adapted artefact kinds will be adopted more readily by an incoming group) she is able to distinguish a geographically meaningful branching signal, as well as evidence for continuous areal diffusion.

In an analogous study not of linguistic vocabulary, but of stylistic variation in a particular material cultural tradition, Cochrane & Lipo (2010) explore the early population history of remote Oceania. They analyse design variation in the characteristic 'Lapita' pottery traditions of these initial colonists, highlighting some limitations of cladistic approaches if the history of such traditions was characterized by considerable inter-societal diffusion, and exploring network methodologies to identify such vectors of lateral transfer.

The topology of the underlying population history on which specific processes of cultural evolution are superimposed comes up in several other contributions. Revisiting 'Galton's Problem',

Fortunato & Jordan (2010) use phylogenetic techniques to fit a tree topology to Indo-European and Austronesian language histories (based on core vocabulary), and introduce methods to estimate ancestral states and stable equilibria for kinship systems within each of these language families. They are explicit that their methodology requires testable assumptions about the appropriateness of phylogenetic reconstructive techniques, and point out that their results will enable better-controlled analyses of the effects of social structure (for instance, sex-biased marital dispersal) on patterns of genetic diversity.

Others have meanwhile started to explore statistical techniques that might exploit parallels between the co-transmission of disparate cultural traits, and the biological processes of host–parasite co-speciation. At the heart of this approach is the assumption of some degree of parallel cladogenesis in two or more cultural lineages. Tehrani *et al.* (2010) introduce co-phylogenetic methods from biology to estimate the degree of parallel evolution of distinct traditions (for example, language and material culture), pointing out that in such situations a simple branching signal of perfect coevolution owing to common vertical descent can be confounded not just by inter-societal diffusion of the more borrowable tradition, but also by the loss of localized variants ('sorting' events) and by heterogeneous innovation rates. Using the 'jungles' algorithm (Charleston 1998) as implemented in TREE-MAP2.0 (Charleston & Page 2002), they illustrate the value of co-phylogenetic methods for teasing out such processes in empirical cases. In a thematically related analysis using different case studies and alternative statistical techniques, Jordan & O'Neill (2010) analyse linguistic and material cultural datasets from the Pacific northwest coast, comparing the results of cladistic reconstructions with those obtained using NeighborNet to estimate the degree of inter-societal diffusion of house-building traditions (and the extent to which such diffusion may have followed ethnolinguistic lines). They also raise the question of how closely inter-societal cultural transfers of house-building techniques may have reflected the marital transfer and residence rules of the gender whose members were most responsible for those techniques' transmission.

Finally, Gray *et al.* (2010) use NeighborNet (Huson & Bryant 2006) to analyse linguistic and material cultural datasets, and propose some new statistical indices of the level of reticulation in a phylogenetic network (in contrast with such cladistic measures as the Retention Index). Their approach recognizes that in historical analyses, anthropologists will typically be interested in both branching and diffusive processes and will wish to estimate the importance of each in any given case. Anthropologists will also typically want to estimate the degree of coupled transmission of disparate traits, to assess (for example) the extent to which material cultural attributes fractionate along ethnolinguistic lines. Gray *et al.*'s worked comparisons of Indo-European and Polynesian language history, and of Polynesian linguistic and material cultural diversity, illustrate the power of these new techniques.

4. FINAL COMMENT

The papers in this special issue illustrate the very significant contributions that evolutionary methods can bring to the cultural sciences, and also some of the key areas in which the greatest innovations are being made in method and theory. These papers also highlight the importance of the continued development of standardized and well-screened comparative datasets of linguistic, material cultural and social structural variation. Online archiving and public availability of both new software and new datasets will be critical for the further development of the field.

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