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CULTURE AND THE DARWINIAN RENAISSANCE IN THE SOCIAL SCIENCES AND HUMANITIES

(For a special issue of the *Journal of Evolutionary Psychology*, "The Darwinian Renaissance in the Social Sciences and Humanities")

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Abstract. A "Darwinian Renaissance" in the social sciences and humanities cannot occur until evolutionary theory can successfully explain rapid and cumulative cultural change. Here I review empirical evidence that much of human behaviour is culturally determined, emphasising the need to incorporate culture into evolutionary analyses of human behaviour. I also review theoretical work which shows that culture is genetically adaptive, belying any simplistic gene-culture dichotomy. Finally, I show how recent work analysing culture as an evolutionary system is beginning to answer the kinds of questions that are of interest to social scientists and humanities scholars. These include phylogenetic reconstructions of the historical relationships between languages, manuscripts, social customs and artifacts, and experimental simulations of the microevolutionary processes underlying patterns of cultural macroevolution.

Keywords: Culture, cultural evolution, evolution, human behaviour, social learning.

1. INTRODUCTION

Before discussing the potential for a Darwinian renaissance in the social sciences and humanities, I would like to briefly mention the actual Renaissance, the one that occurred in 15th and 16th century Europe. During this period, a group of scholars centred around Florence made a series of key discoveries and innovations in the arts and sciences. Artists such as Leon Battista Alberti drew on knowledge of optics and geometry to perfect the representation of perspective, while others refined depictions of light sources to produce hitherto unattained realism in paintings. Leonardo da Vinci, in addition to his great works of art, produced intricately detailed drawings of human anatomy and designs for various technological inventions. Architects and engineers such as Filippo Brunelleschi made key technical innovations in, for

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example, hoisting devices, allowing the construction of impressive structures such as the enormous dome of the Cathedral of Florence. Niccolo Machiavelli developed rational and logical analyses of political action, and in so doing is often said to have founded political science. In the following century these discoveries and innovations spread across the rest of Europe, facilitated by the recently invented printing press, and had a profound influence on the scientific, artistic and social development of various nations.

It seems to me that any effective "Darwinian renaissance" in the social sciences and humanities has to be able to explain the kind of rapid cultural change exemplified by the actual Renaissance. Why did it occur in Florence, rather than, say, Budapest or Paris? Why the 15th century and not the 11th, or the 17th? Was it just luck that the aforementioned inventors and artists were born around the same time and in the same place, or were they each the product of wider social and demographic factors? Did the aforementioned inventions and techniques spread purely because they were functionally superior to previous alternatives, or was there an element of chance in their appearance and subsequent diffusion? These are the kinds of questions that social scientists and humanities scholars want to answer. Unless it can be demonstrated that Darwinian methods provide additional insights into such problems beyond those obtained through traditional social science methods, a Darwinian Renaissance is neither likely to occur nor, indeed, warranted.

My aims in this paper are twofold, and with two distinct audiences in mind. My first aim is to show that culture plays an important role in shaping human behavioural variation, just as the mainstream (non-evolutionary) social sciences have traditionally argued, but against the views of some evolutionary behavioural scientists. In Section 2 I review empirical studies that support this claim, and highlight theoretical analyses which suggest that culture is genetically adaptive, i.e. that it is adaptive for genes to forego direct control over behaviour and let culture take over. My second aim is to demonstrate to social scientists and humanities scholars that evolutionary methods can be useful for analysing cultural change, and can offer something novel above and beyond (and not necessarily instead of) traditional social science methods. In Section 3 I give examples of where this is beginning to occur. A Darwinian Renaissance in the social sciences and humanities is only possible, I think, if evolutionary scholars accept the importance of culture, *and* if it can be demonstrated to social scientists and humanities scholars that evolutionary methods can tell them something useful beyond their current explanations.

2. WHY CULTURE IS IMPORTANT

2.1 Culture shapes human behavioural variation

In recent decades several disciplines have undergone a similar realisation that what once were thought of as human universals are actually rather specific to Western peoples, that non-Western people often show significantly different psychological and behavioural characteristics to Westerners, and that these difference are cultural in origin (HENRICH, HEINE and NORENZAYAN 2010). Of course, socio-cultural anthropologists have long described cultural variation in different societies worldwide. But it is only recently that this variation has been quantitatively and systematically documented. Some of the best work can be found in cross-cultural psychology (HEINE 2008; HEINE and NORENZAYAN 2006). Various psychological characteristics that were once thought to be human universals, such as the Fundamental Attribution Error (the tendency to attribute a person's actions to their stable, underlying dispositions) and cognitive dissonance (anxiety brought about by a mismatch between one's behaviour and one's views), have been found to be weaker or absent in non-Western (typically East Asian) people (HEINE and LEHMAN 1997; MORRIS and PENG 1994). Even basic perceptual and attentional processes have been found to vary culturally: Western and East Asian participants attend to different parts of scenes and faces, for example (BLAIS et al. 2008; MASUDA and NISBETT 2001), while perceptual illusions such as the Müller-Lyer effect that are found in people raised in industrialised environments are absent in people raised in non-industrialised countries (SEGALL, CAMPBELL and HERSKOVITS 1963).

Other experimental studies have employed methods used by economists, such as the Ultimatum Game, to find significant cross-cultural variation in cooperation and punishment across several small-scale societies (HENRICH et al. 2005; HENRICH et al. 2006). Political scientists have shown how values related to "civic duty", such as the tendency to vote or give to charity, vary across the United States according to the civic duty values of a person's European country of origin (RICE and FELDMAN 1997). So Americans who descend from Scandinavians, like present-day Scandinavians, have high levels of civic duty, while Americans who descend from Italy and Spain, like present-day Italians and Spaniards, have lower levels of civic duty. It seems that such values have been culturally transmitted via imitation or teaching from parent to child or teacher to pupil over several successive generations from the original European settlers to present-day Americans.

There are, of course, alternative explanations for this alleged cultural variation: the variation could be genetic (e.g. genes for cooperative behaviour or civic duty), or it could be individual (non-cultural) adaptation to local ecological conditions. Evidence against purely genetic explanations of behavioural variation comes from immigration studies: while East Asian immigrants to North America maintain the psychological traits of their country of origin, their children exhibit psychological traits intermediate between East Asians and Westerners, and their children's children are indistinguishable from Westerners (HEINE and NORENZAYAN 2006). This suggests that the aforementioned psychological variation is the result of horizontally-transmitted cultural norms rather than vertically-transmitted genes. Many technological and social innovations spread even more quickly than a single biological generation over the course of weeks, months and years (ROGERS 1995), far too quickly to be explained purely by genetic evolution.

While behavioural variation cannot be explained in terms of genetic differences between people living in different societies, some evolutionary psychologists hold the more reasonable view that putative cultural variation is the product of "evoked culture" (Gangestad, Haselton and Buss 2006; Nettle 2009). This explanation assumes that people everywhere are broadly genetically identical, and behavioural variation is caused by different genetically-specified responses to different ecological conditions such as resource availability or parasite prevalence, rather than culturally transmitted norms, values, beliefs etc. However, several systematic cross-cultural analyses have shown a double dissociation between behaviour and ecology that counts against the evoked culture hypothesis: the same behaviour can be observed in societies living in different ecological conditions, and different behaviours can be observed in societies living in the same ecological conditions (Guglielmino et al. 1995; Hewlett, De Silvestri and Guglielmino 2002). Furthermore, the existence of adaptation to local ecological conditions does not necessarily conflict with a transmitted culture origin: individual learning biases can generate adaptive responses to local conditions that are then transmitted through the local population via social learning (Richerson and Boyd 2005). A final strand of research that supports the notion that a substantial portion of human behavioural variation is the result of transmitted culture comes from developmental psychology, showing that children are geared to automatically and spontaneously copy the behaviour of others (Csibra and Gergely 2009; Lyons, Young and Keil 2007; Tomasello 1999), often in striking contrast to other great ape species (Herrmann et al. 2007; Horner and Whiten 2005). All of this evidence jointly demonstrates substantial cultural variation in human behaviour, such that any explanation of human behaviour that ignores transmitted culture will be inadequate and incomplete.

2.2 Culture is genetically adaptive

A robust body of formal evolutionary modelling shows that the capacity for culture can be genetically adaptive under a wide range of conditions. This leads to the somewhat non-intuitive, and often overlooked, prediction that it is in the genes' interests (metaphorically speaking) to forego direct control over behaviour and let culture take over (Plotkin 1995). On this view, the evidence reviewed in the previous section which demonstrates that much of human behaviour is culturally determined is rather unsurprising. Several formal analyses have explored the conditions under which social/cultural learning is adaptive relative to genetic inheritance and purely individual, asocial learning (Aoki, Wakano and Feldman 2005; Boyd and Richerson 1995, 1996; Kameda and Nakanishi 2003; Kendal, Giraldeau and Laland 2009; Rogers, 1988). These models, like many formal models constructed by evolutionary biologists, specify a population of organisms each of which possesses one of a set of different genotypes. In this case these genotypes determine whether the organism's behaviour is innate, learned individually or learned socially. The "innate" genotype directly specifies a particular behaviour for that organism, with this behaviour fixed at birth and not subject to modification by learning. The "individual learning" genotype causes its bearer to try out different behaviours during its lifetime and repeat those behaviours that have the highest payoffs. Finally, the "social learning" genotype causes its bearer to copy the behaviour of another organism in the population (either at random or according to some specific social learning strategy, such as preferentially copying the most successful organism: LALAND 2004). These genotypes are then inherited by subsequent generations of organisms in proportion to their bearers' fitness. Modellers can examine the conditions under which genotypes for social learning (i.e. culture) spread in the population at the expense of genotypes for innateness and genotypes for individual learning.

According to these models, learning (either individual or social) is favoured over innateness when environments change relatively rapidly, because genes cannot respond to rapid change that occurs within a single biological generation (AOKI et al. 2005; BOYD and RICHERSON 1988). Konrad Lorenz called this "generational deadtime" - the time in between receiving genes and passing them on during which genes cannot respond to novel environmental change (LORENZ 1969; see also PLOTKIN 1995). Learning allows organisms to adapt to novel environmental change that occurs during generational deadtime and that cannot be anticipated by genes in advance. And *social* learning is favoured over individual learning when environments do not change so rapidly such that copied behaviour is immediately out-of-date, and when it allows organisms to avoid the costs of individual learning. The latter can occur under two conditions (BOYD and RICHERSON 1995). The first is when organisms can selectively switch between individual learning and social learning, only employing social learning when individual learning is difficult or costly. Experimental evidence suggests that humans are particularly good at this (KAMEDA and NAKANISHI 2003; MESOUDI 2008). The second is when culture is *cumulative*, such that increasingly beneficial innovations are accumulated over time with each incremental improvement dependent on previous innovations. Once cumulative culture takes off, it allows organisms to acquire traits from other organisms that they could never have invented on their own. This cumulative property is a defining characteristic of human culture (TOMASELLO 1999): while other species exhibit geographically variable cultural traditions, such as regional differences in chimpanzee nut-cracking techniques (WHITEN et al. 1999) or birdsong dialects (CATCHPOLE and SLATER 1995), none of these traditions appear to be cumulative in the way that human technological, scientific and artistic knowledge are (BASALLA 1988). Indeed, the Renaissance is an excellent example of this accumulation, given that 15th century scholars and artists were explicitly building on the prior discoveries and innovations of the Ancient Greeks. Importantly, once culture becomes cumulative in this way, it can be said to constitute an evolutionary process in its own right that acts partially independently of genetic evolution (MESOUDI, WHITEN and LALAND 2004). This process of cultural evolution allows complex cultural (rather than genetic) adaptations to emerge, from scientific knowledge such as geometry or optics to technological traits such as the aforementioned architectural hoisting devices used during the Renaissance. To summarize, any simplistic dichotomy between genes and culture is flawed. It is often in the genes' interests (metaphorically speaking) to forego direct control over behaviour and allow culture to take over. This is particularly applicable given our species' capacity for cumulative culture, which allows rapid cultural (rather than genetic) adaptation.

3. THE VALUE OF DARWINIAN METHODS FOR THE SOCIAL SCIENCES AND HUMANITIES

At first sight, the empirical and theoretical evidence reviewed above that human behaviour is largely culturally determined suggests that evolutionary theory might be irrelevant in the social sciences and humanities. Indeed, this was the conclusion of many early social scientists (e.g. BOAS 1940) and remains so today (see PERRY and MACE 2010). This conclusion does not necessarily follow, however. First, the capacity for culture remains the product of genetic evolution, and understanding this genetic evolutionary origin can give us important information about how culture operates. Second, as noted above, human culture is uniquely cumulative, with increasingly beneficial innovations successively built up over time. This makes human culture an evolutionary process in its own right. Just as Darwin saw biological change as a process of gradual "descent with modification", with the successive accumulation of beneficial biological traits generating the immense complexity and diversity of the natural world, so too human culture can be seen as an evolutionary process with the same basic properties (MESOUDI et al. 2004). Indeed, this parallel was pointed out by Darwin himself, who drew analogies between the way in which species change and the way in which languages change:

> "The formation of different languages and of distinct species, and the proofs that both have been developed through a gradual process, are curiously parallel … The survival or preservation of certain favoured words in the struggle for existence is natural selection" (DARWIN 1871: 90–91)

In recent decades this informal parallel has been made formal through the application to cultural evolution of quantitative evolutionary methods originally developed by biologists to explain biological change. Although cultural evolution research is still in its infancy, there are indications that Darwinian methods have the potential to explain patterns of rapid cultural change in a way that can valuably supplement traditional social science and humanities research. The following sections present a selection of examples where this potential can be observed.

3.1 Phylogenetic reconstructions of cultural evolution

One of Darwin's key insights was that species are related by descent. To illustrate this in *The Origin* he represented biological evolution as a tree, with living species at the tips of the branches connected by common ancestors. Since then, evolutionary biologists have developed sophisticated quantitative tools for constructing phylogenetic trees that specify the evolutionary relationships between living species. A key assumption is that similarity indicates relatedness: the more similar two species are, the more related they are, because they inherited those similarities from a recent common ancestor. Another assumption is parsimony, whereby the most likely evolutionary tree is the one that contains the fewest number of independent evolutionary changes. For example, if two species share some unusual characteristic that is absent in every other species, then it is more parsimonious to assume that the unusual characteristic evolved just once in the common ancestor of those two species, rather than evolving independently on two separate occasions.

Viewing culture as an evolutionary process has led several groups of researchers to apply the same phylogenetic methods to cultural phenomena, on the assumption that cultural traits form lineages connected by common descent. Phylogenetic methods have been applied to languages (PAGEL 2009), prehistoric artifacts (O'BRIEN, DARWENT and Lyman 2001), social customs (HOLDEN and MACE 2003) and medieval manuscripts (HOWE et al. 2001). The aim is the same as in biology: to reconstruct evolutionary historical relationships between sets of entities. Rather than those entities being species, however, the entities in the cultural case are languages, artifacts, manuscripts and so on. In many cases these phylogenetic analyses have given more reliable answers to historical questions than traditional social science methods.

For example, phylogenetic methods provide a solution to a problem that anthropologists face when comparing the customs and practices of different societies: that two societies may share two or more customs not because of any functional reason, but simply because they both descend from a common ancestral society that happened to have both of those customs (known as "Galton's problem" after Francis Galton pointed it out in 1889). As MACE and PAGEL (1994) argued, biologists face exactly the same problem - two species might share characteristics not for any functional reason, but because they both inherited it from a common ancestral species. Phylogenetic methods were designed by biologists to control for this non-independence of data points, and can solve the same problem in anthropology. MACE and HOLDEN (2003) illustrated this in the case of cattle farming and wealth inheritance in sub-Saharan African societies. Anthropologists (e.g. ABERLE 1961) have long noted that societies which keep cattle also tend to be patrilineal, i.e. inherit wealth along the male lineage from father to son. Non-cattle-keeping societies, on the other hand, tend to be matrilineal, i.e. inherit wealth along the female lineage from mother to daughter. Without properly controlling for common cultural descent, however, this correlation may be a spurious accident of history. MACE and

HOLDEN (2003) therefore mapped the presence or absence of these practices onto a phylogenetic tree of 68 sub-Saharan African societies constructed on the basis of language similarity. Their analysis showed that matriliny plus non-cattle-keeping was the most likely ancestral state and that there were several independent shifts to a combination of patriliny plus cattle-keeping. This suggests that there is indeed some functional link between patriliny and cattle-keeping. Holden and Mace suggest that cattle are more useful to sons because they can be used to pay a larger bridewealth to a bride's family and make him more likely to marry, thus favouring patrilineal inheritance.

Phylogenetic methods have also been used to answer questions concerning the origin of different language groups. For example, a much-debated issue in anthropology and linguistics is the origin of the similar languages spoken by several groups of people across Austronesia, from the Philippines to Hawaii and New Zealand. One hypothesis is that rice farmers from mainland China rapidly spread out from Taiwan around 9000 years ago to colonize the islands of the Pacific in just 2000 years taking their language with them (DIAMOND 2000). An alternative hypothesis is that Austronesian languages originated not from Taiwan but in eastern Indonesia, and long before agriculture appeared (OPPENHEIMER and RICHARDS 2001). To test these competing hypotheses, GRAY and JORDAN (2000) constructed a phylogenetic tree from the basic vocabulary of 77 Austronesian languages, finding that this tree best matched the out-of-Taiwan scenario: contemporary Taiwanese languages were shown to be older than Indonesian languages. A similar study by GRAY and ATKINSON (2003) showed that Indo-European languages originated around 7800-9800 years ago, consistent with having spread with Anatolian farmers, rather than having been spread by non-farming Kurgan horsemen several thousand years later (see RENFREW 1990). Phylogenetic methods have also been used to reconstruct the evolutionary relationships between different versions of Medieval manuscripts such as *The Canterbury Tales* (BARBROOK et al. 1998). The resulting trees bear several similarities to the trees reconstructed by manuscript scholars using informal, subjective judgements of similarity, such as agreement on which is the earliest, original manuscript version. However, the quantitative phylogenetic methods generated several novel findings, such as the identification of a group of manuscripts closely related to the original manuscript that are typically ignored by historians and may warrant closer attention. In all of these cases phylogenetic methods borrowed from evolutionary biology and deriving from viewing culture as a Darwinian evolutionary process have been used to provide more reliable answers to outstanding questions in the social sciences and humanities.

Of course, linguists and historians have been reconstructing the historical relationships between languages and manuscripts for a very long time (indeed, even before Darwin wrote The Origin: VAN WYHE 2005). Linguists use the comparative method (not to be confused with the comparative method used in biology) to draw language trees, while historians do the same when generating tree-like "stemmata" of manuscripts. And the underlying logic behind these methods is often the same as that underlying phylogenetic analyses: that similar languages/manuscripts are more likely to be related to one another than dissimilar languages/manuscripts. But while the underlying logic is the same, the traditional methods for reconstructing cultural histories are far more subjective than the rigorous statistical and phylogenetic methods developed by biologists. Consider, for example, the linguistic comparative method (MCMAHON and MCMAHON 2003). Typically, language trees are reconstructed based on linguists' intuitions about what kinds of changes were more likely, and in what directions. This is problematic because there is no widely agreed-upon set of rules for the linguistic comparative method, and different researchers have different criteria for judging relatedness. Consequently, different linguists produce different historical relationships, and with no objective criteria or statistical tests for measuring relatedness, there is no way of deciding which historical tree is best supported by the data. Phylogenetic methods provide just such a quantitative solution to this problem. Rigorous statistical techniques such as maximum parsimony, maximum likelihood or Bayesian methods can be used to quantify the likelihood that different trees accurately resemble actual evolutionary history, according to explicit and objective assumptions and algorithms. This is not to say that phylogenetic methods will always produce a single, definitive tree with 100% accuracy. However, this uncertainty can be quantified and consequently minimized in a way that is not possible with traditional linguistic tree-building methods. Another advantage is tractability: computational phylogenetic methods can analyse manuscript texts more comprehensively and in a fraction of the time that it takes historians to generate stemmata (HOWE et al. 2001).

3.2 Linking cultural macroevolution and cultural microevolution

The patterns and trends in long-term and large-scale cultural change described in the previous section, such as the spread of Austronesian languages from Taiwan to the Pacific islands, can be described as cultural macroevolution. Although the accurate description of cultural macroevolution, such as through the use of phylogenetic methods, is important, we also need to explain patterns and trends in cultural macroevolution in terms of underlying individual-level processes. Biologists explain patterns and trends in the fossil record or in different biogeographical regions in terms of underlying microevolutionary processes such as natural selection, sexual selection, mutation and drift. So, for example, finch beak diversity is explained in terms of selective responses to different sized seeds, and elaborate traits such as peacocks' tails are explained in terms of runaway sexual selection[1]. Viewing culture

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[1] This is not to say that all biologists agree that biological microevolution and macroevolution have been linked satisfactorily: proponents of evolutionary developmental biology ("evo-devo") argue that developmental constraints provide a crucial yet often-overlooked link between micro- and macro-evolution (e.g. CARROLL 2000), while proponents of punctuated equilibrium

as an evolutionary process allows similar micro-macro links to be made for cultural change (MESOUDI 2007; MESOUDI, WHITEN and LALAND 2006). The microevolutionary processes that drive cultural evolution are not necessarily the same as those that drive biological evolution, and in many cases may be very different. Nevertheless, evolutionary theory provides the tools and conceptual framework for making these micro-macro links.

A specific example illustrates this point. Prehistoric projectile points (e.g. arrowheads or dart tips) are commonly found at various sites in the Great Basin region of the south-western United States. BETTINGER and EERKENS (1999) documented an interesting difference between two specific archaeological sites dating to around 300–600 AD in projectile point characteristics. One site, in central Nevada, contained points that varied little in their designs due to tight links between their dimensions, such as length, width, thickness and shape. So, for example, points that were narrow were also almost always thin, such that width and thickness were linked. Another site, in eastern California, contained points made of the same material and from the same period but much more diverse in their designs. No links between dimensions were apparent: narrow points were no more likely to be thin and light than to be thick and heavy. BETTINGER and EERKENS (1999) explained these macroevolutionary differences in terms of the microevolutionary processes concerning how point designs originally spread within these two societies. In Nevada they argued that points spread via “prestige bias” (HENRICH and GIL WHITE 2001), where every point manufacturer copied the entire design of a single successful and prestigious hunter. Consequently, dimensions will be copied in a linked manner, thus reducing diversity. In California, in contrast, Bettinger and Eerkens argued that points spread via “guided variation” (BOYD and RICHERSON 1985), where point manufacturers copy a new design from another hunter but then modify that design according to individual trial-and-error learning. This latter trial-and-error phase would have increased point design diversity relative to the Nevadan site. So Bettinger and Eerkens linked population-level patterns - high and low diversity in point design - to individual-level learning biases - guided variation and prestige bias, respectively.

Of course, without a time machine we cannot go back in time and directly observe point manufacturers’ learning biases, so this hypothesis remains somewhat speculative. However, we can test the hypothesis indirectly by simulating the learning biases experimentally in the psychology lab, where we can directly observe and even manipulate microevolutionary learning processes. Michael O’Brien and I con-

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theory (GOULD and ELDREDGE 1977) have sometimes argued that rapid macroevolutionary mass-speciation events observed in the fossil record are inconsistent with gradual microevolutionary change (although see ARNOLD, PFRENDER and JONES 2001). Yet despite these more recent additions and revisions, it remains the case that the integration of micro- and macro-evolutionary branches of the biological sciences was a hugely significant advance in the history of evolutionary biology (MAYR and PROVINE 1980), and subsequent refinements were only possible once an initial integration had been made.

ducted such experiments in which participants designed and copied arrowhead designs in a computer-based virtual hunting task (MESOUDI 2008; MESOUDI and O'BRIEN 2008). We showed that the hypothesised microevolutionary biases (prestige bias and guided variation) do indeed generate the predicted patterns of variation (low and high respectively), but only under certain conditions. Specifically, guided variation only generates high diversity when there are multiple locally optimal point designs. This causes different individuals to converge on different local optima (or "peaks" in the adaptive landscape that determines point fitness, to use a biological analogy) thus maintaining diversity. Conversely, a single optimal point design would cause all of the individual learners to converge on that single design, reducing (not increasing) diversity. This fits with other experimental work suggesting trade-offs between design characteristics of projectile points which would generate multiple locally optimal designs (CHESHIER and KELLY 2006).

Cultural evolutionary research has linked other real-world cultural patterns to underlying microevolutionary biases. HENRICH (2001) showed that the S-shaped cumulative distribution curves that sociologists have shown typify the diffusion of novel technological and social innovations through societies (ROGERS 1995) are consistent with the operation of conformist cultural transmission, where people preferentially copy the most popular trait in the population. Specifically, the slow initial take-off of beneficial innovations (the first part of the S-curve) results from conformity to the pre-existing technology/practice inhibiting transmission of the novel, beneficial trait. Other work has used the ethnographic method to identify the microevolutionary (within-society) processes that are responsible for macroevolutionary (cross-cultural) patterns identified by phylogenetic analyses. For example, TEHRANI and COLLARD (2009) found that weaving techniques and textile patterns exhibited by Iranian tribal women were transmitted either vertically (from mother to daughter) or horizontally (between unrelated women), but in the latter case strictly within local communities due to social prohibitions on women visiting other communities. This strictly within-community transmission generated a branching, tree-like pattern of increasingly divergent textile patterns at the macroevolutionary level that was detectable using phylogenetic analyses.

4. CONCLUSIONS

The previous section presented examples where viewing culture as a Darwinian evolutionary process, and using Darwinian evolutionary methods to analyse cultural change, has yielded significant and novel insights that valuably add to existing social science and humanities research. Phylogenetic methods solve Galton's problem in anthropology and allow more reliable cross-cultural comparisons than traditional non-evolutionary methods. Phylogenetic methods can also be used to reconstruct more reliable historical relationships between languages, manuscripts, customs and artifacts than traditional historical methods. Evolutionary theory also provides a formal framework for explaining macroevolutionary patterns in human culture in terms of specific underlying microevolutionary processes. Patterns in the archaeological, ethnographic and sociological record can be explained in terms of different learning biases (prestige bias, conformity, random copying, vertical vs. horizontal transmission etc.), each of which has been subject to formal evolutionary modelling (BOYD and RICHERSON 1985; CAVALLI-SFORZA and FELDMAN 1981). These models provide specific, quantitative predictions concerning population-level patterns that can be tested against real-world cultural datasets, such as regional variation in prehistoric projectile points or inter-tribal variation in Iranian textile patterns.

This work reveals a final benefit of adopting an evolutionary approach to the study of human culture: interdisciplinary synthesis. Traditionally, the different branches of the social sciences and humanities have been isolated from one another, each harbouring mutually incompatible theoretical assumptions and with little exchange of ideas, findings and concepts across disciplinary boundaries. The cultural evolutionary studies discussed above, in contrast, fuse multiple methods (mathematical models, laboratory experiments, historical analyses, ethnographic field studies) and multiple social science and humanities disciplines (anthropology, archaeology, sociology, psychology, economics, history). This is beginning to resemble the synthetic structure of evolutionary biology, which, since the 1940s, has integrated diverse methods and disciplines within a single framework unified by Darwinian evolutionary theory. We can take advantage of the fact that culture is also a Darwinian evolutionary system to forge a similar synthesis in the social sciences and humanities (MESOUDI 2007; MESOUDI et al. 2006). Real benefits emerge from this interdisciplinary synthesis, some of which have already been hinted at. For example, experimental simulations of projectile point transmission (MESOUDI and O'BRIEN 2008) can test archaeological hypotheses such as those of BETTINGER and EERKENS (1999) in a way that is impossible to do with purely historical data: in experiments we can manipulate variables, we can directly measure behaviour, we can "re-run" history to see whether trends are significant or just due to chance, etc. There is, of course, a corresponding drop in external validity associated with experiments, but explicitly tying experimental situations to real-world data can reduce this problem.

So perhaps in the future evolutionary tools might be used to explain phenomena such as the actual Renaissance. Phylogenetic methods might be used to reconstruct the history of the different scientific, architectural and artistic traditions involved. The Renaissance might be studied as an example of an adaptive radiation – a punctuated burst of variation following a period of stasis – as has been shown to occur for languages (ATKINSON et al. 2008). Models and experiments might simulate the possible microevolutionary biases that contributed to the rapid spread of innovations, such as prestige bias facilitating the transmission of innovations exhibited by prestigious individuals such as Leonardo da Vinci, or how the invention of the printing press increased the fidelity of horizontal cultural transmission, or how population size or structure might have promoted innovation by providing a larger pool of models from whom subsequent generations could acquire beneficial cultural innovations (e.g. POWELL, SHENNAN and THOMAS 2009). Social scientists and humanities scholars should not see the application of these methods as attempts to "biologise" their disciplines, merely as useful tools to better explain the cultural phenomena that they seek to understand.

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