Blute, M., & Jordan, F. (2018). The evolutionary approach to history: sociocultural phylogenetics. In R. L. Hopcroft (Ed.), *Oxford Handbook of Evolution, Biology, and Society* Oxford University Press. https://doi.org/10.1093/oxfordhb/9780190299323.013.32

The Evolutionary Approach to History: Sociocultural Phylogenetics

Marion Blute*

Sociology, University of Toronto

Fiona Jordan*

Archaeology & Anthropology, University of Bristol

*The authors contributed equally to this paper.

This paper on cultural or sociocultural evolution begins with a discussion of the Darwinian-inspired evolutionary approach to history. It then outlines modern evolutionary phylogenetic methods borrowed from Biology but now used extensively in the social sciences and humanities. We provide examples of how language trees may be inferred; phylogenetic comparative methods that use language trees to answer questions about aspects of geographical, social, political, cultural or economic organization; and phylogenetic investigations of material culture and oral traditions..The conclusion is drawn that culture does indeed "descend with modification".

Keywords: evolution and history, cultural evolution, sociocultural evolution, cultural phylogenetics, phylolinguistics

Modern Darwinian evolutionism in the social sciences and humanities comes in three forms - the gene-based biological, the social learning-based sociocultural, and gene-culture coevolution dealing with their interaction. This paper is about the second - about sociocultural evolution (for some books on the general subject see Cavalli-Sforza & Feldman 1981, Boyd & Richerson 1985, Basalla 1988, Hull 1988, Plotkin 1994, Fog 1999, Richerson & Boyd 2005, Turner& Maryanski 2008, Runciman 2009, Blute 2010, Hodgson & Knudsen 2010, Distin 2011, Mesoudi 2012, and Richerson & Christiansen 2013). Some prefer to think of this process as analogous to biological evolution. Others see both biological and sociocultural evolution as tokens of the same general type (variously termed evolutionary epistemology, generalized Darwinism, universal Darwinism, selection processes etc.). Some prefer to speak of cultural evolution, some of social evolution and some of sociocultural evolution. The substantive focus also varies - linguistics, archaeology, cultural anthropology, political science, economics, sociology, science and technology or literary studies. Whatever such differences in terminology or substantive focus, as Donald T. Campbell was always fond of pointing out, they have all descended from Darwinism (personal communication). Such evolutionists generally agree that there are four basic kinds of evolutionary explanations for stability or change and diversity but sometimes differ in their emphasis. The four are 1) constraints (e.g. the laws of physics and chemistry); 2) chance or “drift” (sampling error in finite populations where random effects are propagated through time); 3) what Darwin called the “unity of types” (shared ancestry); and 4) what he called “the conditions of existence” (selection). This paper is focused on the third - on history - on the ways in which history or shared descent from common ancestors can structure diversity in social and cultural phenomena.

From here on, in order, sections are included on i) history; ii) contemporary methods; iii) language trees and networks; iv) testing hypotheses about cultural evolution using phylogenetic comparative methods (including ancestral state, tracking history, models of transformation, correlated evolution, and patterns and processes of change); v) phylogenetic approaches to cultural artefacts (including material culture and folk tales); and vi) some conclusions.

History

There are two (not mutually exclusive) ways to study the effects of history on sociocultural diversity. One can study what has been called the “relics” - just as paleontologists study biological fossils, archaeologists study the material remains of prehistoric human settlements and activities, and historians and other kinds of historically-oriented social scientists study documents and other artifacts from the past. This approach gives direct insight into the behaviours and material culture of particular human populations at particular points in time but the archaeological and relic record is patchy and not comprehensive across time and space. The other way is to compare contemporary forms and use that information to draw historical inferences. Classically, sociology and anthropology took that approach (e.g. Morgan 1871 on kinship terminologies) but it was recognised early on in the history of both disciplines that this approach was problematic. Their taxonomies were commonly only one layer deep based on geographic or cultural areas and they lacked suitable methods for drawing historical inferences from present forms. The result was “developmentalism” or unilineal “evolutionism”, as in the work of Herbert Spencer for example - stage theories of historical “progress” which, as Lovejoy (1936) showed, had its roots in the pre-Darwinian medieval idea of “a great chain of being”. Present forms were arranged in a sequence from simpler to more complex, e.g. “savage” to "civilisation" as in Morgan (1877) and then placed on an escalator. True Darwinian evolutionary thinking is not sequential or ladder-like, whether singular or "multilineal" (Blute 1979). By contrast with such sequences, Darwin represented his view of history by a tree (first on page 36 of his Notebook B on the transmutation of species). Darwin's "unity of types" was his historical interpretation of Linnaeus' "natural system" by which he viewed species in the same genus as literally more closely related historically than those in different genera, those in the same family as more closely related historically than those in different families and so on through the natural taxonomic hierarchy of Linnaeus' groups within groups.

In the social sciences, cultural inheritance ranges from the most micro foundations (social learning by observation or by linguistically-encoded instructions) to the most macro, for example, the anthropologists "way of life of a people". Transmission is not always accurate and there are many modes of variation or innovation in evolution (Blute, 2015) but all are said to be "random". Random does *not* mean uncaused, necessarily unique, equiprobable, or the absence of the transmission of acquired characteristics. All it means is that innovations are non-prescient as Donald T. Campbell always emphasized. There is much evidence that sociocultural innovations, just as biological mutations, similarly are not statistically biased in the direction required for them to spread. In that sense, sociocultural evolution is Darwinian not Lamarckian. As well as transmission and variation there is selection, i.e. some variants are transmitted further while others are not, and among those that are, some are transmitted at faster rates or for longer than others.

The dynamics of cultural transmission can differ from biological inheritance in particular ways, but the distinctions are not as straightforward as some commentators have claimed (Borgerhoff Mulder et al 2006). According to some, cultural evolution–biological evolution analogies are simply useful tools with which to think (Gray et al 2007, Lewens 2015, Pagel 2016). Applying particular methodologies to particular data sets does not rely on isomorphic mapping of cultural and biological "units" such as genes or cultural traits. It relies instead on the the Darwinian evolutionary criteria (variation, inheritance, differential survival and reproduction) be justified for the particular case at hand. The relative ease by which ideas may be horizontally transmitted between individuals within a social group versus inherited vertically from parents depends on the sort of cultural feature one is modelling (e.g. grammar versus words), as does the "borrowability" and subsequent transmission and survival of cultural and linguistic features between populations (Gray et al 2007). In addition, a rich body of theory and modelling has emerged in recent years to describe the social learning biases that are at work to influence the rise and fall of cultural features in human populations (e.g. Boyd & Richerson 1985, Richerson & Boyd 2005; Henrich and Boyd 1998). Mechanisms such as model bias (e.g. copying prestigious or successful individuals), frequency-dependence (e.g. copying majority or rare behaviours), and content biases (e.g. preferences for socially-relevant information in certain contexts) all constitute important forces of cultural evolution alongside drift, natural selection, and the other traditional biological "forces of evolution". These forces work primarily at the micro-evolutionary level on individual social learning and cultural transmission at the small-scale, but are not in themselves the generators of sociocultural variation. The innovation of cultural features is currently an under-theorised aspect of cultural evolution theory, intersecting work between anthropology and psychology (see for example Sperber's (1996) work on "cultural attractors"). There is little evidence to suggest that cultural evolution is Lamarckian—that we as a species are particularly successful at innovating behaviours or beliefs that are inherently "spreadable". Indeed given the creative agency and imagination afforded by our big brains, dense social networks, and long lives, it is unclear just how much individuals add to the cultural pool on average.

Contemporary Methods

While Darwin's tree metaphor for biological history was revolutionary, ambiguities remained for a long time. In the 1970's biological taxonomy was revolutionized beginning with Hennig's (1966) cladistics or phylogenetic systematics. He formulated his phylogenetic principle, making assumptions that classification should be strictly historical, that branching is bivariate, and that some changes are recent, some older and some older still. Two groups A and B can be inferred to have come via the same unique path, only if they share characters which are *not* shared with an outgroup C. Hence a phylogenetic or cladistic classification is a nested set of such *shared, derived* characters which he called "synapomorphies". In his *Science as a Process*, David Hull (1988) used a variety of historical and sociological methods to tell the story of the three schools of taxonomic thought which subsequently vied for dominance in the 1970's and 1980's and to some extent still do - Hennig's cladistics or phylogenetic systematics, evolutionary taxonomy, and phenetics. These can be distinguished by the groups recognized and the characters used (see Figure 1). Since then, many applications of various computational tree-building methods borrowed from Biology have been used in the social sciences and humanities to answer basic historical questions such as the origins and relationships among populations, languages or other socio-cultural entities (including material culture) as well as the dynamics of cultural evolution itself.

The basic concepts of the four major classes of methods are well explained in Baum & Smith (2013) and Nunn (2011).

a) Distance. Distance based methods have descended from phenetics. They calculate a measure of feature distance between all pairs of taxa (such as shared vocabulary). A tree is generated from these distances that is most consistent with the distance matrix. Neighbour-joining is the most common instantiation of this approach.

The other methods are "character-based" and work on the "raw" data, that is they do not calculate distances between taxa but have an underlying set of assumptions about the model of evolutionary change. They are more computationally intensive:

b) Parsimony. Parsimony has descended from Hennig's cladistics. It selects the tree that can account for the data with the fewest evolutionary changes. While intuitive, parsimony does not deal efficiently with variations in the rate of evolution.

c) Maximum Likelihood. Given explicit modelling assumptions, it searches for the tree that has the highest probability of giving rise to the observed data.

d) Bayesian Methods. Given explicit prior beliefs ("subjective probabilities") as well as an explicit model and the data, it yields a range of trees in proportion to their probability.

The topic of phylogenetic inference is complex because not only are there different classes of methods (Felsenstein 2004), but there are also a number of algorithms for each, and sometimes many computer programmes for each of those. Wikipedia (2016) has a list of more than 50 programmes and Felsenstein's (2016) website "phylogeny programmes" currently includes 392 programmes.

To infer phylogenies from linguistic and cultural data, researchers are increasingly adopting Bayesian inference methods, for three reasons. They build on the strengths of maximum likelihood in that they force researchers to think carefully about an explicit model of cultural change and use models that allow for sources of variation such as rate heterogeneity (Greenhill and Gray 2009). Prior knowledge, such as known dates of linguistic splits, or evidential inference from archaeology or human genetics may be incorporated alongside reasoned models of evolutionary change. Finally, they produce a posterior sample of phylogenetic trees that represent aspects such as branching patterns and branch lengths in proportion to their probability. This allows the researcher to incorporate uncertainty by drawing conclusions based on a range of phylogenetic hypotheses. Newcomers can be guided by the ever-increasing cultural phylogenetic literature to appropriate methods - Bayesian tree-inference software such as BEAST and RevBayes have appropriate models for non-genetic data and good introductions to theory and methods are given in Felsenstein (2004), Lemey, Salemi & Vandamme (2009) and Drummond & Bouckaert (2015). The remainder of this paper will provide empirical examples to give readers a sense of the kinds of possibilities that exist.

Language Trees and Networks

Darwin used the then known Indo-European language family as an analogy to explain his biological evolutionary theory. Over generations, historical linguists have constructed some 200 language families in each of which the languages have descended with modification from a common ancestral language (Crowley & Bowern 2010). The evolutionary biologist Maynard-Smith once expressed amazement at how this had been accomplished without the use of quantitative methods (personal communication). However, in recent years, various computational tree-building methods borrowed from Biology have been applied to languages to answer various kinds of questions. For example:

Gray & Jordan (2000) used parsimony methods to infer a phylogeny of 77 languages of the Austronesian family testing a hypothesis of the sequence of population movements that spread from Taiwan all the way to Eastern Polynesia. Gray, Drummond & Greenhill (2009) improved on this with Bayesian methods and an extended vocabulary dataset (Greenhill, Blust & Gray 2008) to show that this expansion took place in a “pulse-pause” pattern. Four major expansion pulses and two pauses took place - the pauses being before the settlement of the Philippines around 3800-4500 years BP and after the settlement of western Polynesia by 2800 years BP.

Stimulated by a longstanding archaeological debate, “the most intensively studied, yet still the most recalcitrant problem of historical linguistics” (Diamond & Bellwood 2003) was tackled with Bayesian methods by Gray & Atkinson (2003). They tested two theories of the origin of the Indo-European language family - the Kurgan hypothesis (from the Pontic steppes north of the Caspian sea by semi-nomadic horsemen around 6th years ago) and the Anatolian hypothesis (from Turkey by farmers around 8-9th years ago). Results supported the latter date (7899-9500 years ago). Bouckaert et. al. (2012) improved on this with a Bayesian phylogeographic inference framework developed to study viral outbreaks using improved data which also supported the Anatolian origin. However, Chang et. al. (2015) employed the same model and data as Bouckaert et. al. but incorporated ancestry constraints from ancient and medieval languages. Their results inferred an older age for the root of the tree supporting the steppe hypothesis. Recent genetic work suggests both steppe and Anatolian origins can be integrated in an emerging multi-phase Indo-European story (Haak et. al. 2015).

Large language families associated with Neolithic or agricultural dispersals of speakers have been a popular object of enquiry for phylolinguistic analysis. Besides Austronesian and Indo-European, the family relationships of the Bantu languages of sub-Saharan Africa (Holden 2002; Grollemund et. al. 2015) and the Uto-Aztecan languages of Mesoamerica (Dunn et. al. 2011) have been inferred, offering opportunities to test hypotheses about homelands, migration routes, timing and dating of roots and splits, and the social and ecological triggers for population movements. For example, Grollemund et. al. (2015) used a time-calibrated tree of some 400 Bantu languages and mapped onto it the probable geographical location of each of the internal nodes of the tree. They showed that the Bantu expansion (beginning about 5,000 years ago) spread preferentially along emerging savannah corridors avoiding rainforest habitats. When the latter did take place, expansion was slowed by an average of 300 years relative to the former. The list of language families to which computational phylogenetic methods have been applied has expanded greatly in the last decade including Aslian (Dunn, Kruspe & Burenhult 2013), Alor-Pantar (Robinson & Holton 2012) Arawak (Walker & Ribero 2011), Chapacuran (Birchall et. al. 2016), Japonic (Lee & Hasegawa 2011), Pama-Nyungan (Bowern & Atkinson 2012), Semitic (Kitchen et. al. 2009), Tupi-Guarani (Michael et. al. 2015), and Uralic (Honkola et. al. 2013). Many of these studies have used cognate-coded basic vocabulary as their data. Two notable exceptions are Dene-Yenesian (Sicoli and Holton 2014) and Papuan languages in Dunn et. al. (2005), both of which use typological features as their data, incorporating structural aspects of language such as word order, the presence of tense marking, etc.

Finally on phylolinguistics, while many scholars are sceptical of the ability of both traditional and computational methods to infer deeper phylogenies (Campbell & Poser 2008), some recent works attempts to infer larger-scale trees of human languages. From a database of reconstructed vocabulary, Pagel and colleagues (2013) inferred a "superfamily" that linked seven families across the Eurasian continent to a root of around 14,400 years ago. Their results pointed to some suggestions for "ultraconserved" word meanings. At the global scale, Jaeger & Wichmann (2016) applied weighted sequence alignment and distance-based phylogenetic methods to word lists in phonetic transcription from more than 6,000 languages and dialects to infer a global tree of languages. The results not only recaptured established language families and their subgroupings but also revealed large-scale patterns which they interpret as a statistical signal from deep time.

One common critique of phylolinguistics is the observation that aspects of language are not tree-like - that is words, sounds, morphosyntax and even grammatical structures can be transmitted horizontally between languages by borrowing and contact, thus adding conflicting signals to phylogenetic inference (Moore 1994). This point is an empirical one at bottom, and the extent and likelihood of borrowing can differ for kinds of vocabulary: compare pronouns versus words that name trade items to give a trivial example (Gray et. al. 2007; Gray, Bryant & Greenhill 2010). Simulations of feature borrowing have shown that phylogenetic inference can perform well under conditions of moderate realistic borrowing i.e. between sister populations (Greenhill et. al. 2009). Operationally, biologists deal with horizontal or lateral gene transfer in microbial populations as a matter of course, and measures such as the delta score (Holland et. al. 2002) can give comparable measures of how reticulate or tree-like a data set is (see Gray et. al, 2010 and Wichmann et. al, 2011 for examples). Phylogenetic networks (Huson & Bryant 2006) can be inferred in programmes such as NeighbourNet and Network and allow for graphical representation of the conflicting or reticulate signal in a data set. Walker & Ribiero (2011) use

NeighbourNet to show that Arawak languages have both well-formed subgroupings and evidence of reticulation among early-splitting lineages.

Language Trees as Population Histories: Testing Hypotheses About Cultural Evolution Using Phylogenetic Comparative Methods

As we have seen, inferring a phylogeny from language data affords investigators ways to answer questions such as the following. What are the relationships among languages? When and where did they originate? What is the rate of language change? How reticulate or tree like is linguistic evolution? The answers to a host of other questions are made possible by using language phylogenies as a scaffold for the history of speaker populations. Mapping social, cultural, political, economic organization or other geographic, ethnographic or biocultural data onto the tips of a (usually) language tree allows investigators to use phylogenetic comparative methods (PCMs) to examine the dynamics of cultural change. This suite of methods all employ a phylogeny, a set of “tip data” and a model of change for the feature under study and were developed in evolutionary biology to avert the problem of statistical non-independence between species (Felsenstein 1985). Mace and Pagel (1994) then introduced them to anthropologists and linguists as a formal answer to Galton’s Problem - the similar objection for comparative cross-cultural analyses that societies may share traits not due to any functional correspondences or universality of human cognition, but rather simply due to inheritance from a common parental population.

Beyond rectifying statistical properties, PCMs allow new kinds of questions to be asked about cultural and linguistic evolution because the diachronic (timed) nature of a phylogeny gives insight into process as well as pattern. Answers to questions such as the following are possible (combined, modified and added to from Currie 2013 and Jordan 2013). What was the ancestral state of a feature? Does a trait track historical ancestor-descendant relationships or some other process such as cultural contact? If two traits change together, does one follow the other? Have trait changes followed a particular order? Is there an overall trend in the direction in which traits change? Are patterns of change gradual or punctuational and do rates of change differ? Below we describe some empirical examples from this growing body of literature.

a) *Ancestral state:* Many features of human social and cultural life leave no material trace. Archaeologists may sometimes infer social norms and behaviours from remains, but PCMs provide another window into the past. Jordan et. al. (2009) mapped post-marital residence norms of 135 Austronesian-speaking populations onto the language phylogeny and inferred that matrilocal residence (where a husband moves to live with the wife's kin) was likely the ancestral state c. 5000 years ago. The inferred model of cultural change showed that marriage systems had unequal likelihoods of change such that shifts to patrilocality became more common over time. This work was extended to other language families (Fortunato & Jordan 2010, Fortunato 2011a) showing similarities in the models of change but differences in the ancestral states. Fortunato (2011b) inferred ancestral marriage payment strategies in Indo-European populations, and Jordan (2013) inferred ancestral sibling term systems in Bantu and Austronesian languages. Linguists have also used PCMs to infer ancestral states of typological features. For example, Calude & Verkerk (2016) investigated the ways in which Indo-European languages combine base numerals to form higher numeral terms. For example, English *eighty-nine* is (8 x 10 + 9) whereas French *quatre-vingt neuf* is (4 x 20 + 9). Across a range of numeral features, they inferred all ancestral nodes including Proto-Indo-European, demonstrating for instance that "teen" numerals were formed as atom + 10 like English *eighteen*, with subsequent changes in different subgroups. Finally, other studies have used ancestral state inference beyond the time depth of a single language family. Using a global “supertree” derived from a combination of genetic and linguistic data from 133 published studies, Peoples et. al. (2016) mapped seven different religious traits of 33 worldwide hunter-gather societies and inferred that one trait, animism, was ancestral in the most recent common ancestor.

b) *Track history:* PCMs allow investigators to measure phylogenetic signals, i.e. the extent to which variation in a cultural trait is predicted by the phylogeny. These measures are a good indication of the importance of shared ancestry in structuring cultural diversity. Kushnick et. al. (2014) mapped land tenure (resource ownership) norms from 97 Austronesian societies onto language phylogenies to infer ancestral states and test sequential models from behavioural ecology about resource and risk management. The historical signal in four different kinds of tenure norms (none, versus ownership by village, kin-group or individuals) were tracked for their degree of “clumping” through shared ancestry on the one hand or random distribution on the phylogeny on the other. Norms of no tenure and kin-group ownership displayed moderate and strong signals. This study also tested phylogenetic versus geographical/spatial clustering, and found that for all four norms, history was more important in structuring diversity. Bentz et. al. (2015) used measures of phylogenetic signal in their study relating lexical diversity (the number of word forms in a language that convey the same information) to the proportion of non-native speakers in a language. Lexical diversity showed a “deep” phylogenetic signal across three large language families and multiple measures, indicating this property of lexicons to be strongly subject to inheritance.

c) *Models of transformation:* Embedded in the statistical machinery of PCMs for inferring ancestral states is a flexible method for simultaneously estimating the model of change between traits, and this property can be used to both infer and test particular models for their fit. Currie et. al. (2010) examined how norms of Austronesian political complexity (acephalous societies, simple chiefdom, complex chiefdom and state) evolved on language phylogenies, testing long-standing assertions in archaeology and anthropology about "unilinear" cultural evolution in this trait. They showed that the model of political complexity that best fit Austronesian societies arises in a sequence of small steps but can fall by bigger jumps. Kushnick et. al. (2014) showed similarly that a sequential model of land-tenure norms applied to Austronesian societies, but that the best-supported model was one in which group and kin-group ownership evolved from individual tenure, rather than individual ownership being the "end-point". Peoples et. al. (2016) in the study cited above modelled the ways in which hunter-gatherer religious beliefs changed on the phylogeny. From an animistic state, belief in an afterlife, then shamanism, then ancestor worship emerged subsequently, while a belief in high gods stood apart and could emerge regardless of other properties. Returning to typological studies of language, Zhou & Bowern (2015) used Bayesian methods to investigate number terms in the Pama-Nyungan family (containing about 70% of Australian languages). They found that upper limits on number extent commonly vary between three and five, and beyond these as lower limits, languages can lose as well as gain numerals. Above the limits, Pama-Nyungan languages tend to add numerals by combining (e.g. 4 is 2 + 2) rather than inventing new words. Similar approaches were taken by Haynie & Bowern (2016) to model the evolution of colour term systems in Pama-Nyungan languages. Some languages have minimal basic colours as low as three terms (e.g. dark-light-red), while others have up to 12, and influential models of sequential development have been long established. Here the authors tested the sequential model, showing both support for, and departures from (i.e. that languages could lose terms) in these Australian languages.

d) *Correlated evolution:* The "original" reason for introducing phylogenetic comparative methods to anthropology was the robust testing of functional relationships (adaptation and/or correlated evolution) while controlling for autocorrelation due to shared descent (Mace & Pagel 1994). Pagel's "Discrete" method (Pagel 1994) is widely used in cultural phylogenetics as it allows not only the testing of correlations between categorical features (a "dependent" model) but outputs the rates of trait changes, enabling directional models to be specified. Holden & Mace (2003, 2005) mapped mode of subsistence and descent system onto the language tree of Bantu societies to test the hypothesis that matrilineal descent did not persist when societies acquired cattle, because men acquired defensible resources that could be passed on to sons and thus increase reproductive success. In Bantu societies, the acquisition of pastoralism across the tree was associated with and led to patriliny, supporting the idea that "the cow is the enemy of matriliny". Again in Bantu societies, Opie et. al. (2014) used PCMs to test for correlated evolution between modes of postmarital residence and descent, challenging a broadly held notion that residence changes act as a precursor to changes in descent and other forms of kinship social organization. Their results supported correlated evolution throughout the course of the Bantu expansion, but in opposite trajectories to those proposed by Murdock (1969) and described by Jordan and Mace (2007) for Austronesian societies.

Linguists have used phylogenetic correlations across multiple language families to test for putative universal dependencies in typological features. Dunn et. al. (2011) explored the functional links between a suite of different features of word order (e.g. the positions of subjects, verbs, adpositions) to explore the extent to which dependencies could be explained by either cognitive constraints (universals) or shared historical paths. Across four large language families (Austronesian, Bantu, Uto-Aztec, and Indo-European) they found lineage-specific correlations– and when correlations were shared, the directionality differed between families. Finally, driving factors in the evolution of religious beliefs and behaviours (Peoples et. al. 2016, Watts et. al. 2015, Watts et. al. 2016) have been investigated with these methods. Watts et. al. (2015) examined how moralising high gods and broad threats of supernatural punishment interacted in the evolution of political complexity in Austronesian societies. Counter to influential theories positing that moralising high gods drove societies towards political complexity (e.g. Norenzayan), Watts and colleagues showed that high gods followed complex societies, while supernatural punishment norms appeared to be the preceding factor.

e) *Patterns and processes of change:* Mace & Jordan (2011) measured how well the phylogenetic versus geographic nearest neighbours of Austronesian societies predicted what cultural features they shared. While both historical and spatial associations were important in structuring diversity, phylogenetic nearest neighbours better predicted traits associated with kinship and heritable social and material resources, such as slavery or domesticated animals. Walker et. al. (2012) created a distance-based phylogeny of the Tupi language family of lowland South America which supported a homeland in west central Brazil. Onto this, they mapped 11 locally-varying cultural features such as shamanism, residence patterns and paternity beliefs. By estimating the gains and losses of these features across the language family and the transition rates per 10,000 years they showed that variety has decreased with time, associated not only with European contact but with the independent emergence of nomadic hunter-gatherer societies.

Currie & Mace (2014), using the same set of traits as Mace & Jordan above, compared cultural trait evolution in i) island southeast Asian and the Pacific and ii) sub-Saharan Africa. They found similar rates of evolution across both regions and also found that features of social organisation such as kinship evolved more rapidly than ecological features such as the mode of subsistence.

Atkinson et. al. (2008) found that across three major language families (Bantu, Indo-European and Austronesian) languages tend to evolve in punctuational bursts i.e. word replacement rates increase just after splits rather than along branches. Similar "burst" dynamics were found by Valverde & Solé (2015) in their study of programming language diversification and Bromham et. al. (2015) demonstrated that in Polynesian languages, those with small populations lose words faster while larger populations gain new words at higher rates.

Phylogenetic Approaches to Cultural Artefacts

A third category of cultural phylogenetic studies draws on both tree-building and PCM techniques and applies these to aspects of material culture and cultural artefacts. Archaeologists in particular were quick to see the possibilities for these methods. Buchanan & Collard (2007) provide a recent example of phylogenetic analyses of Paleoindian projectile tools that provide insights into the peopling of North America. They used landmark measurements of projectile points across the continent as data in cladistic analyses and tested their trees against expectations from models of population migrations. Schillinger et. al. (2016) used a novel approach to draw on data produced in cultural transmission studies where participants were instructed to replicate a form model of a stone tool, an Acheulean hand-axe, down a transmission chain. They showed experimentally that phylogenetic reconstruction is more accurate in artefactual lineages where copying error is lower. For further work on archaeological artefacts, readers are directed to the collected papers in Lipo et. al. (2006) for example.

Material culture craft and design: Tehrani & Collard (2002) studied the characteristics of preparation and fabrication (flat-weave designs and pile-weave designs) of Turkmen tribal textiles from Iran. Permutation tests for phylogenetic signal and parsimony methods for inferring the best tree from this data were used to conclude that branching processes played a significant role over blending in the five populations under study. Matthews et. al. (2011) extended this work using Bayesian tree-inference methods to show that pile-weave designs have a different phylogenetic history compared to other textile characteristics. These different histories could be reconciled with ethnographic information on the socio-economic histories of the groups. Rogers et. al. (2009) applied distance-based methods to a dataset of traditional Polynesian canoes that similarly represented both design motifs and construction techniques. In their study they inferred a Fijian ancestry for canoe forms and a sequence of cultural origins throughout Polynesia. They observed a serial founder effect and indicated that population history was more strongly reflected by functional than by stylistic traits. Subsequent analyses of the Polynesian canoe dataset show that more accurate inferences about population history overall can be made by using PCMs and language trees as a scaffold for the canoe traits. Both functional and design traits display limited phylogenetic signal, with stylistic design features tracking history marginally more closely (Gray et. al. 2010) perhaps as a symbol of cultural group identity.

Buckley (2012) used Bayesian and neighbour net techniques to study 36 characteristics of Southeast Asian Warp Ikat weaving. He showed that they have a common ancestry and one much older than had been thought - associated with Neolithic pottery motifs from the Asian mainland rather than with Bronze Age drums of the Dong-Son culture in coastal Vietnam between 500BC and 100 AC.

Narrative artefacts and folk tales: Tehrani (2013) drew on data from comparative folklore to study global variants of the stories "Little Red Riding Hood" and "The Wolf and the Kids" in an attempt to discover if they were different lineages of the same story or independent narratives. With a range of phylogenetic inference methods, Tehrani used the plot variations and tale motifs in 58 variants of the tales across 33 global populations. Results showed that although related, the two stories could be distinguished as distinct international tale types but that the East Asian "tiger grandmother' variant was a probable hybrid of the two. Da Silva & Tehrani (2016) extended this approach to uncover the ancient roots of the Indo-European folktale "Tales of Magic" and used ancestral state inference methods that plotted different tale types on the Indo-European language phylogeny. They found evidence that these oral traditions antedate written records and that over 75% showed a phylogenetic signal correlated with the language tree. Four tales were likely present in Proto-Indo-European, and one tale, "The Smith and the Devil" likely goes back to the early Bronze Age. Similar phylogenetic approaches to folk tales have been taken by Ross et. al. (2013) who used a phylogenetic control to characterise the strong geographic structuring of a set of variants of one folktale across Europe, and by Ross & Atkinson (2016) who found that both spatial distance and historical shared ancestry structure the diversity of folktales in 18 Arctic hunter-gatherer populations.

Some Conclusions

Do not only living things but also culture and social organization “descend with modification’? The examples described above from the burgeoning field of cultural phylogenetics suggest a resounding yes. The Darwinian principles of descent, innovation, and differential survival are present in the business of science as well. Yong (2013) published a “family tree” of over 300 of the student descendants (i.e. students, grand students and great-grand students) of the ecologist R. T. Paine. Paine invented the concept of a “keystone species”, one whose removal yields drastic change in eco-systems. The 300 individuals on that tree did not even include the peers he influenced horizontally and the students of peers he influenced obliquely. While influenced by him in “attitudes, philosophies and technical skills”, he encouraged freedom and individuality in his students, so not surprisingly, this example of cultural descent included innovations. Some cultural descendants moved on from small scale field experiments to large multi-lab collaborations studying hundreds of miles of coastline for example. And of course, some students gave rise to many more grand- and great-grand-students than others.

Cultural or sociocultural evolutionary theory can reconcile many of the dilemmas in cultural and social theory - the relationship between history and science, conflict and cooperation, the ideal and the material, and the problems of agency, subjectivity and the nature of social structure (Blute, 2010). This is a young field, however, and much remains to be done. As well as differences among the three philosophical-theoretical schools of thought about systematics illustrated in Figure 1, it is well known that Darwin did not solve the problem of the *origin* of species. Nor does sociocultural evolutionary theory obviously solve the problem of the origin of sociocultural entities. While many definitions of species have been proposed, the most widely accepted remains that of Ernst Mayr that members of a species are actual or potential interbreeders - i.e. recombination among members is possible. Setting aside the issues of defining cultural populations, it is true that in the sociocultural as in the biological realm, new variants commonly arise by recombination - as has been shown for technology by Arthur (2009) for example. It is commonly thought that recombination,is more promiscuous, and multiple cultural parents are more common socioculturally than they are biologically, but this is an empirical issue of scale and boundaries. "One may get an idea for a handle shape for a pot from a basket, but when was the last time characteristics among tables and curtains or staplers and rugs, say, were recombined" (Blute, 1979). While it now seems likely that barriers to recombination can originate by any of geographical, ecological or social means, what is most common remains unclear. For example, see Shennan et. al. (2015) on the archaeological "population structure" of pottery and personal ornaments from Neolithic central Europe.

On the scientific selectionist "with modification" side of Darwin's theory, it seems likely that some general principles similar to the biological apply socioculturally - principles pertaining to density, scale, patchiness, uncertainty (with or without reliable cues) and so on. But many problems there too remain unresolved. What exactly is the relationship between somatic and reproductive functions (in the social sciences, between individual and social learning)? How do new levels of selection arise? Biologically, how does evolution go from prokaryotic to eukaryotic cells, from the single-celled to the multi-celled, and from the multi-celled to eusocial colonies? Similarly socioculturally, how does evolution go from individual norms and values, to aggregates of these in social roles or statuses, and to aggregates of those in turn in organizations and institutions?

Returning to the historical "descent" side of Darwin's theory of "descent with modification", one thing about sociocultural evolution is clear. As the examples summarized in this paper (and others that could have been) illustrate, many of the computational tree-building methods developed in systematic biology can be utilized in the social sciences to answer a host of kinds of questions about history that we could not answer in any other way. Many too are the kinds of cultural phenomena they can be asked of in the future. What about variants of Abrahamic religions, financial occupations or rap music? We are limited only by our imaginations and sources of data.

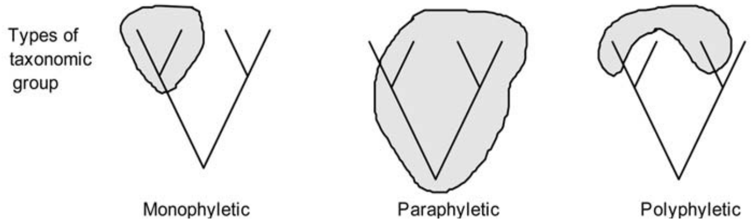

Figure 1. Differences among cladistic, evolutionary and phenetic systematics*

	Groups Recognized			Characters Used		
	Mono-phyletic	Para-phyletic	Poly-phyletic	Derived	Ancestral	Analogies
Cladistic	Yes	No	No	Yes	No	No
Evolutionary	Yes	Yes	No	Yes	Yes	No
Phenetic	Yes	Yes	Yes	Yes	Yes	Yes

(*Source Modified from Ridley, M. *Evolution*, Second Edition. 1996, p. 381-2).

References

Arthur, W. B. (2009). *The Evolution of Technology: What It Is and How It Evolves*. New York, The Free Press.

Atkinson, Q. D., Meade, A., Venditti, C., Greenhill, S. J., & Pagel, M. (2008). Languages evolve in punctuational bursts. *Science,* 319, 588.

Basalla, G. (1988). *The Evolution of Technology*. Cambridge, Cambridge University Press.

Baum, D. A., & Smith, S. D. (2013). *Tree Thinking: An Introduction to Phylogenetic Biology*. Greenwood Village, CO, Roberts and Company Publishers, Inc.

Bentz, C., Verkerk, A., Kiela, D., Hill, F., & Buttery, P. (2015). Adaptive communication: Languages with more non-native speakers tend to have fewer word *forms. PloS one*, 10(6), e0128254.

Birchall, J., Dunn, M., & Greenhill, S. (2016). A combined comparative and phylogenetic analysis of the Chapacuran language family. *International Journal of American Linguistics*, 82, 255-284.

Blute, M. (1979). Sociocultural evolutionism: An untried theory. *Behavioral Science* 16, 46-59.

Blute, M. (2010). *Darwinian Sociocultural Evolution: Solutions to Dilemmas in Cultural and Social Theory*. Cambridge: Cambridge University Press.

Blute, M. (2015). Modes of variation and their implications for an extended evolutionary synthesis. In J. H. Turner, R. Machalek, & A. Maryanski (Eds.), *Handbook on Evolution and Society: Toward an Evolutionary Social Science* (pp. 59-75). Boulder, Paradigm Publishers.

Borgerhoff Mulder, M., Nunn, C. L., & Towner, M. C. (2006). Cultural macroevolution and the transmission of traits. *Evolutionary Anthropology: Issues, News, and Reviews*, 5(2), 52-64.

Bouckaert, R., Lemey, P., Dunn, M., Greenhill, S. J., Alekseyenko, A. V., Drummond, A. J., Gray, R. D., Suchard, M. A., & Atkinson, Q. D. (2012). Mapping the origins and expansion of the Indo-European language family. *Science,* 337, 957-960.

Bowern, C., & Atkinson, Q. (2012). Computational phylogenetics and the internal structure of Pama-Nyungan. *Language*, 88(4), 817-845.

Boyd, R. & P. J. Richerson. (1985). *Culture and the Evolutionary Process*. Chicago, The University of Chicago Press.

Bromham, L., Hua, X., Fitzpatrick, T. G., & Greenhill, S. J. (2015). Rate of language evolution is affected by population size. *Proceedings of the National Academy of Sciences*, 112(7), 2097-2102.

Buchanan, B., & Collard, M. (2007). Investigating the peopling of North America through cladistic analyses of Early Paleoindian projectile points. *Journal of Anthropological Archaeology*, 26(3), 366-393.

Buckley, C. D. (2012). Investigating cultural evolution using phylogenetic analysis: the origins and descent of the southeast Asian tradition of Warp Ikat weaving. *PLoS One,* 7, 1-20.

Calude, A. S., & Verkerk, A. (2016). The typology and diachrony of higher numerals in Indo-European: a phylogenetic comparative study. *Journal of Language Evolution*, 1(2), 91-108.

Campbell, L., & Poser, W. J. (2008). *Language classification: History and method*. Cambridge, Cambridge University Press.

Cavalli-Sforza, L. L., & Feldman, M. W. (1981). *Cultural Transmission and Evolution: A Quantitative Approach*. Princeton, Princeton University Press.

Chang, W., Cathcart, C., Hall, D., & Garrett, A. (2015). Ancestry-constrained phylogenetic analysis supports the Indo-European steppe hypothesis. *Language*, 91, 194-244.

Crowley, T., & Bowern, C. (2010). *An introduction to historical linguistics*. Oxford, Oxford University Press.

Currie, T. E. (2013). Cultural evolution branches out: the phylogenetic approach in cross-cultural research. *Cross-Cultural Research,* 47, 102-130.

Currie, T. E., Greenhill, S. J., Gray, R. D., Hasegawa, T., & Mace, R. (2010). Rise and fall of political complexity in island South-east Asia and the Pacific. *Nature,* 467, 801-804.

Currie, T. E., & Mace, R. (2014). Evolution of cultural traits occurs at similar relative rates in different world regions. *Proceedings of the Royal Society B*, 281, 1622-1629.

da Silva, S. G., & Tehrani, J. J. (2016). Comparative phylogenetic analyses uncover the ancient roots of Indo-European folktales. *Royal Society Open Science*, Jan. 20, DOI: 10.1098/sos.150645.

Diamond, J., & Bellwood, P. (2003). Farmers and their languages: the first expansions. *Science*, 300(5619), 597-603.

Distin, K. (2011). *Cultural Evolution*. Cambridge, Cambridge University Press.

Drummond, A. J., & Bouckaert, R. R. (2015). *Bayesian evolutionary analysis with BEAST*. Cambridge, Cambridge University Press.

Dunn, M., Greenhill, S. J., Levinson, S. C., & Gray, R. D. (2011). Evolved structure of language shows lineage-specific trends in word-order universals. *Nature*, 473(7345), 79-82.

Dunn, M., Kruspe, N., & Burenhult, N. (2013). Time and place in the prehistory of the Aslian languages. *Human biology*, 85(3), 383-400.

Dunn, M., Terrill, A., Reesink, G., Foley, R. A., & Levinson, S. C. (2005). Structural phylogenetics and the reconstruction of ancient language history. *Science*, 309(5743), 2072-2075.

Felsenstein, J. (1985). Phylogenies and the comparative method. *American Naturalist*, 1-15.

Felsenstein, J. (2004). *Inferring Phylogenies*. Sunderland: Sinauer Associates.

Felsenstein, J. (2016). *Phylogeny programs*. Retrieved, March 23, 2016. http://evolution.genetics.washington.edu/phylip/software.html

Fog, A. (1999). *Cultural Selection*. Dordrecht, Kluwer Academic Publishers.

Fortunato, L. (2011a). Reconstructing the history of residence strategies in Indo-European-speaking societies: neo-, uxori-, and virilocalitry. *Human Biology*, 83, 107-128.

Fortunato, L. (2011b). Reconstructing the history of marriage strategies in Indo-European-speaking societies: monogamy and polygamy. *Human Biology*, 83, 87-105.

Fortunato, L. & Jordan, F. (2010). Your place or mine? A phylogenetic comparative analysis of marital residence in Indo-European and Austronesian societies. *Philosophical Transactions of the Royal Society B*, 365, 3913-3922.

Gray, R. D., & Atkinson, Q. D. (2003). Language-tree divergence times support the Anatolian theory of Indo-European origin. *Nature,* 426, 435-439.

Gray, R. D., Bryant, D., & Greenhill, S. J. (2010). On the shape and fabric of human *history. Philosophical Transactions of the Royal Society B: Biological Sciences,* 365(1559), 3923-3933.

Gray, R. D., Drummond, A. J., & Greenhill, S. J. (2009). Language phylogenies reveal expansion pulses and pauses in Pacific settlement. *Science,* 323, 479-483.

Gray, R. D., Greenhill, S. J., & Ross, R. M. (2007). The pleasures and perils of Darwinizing culture (with phylogenies). *Biological Theory*, *2*(4), 360-375.

Gray, R. D., & Jordan, F. M. (2000). Language trees support the express-train sequence of Austronesian expansion. *Nature*, 405, 1052-1055.

Greenhill, S. J., Blust, R., & Gray, R. D. (2008). The Austronesian basic vocabulary database: from bioinformatics to lexomics. *Evolutionary Bioinformatics*, 4, 271-283.

Greenhill, S. J., Currie, T. E., & Gray, R. D. (2009). Does horizontal transmission invalidate cultural phylogenies?. *Proceedings of the Royal Society B: Biological Sciences*, 276(1665), 2299-2306.

Greenhill, S. J., & Gray, R. D. (2009). Austronesian language phylogenies: Myths and misconceptions about Bayesian computational methods. *Austronesian historical linguistics and culture history: a festschrift for Robert Blust.* Canberra: Pacific Linguistics, 375-397.

Grollemund, R., Branford, S., Bostoen, K., Meade, A., Venditti, C. & Pagel, M. (2015). Bantu expansion shows that habitat alters the route and pace of human dispersals. *Proceedings of the National Academy of Sciences*, 112, 13296-13301.

Haak, W., Lazaridis, I., Patterson, N., Rohland, N., Mallick, S., Llamas, B., & Fu, Q. (2015). Massive migration from the steppe was a source for Indo-European languages in Europe. *Nature*, 522(7555), 207-211.

Haynie H. J., Bowern C. (2016). Phylogenetic approach to the evolution of color term systems. *Proceedings of the National Academy of Sciences USA* 113(48):13666-13671.

Hennig, W. (1966). *Phylogenetic Systematics*. Urbana, University of Illinois Press.

Henrich, J., & Boyd, R. (1998). The evolution of conformist transmission and the emergence of between-group differences. *Evolution and Human Behavior,* 19(4), 215-241.

Hodgson, G. M., & T. Knudsen (2010). *Darwin's Conjecture: The Search for General Principles of Social & Economic Evolution*. Chicago, The University of Chicago Press.

Holden, C. J. (2002). Bantu language trees reflect the spread of farming across sub-Saharan Africa: a maximum-parsimony analysis. *Proceedings of the Royal SocietyB: Biological Sciences*, 269(1493), 793-799.

Holden, C. J., & Mace, R. (2003). Spread of cattle led to the loss of matrilineal descent in Africa: a coevolutionary hypothesis. *Proceedings of the Royal Society of London* B, 270, 2425-2433.

Holden, C. J., & Mace, R. (2005). The cow is the enemy of matriliny: using phylogenetic methods to investigate cultural evolution in Africa. In R. Mace, C. J. Holden & S. Shennan (Eds.) *The Evolution of Cultural Diversity: A Phylogenetic Approach*. (pp. 217-234). London, UCL Press.

Holland, B. R., Huber, K. T., Dress, A., & Moulton, V. (2002). δ plots: a tool for analyzing phylogenetic distance data. *Molecular Biology and Evolution*, 19(12), 2051-2059.

Honkola, T., Vesakoski, O., Korhonen, K., Lehtinen, J., Syrjänen, K., & Wahlberg, N. (2013). Cultural and climatic changes shape the evolutionary history of the Uralic languages. *Journal of evolutionary biology*, 26(6), 1244-1253.

Hull, D. L. (1988). *Science as a Process: An Evolutionary Account of the Social and Conceptual Development of Science*. Chicago, The University of Chicago Press.

Huson, D. H. & Bryant, D. (2006). Application of phylogenetic networks in evolutionary studies. *Molecular Biology & Evolution*, 23(2), 254-267.

Jaeger, G., & Wichmann, S. (2016). Inferring the world tree of languages from word lists. In S. G. Roberts, C. Cuskley, L. McCrohon, L. Barceló-Coblijn, O. Feher & T. Verhoef (Eds.) Evolang 11 http://evolang.org/neworleans/papers/147.html

Jordan, F. M. (2013). Comparative phylogenetic methods and the study of pattern and process in kinship. In P. McConvell, I. Keen & R. Hendery (Eds.) *Kinship Systems: Change and Reconstruction* (pp. 43-58). Salt Lake City, The University of Utah Press.

Jordan, F. M., Gray, R. D., Greenhill, S. J., & Mace, R. (2009). Matrilocal residence is ancestral in Austronesian societies. *Proceedings of the Royal Society B: Biological Sciences* 276, 1957-1964.

Jordan, F. M. & Mace, R. (2007) Changes in post-marital residence precede changes In descent systems in Austronesian societies. Presented at: The European Human Behaviour and Evolution Conference (EHBE 2007), London School of Economics, London, UK.

Kitchen, A., Ehret, C., Assefa, S., & Mulligan, C. J. (2009). Bayesian phylogenetic analysis of Semitic languages identifies an Early Bronze Age origin of Semitic in the Near East. *Proceedings of the Royal Society B: Biological Sciences* 276(1668), 2703–2710.

Kushnick, G., Gray, R. D., & Jordan, F. M. (2014). The sequential evolution of land tenure norms. *Evolution & Human Behavior*, 35, 309-318.

Lee, S., & Hasegawa, T. (2011). Bayesian phylogenetic analysis supports an agricultural origin of Japonic languages. *Proceedings of the Royal Society B: Biological Sciences* 278, 3662–3669.

Lemey, P., Salemi, M., & Vandamme, A. M. (2009). *The Phylogenetic Handbook: a practical approach to phylogenetic analysis and hypothesis testing*. Cambridge, Cambridge University Press.

Lewens, T. (2015). *Cultural Evolution: Conceptual Challenges*. Oxford, Oxford University Press.

Lipo, C. P., O'Brien, M. J., Collard, M., & Shennan, S. J. (2006). *Mapping our ancestors.* New Brunswick and London: Aldine Transactions.

Lovejoy, A. O. (1936). *The Great Chain of Being: A Study of the History of an Idea*. Boston, Harvard University Press.

Mace, R., & Jordan, F. M. (2011). Macro-evolutionary studies of cultural diversity: A review of empirical studies of cultural transmission and cultural adaptation. *Philosophical Transactions of the Royal Society of London B: Biological Sciences*, 366(1563), 402-411.

Mace, R., & Pagel, M. (1994). The comparative method in anthropology. *Current Anthropology*, 35(5), 549-564.

Matthews, L J., Tahran, J. J., Jordan, F. M., Collard, M., & Nunn, C. L. (2011). Testing for divergent transmission histories among cultural characters: a study using Bayesian phylogenetic methods and Iranian tribal textile data. *PLoS One,* 6(4), e14810.

Mesoudi, A. (2012). *Cultural Evolution: How Darwinian Theory Can Explain Human Culture & Synthesize the Social Sciences*. Chicago, The University of Chicago Press.

Michael, L., Chousou-Polydouri, N., Keith, B., Donnelly, E., Meira, S., Wauters, V., O'Hagan, Z. (2015). A Bayesian Phylogenetic Classification of Tupí-Guaraní. *LIAMES - Línguas Indígenas Americanas,* 15(2), 193 – 221.

Moore, J. H. (1994). Putting anthropology back together again: the ethnogenetic critique of cladistic theory. *American Anthropologist*, 96, 925-948.

Morgan, L. H. (1871). *Systems of consanguinity and affinity of the human family* (Vol. 218). Smithsonian institution.

Morgan, L. H. (1877). *Ancient society; or, researches in the lines of human progress from savagery, through barbarism to civilization*. H. Holt.

Murdock, G. P. (1969). *Outline of World Cultures*. Yale: Human Relations Area Files.

Nunn, C. L. (2011). *The comparative approach in evolutionary anthropology and biology*. Chicago, University of Chicago Press.

Opie, C., Shultz, S., Atkinson, Q. D., Currie, T., & Mace, R. (2014). Phylogenetic reconstruction of Bantu kinship challenges Main Sequence Theory of human social evolution. *Proceedings of the National Academy of Sciences*, *111*(49), 17414-17419.

Pagel, M. (1994). Detecting correlated evolution on phylogenies: A general method for the comparative analysis of discrete characters. *Proceedings of the Royal Society B: Biological Sciences* 255(1342), 37-45.

Pagel, M. (2016). Darwinian perspectives on the evolution of human languages. *Psychonomic Bulletin & Review*, 1-7.

Pagel, M., Atkinson, Q., Calude, A., & Meade, A. (2013). Ultra-conserved words point to deep language relationships across Eurasia. *Proceedings of the National Academy of Sciences,* 110(21), 8471–8476.

Peoples, H. C., Duda, P., & Marlowe, F. W. (2016). Hunter-gatherers and the origins of religion. *Human Nature,* 27, 261-282.

Plotkin, H. (1994). *Darwin Machines and the Nature of Knowledge*. Cambridge, Harvard University Press.

Richerson, P. J., & Boyd, R. (2005). *Not by Genes Alone: How Culture Transformed Human Evolution*. Chicago, The University of Chicago Press.

Richerson, P. J. & Christiansen, M. (2013). *Cultural Evolution: Society, Technology, Language and Religion*. The MIT Press.

Ridley, M. (1996). *Evolution*. Second Edition. Hoboken, Blackwell Science, Inc.

Robinson, L. C., & Holton, G. (2012). Internal classification of the Alor-Pantar language family using computational methods applied to the lexicon. *Language Dynamics and Change*, *2*(2), 123-149.

Rogers, D. S., Feldman, M. W., & Ehrlich, P. R. (2009) Inferring population histories using cultural data. *Proceedings of the Royal Society B: Biological Sciences* 276, 3835-3843.

Ross, R. M., & Atkinson, Q. D. (2016). Folktale transmission in the Arctic provides evidence for high bandwidth social learning among hunter–gatherer groups. *Evolution and Human Behavior*, 37(1), 47-53.

Ross, R. M., Greenhill, S. J., & Atkinson, Q. D. (2013). Population structure and cultural geography of a folktale in Europe. *Proceedings of the Royal Society B: Biological Sciences*, 280(1756), 20123065.

Runciman, W. (2009). *The Theory of Cultural and Social Selection*. Cambridge, Cambridge University Press.

Schillinger, K., Mesoudi, A., & Lycett, S. J. (2016). Copying error, evolution, and phylogenetic signal in artifactual traditions: An experimental approach using 'model artifacts'. *Journal of Archaeological Science*, 70, 23-34.

Shennan, S. J., Crema, E. R., & Kerig, T. (2015). Isolation-by-distance, homophily, and "core" vs. "package" cultural evolution models in Neolithic Europe. *Evolution and Human Behavior*, 36, 103-109.

Sicoli, M. A., & Holton, G. (2014). Linguistic phylogenies support back-migration from Beringia to Asia. *PloS one*, 9(3), e91722.

Sperber, D. (1996). *Explaining culture: A naturalistic approach*. Oxford, Blackwell.

Tehrani, J. (2013). The phylogeny of little red riding hood. *PLoS One,* 8, 1-11.

Tehrani, J. & Collard, M. (2002) Investigating cultural evolution through a phylogenetic analysis of Turkmen textiles. *Journal of Anthropological Archaeology*, 21, 443-463.

Turner, J. H., & Maryanski, A. (2008). *On the Origin of Societies by Natural Selection*. Boulder, Paradigm Publishers.

Valverde, S., & Solé, R. V. (2015). Punctuated equilibrium in the large-scale evolution of programming languages. *Journal of The Royal Society Interface*, 12(107), 20150249.

Walker, R., Robert, S., & Ribeiro, L. A. (2011). Bayesian phylogeography of the Arawak expansion in lowland South America. *Proceedings of the Royal Society B: Biological Sciences* 278(1718), 2562–2567.

Walker, R. S., Wichmann, S., Mailund, T., & Atkisson, C. J. (2012). Cultural phylogenetics of the Tupi language family in lowland south America. *PLoS One,* 7, 1-9.

Watts, J., Greenhill, S. J., Atkinson, Q. D., Currie, T. E., Bulbulia, J., & Gray, R. D. (2015). Broad supernatural punishment but not moralizing high gods precede the evolution of political complexity in Austronesia. *Proceedings of the. Royal Society B*: Biological Sciences (Vol. 282, No. 1804, p. 20142556).

Watts, J., Sheehan, O., Atkinson, Q. D., Bulbulia, J., & Gray, R. D. (2016). Ritual human sacrifice promoted and sustained the evolution of stratified societies. *Nature*, *532*, 228-231.

Wichmann, S., Walker, R., Rama, T., & Holman, E. W. (2011). Correlates of reticulation in linguistic phylogenies. *Language Dynamics and Change*, 1(2), 205-240.

Wikipedia. (2016). Outline of Evolution; Taxonomy, systematics and phylogeny; List of phylogenetics software. Retrieved March 23, 2016. http://en.wikipedia.org

Yong, E. (2013). Dynasty: Bob Paine fathered an idea - and an academic family - that changed ecology. *Nature*, 493, 286-289.

Zhou, K. & Bowern, C. (2015). Quantifying uncertainty in the phylogenetics of Australian numeral systems. *Proceedings of the Royal Society B: Biological Sciences*, 282, 1278-1283.