

Insights from evolutionary anthropology
on the (pre-)history of the nuclear family

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Abstract

My aim in this paper is to elucidate the relevance of the evolutionary paradigm to the study of kinship and marriage systems. I begin with a discussion of conceptual and methodological issues that arise in approaching human social systems from an evolutionary perspective. I then narrow the focus on key tools used in contemporary cross-cultural research within evolutionary anthropology. Next, as a case study, I provide an overview of work aimed at reconstructing the (pre-)history of the nuclear family in Indo-European-speaking societies, focusing on the interplay between monogamous marriage and neolocal residence. I conclude with musings on the prospect of a biologically based social anthropology.

Keywords Evolutionary anthropology, cross-cultural research, nuclear family, monogamous marriage, neolocal residence, kinship and marriage systems, Indo-European-speaking societies.

1 Introduction

In *The history of human marriage*, Westermarck (1921, p. 104) wrote

Monogamy is the only form of marriage that is permitted among every people. Wherever we find polygyny, polyandry, or group-marriage, we find monogamy side by side with it. On the other hand, it is also in many cases the only form of marriage which is permitted by custom or law. This may be due to the mere force of habit ; or, possibly, to the notion that some men must not appropriate a plurality of wives when others in consequence can get none at all ; or to the feeling that polygyny is an offence against the female sex ; or to the condemnation of lust.

This excerpt, from the third volume of Westermarck’s monumental opus, illustrates some of the problems that have marred the study of kinship and marriage systems since its inception in the nineteenth century. For example, group-level norms are confounded with individual behaviour, such that variation in behavioural strategies within societies is contrasted with variation across societies. In the following decades, these difficulties precipitated the field into “a subject in which specialists talked only to each other (and some talked only to God)” (Fox 1983, p. 10). Couched in arcane language and obscure conceptual categories, its basic assumptions came under severe scrutiny during the second half of the twentieth century; by the end of the century, anthropology had essentially repudiated what it once viewed as its “basic discipline” (Fox 1967, p. 10; see discussion in Holy 1996, pp. 1–8).

As in other domains in the behavioural sciences, an evolutionary approach offers a unified conceptual and analytical framework to overcome these difficulties (see discussion in Mesoudi 2011). After all, kinship and marriage systems represent “one form of assortative mating which has the interesting component of culturally defined categories” (Fox 1983, p. 3). Thus, the study of these features of social organization can take advantage of the suite of theoretical and methodological tools used in the analysis of social behaviour, both human and non-human. In turn, to the extent that networks based on kinship and marriage created the social niche in which our species evolved, understanding their workings becomes crucial for understanding the evolution of human behaviour. Ultimately, a comprehensive evolutionary account of the human phenomenon must be able to explain why individuals organize relatedness and reproduction in the ways they do (Fortunato 2015).

Anthropologists have generally resisted application of the evolutionary paradigm to the analysis of kinship and marriage systems, the classic complaint being that “social” and “biological” categories overlap but are not identical (Fox 1983, p. 3; see e.g. Sahlins 2013, 1976). At the same time, those advocating an evolutionary approach have perhaps failed to provide compelling explanations to account for these discrepancies. For example, one of the most powerful insights afforded by the evolutionary approach to the study of human behaviour is the asymmetry that characterizes sexually reproducing species, deriving from the higher potential rate of reproduction of males relative to females (see review in Brown et al. 2009). The cross-cultural prevalence of polygynous marriage is readily explained on this notion; why a small but substantial proportion of societies prescribe monogamous marriage is however not clear (Fortunato and Archetti 2010). A norm enforcing monogamous marriage is especially puzzling where mating is effectively polygamous (e.g. through pre- and extra-marital sexual relationships). The discrepancy between the “social” category of marriage and the “biological” category of mating would seem to disprove claims to the relevance of evolutionary explanations to these aspects of human social life (Fortunato 2015).

My aim in this paper is to elucidate the relevance of the evolutionary paradigm to the study of kinship and marriage systems. I begin with a discussion of conceptual and methodological issues that arise in approaching human social systems from an evolutionary perspective. I then narrow the focus on key tools used in contemporary cross-cultural research within evolutionary anthropology. Next, as a case study, I provide an overview of work aimed at reconstructing the (pre-)history of the nuclear family in Indo-European-speaking societies. This exercise can help us evaluate theoretical claims to the centrality of the arrangement to European social organization and, by extension, to “western” social organization. Such claims abound in the social sciences, typically outside anthropology (Goody 1996; Sear 2016; Smith 1993). The results also speak to renewed interest from across the social sciences in how family systems, and their historical trajectories, have contributed to shaping the contemporary world (e.g. Alesina and Giuliano 2010; Duranton et al. 2009).

1.1 Levels of explanation

Following a schema introduced in biology by Tinbergen (1963), researchers investigating a given behaviour may focus on one of four levels of explanation. Those interested in *why* the behaviour evolved may ask questions about (i) its adaptive function, and about (ii) its evolutionary history. Those interested in *how* the behaviour comes about within an individual may ask questions about (iii) the mechanisms underpinning it, and about (iv) its ontogeny, or development, over the individual’s life course. Function and history represent the *ultimate* causes of the behaviour, mechanisms and ontogeny its *proximate* causes (Mayr 1961).

In the analysis of kinship and marriage systems, at the ultimate level we may ask why societies vary with respect to a particular set of norms (function), and how this variation arose (history). For example, does monogamous marriage benefit individuals under specific conditions, and does this explain why the arrangement is prescribed in some societies, while the majority of societies allow polygynous marriage? Does the prevalence of monogamous marriage among European societies reflect social or ecological determinants, or is it simply an artefact of history? At the proximate level, we may ask about the “machinery” (e.g. physiological or psychological) underpinning the behaviour within an individual (mechanism), and about the developmental pathways involved (ontogeny). For example, do men vary in the propensity to seek multiple sexual partners (e.g. in their hormonal profiles), and is this related to whether they engage in multiple marriages? And what are the respective roles of genetic and environmental effects in this process over the course of an individual’s lifetime?

Tinbergen’s (1963) schema, coupled with Mayr’s (1961) ultimate/proximate distinction, has proven extremely fruitful in the study of behaviour over the past 50 years (see discussion in Bateson and Laland 2013). In particular, it served to clarify that the four levels of explanation — function, history, mechanism, and ontogeny — are logically independent, in the sense that alternative hypotheses compete *within* levels, not *across* them (Sherman 1988). In biology, this insight helped resolve heated debates between researchers effectively arguing over supposedly alternative hypotheses, which sat instead at different levels of explanation (see Sherman 1988, for examples drawn from the biological literature).

In practice, conceptual separation of the four levels implies that we can ask questions at one level (e.g. about function), even if we are ignorant of the answer at another (e.g. about

mechanism) (Dunbar 2008, p. 132). It does not follow that one level can be ignored in favour of others, or that — as is sometimes implied — ultimate questions are more insightful than proximate ones. Full understanding of any phenomenon requires answers at all levels of explanation — indeed, their integration into a “biology of behaviour” was a key aim of Tinbergen’s (1963) proposal (Bateson and Laland 2013). Consistently, over the years researchers have increasingly come to recognize the importance of questions that lie at the interface between levels (e.g. Autumn et al. 2002; Müller 2007). Fifty years on, there are calls within biology to explicitly update and extend the Tinbergen/Mayr framework. Advocates argue for a shift in focus from distinct levels of explanation, and the strict dichotomy between ultimate and proximate questions, to their integration into an “extended evolutionary synthesis” (e.g. Bateson and Laland 2013; Laland et al. 2014; Laland 2015; Laland et al. 2013, 2011, 2015; Mesoudi et al. 2013).

These calls remain controversial (e.g. Dickins and Barton 2013; Dickins and Rahman 2012; Scott-Phillips et al. 2011; Welch 2016; Wray et al. 2014). The details of the debate are beyond the scope of the present discussion, yet one point of controversy is especially relevant to evolutionary anthropology. This relates to the role of cultural transmission — one of the known pathways for the non-genetic transmission of information (others being epigenetic inheritance and “ecological” inheritance, or niche construction; see references above for details). Beginning with seminal work by e.g. Cavalli-Sforza and Feldman (1981) and Boyd and Richerson (1985), a large body of theoretical and empirical insights has now accumulated, showing that the process of cultural inheritance operates through different dynamics than the process of genetic inheritance. This notion is uncontroversial; what is controversial is how to accommodate it within the Tinbergen/Mayr framework.

At one extreme, some maintain that how a given behaviour is transmitted, whether genetically or culturally (i.e. through social learning), is a proximate question (e.g. West et al. 2007). Thus, we can ask ultimate questions about cultural behaviours without reference to the underlying mechanism of transmission (Dunbar and Barrett 2007, p. 5). Others explicitly acknowledge the role of cultural transmission in the evolutionary process, distinct from the role of genetic transmission. Within this camp, some have characterized investigating the interactions between the processes of genetic and cultural change as answering proximate questions (e.g. Henrich and McElreath 2003), some as answering both proximate and ultimate questions (e.g.

Richerson and Boyd 2005). At the other extreme, some argue that this confusion stems from limitations of the Tinbergen/Mayr framework, which is in fact hampering progress in the field (e.g. Laland et al. 2011, and other references above).

This controversy is potentially relevant to those working at the interface of biology and other disciplines, but it is irrelevant to researchers in the social sciences who have never heard of the Tinbergen/Mayr framework — and that is perhaps the majority. Against this background, there is still scope for application of the framework to questions about human behaviour. In my view, one key advantage of starting by addressing ultimate questions is that it forces us to treat the behaviour of our species in the general terms used to characterize the behaviour of other species; this, in turn, forces us to think *explicitly* about where and how our species departs from the predictions of the “biological” paradigm. For instance, placing kinship and marriage systems in the wider context of animal social behaviour provides a set of first principles for devising analytical traits and categories that are theoretically justifiable and empirically useful. This is crucial for clearing up the terminological confusion that has dominated the study of kinship and marriage systems within anthropology, eventually leading to its demise (Section 1), and which has fostered more confusion in other fields that have relied on previous anthropological theorizing (see discussion in Fortunato 2011a,b, 2015, for examples).

So, to continue the example introduced above, in investigating the evolution of monogamous marriage we can start with ultimate questions about its function. For instance, theoretical work in Fortunato and Archetti (2010) asks under what conditions monogamous marriage can maximize inclusive fitness, where fitness is linked to resources and resources are transferred across generations. Of course, variation in marriage strategies across societies, or in other features of social organization, is unlikely to be based on genetic differences (Hughes 1988, pp. 6–7). The inclusive fitness metaphor is used in this case as shorthand for the assumption that social norms effect the “biological” paradigm — that is, that they encode the cumulative outcomes of the inclusive-fitness-maximizing behavioural tendencies of individuals (Alexander 1979, p. 68). Irrespective of its validity, this assumption provides a useful starting point for investigating the diversity of human social systems, at least to the extent that it helps us conceptualize previous anthropological observations about the distribution of marriage strategies, and that it focuses further theoretical and empirical work (Fortunato 2012; Fortunato and Archetti 2010). Next,

we can ask through what proximate mechanisms these inclusive-fitness-maximizing behavioural tendencies are realized. For example, in societies with status differentiation based on ownership of resources, monogamous marriage and the transfer of property to lineal heirs may reflect the conscious concern of individuals with the preservation of status through the concentration of wealth (Rogers 1995; see e.g. Goody 1976); status and ownership of resources are typically linked to fitness in these societies (see review in Hopcroft 2006). Finally, we can ask to what degree the process of cultural inheritance can lead to patterns of behaviour that are inconsistent with the predictions of the “a-cultural” model (Rogers 1988). For instance, we can investigate how the evolutionary dynamics are affected by different pathways for the transmission of mating preferences between individuals (e.g. Mesoudi and Laland 2007). From the perspective of the social sciences, this particular example gains in clarity through application of the Tinbergen/Mayr framework.

1.2 Explaining cross-cultural variation

To the extent that kinship and marriage systems determine the structure of human societies, they likely played a role in the unfolding of (pre-)history. At the same time, long-term population processes such as migration, or the diffusion of cultural traits between neighbouring populations, likely shaped the observed pattern of variation in kinship and marriage systems. Unravelling the interactions between these facets of (pre-)history becomes crucial for understanding the evolution of human social organization, and of human behaviour more generally (Jones 2003; see e.g. Gamble 2008; Gowlett 2008).

This task is hampered by a key methodological difficulty. Some societies are more closely related than others, either by way of descent from a common ancestor or through contact. Consequently, the statistical assumption of independence of sample units is untenable for any cross-cultural dataset (Dow 1993). Kinship and marriage systems appear to be “conservative” features of social organization (Murdock 1949, p. 196); in the context of linguistic and genetic variation, the effect of descent is strongest at the supra-regional level, while the effect of contact prevails within regions (Borgerhoff Mulder et al. 2001, 2006; Burton et al. 1996; Guglielmino et al. 1995; Hewlett et al. 2002; Holden and Mace 1999; Jones 2003; Moylan et al. 2006).

The issue of the non-independence of sample units in cross-cultural analysis was first rec-

ognized by Galton in response to the earliest application of a quantitative approach to cross-cultural data — coincidentally, Tylor’s (1889) study of norms relating to marriage and descent (Jorgensen 1979). Tylor’s contribution has been described as “[p]erhaps the greatest anthropological paper of the nineteenth century” (Harris 2001, p. 158). Yet a different view of comparative approaches has come to prevail within anthropology — seemingly a reaction to the excesses of its nineteenth century forebear, cultural evolutionism, and its abuse of ethnographic material (see discussion in Fortunato 2016). As a result, the majority of “mainstream” anthropologists today are wary of, if not outright hostile to, cross-cultural approaches to the ethnographic record. Comparative analysis is an inevitable technique in anthropological enquiry — societies are routinely compared and contrasted to make sense of the diversity of human social systems (see discussion in Legros 2013, Chapter 1). However, efforts to formalise this line of enquiry typically involve focusing on variation across societies in a small number of traits, isolated from their context, so that the data are amenable to systematic analysis. To many anthropologists this approach is, at best, too reductionist and, at worst, too close to the comparative method of evolutionism (see discussion in Fortunato 2016). For example, as we shall see below, Murdock dedicated a substantial part of his 50-year career, between the early 1930s and the early 1980s, to addressing some of the key conceptual and methodological issues with cross-cultural research. The resistance he endured from within anthropology in the face of these efforts led to a rather pessimistic outlook on the field, and on the discipline more generally, towards the end of his career (e.g. Murdock 1971, 1977).

The refusal of anthropology to engage with cross-cultural research has not prevented other disciplines from doing so, however. For example, since the 1970s researchers interested in the study of human social behaviour from an evolutionary perspective have embraced cross-cultural comparison, contributing both hypotheses (e.g. Alexander et al. 1979) and methods (e.g. Mace and Pagel 1994) to the approach. Increasingly, cross-cultural databases developed in anthropology are being used in empirical research across the social sciences (e.g. Alesina et al. 2011). This paradoxical situation has one unfortunate consequence for practitioners: the extensive discussions surrounding the approach that occurred within anthropology since the late nineteenth century have been lost to contemporary practice — including discussions about subtle conceptual and methodological issues, such as definition of the units of analysis (e.g.

Naroll 1964), that anthropologists are best placed to resolve (Fortunato 2016).

In any case, cross-cultural research has come to feature prominently in the toolkit of those bringing an evolutionary approach to human behaviour, to investigate variation in cultural practices across societies. Below I introduce two key tools in contemporary cross-cultural research within evolutionary anthropology.

1.2.1 Cross-cultural databases

The first tool originated with Murdock’s intuition of developing a set of standardized resources for cross-cultural analysis. In an explicit effort to address the shortcomings of earlier comparative work (including his own, e.g. Murdock 1949), Murdock developed the *World Ethnographic Sample* in 1957, with two key objectives: “(1) to present a carefully selected sample of all the cultures known to history and ethnography, and (2) to classify each selected culture according to certain standard ethnographic categories” (Murdock 1957, p. 664). Refinement of this resource culminated in the *Ethnographic Atlas*, a collection of coded ethnographic data published in installments in the journal *Ethnology*, starting with Murdock (1962) and summarized in Murdock (1967a,b). The aspiration was “that the Atlas may ultimately develop into a cumulative encyclopedia of classified ethnographic information” (Murdock 1962, p. 114). Data on the 1267 societies covered over the years are collated in Gray (1999).

In a later development, Murdock and White (1969) produced the *Standard Cross-Cultural Sample*, with the aim to adequately represent the range of known cultural variation (that is, avoiding biases towards regions that are overrepresented in the ethnographic record), while minimizing the effects of descent and contact on the distribution of cultural practices across societies (Murdock 1977). To these ends, Murdock (1963, 1966, 1967b, 1968) had previously divided entries in the *Ethnographic Atlas* into sets including societies that he believed to share similarities through descent and/or contact (see discussion in Jorgensen 1979). From each set, Murdock and White (1969) sought to include in the *Standard Cross-Cultural Sample* the society with the most extensive coverage; in any case, they excluded entries that could not be focused (“pinpointed”) to a specific date and locality of observation. This strategy produced a sample including 186 societies; empirical estimates indicate that it was successful in reducing the degree of non-independence within the sample (Dow 1989, 1993; Dow and Eff 2008; Murdock and White

1969), and in reducing the amount of random error that derives from the use of “unfocused” data (Divale 1975). Finally, by establishing a standard sample, Murdock and White (1969) aimed to facilitate integration of data and findings across studies. Currently, the *Standard Cross-Cultural Sample* codebook includes coded data for approximately 2000 variables (White et al. n.d.) across 186 societies; for comparison, the *Ethnographic Atlas* codebook includes coded data for approximately 100 variables across 1267 societies (Gray 1999).

1.2.2 The phylogenetic comparative approach

The second key tool in contemporary cross-cultural research within evolutionary anthropology involves application of phylogenetic comparative methods developed in biology. Like human societies, species and other biological groups, or taxa, are hierarchically related by way of descent from a common ancestor. Evolutionary biologists use phylogenetic comparative methods to control for the resulting non-independence in analyses of attributes across taxa (Felsenstein 1985; Harvey and Pagel 1991). Using a phylogenetic tree to represent how the taxa are related, these methods infer likely evolutionary scenarios that produced the observed distribution of the attribute(s) of interest across the taxa. Besides testing for correlated evolution between traits, they can be used to infer evolutionary pathways, to estimate rates of evolutionary change, and to reconstruct ancestral states of the traits (see overviews in Felsenstein 2004, Chapter 25, and in Pennell and Harmon 2013).

Mace and Pagel (1994) advocated the use of phylogenetic comparative methods in cross-cultural analysis, to control for the component of non-independence resulting from the descent of societies from a common ancestor. The component resulting from contact comprises instances of “horizontal transmission” of traits across societies, for example through copying. Societies lose or acquire cultural traits either through original invention or through horizontal transmission; both represent pathways through which functional associations between traits can arise. However, phylogenetic comparative methods assume that traits are transmitted vertically, i.e. from parent to daughter groups, along the branches of the phylogenetic tree used to represent how the taxa are related; consequently, high rates of horizontal transmission may invalidate application of the methods to cross-cultural data. There has been substantial debate around this and related issues (e.g. Borgerhoff Mulder 2001; Borgerhoff Mulder et al. 2006; Nunn et al. 2006;

Rogers and Cashdan 1997), with a small number of simulation studies aimed at evaluating the performance of phylogenetic comparative methods in the presence of horizontal transmission (e.g. Currie et al. 2010; Nunn et al. 2006).

The details of the debate are beyond the scope of the present discussion, but it is worth emphasizing one aspect here, which has been largely overlooked in this context. High rates of horizontal transmission, in a process of “cultural infection” (Mace 2005, p. 203) where two or more traits spread together across societies even though they are not functionally related, are by definition problematic for *any* method used in cross-cultural research — not just for phylogenetic comparative methods! This is because the basic assumption of cross-cultural hypothesis testing is that traits tend to occur together if they are functionally related (Murdock and White 1969). Phylogenetic comparative methods provide one approach to resolve empirically the relative roles of descent, horizontal transmission mediated by geographical proximity, and adaptation to the local ecology, in shaping the distribution of cultural practices across societies (e.g. Saslis-Lagoudakis et al. 2014).

1.2.3 Murdock vindicated

Despite the widespread resistance to cross-cultural research within anthropology, impetus from other disciplines has now firmly re-established this approach as an essential tool to uncover patterns in behavioural diversity across human societies, including diversity in kinship and marriage systems. Murdock’s intuition and contributions stand vindicated, as his databases are routinely used as a source of coded comparative data across the biological and social sciences (see e.g. Kirby et al. 2016, for a recent development).

Of course, neither tool introduced above addresses all potential shortcomings, and awareness of the limitations of each is key. For example, the quality and quantity of data in the *Standard Cross-Cultural Sample*, coupled with reduction in the degree of non-independence due to descent from a common ancestor and/or contact, make use of this sample the strategy of choice in many applications (Gray 1996). At the same time, clustering of variables still obtains in the sample, both by language family and by region (Dow 1989, 1993; Dow and Eff 2008; Eff 2004; Murdock and White 1969; Murdock et al. 1978); consequently, caution is required in interpretation of results derived from its analysis. Phylogenetic comparative methods control for, rather than

merely minimize, the component of non-independence due to descent. Whether, and how, the component resulting from contact affects the application of these methods to cross-cultural data is however a point of dispute within evolutionary anthropology.

Ultimately, which approach is used is often driven by practical considerations. These include, for example, whether the traits of interest show sufficient variation at the relevant scale of analysis (typically, at the global level in analysis of the *Standard Cross-Cultural Sample*, and at the language family level in phylogenetic comparative analysis), and/or the availability of trees representing human population history for use in phylogenetic comparative analysis (see overview in Dunn 2015).

2 Reconstructing the (pre-)history of the nuclear family

Having discussed some key conceptual and methodological issues that arise in approaching kinship and marriage systems from an evolutionary perspective, I now illustrate the approach with a brief overview of work aimed at reconstructing the (pre-)history of the nuclear family in societies speaking Indo-European languages (see Fortunato 2009, Chapter 6, for details).

It is useful to start with definitions, as these vary across disciplines, and between technical and everyday usage. In anthropology, the nuclear family designates a family unit comprising parents and their dependent children (Fox 1983, p. 36; Keesing 1975, p. 150; Parkin 1997, p. 28); technically, therefore, this arrangement can be associated with either monogamous or polygamous marriage (Murdock 1949, pp. 1–2; see discussion in Fox 1983, pp. 36–40). In other disciplines, as in everyday usage, the concept is typically used rather vaguely to designate the small isolated (i.e. monogamous and non-extended) family type characteristic of “western” social organization (Smith 1993). I enclose instances of the latter definition in quotes.

Is the “nuclear family”, so defined, a coherent arrangement, possibly conveying an advantage over alternative arrangements? For example, within anthropology it has long been suggested that both monogamy and neolocality serve to reduce potential conflicts of interests between spouses (e.g. Lowie 1920; Murdock 1949). Monogamous marriage eliminates the possibility of additional spouses and their children, whereas neolocal residence limits biases in access of husband and wife to their respective kin. Within the Tinbergen/Mayr framework (Section 1.1), this provides a possible explanation in terms of function (e.g. Alexander 1987, pp. 70–73). More

broadly, monogamy and neolocality have been variously linked to features of social organization viewed as markers of “complexity”, including industrialization, commercialization, modernization, and so on (Levinson and Malone 1980, pp. 37–38; e.g. Blumberg and Winch 1972; de Leeuwe 1971; Ember 1967; Lee 1979; McNett 1973; Osmond 1965, 1969; Sheils 1971). The co-occurrence of the two traits in the “nuclear family”, and the preeminence of this arrangement in “western” societies, would seem to uphold this view (Smith 1993).

Enter what has come to be known in anthropology as “Galton’s problem” — the issue of the statistical non-independence of human societies (Section 1.2). The observation that two traits tend to co-occur provides necessary but not sufficient evidence that they are functionally related — that is, that they convey an advantage over alternative combinations of traits. Societies may share practices through descent from a common ancestor and/or through contact, hence the co-occurrence of traits in a cross-cultural sample may effectively be a historical artefact. Conversely, if changes in one trait tend to be associated with changes in the other trait, then this can be taken as evidence that the two traits co-evolve, indicating that they may be functionally related. For example, it may be that societies with neolocal residence are more likely to acquire monogamous marriage from neighbouring societies. Alternatively, it may be that where monogamous marriage emerges as an independent innovation, it is more likely to “stick” in the presence of neolocal residence. Evidence along these lines would suggest that the “nuclear family” is indeed a coherent arrangement, possibly conveying an advantage over alternative ones, and justifying its preeminent role in “western” social organization.

Discriminating between these scenarios in the absence of detailed information about the history of the traits is problematic. Phylogenetic comparative methods offer one solution (Section 1.2.2). Using a phylogenetic tree to represent how the societies are related by way of descent from a common ancestor, they infer likely evolutionary scenarios that produced the observed distribution of traits across the societies. In testing for co-evolution between two traits, the aim is to determine whether they have tended to change in correlated fashion over time. I used this approach to investigate the interplay between marriage and residence strategies in the history of Indo-European-speaking societies (Fortunato 2009). Related results are reported in Fortunato (2011a,b,c), where I used a phylogenetic comparative approach to reconstruct the history of the traits.

There are two steps to a phylogenetic comparative analysis. The first is to obtain a phylogenetic tree, or a sample of trees, and the matching comparative data. The second step is the statistical analysis. I used a sample of trees generated by Pagel et al. (2007) through application of a phylogenetic tree-building method to vocabulary data for Indo-European languages; the data were collated by Dyen et al. (1992). In previous analyses of these data, Gray and Atkinson (2003) used the same approach to test between the two main competing hypotheses for the origin of the language family (see also Atkinson et al. 2005; Atkinson and Gray 2006a,b; Bouckaert et al. 2012), providing support for the scenario proposed by Renfrew (1987). This posits the expansion of Indo-European languages from Anatolia with the spread of agriculture beginning around 7000 to 6000 BCE. The alternative scenario, proposed by Gimbutas (1973a,b), places the homeland of the language family in the Pontic steppes north of the Black Sea, with expansion driven by nomadic horse-riding pastoralists starting after 4000 BCE (see discussion in Diamond and Bellwood 2003).

With the tree sample in hand, I matched speech varieties in the vocabulary database with societies in the *Ethnographic Atlas*, to obtain comparative data on marriage and residence strategies. This resulted in a sample of 27 societies, with marriage scored as monogamous vs. polygamous, and residence as neolocal vs. non-neolocal (Figure 1). As expected, monogamy and neolocality tended to co-occur in the sample, with monogamy present in 93.8% of neolocal societies (15 of 16 societies) vs. 27.3% of non-neolocal ones (3 of 11 societies).

This pattern is suggestive of a functional association between the two traits, but mapping the comparative data onto the phylogenetic trees reveals clustering in specific “branches”, corresponding to linguistic sub-groups (Figure 1). With few exceptions, monogamy and neolocality are found in the European branches, and their co-occurrence is exclusive to them. Overall, the distribution of marriage and residence strategies at the “tips” of the trees can be accounted for through a limited number of instances of correlated change in the traits. These do not provide sufficient evidence that the traits have tended to change in correlated fashion. In other words, the co-occurrence of monogamy and neolocality in this sample can be accounted for by the patterning of descent of the societies from a common ancestor, which likely practiced monogamous marriage (Fortunato 2011a) and neolocal residence (alongside virilocal residence as the prevailing mode; Fortunato 2011b). In testing for co-evolution, two models were fitted to the data:

a model of independent evolution, in which the traits change independently of each other, and a model of dependent evolution, in which they change in correlated fashion. Statistically, the dependent model did not provide a better fit to the data than the independent model; hence, there was no support for a scenario of correlated change. While investigation of a larger sample may provide stronger support for the hypothesis of co-evolution, this seems unlikely given the tight clustering of marriage and residence strategies within linguistic sub-groups (Fortunato 2009).

3 Towards a biologically based social anthropology

Previous theorizing about human family systems has often assumed, or at least implied, a functional association between monogamous marriage and neolocal residence, in what is commonly referred to as the “nuclear family”. This assumption is based on the observation that the two practices tend to occur together, and it underlies theories that make this family type central to “western” social organization. However, the co-occurrence of traits across societies may reflect the history of the traits, rather than a functional relationship between them (Fortunato 2008).

I have provided an overview of phylogenetic comparative analyses, applied to cross-cultural data, aimed at reconstructing the history of marriage and residence strategies in Indo-European-speaking societies, with a focus on the interplay between monogamy and neolocality (Fortunato 2009, 2011a,b,c). Results show that any evidence of association between the two traits cannot be untangled from the patterning produced by the phylogenetic relationships among societies in the sample. These results challenge the notion, prevalent in history and sociology of the family and in demography, of the centrality of the “isolated nuclear family” to the social organization of Europe, and of western Europe in particular (Goody 1996; Smith 1993; see e.g. Hajnal 1965, 1982). They imply that the widespread co-occurrence in the region of two key elements of this family type — monogamy and neolocality — may be an artefact of history, rather than the result of “the individualistic or nuclear tendencies of the European family system” (Smith 1993, p. 328). Consistently, phylogenetic ancestral state reconstructions reported in Fortunato (2011b) show that neolocal residence occurred alongside virilocal residence throughout the history of Indo-European-speaking societies; by definition, virilocality results in extended family organization.

As noted above, the occurrence of the “nuclear family” is often linked to features of social organization viewed as indicators of “societal complexity” and “modernization”, based on the prevalence of this family type among the “complex”, “modern” societies of Europe. Yet the historical evidence (discussed in Smith 1993; see e.g. Laslett 1977) and the phylogenetic reconstructions in Fortunato (2011a,b) point to an “early” origin of this family type across European societies, and across Indo-European-speaking societies more generally. Unless social and/or ecological determinants can be identified that account for both its distribution and its history, then the occurrence of this arrangement across Europe is best viewed as a result of the nexus of descent linking societies in the region. Detailed historical demographic data (e.g. Szoltysek and Gruber 2015) will likely play a role in identifying possible social and ecological determinants.

An “early” origin of this family type also suggests revisiting explanations that ascribe the “nuclear tendencies” of the European family to the influence of Christian ideology on kinship and marriage systems (Smith 1993; e.g. Goody 1983). The available evidence is, at present, anecdotal; detailed historical and ethnographic data will be required to formally evaluate the alternative pathways that may have produced the posited associations between Christianization and specific features of social organization (see discussion in Fortunato 2009).

Finally, together with previous analyses (Fortunato et al. 2006; Fortunato and Mace 2009), the reconstructions of Indo-European social organization in Fortunato (2011a,b) point to a society practising monogamy, virilocality with neolocality, and dowry. On the ethnographic evidence, this type of social structure is compatible with interpretations of the linguistic evidence that attribute to Indo-European society an economy based on domesticated plants and animals, with use of the plough, a settled lifestyle, and possibly some form of social ranking based on social status differentiation (Mallory and Adams 2006, p. 284). The reconstructions seem harder to reconcile with interpretations of the linguistic evidence that tend to emphasize elements pointing to a pastoral economy and a nomadic lifestyle; these interpretations provide the basis for the traditional view that Indo-European languages propagated across Eurasia with warlike nomadic pastoralists (e.g. Anthony 2007; Gimbutas 1991; Mallory 1989). In fact, the traditional view has strongly influenced reconstructions of other aspects of early Indo-European social life; in turn, these reconstructions have been used to substantiate the traditional view of Indo-European origin (Renfrew 1987, pp. 260–262). The analyses in Fortunato (2009, 2011a,b)

avoid this circularity because the inferences are derived entirely from the cross-cultural data, in conjunction with the model of population history captured by the linguistic evidence; consequently, the inferential process is relatively assumption-free with regards to early Indo-European social organization. One implicit assumption is that practices observed in the “ethnographic present” can be used to characterize early Indo-European social structure. The analytical categories used in these analyses are based on the simplest possible conceptualization of marriage and residence strategies; as such, they apply to the range of social systems found in the ethnographic record. They are therefore likely to apply also to the range of social systems involved in the history of dispersal of Indo-European-speaking societies from a common ancestor.

Overall, the findings reviewed here emphasize the importance of using systematic and, where possible, explicitly historical approaches to cross-cultural comparison. The formulation of analytical categories that are theoretically justifiable and empirically useful is one of many advances that derive from extension of the philosophical, theoretical, and methodological foundations of the evolutionary paradigm to the study of kinship and marriage systems (Section 1). More generally, placing variation in human social systems within this paradigm offers a unique opportunity for progressing the study of human behaviour towards what Hughes (1988, p. 21) envisioned as “a biologically based social anthropology” — a discipline focused on understanding the social system of the human species, while at the same time situating human behaviour within a broad cross-specific perspective.

A “mature science of society” will comprise general principles applicable to any species, and specific principles applicable to individual taxonomic groups (Hughes 1988, p. 141); together, they will need to account for the ultimate causes of behaviour and for its proximate determinants, including any interactions between genetic and non-genetic pathways for the transmission of information (Rogers 1988; Section 1.1). Given the emphasis on cultural transmission in the study of human behaviour (e.g. Boyd and Richerson 1985; Cavalli-Sforza and Feldman 1981), this will likely involve “a mutual transformation” of biology and anthropology (Wilson 1979). In turn, this will represent an indispensable step towards integration of evolutionary approaches to human behaviour (see Laland and Brown 2011), culminating in the development of a biologically based social anthropology.

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