

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

Laura Fortunato

Institute of Cognitive and Evolutionary Anthropology

University of Oxford

64 Banbury Road, Oxford OX2 6PN, UK

`laura.fortunato@anthro.ox.ac.uk`

+44 (0)1865 284971

Santa Fe Institute

1399 Hyde Park Road

Santa Fe, NM 87501, USA

DRAFT

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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 (e.g. Mesoudi et al. 2006), an evolutionary approach offers a unified conceptual and analytical framework to overcome these difficulties: 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; e.g. Sahlins 1976). At the same time, those advocating an evolutionary approach have at times 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 — in fact, mating is typically polygamous in these societies. 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 in contemporary cross-cultural research. 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; Smith 1993). It also speaks to renewed interest from across the social sciences in how family systems, and their historical trajectories, have contributed to shaping the contemporary world.

1.1 Levels of explanation

Investigating the evolution of a given behaviour involves asking questions about its function and about its history. In the analysis of kinship and marriage systems, we may ask why societies vary with respect to a particular set of norms, and how this variation came about. For example, why do some societies prescribe monogamous marriage, while the majority allow polygyny? Does the

prevalence of this strategy among European societies reflect social or ecological determinants, or is it simply an artefact of history?

In Tinbergen's (1963) schema, these represent two of four levels at which we may aim to explain a given behaviour. The other two involve questions about the mechanisms, physiological or psychological, resulting in the behaviour, and questions about its ontogeny, that is, about the respective roles of genetic and environmental effects in this process. For example, what induces some men to take a second wife in societies that allow polygynous marriage, while other men settle for monogamy? Do men vary in the propensity to seek multiple sexual partners, and is this related to whether they engage in multiple marriages?

Function and history represent the ultimate causes of behaviour, mechanisms and ontogeny its proximate causes (Mayr 1961). The four levels of explanation are logically independent, in the sense that ignorance of the answer at one level does not preclude us from asking questions at another (Dunbar 2008, p. 132): alternative hypotheses compete within levels, not across them (Sherman 1988). Crucially, this implies that even though the process of cultural inheritance is known to operate through different dynamics than the process of genetic inheritance (e.g. Boyd and Richerson 1985; Cavalli-Sforza and Feldman 1981), we can ask evolutionary questions about cultural behaviours without reference to the underlying mechanism of transmission (Dunbar and Barrett 2007a, p. 5). How a given behaviour is transmitted, whether genetically or through social learning, is a proximate question (West et al. 2007).¹

Of course, full understanding of any phenomenon requires answers at all levels of explanation; for humans, as for other species with social transmission of behaviour, this involves taking into account both genetic and cultural evolution (Rogers 1988; see Laland 2008 for discussion of the issue of non-human culture). One key advantage of starting by addressing ultimate questions is that it forces us to treat human behaviour 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. Approaches that focus on the proximate determinants of human behaviour typically sidestep this crucial issue (Henrich and McElreath 2003; West et al. 2007). Further, placing kinship and marriage systems in the wider context of animal social behaviour provides a set of first principles for devising analytical traits

¹Within this framework, understanding the interactions between the processes of genetic and cultural evolution has been characterized as answering proximate questions about human behaviour (e.g. Henrich and McElreath 2003), or as answering both proximate and ultimate questions (e.g. Richerson and Boyd 2005).

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, for examples).

For example, 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 represents 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 in this area (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; e.g. Goody 1976); status and ownership of resources are typically linked to fitness in these societies (see review in Hopcroft 2006; e.g. Nettle and Pollet 2008). Finally, we can ask to what degree the process of cultural evolution can lead to patterns of behaviour that are inconsistent with the predictions of the “acultural” model (Rogers 1988). For instance, we can investigate how the evolutionary dynamics are affected by proximate considerations relating to the transmission of mating preferences or of norms regulating sexual behaviour (e.g. Mesoudi and Laland 2007). Importantly, these specific questions about human social life become meaningful only within the wider context of variation in animal social behaviour.

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; 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 recognized by Galton in response to the earliest application of a statistical 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 sociocultural anthropology — seemingly a reaction to the excesses of its nineteenth century forebear, cultural evolutionism, and its abuse of the ethnographic record (see discussion in Fortunato 2017b). 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 organization (see discussion in Legros 2013, Chapter 1). However, attempts to formalise this line of enquiry typically involve focusing on variation across societies in a small number of traits, so that data are amenable to quantitative analysis. To many anthropologists this approach is, at

best, too reductionist and, at worst, too close to the the comparative method of evolutionism (see discussion in Fortunato 2017b). 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 (Murdock 1971, 1977).

The refusal of sociocultural 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 comparison is being used in empirical research across the social sciences, for instance to test hypotheses derived from theory. One unfortunate consequence of this paradoxical situation is that the extensive discussions surrounding the approach that occurred within anthropology since the late nineteenth century have been lost to contemporary cross-cultural research — including discussions about subtle conceptual and methodological issues (e.g. definition of the units of analysis) that anthropologists are best placed to resolve (see discussion in Fortunato 2017b). Below I introduce two key tools in contemporary cross-cultural research.

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 (1957, p. 664) developed the *World Ethnographic Sample*, 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.” 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).

In a later development, Murdock and White (1969) collated 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 (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.); for comparison, the *Ethnographic Atlas* codebook includes coded data for approximately 100 variables for the 1267 societies in the sample (Gray 1999).

1.2.2 The phylogenetic comparative approach

The second tool that is gaining momentum within contemporary cross-cultural research rests on application of phylogenetic comparative methods developed in biology. Like human societies, species and other biological 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 review in Felsenstein 2004, Chapter 25).

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 populations, along the branches of the phylogenetic tree model used to represent how the taxa are related; consequently, high rates of horizontal transmission may invalidate their application to cross-cultural data (Borgerhoff Mulder 2001; Borgerhoff Mulder et al. 2006; Nunn et al. 2006; Rogers and Cashdan 1997). Yet 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, since the basic assumption of cross-cultural hypothesis testing is that traits tend to occur together if they are functionally related (Murdock and White 1969). By contrast, phylogenetic comparative methods outperform non-phylogenetic methods under a wide range of simulated scenarios and levels of horizontal transmission (Currie et al. 2010; Nunn et al. 2006).

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 kinship and marriage systems. Ultimately, Murdock’s intuition and contributions stand vindicated, as his databases are routinely used as a key source of coded comparative data across the biological and social sciences (see e.g. Kirby et al. 2016, for a recent development).

Of course, none of the available tools 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*, combined with the 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 this 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 non-independence due to descent, one of two facets of what has come to be known as “Galton’s problem”. The effect of its other facet — non-independence due to contact — on applicability of these methods to cross-cultural data is yet to be settled.

Ultimately, which approach is used is often driven by practical considerations, 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 analyses), and/or the availability of trees representing human population history for use in phylogenetic comparative analysis.

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.

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 (e.g. 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, while neolocal residence limits biases in access of husband and wife to their respective kin. More broadly, the two traits have been variously linked to features of social organization viewed as markers of “complexity”, including industrialization, commercialization, modernization, and so on. The co-occurrence of monogamy and neolocality in the “nuclear family”, and the preeminence of this arrangement in “western” societies, would seem to uphold this view.

Enter 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 arrangements, 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 the traits 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 2017a). This work builds on results 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 statistical analysis. I used a sample of trees generated by Pagel et al. (2007) through application of a phylogenetic tree-building method to basic vocabulary data, collated by Dyen et al. (1992) for Indo-European languages. 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), 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 (Diamond and Bellwood 2003). 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 (Diamond and Bellwood 2003).

With the tree sample in hand, I matched speech varieties in the basic 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. As expected, monogamy and neolocality tended to occur: monogamy was present in 93.8% of neolocal societies (15 of 16 societies) vs. 27.3% of non-neolocal ones (3 of 11 societies).

While this pattern is suggestive of a functional association between the two traits, mapping the comparative data onto the phylogenetic trees reveals clustering in specific “branches”, corresponding to linguistic sub-groups. 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 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 (albeit secondary to virilocal

residence; Fortunato 2011b). In testing for co-evolution, two models were fit 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, there is no evidence that the dependent model provides a better fit to the data than the independent model, and hence 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 2017a).

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 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 2011a,b,c, 2017a). 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; 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 was secondary to 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; e.g. Laslett 1977) and the phylogenetic reconstructions outlined above point to an earlier 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 history, confirmed by detailed historical demographic data (e.g. Szoltysek and Gruber 2015), then the occurrence of this arrangement across Europe must be seen as contingent upon the nexus of descent linking societies in the region.

This 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). In particular, the standard “cultural infection” scenario, whereby features of social organization spread “passively” alongside Christianity, seems too simplistic. The available evidence is, at present, anecdotal; quantitative 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 early 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 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 (2011a,b, 2017a) 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. More generally, placing variation in human social systems in the wider context of variation in animal social systems 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 whose concern is the social system of the human species, while at the same time situating human behaviour within a 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, as well as for the interactions between genetic and cultural processes in *any* species with social transmission (Rogers 1988). Given the emphasis on cultural evolution 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). This, in turn, will represent an indispensable step towards integration of evolutionary approaches to the analysis of human behaviour (reviewed in Laland and Brown 2011), culminating in the development of a biologically-based social anthropology.

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