

The nuclear family  
in the history of Indo-European-speaking societies:  
a phylogenetic comparative approach

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# 1 Introduction

## 1.1 Background

The “socially imposed monogamy” model views monogamous marriage as a mechanism of reproductive levelling, which evolved because of the benefits accrued to groups from minimizing male–male conflict over access to females (Alexander 1987, pp. 71–73; see review and discussion in Fortunato 2015). In addition, monogamous marriage is argued to minimize male–female conflict over the production and rearing of offspring, especially where features of social organization limit opportunities for husbands and wives to divert resources to their respective kin. Residence strategies determine the pattern of access of individuals to kin: in this context, neolocality may have favoured the evolution of monogamous marriage by reducing the degree of differential access of husbands and wives to their own relatives (Alexander 1987, pp. 70–71). On this view, monogamous marriage represents the outcome of “complete cooperation” (Alexander 1987, p. 70) between spouses.

The association between monogamy and neolocality assumed by the “socially imposed monogamy” model largely rests on the observation that both practices prevail across societies organized in nation-states (e.g. Alexander 1987, p. 71), that is, across “the most complex of human social groups” (Alexander 1979, p. 259). However, ahistorical reasoning about the association between traits, based on their distribution, can easily lead to spurious inferences, just like distributional arguments can lead to spurious inferences about the pattern of change in the traits (Fortunato 2008).

Here I use a phylogenetic comparative approach to investigate the interaction between marriage and residence strategies in the history of societies speaking Indo-European (IE) languages. Indirectly, this assesses the validity of the notion of association between monogamy and neolocality, the defining features of the “nuclear family”, implicit in theories that make this family type central to European social organization. Such theories dominate the social sciences (Goody 1996; Smith 1993).

## 1.2 Related research

To my knowledge, no formal test exists of the association between monogamous marriage and neolocal residence. Yet the potential divergence of interests between spouses in societies practis-

ing non-neolocal residence was noted as early as by Lowie (1920, p. 71), who remarked that “the rule of residence may produce a stressing of one side of the family and in so far forth interfere with the bilateral symmetry of family relations.” This is because under non-neolocal residence, and in particular where marriage is exogamous with respect to the community, individuals of the dispersing sex come to rely on their spouse’s kin for resources, as opposed to their own. Coupled with the fact that, by definition, non-neolocal residence results in the aggregation of individuals in extended families, this may create an asymmetry of interests between spouses (Murdock 1949, pp. 18, 202).

For example, polygyny is “particularly congenial” (Murdock 1949, p. 206) to virilocality, where men live with their relatives while their wives are isolated from their own kin: in such a system the corporate interests of related males, for instance where property is owned collectively, may increase the payoffs to husbands from investing in their kinsmen at the expense of their wives’ offspring (Murdock 1949, pp. 206–208; e.g. Goody 1970). It follows that neolocality will minimize opportunities for diverting resources to one’s own relatives, by isolating both husbands and wives from their respective kin, and by preventing the formation of extended kin groups (Murdock 1949, pp. 203–204). Alexander’s (1987, pp. 70–71) conjecture extends the reasoning to argue that the confluence of interest between spouses will be maximized under these conditions, leading to the co-occurrence of monogamy and neolocality across societies.

### **1.3 Rationale and objective**

Previous theorizing about human family systems has assumed a functional association between monogamous marriage and neolocal residence, as these practices tend to occur together. However, the co-occurrence of traits across societies may reflect the history of the traits rather than a functional relationship between them.

Building on the ancestral state reconstructions in Fortunato (2011a,b), here I use a phylogenetic comparative approach, in a Bayesian reversible jump (RJ) Markov chain Monte Carlo (MCMC) framework, to perform a co-evolutionary analysis of marriage and residence strategies in the history of IE-speaking societies. This approach provides a stringent test of presumed functional associations: two traits are taken to have co-evolved, suggestive of a functional relationship, only if they can be shown to have tended to change together throughout the history

of the taxa under investigation. In other words, this approach discounts any evidence of association between traits that cannot be distinguished from associations arising from the pattern of descent of the taxa from a common ancestor.

## 2 Data and methods

### 2.1 Phylogenetic comparative analysis

Following the procedure set out in Fortunato (2011a,b,c), I used data on marriage and residence strategies from the *Ethnographic Atlas* database (Gray 1999; Murdock 1967) for a sample of societies speaking IE languages (Section 2.1.1). The cross-cultural data were mapped onto a sample of phylogenetic trees representing how the societies are related, obtained by Pagel et al. (2007) through tree-building analysis of Dyen et al.'s (1992) IE basic vocabulary database (Section 2.1.2). On the cross-cultural data and tree sample, I used the phylogenetic comparative method developed by Pagel and colleagues (Pagel and Meade 2005, 2006; Pagel et al. 2004) to test the hypothesis of co-evolution between monogamous marriage and neolocal residence (Section 2.1.3).

#### 2.1.1 Cross-cultural data

I obtained the cross-cultural sample by matching societies in the cross-cultural database with speech varieties in the linguistic database. The phylogenetic comparative method used requires data in binary form (Section 2.1.3). For marriage strategy I coded societies as polygynous (state 0) or monogamous (state 1). For residence strategy I combined information on prevailing and alternative modes of residence into a binary variable, with societies coded as non-neolocal (state 0) or neolocal (state 1). Additional information is in Section S1.1.1 in the SM, including the data in binary form and maps of their geographical distribution.

#### 2.1.2 Tree sample

I used a sample of 750 trees obtained by Pagel et al. (2007) through Bayesian MCMC phylogenetic tree-building analysis of the linguistic database. Trees are represented in the sample in proportion to their posterior probabilities. Each tree in the sample captures a possible scenario for how the speech varieties at its tips are related by way of descent from a common ancestor.

Effectively, the posterior probability distribution of trees in the sample provides an indication of the degree of uncertainty in reconstruction of the phylogenetic relationships. By using a sample of trees, as opposed to a single “best” tree, this uncertainty is incorporated into the comparative analysis (Section 2.1.3).

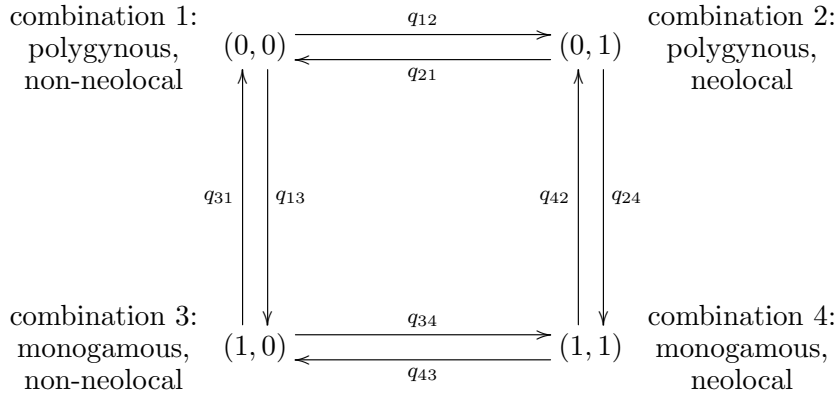
I obtained the tree sample from the authors. I “pruned” the trees to retain only the speech varieties corresponding to the 27 societies in the cross-cultural sample (Section 2.1.1). An additional speech variety, Hittite, was retained as the outgroup, but it was assigned no marriage or residence data in the comparative analysis (Section 2.1.3). Additional information is in Section S1.1.2 in the SM.

### 2.1.3 Comparative analysis

Co-evolutionary analysis using the phylogenetic comparative method developed by Pagel and colleagues (Pagel and Meade 2005, 2006; Pagel et al. 2004) is performed using `BayesDiscrete`, available as part of the `BayesTraits` package (Pagel and Meade n.d.) from <http://www.evolution.rdg.ac.uk/BayesTraits.html>. The method is outlined below; additional information is in Section S1.1.3 in the SM.

**Models of trait evolution** Given the cross-cultural data and tree sample, `BayesDiscrete` estimates parameters in the model of trait evolution for two binary traits. As discussed in Section 2.1.1 and illustrated in Figure 1, here one trait is the marriage strategy, with states 0 (polygynous) and 1 (monogamous), the other trait is the residence strategy, with states 0 (non-neolocal) and 1 (neolocal). This produces four combinations of states for the two traits, e.g. combination 2 (0, 1) represents polygynous marriage with neolocal residence.

A series of transition rate parameters  $q_{ij}$  describes the joint evolution of the two traits on a tree. These rate parameters measure the instantaneous rate of change from combination “i” to combination “j”, which corresponds to the rate of change between two states of one trait while holding the state of the other trait constant. For example, rate parameter  $q_{12}$  describes transitions from combination 1 (0, 0) to combination 2 (0, 1), that is, changes from non-neolocal to neolocal residence against a background of polygynous marriage (Figure 1). Similarly, rate parameter  $q_{34}$  describes transitions from combination 3 (1, 0) to combination 4 (1, 1), that is, changes from non-neolocal to neolocal residence against a background of monogamous marriage.



**Figure 1:** Rate parameters describing the evolution of marriage and residence strategies.

The rate parameters are used to define the probabilities of the corresponding changes, the probabilities of the two states at internal nodes on the tree, and the likelihood of the data. Tips that are not assigned comparative data for a given trait are treated in the likelihood calculations as taking either state for the trait with equal probability. This applies to the outgroup Hittite, which was assigned no marriage or residence data (Section 2.1.2).

**Independent vs. dependent trait evolution** The eight rate parameters yield 21,146 model categories, in which two or more rate parameters are set to take equal or distinct positive values, or one or more of them can be set to zero. Of the 21,146 possible categories, 51 (0.24%) conform to independent trait evolution. In these categories the rate of change in one trait is not affected by the state of the other trait, that is,  $q_{12} = q_{34}$ ,  $q_{13} = q_{24}$ ,  $q_{21} = q_{43}$ , and  $q_{31} = q_{42}$ . For example,  $q_{12} = q_{34}$  specifies that the rate of change from non-neolocal to neolocal residence does not depend on whether marriage is polygynous vs. monogamous (Figure 1). All other model categories conform to dependent trait evolution, because they assign rates within one or more of the four pairs above to different rate classes. This means that the rate of change in one trait does depend on the state of the other trait. For example,  $q_{12} \neq q_{34}$  specifies that the rate of change from non-neolocal to neolocal residence does depend on whether marriage is polygynous vs. monogamous (Figure 1).

**Estimation of support for dependent evolution and implementation** I used BayesDiscrete in Bayesian RJ-MCMC mode. In this mode BayesDiscrete uses RJ-MCMC chains to produce a posterior probability sample of states in the model of trait evolution. A state in the

model consists of model category, values of the rate parameters, and ancestral state probabilities. Schematically, the distributions are estimated by running RJ-MCMC chains that sample states in the model of trait evolution in proportion to their posterior probability, across trees in the tree sample (Section 2.1.2). Effectively, the posterior probability distribution of states sampled by a chain provides an indication of the degree of uncertainty in reconstruction of the model of trait evolution. Combining estimates over the sample produced by the chain amounts to “averaging” inferences over uncertainty in the phylogeny, in the parameters of the model of trait evolution, and in the model itself (see Section S1.1.3 in the SM).

I used two approaches to estimate support for dependent vs. independent trait evolution, which involved running two sets of analyses. In the first set, termed RJ-unconstrained, the RJ-MCMC chains were free to visit all model categories. The proportions of model categories conforming to dependent vs. independent evolution sampled by the chains provide an estimate of the posterior probability of the two evolutionary models. In the second set, termed RJ-constrained, the RJ-MCMC chains were constrained to visit model categories conforming to independent evolution. The posterior probability distribution returned by a chain constrained in this way is then compared to the distribution returned by an unconstrained chain (having removed visits to model categories conforming to independent evolution). The two approaches use different implementations of the Bayes factor to determine the strength of the evidence in favour of one model over the other, as detailed in Section S1.1.3 in the SM. The Bayes factor for dependent vs. independent evolution is denoted  $B_{DI}$ .

For each set of analyses I ran five separate chains started from random seeds. Chain specifications were determined as described in Section S1.1.3 in the SM. Convergence of the chains to the target distributions and near-independence of sampling events were assessed as described in Section S1.1.3 in the SM. In all cases, the diagnostics indicated that the chains sampled the target distributions adequately.

## 3 Results

### 3.1 Phylogenetic comparative analysis

For each sets of analyses, I compared  $\log_e[H(\text{likelihood})]$  values for the states in the model of trait evolution sampled by the five separate chains at convergence, where  $\log_e[H(\text{likelihood})]$  is

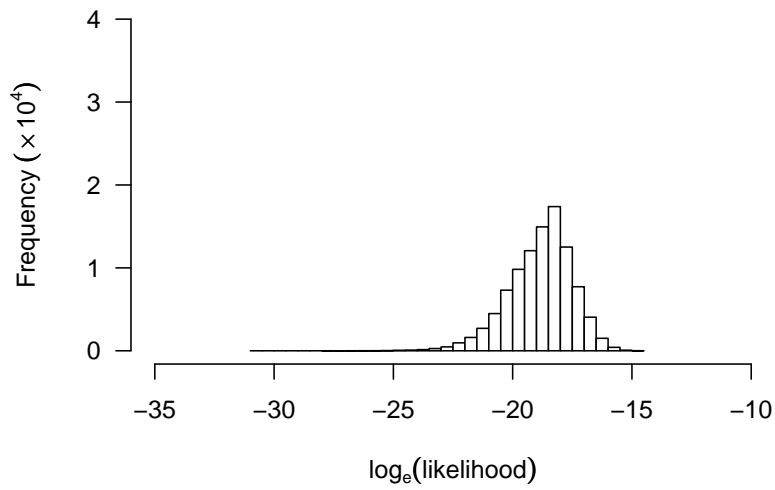
the natural logarithm of the harmonic mean of the likelihood values. I present results for the chain that returned the median value of  $\log_e[H(\text{likelihood})]$ .

The posterior probability distribution of model categories sampled by the RJ-unconstrained chain at convergence is described in Section S2.1.1 in the SM. In summary, the chain sampled 2,855 model categories of the possible 21,146, with rates assigned to  $1.86 \pm 0.45$  non-zero classes (mean  $\pm$  SD; range: 1–4 non-zero classes) of the possible eight. Thus, the processes underlying the evolution of the two traits likely involved fewer than the eight transitions specified by rate parameters  $q_{ij}$  in Figure 1. Of the  $10^5$  points sampled by the RJ-unconstrained chain, 98.67% corresponded to model categories conforming to dependent evolution and 1.33% to categories conforming to independent evolution, yielding a posterior odds of 74.36. Comparison of the posterior odds to the theoretical prior odds of 413.63 yields  $B_{\text{DI}} = \frac{74.36}{413.63} = 0.18$  or, on a logarithmic scale,  $2\log_e(B_{\text{DI}}) = -3.43$ . This corresponds to no evidence for dependent trait evolution or, equivalently, to positive evidence for independent trait evolution (Section S2.1.2 in the SM).

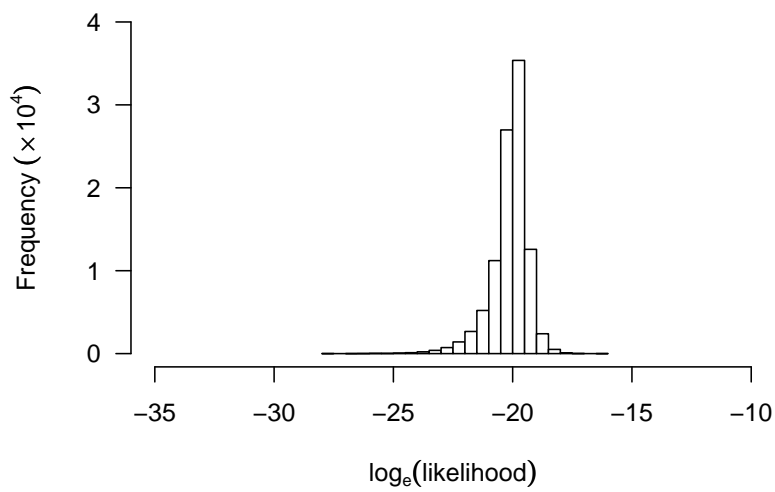
Because the RJ-unconstrained chain sampled a restricted sub-set of all possible model categories, the posterior to prior odds  $B_{\text{DI}}$  may underestimate the evidence for dependent trait evolution. As discussed in Section S1.1.3 in the SM, the alternative implementation of the Bayes factor may provide a more accurate estimate of support for dependent trait evolution. In this case, the posterior probability distribution sampled by the RJ-unconstrained chain (Figure 2a), having excluded categories conforming to independent evolution, is compared to the posterior probability distribution sampled by the RJ-constrained chain (Figure 2b). Comparison of the  $\log_e[H(\text{likelihood})]$  values yields  $2\log_e(B_{\text{DI}}) \approx 2[(-20.56) - (-20.78)] = 0.44$ , and thus no evidence for dependent evolution (Section S2.1.2 in the SM). This reflects the substantial overlap in the distributions of  $\log_e(\text{likelihood})$  values for the states in the model of trait evolution sampled by two chains (Figure 2).

In sum, both implementations of the Bayes factor returned no support for dependent trait evolution, indicating that there is no evidence for the hypothesis of co-evolution of monogamy and neolocality in the history of IE-speaking societies. This means that any evidence for correlated change in the two traits that may exist in the data cannot be untangled from the patterning produced by the phylogenetic relationships among societies in the sample. The ancestral state





(a) Model categories conforming to dependent trait evolution



(b) Model categories conforming to independent trait evolution

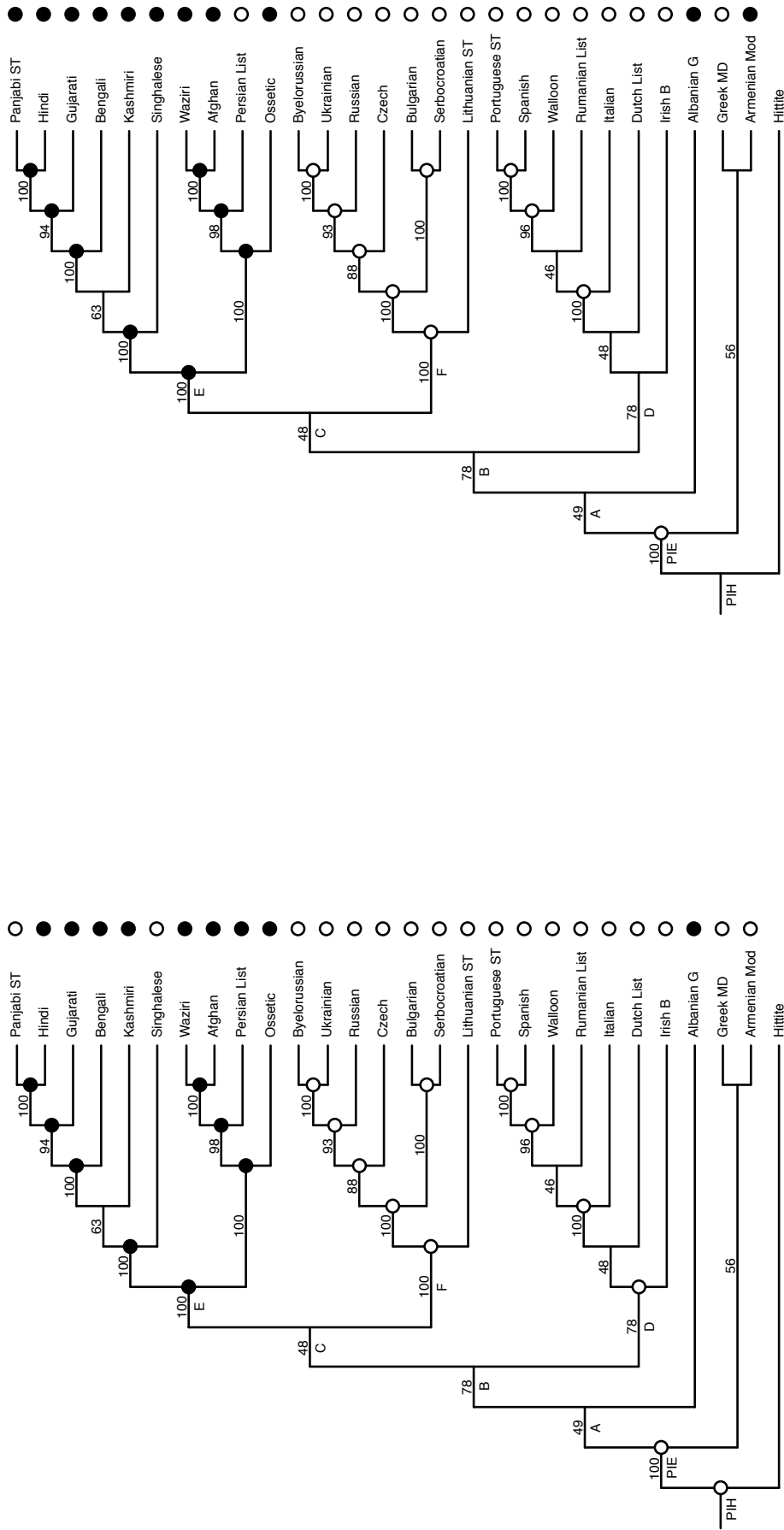
**Figure 2:** Distributions of  $\log_e(\text{likelihood})$  values for the states in the model of trait evolution sampled by (a) the RJ-unconstrained chain and (b) the RJ-constrained chain.

reconstructions for the two traits (Fortunato 2011a,b), summarized in Figure 3, imply only one instance of potentially correlated change, between nodes PIE and E, leading from the presence of monogamy and neolocality in “Proto-Indo-European” (PIE) to the absence of both in the ancestor of societies speaking Indo-Iranian languages (node E). A second instance is possible between node PIE and Albanian G, leading to the absence of monogamy and neolocality in the latter, but existence of the intervening node is itself uncertain (node A). In contrast, the co-occurrence of monogamy and neolocality in societies speaking Balto-Slavic languages is explained away by the presence of both practices in their ancestor (node F). Similarly, co-occurrence of these practices in societies speaking Italic languages (Portuguese ST, Spanish, Walloon, Rumanian List, Italian) is explained away by their presence in the ancestor of the Italic sub-group. This pattern may extend back to include societies speaking Germanic and Celtic languages (Dutch List and Irish B), but phylogenetic uncertainty limits the confidence that can be placed in the reconstruction of neolocality for the ancestor of the Italic-Germanic-Celtic sub-group (node D).

## 4 Discussion

The phylogenetic comparative analysis of marriage and residence strategies across IE-speaking societies indicates that the observed association between monogamy and neolocality may be tracking the descent of societies from a common ancestor rather than a functional link between the two practices. 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.

Thus, the analysis provides no evidence to support Alexander’s (1987, pp. 70–71) conjecture that neolocal residence favoured the evolution of monogamous marriage by increasing the payoffs to husbands and wives from attending to their shared reproductive interests. More generally, this challenges 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). Together with the reconstructions in Fortunato (2011a,b), the present analysis suggests that the widespread co-occurrence in the region of the defining elements of this family type — monogamy and neolocality — may be an artefact of descent, rather than the result of “the individualistic or



(a) Marriage strategy

(b) Residence strategy

**Figure 3:** Majority-rule consensus tree of Pagel et al.’s (2007) sample of 750 trees, pruned to 27 IE speech varieties plus the outgroup Hittite (Section 2.1.2). The value above each node represents the node’s posterior probability as a percentage. Node labels PIH (Proto-Indo-Hittite), PIE (Proto-Indo-European), and A–F are used in the text to refer to specific nodes. Tips are colour-coded to represent (a) the marriage strategy (white: monogamous; black: polygynous) and (b) the residence strategy (white: neolocal; black: non-neolocal) of the corresponding societies (Table S1 in the SM). Nodes are colour-coded to indicate that the combined probability for a state at the node is  $\geq 0.70$ , using the same colour schemes. See Fortunato (2011a,b) for details; the residence strategy data and reconstructions were combined as non-neolocal/neolocal and over the two modes of residence (prevailing and alternative; Section 2.1.1).

nuclear tendencies of the European family system” (Smith 1993, p. 328). Consistently, the reconstructions in Fortunato (2011b) show that neolocal residence was secondary to virilocal residence throughout the history of IE-speaking societies; by definition, virilocality results in extended family organization.

The emergence of monogamous marriage is typically attributed to the development of features of social organization viewed as indicators of “societal complexity” and “modernization”, based on the prevalence of this marriage strategy among the “complex”, “modern” societies of Eurasia. The emergence of neolocality is similarly attributed to features of social structure characteristic of “complex”, “modern” societies (Levinson and Malone 1980, pp. 37–38; e.g. van den Berghe 1990, pp. 109–110): cross-cultural analyses have focused, for example, on the relationship of neolocal residence with commercialization and industrialization (e.g. de Leeuwe 1971; Ember 1967). Yet the historical evidence (discussed in Smith 1993; e.g. Laslett 1977) and the reconstructions in Fortunato (2011b) point to an earlier origin for this residence strategy across European societies, and across IE-speaking societies more generally. Unless social and/or ecological determinants of neolocality can be identified that account for both its distribution and history, the widespread occurrence of this practice across Europe must be seen as contingent upon the nexus of descent linking societies in the region.

We currently lack a theoretical framework for understanding variation in residence strategies, both across and within societies. Theoretical work on the evolution of sex-biases in dispersal across mammals focuses on the complex interactions between (i) the costs of inbreeding, (ii) the inclusive fitness benefits of co-operating with kin, for example in the acquisition of resources (e.g. mates or food), and (iii) the inclusive fitness costs of competing with kin for those same resources (see review in Lawson Handley and Perrin 2007); extension of this framework to residence strategies may shed light on the evolutionary significance of this feature of social organization. Within this framework, various aspects of human dispersal *across* communities (that is, not necessarily in the context of residence changes at marriage) have been shown to vary in predictable ways with social and ecological factors affecting the availability of resources: for example, in agrarian societies the availability of land affects the sex of the disperser and the timing and rate of dispersal (e.g. Beise and Voland 2008; Clarke and Low 1992; Strassmann and Clarke 1998; Towner 1999, 2001, 2002; Voland and Dunbar 1995). This suggests that in humans,

as in other species, dispersal is linked to the acquisition of resources; unlike in other species, however, the acquisition of resources may be partly effected through marriage and inheritance (Fortunato 2012; Fortunato and Archetti 2010). Across species of birds and mammals, female-biased dispersal characterizes social systems in which males compete over access to females based on their ability to defend resources critical for reproduction: in these “resource-defence” mating systems, the benefits of philopatry (e.g. familiarity with the natal territory) are greater to males than to females (Greenwood 1980). This notion has been invoked to explain female biases in dispersal in the land-based societies of Europe (e.g. Beise and Volland 2008; Clarke and Low 1992; Volland and Dunbar 1995); analogous considerations may explain the prevalence of virilocal residence throughout the history of IE-speaking societies (Fortunato 2011b), and across human societies more generally (Koenig 1989). Sixty-four percent of societies in the *Standard Cross-Cultural Sample (SCCS)* practise prevailing virilocality (Murdock and Wilson 1972), and the incidence of this strategy is higher among societies with subsistence based on agriculture and pastoralism compared to foragers (Marlowe 2004; Wilkins and Marlowe 2006).

Intra-societal variability in residence strategies may also be explained within this framework; the reconstructions in Fortunato (2011b) indicate that such variability likely characterized early IE society, with neolocality practised alongside virilocality in several descendants of PIE. As discussed in Section 1.2, Alexander’s (1987, pp. 70–71) hypothesis views neolocality as reducing the conflict of interests between spouses, by limiting opportunities for co-operation of spouses with their respective kin. A factor not considered by Alexander (1987) is that, at the same time, neolocality limits opportunities for competition of spouses with their kin; competition between relatives can alter the evolutionary dynamics in important ways, even to the point of negating the effect of kin selection for co-operation where local competition is intense (West et al. 2002). Crucially, the relative costs and benefits of foregoing co-operation and avoiding competition with kin will depend on other aspects of social organization besides the marriage strategy itself, notably the pattern of marital endo- and exogamy across groups, and the ability of individuals within groups to monopolize reproductive opportunities (i.e. the degree of reproductive skew; Emlen 1995, 1997). Recent developments in the theory of social evolution stress the need to focus on the net effect of co-operation and competition between relatives in the study of social interactions (see review in West et al. 2007); incorporating these developments into the analysis

of kinship and marriage systems holds great promise for furthering our understanding of the evolution of human social behaviour.

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