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Controlled Simulation of Marriage Systems

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Abstract

This article presents and illustrates a new methodology for testing hypotheses about the departure of marriage choices from baseline models of random mating in an actual kinship and marriage network of a human population. The fact that demographic constraints can drastically affect the raw frequencies of different types of marriage suggests that we must reexamine or even throw out - as methodologically flawed - statistical conclusions regarding marriage "rules" from most of the existing empirical case studies. The development of the present methods, in contrast, enables researchers to decompose those behavioral tendencies that can be taken as agent-based social preferences, institutional "rules" or marriage structure from those behaviors whose divergent frequencies are merely a by-product or epiphenomena of demographic constraints on the availability of potential spouses. The family of random baseline models used here enables a researcher to identify overall global structures of marriage rules such as dual organization as well as more local of egocentric rules such as rules favoring marriage with certain kinds of relatives. Based on random permutations of the actual data in a manner that controls for the effects of demographic factors across different cases, the new methods are illustrated for three case studies: a village in Sri Lanka with a novel form of dual organization detected by this methodology, a cross-class analysis of a village in Indonesia, and an analysis of a farming village in Austria in which a structurally endogamous subset of villages is identified by the method and shown to form the backbone of a class-based landed property system.

Keywords:

Population studies, Marriage rules, Demographic constraints on choice behavior, Social class, Social anthropology

Introduction

1.1

One of the issues in the study of family systems is how to identify rules, structures, and strategies that give non-random inflections to mating systems. Probability models include (uniform) *random partner selection*, in which each person in a group has an equal opportunity of being selected, as distinguished from *probabilistic partner selection*, a process that takes place randomly with certain probabilities. One of the questions raised by anthropological studies is whether there are determined structures, related to marriage rules and/or strategies, within which random marriage choices occur, such as uniform random partner selection for any given pair of positions in the structure. This article proffers a quantitative strategy for examining such a question. To the extent that it is successful, it could help to explain certain of the ties between kinship, economics, and political structure in more empirical terms.

A Network Approach

2.1

The problem of evaluating marriage structures in relation to marriage rules is complex because we may need to specify positions within a network of kinship and marriage relations that exists prior to any given marriage. Adding to the complexity is the variety of mating and marriage behaviors, including sequential marriages or polygamy. This complexity is further augmented by the fact that language categories, verbal and normative statements and differential sanctions may exist for proper or improper marriage choices and these different aspects of marriage "rules" may not correspond. To deal with this complexity, an approach to random baseline models is proposed that establishes for each case study a partially ordered classification of potential marriage partners stemming from their position within a network of kinship and marriage relations, and specifying those classes within which uniform random partner selection occurs. This is done by a simulation of marriage choices that imposes constraints on marriagability by classificatory or positional network relationships, and then assigns spouses within marriagability classes by random permutations under uniform probability of assortment.

2.2

The major hypothesis of the simulation is that once normalization is made against a random baseline suitable for each individual

case, the observed agreement between the positions in the existing kinship marriage network, language categories, and verbal norms may be greater than previously thought to be the case. Some verbal formulae are models "of" behavior, while others are models "for" behavior and may include adjustments for departures from established norms. Internal cultural variability may also turn out to be a key factor for understanding marriage patterns. Case studies drawn from Indonesia, Sri Lanka, and Austria are analyzed to test these ideas about random baseline norms in the context of establishing evidence for different marriage rules and strategies.

The Model

3.1

The key innovation of this study is a method for identifying a partially ordered structure of social groupings on which to map uniform partner selection probabilities between pairs of positions in the structure and, by extension, how to decompose the statistical variance in marriage structures. A *uniform marriage structure* is a partition P of the marriages in U , the observed population of marriages, into subgroups in which uniform probabilities of partner selection are assigned as a function of the subgroup memberships of potential pairs of partners. Some models will take the form of a *partially ordered uniform marriage structure* where for a series S of subsets of marriages in U , any pair of distinct subsets X and Y in S will either be mutually exclusive or the set of elements of one subset will be contained in those set of the other, e.g., $X \dot{\bar{\cap}} Y$. S will relate to P in that S is made up of sets that are either a subset in a partition P or the union of two or more subsets in the partition P .

An Idealized Example for "Simple" Systems

4.1

[Figure 1](#) gives in diagrammatic form an example of a "simple" partially ordered marriage classification structure of a matrimonial moiety system. The oval in [Figure 1](#) is a maximal set E of marriages that are *structurally endogamous* in that every marriage in E has parent-child links to at least two other marriages in E (to parents of the husband, parents of the wife, and/or to one or more children's marriages - where at least two of these are also in E). Sets $1, 2, \dots, n$ (horizontal boxes in [Figure 1](#)) represent mutually exclusive genealogical generations within U and E , and the sets a, b (semi-ovals in [Figure 1](#)) represent a moiety division within E such that for any marriage in E , if the parents of the husband come from one moiety, the parents of the wife come from the other moiety, and vice versa (hence sets a and b are also mutually exclusive). The sets $a_1, b_1, a_2, b_2, \dots, a_n, b_n$ are mutually exclusive subsets of E that represent the intersection of the moiety division and the generational division. More precisely, let the set of sets $M = \{a_1, b_1, a_2, b_2, \dots, a_n, b_n\}$ consist of the Cartesian products of the set of sets $A = \{a, b\}$ and the set of sets $G = \{1, 2, \dots, n\}$; that is, $M = A \times G = \{a, b\} \times \{1, 2, \dots, n\}$. The structure satisfies one set of criteria for a partially ordered marriage structure if we take the partition P to consist of the sets in M , all of which are in E , and the residual set $U-E$ (and, if wanted, its generational subsets). All the sets of marriages in A, G and M are either subsets in partition P or the union of two or more subsets in P .

4.2

The crucial feature of the model for statistical testing purposes is a moiety rule that allow us to place observed marriages in the structure and to determine how well observed behavior fits the uniform probability model in comparison to any other models that posit a simpler structure. Let us assign the moiety rule that children are members of their father's moiety and belong to the succeeding generation. By this criterion each person can be placed in a premarital category included in the set $M = \{a_1, b_1, a_2, b_2, \dots, a_n, b_n\}$, which, in the case of males, is predicted by the moiety rule to be the same as their postmarital category. Females, though, will preserve generation but switch moieties at marriage. In other words, males preserve generation and moiety whereas females preserve generation but switch moiety relative to their fathers.

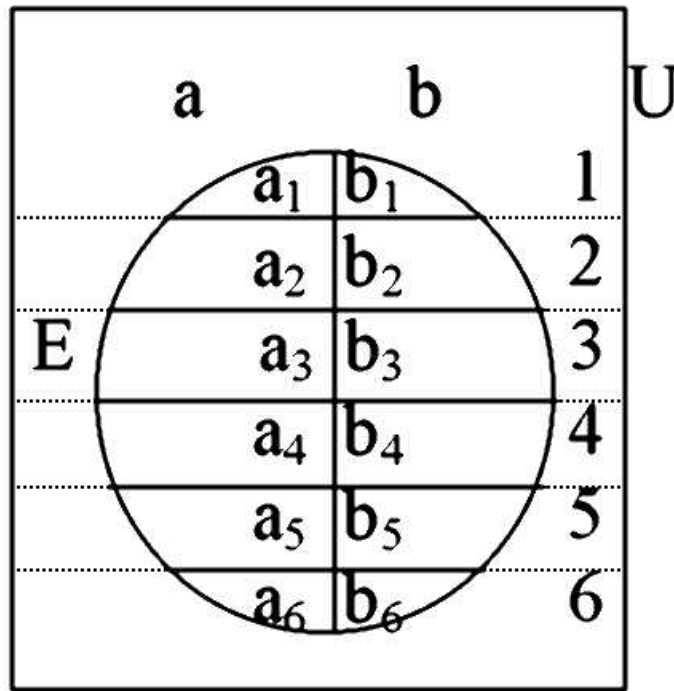


Figure 1: Illustration of a "Simple" Partially ordered uniform marriage structure

4.3

A strict moiety model, with no other criteria affecting marriages, sets a uniform probability of marriage between any opposite sex pair of individuals x, y such that $x \in a_g$ and $y \in b_g$ where $g \in \{1, 2, 3, 4, 5, 6\}$, and $a_g, b_g \in M$; and all other marriage probabilities are zero. Given data for a marriage network, P , generated by a strict moiety model, we could determine inductively the set E of endogamous marriages and the subset G of generations, and within E we could determine inductively the moiety rules for $A = \{a, b\}$. Note that for marriages in E with one or more known parents, the structure of subsets G and $A \times G$ is partially ordered. Holding E and G constant, we can test the hypothesis that P is *not* a moiety structure by the null model where for any opposite sex pair of individuals x, y such that $x \in a_g$ and $y \in b_g$ the marriage probability is uniform. This is most easily done using a permutation test where married individuals in generation g are decoupled, and their couplings randomly permuted. Since individuals are classified by the set of moieties $A = \{a, b\}$, the null model for "no moieties" can then be compared statistically with the observed data and an appropriate correlation ("strength of the moiety tendency"), as well as significant tests, can be made. Another null model could be constructed for comparisons with different kinds of generational marriage structures.

4.4

The remainder of this paper provides a generalization of this approach to determining marriage structures inductively regardless of the type of structure, with the moiety structure as a special case.

Limitations of the Classical Approaches to Studying Marriage Systems

5.1

Anthropology has long concerned itself with marriage patterns, especially where variable cultural rules and marriage strategies shape mating regimes. Some of humanity's fundamental social concerns are with marriage rules and strategies - ranging from incest and exogamy on the one hand to social norms and strategic interest on the other. Alliance theory takes the study of these features as central to understanding social organization. Their discussion in ethnographic case studies is nearly mandatory, and structuralists like Lévi-Strauss define them as paradigmatic to cultural systems. Lévi-Strauss's theory of elementary, complex, and semi-complex kinship systems, briefly put, is that elementary systems prescribe "positive rules" of marriagability in terms of classes of relatives (including sections, moieties, etc.). Complex systems are characterized by "negative rules" such as incest prohibitions. Intermediate between them, semi-complex systems are defined by such extensive proliferation of "negative" proscriptions that individuals in similar kinship lines must disperse their marriage with other lines ^[1] in a series of residual categories. This residue of marriageable relatives takes on the flavor of a prescriptive "elementary" system, but disperses marriages.

5.2

In spite of the centrality of these concerns with rules for marriage and against incest, anthropology has no established methodology for evaluating marriage strategies against random baselines. Lévi-Strauss understood correctly that terms such as marriage "preference" or marriage "avoidance" were relative terms when speaking statistically. If evidence for marriage preferences is established by "occurrence with greater frequency than expected by chance under the null hypothesis" then this evidence is entirely dependent on what probabilistic model is used for the null hypothesis. Thus, Lévi-Strauss preferred to speak of ideal models and to describe the models either as "simple" or "elementary systems" if they contained only deterministic rules (probability 1 or 0, respectively, of an individual marrying within a category), or as "complex systems" if all of their rules were probabilistic. Prescriptive marriage rules that imply proscription or avoidance of alternative marriage possibilities are thus "elementary" systems

as ideal models, but Lévi-Strauss considered it improper to speak of "elementary" systems as having only certain preferences towards various marriage rules. Proscriptive marriage rules ("avoidance" of marriage with certain types of relatives), however, may proliferate to such an extent that they almost imply the existence of unstated prescriptive categories. Lévi-Strauss defines his "semi-complex" systems thusly. Lévi-Strauss's reluctance to enter into a statistical evaluation of marriage structures in terms of "preferences" is similar, if not identical, to the problem of which "random baseline" model should be used to evaluate departures from null hypotheses.

5.3

Hammel (1976b), drawing on Reed (1974), challenged Lévi-Strauss somewhat naively, by raising the problem of interpreting marriage frequencies. What he actually challenges is the use of raw frequencies of matrilineal cross cousin marriage (often taken as indexical of asymmetric and generalized exchange in "elementary systems"), relative to frequencies of other marriage types as evidence of marriage preferences. Evidence for preference or strategic behavior in marriage choices, however, is complicated by demographic constraints on marriage choices. Hammel shows the defects of reaching conclusions based on comparing raw frequencies of observed behavior. He concluded from simulation studies that many of the observed raw frequencies of matrilineal cross cousin marriage, upon which monographs and comparative theories have been built, are well within the range expected from a random distribution of marriages within a population if certain demographic features are held constant. Following Reed (1974), he showed that age, status, or other systematic differences between potential husbands and wives create a relative age demographic bias that skews the potential marriage pool under a random mating regime given these demographic constraints so as to raise the raw frequency of matrilineal above that of patrilineal cross cousin marriage. This result undermines many of the writings on alliance theory in the U.S. and Britain, where marriage structures are often interpreted in terms of frequencies of different kinds of marriage choices. Given this kind of interpretation, to the extent that certain kinds of marriage frequency outcomes are shown to be the result of demographic effects or biases, the edifice of an empiricist alliance theory would seem to fall along with the demise of cherished assumptions about marriage rules and strategies that derive from behaviorist interpretations of Lévi-Strauss's theory of marriage structures.

5.4

What, then, is a marriage rule or strategy? As in the moiety example given above shows, the question of how frequencies of behavior can provide evidence of marriage rules or strategies can be approached hierarchically within the partial order model (see also Barry 1998). At a first level, for example, we might have rules of impossibility - proscriptions against marriage with dead people, for example, or people who have no interaction with members of the population. A second level might specify rules that establish an effective breeding population. Ethnicity or social class, for example, might establish high probabilities of endogamous marriages compared to low probabilities across such social boundaries. Within an effective breeding population there might be further specification of marriage probabilities given the respective ages or age classes of the potential partners, and so on.

5.5

Hammel's (1976b) critique of Lévi-Strauss appears to be against "social choice" in marriage in favor of the idea that demographic structure affects partner selection. I address here two problems. One is how to assess the evidence for "social choice" (preferred marriage rules or strategies) given demographic baseline models that skew the probabilities of selecting different types of partners. Since demographic constraints and "social choice" are not mutually exclusive of one another, this aspect of the present work incorporates Hammel's idea and is a continuation and extension of it. The other problem is a subtler one. It is not simply that network structures affect partner selection, as one anonymous reviewer put it. Rather, it is how "social choices" (preferred marriage rules or strategies) are aggregated, under demographic constraints, into network structures, and how the network structures of kinship and marriage structure can be statistically disaggregated into components, including those of social choice versus demographic factors.

5.6

At each successive level in a partially ordered marriage model, goodness of fit can be established between *probabilistic partner selection* given the relative social positions of the potential partners as defined at that level, and the observed marriage frequencies. For the fixed probability of selection given these positions, partner selection is assumed to be random. Significant departures - rejection of the null hypothesis for the model at a given level - from uniform probabilities (in which each pair of persons in the respective groups have an equal opportunity of being selected as partners) may represent evidence of additional, as yet unspecified marriage rules or strategies. *Preferences or avoidances are thus always relative to some prior marriage probability model.* Two possibilities present themselves: (1) observed data may have a higher or lower uniform probability than predicted by a given model, or, (2) a further preferential or avoidance rule not already specified may demonstrate nonuniform probabilities between two categories of potential partners. Thus, a 'preferential' strategy needs to be evaluated by rejection of the null hypothesis by positive deviation from a given random baseline; an 'avoidance' strategy by a similar but negative deviation (and, potentially, a 'randomizing' strategy needs to be evaluated by its fit to a random baseline).

5.7

How are the categories of partners specified in such models? One possible answer is *attributional*: people with bundle *X* of attributes tend to marry those with bundle *Y* of attributes with a certain probability. A second possible answer stems from the *relations* of the social network. People related to others by relationship *X* tend to marry one another with a certain probability. Difficulties with the former and advantages of the latter are discussed in turn.

Defining the General Phenomena: Difficulties of the Attribute Approach

6.1

The attribute approach usually entails a typological classification of a population, and analysis of various tendencies towards

endogamy, exogamy, isogamy, anisogamy (hypergamy, hypogamy), or "alliances" between particular groups, based on such categories. Many models of marriage rules are formulated at this level, especially where lineages provide the typological attributes that classify the population. Attributional models, if they are handled statistically, are usually analyzed by one of two means. The first is straightforward regression analysis that considers how much of the variance in *whom one marries* (the dependent variable) is due to a specified set of attributes and interactions (the independent variables). A second approach developed by Romney (1971) takes into account demographic differences in the sizes of the various groups involved. Romney considers the *aggregate intermarriage matrix* for a given categorical typology (a matrix of marriage frequencies, say, between lineages, with wife-givers as rows and wife-takers as columns), in which different row and column sums reflect the relative demographic strengths of the social units in terms of numbers of men and women. He observes that if a large group were to have a preference to marry into a small group, they could not do so fully because of their numerical imbalance (for an optimization model approach relating more directly to preference orderings, see White 1973: 402-410). Therefore, Romney removes the effects of demographic imbalance by a double-normalization of the matrix to produce uniform marginal totals with proportional rates in the cells relative to "demographic balance" assumptions. This is a form of simulation or random baseline comparison since under independence assumptions the expected value is uniform in every cell in a double-normalized matrix. For any 2 by 2 diagonal sub-table of this matrix, such as Table 1, the cross product ratio alpha, $a = ad/bc$, is a measure of the tendency towards endogamy ($a \gg 1$) versus exogamy ($a \ll 1$), with $a=1$ as the random baseline.

Table 1: Normalized Endogamy (diagonal) $a = ad/bc$, endogamy ratio

	women of A	women of B
Marry:		
Men of A	a	b
Men of B	c	d

6.2

Further, with an off diagonal sub-table such as Table 2, alpha is a measure of tendency of the *X-A* and *Y-B* pairs to ally by intermarriage ($a \gg 1$) or to avoid intermarriage ($a \ll 1$). Romney's method takes only one type of demographic control into account: numeric imbalance between groups.

Table 2: Normalized Alliance (off-diagonal), $a = ad/bc$, endogamy ratio, $1/a$ is the exogamy ratio

	women of A	women of B
Marry:		
men of X	a	b
men of Y	c	d

6.3

There is a more general approach, however, that can take other controls into account by a simulated random baseline, as shown in Table 3, and computation of a baseline-adjusted ratio, alpha-star, $a^* = (ad/bc)/(eh/fg) = adfg / bceh$.

Table 3: Simulated Normalization, $a^* = adfg / bceh$, endogamy ratio

Actual data		Simulated data	
a	b	e	f
c	d	g	h

6.4

These exercises raise two fundamental problems with the attribute approach. One is that all of these approaches involve *aggregation* of individual level data in which there are a multitude of ways to aggregate people into groups on the basis of attributes. Even in the case of kinship groups it is not always clear where the boundaries of the exogamous sub-lineages might be located within the larger clans or lineages (e.g., How many generations deep does the prohibition extend? How to break the sub-lineages when they are hierarchically nested with different ranges of proscriptions for different members?). The only possibility of clear specification is (1) if people in the society have very precise rules demarcating the boundaries of endogamy, exogamy and alliance groupings, (2) if people, moreover, follow these rules to a high degree, and (3) if the marriage prohibitions fall into mutually exclusive sociological groupings, which is not usually the case even in lineage societies! If each of these conditions were met, however, we are approaching something like the "elementary" pole of marriage systems.

6.5

In the general case, the attribute approach ought to be able to model the underlying assumption of a complex marriage system,

namely, that people's marriage choices vary probabilistically across different categories of people. Trying to specify "rules or strategies" with appropriate attribute categories for such systems is fraught with the difficulties of potential specification errors resulting from incorrect aggregation, nested hierarchies or non-exclusive categories, and lack of consideration of relational or network-based rules or strategies.

Specifying the General Phenomena in Network Terms

7.1

The bias of our society - a complex marriage system, in Lévi-Strauss's terms - and our liberal professions is to see marriage in terms of different social categories within a universalistic, anti-particularistic, egalitarian perspective. Yet most marriage rules and strategies are formulated in terms of marriage with those with whom a pre-existing link is recognized such as common ethnicity, class, kinship, community, neighborhood, school ties, etc. Some of these links, like connections through prior kinship or affinity, are directly *relational*. Some, like neighborhood, are *category proxies* for spatial proximity, that are more clearly specified in terms of pairwise proximities (distances) that create probability distributions of interaction. Interaction is a clear prerequisite to acquaintance, courtship, marriage, having children, etc. As for many of the remaining links that appear to be categorical (ethnicity, class, community, etc.), it would be extremely interesting in the general case (including "complex" marriage systems) to know whether ethnicity, class, and community (hence school ties varying in accordance with these three sociological variables) are not themselves constituted to a large extent by *intermarriage*. We can generalize and universalize Lévi-Strauss's insight about the "closed form" of elementary systems by saying that the canonical forms of marriage alliance, marriage rules, and marriage strategies are those individual marriages that *relink* families already linked. To be more precise, *marital relinking* exists when partners are already related prior to their marriage. The concept of marital relinking was invented by French ethnographers such as Jola, Verdier and Zonabend ([1970](#)), and further explored by Segalen ([1985](#)), Richard ([1993](#)) and others.

7.2

Indeed, Lévi-Strauss ([1966](#)) speculated on the possibility of endogamous "demes" on a scale, say, of 2-20,000 or more persons, as characteristic of modern urban populations and rural villages of modern states. His speculations motivated French ethnographers to investigate and identify matrimonial relinking as a marriage alliance strategy employed in the "complex marriage systems" of French farming villages. Richard ([1993](#)) developed a statistical method for assessing the occurrence of relinking in a population. Brudner and White ([1997](#)) identify class formation in rural Austria with the marriage strategy of relinking.

7.3

To articulate the concept of marital relinking to marriage rules, strategies or structure, it can be said that *the minimum necessary form of marriage alliance, rule or strategy, at the broadest level, involves some kind of endogamy*, and that *endogamy is minimally constituted through relinking*. Note here the similarity to Lévi-Strauss's idea that a marriage is not an *alliance*, an elementary form, unless it is in recognition of some preexisting relationship between the families. An alliance is not instituted by a simple marriage contract between man and wife but constituted upon a preexisting set of social relations, expectations, obligations, and/or privileges, existing between two groups, the givers and takers of the bride and reciprocally of the groom.

Decomposing Endogamy into its Constituent Relational Structures

8.1

The concrete form of endogamy that is constituted through marital relinking is not categorical endogamy but *structural endogamy* ([White 1997](#); [Brudner and White 1997](#)). To be more precise, structural endogamy consists of a bounded set of marriages within which each pair of marriages is connected by two or more independent paths of parent/child links, and such that the set is maximal, that is, there are no other marriages that could be included in the set and satisfy the definition.

8.2

Structural endogamy provides the starting point for a simpler solution to the problem of specifying marriage rules and strategies than the attributional approach because it is a concept that implies emergent social boundaries. To apply the concept of structural endogamy we must resist the temptation to immediately aggregate our data. By doing so, and by retaining a definition of endogamy in terms of links among individual marriages, we can adopt techniques of network analysis to identify the boundaries of structural endogamy.

8.3

Structural endogamy is a relational concept that yields a unique decomposition or classification of sets of endogamous marriages in a population graph in which *marriages* - more generally, sexual unions - are represented by the nodes of a graph, and *persons* are represented by lines connecting marriages via parent-child links. The existence of sexual unions in a population implies that each of the two spouses in a given marriage links the marriage to a sexual union of their respective parents. In sociology a *family of orientation* is the unique, ordinary parental node of an individual, while the *family of procreation* is one of the several possible nodes of ego's activity as parent. Every married person links a *family of orientation* to one or more *families of procreation*. If we generalize this idea and add extra nodes for *unmarried children* who link their "personal node" to that of their parents as their node of origin, we have the graph theoretic construction known as a *p-graph* ([White and Jorion 1992](#)).

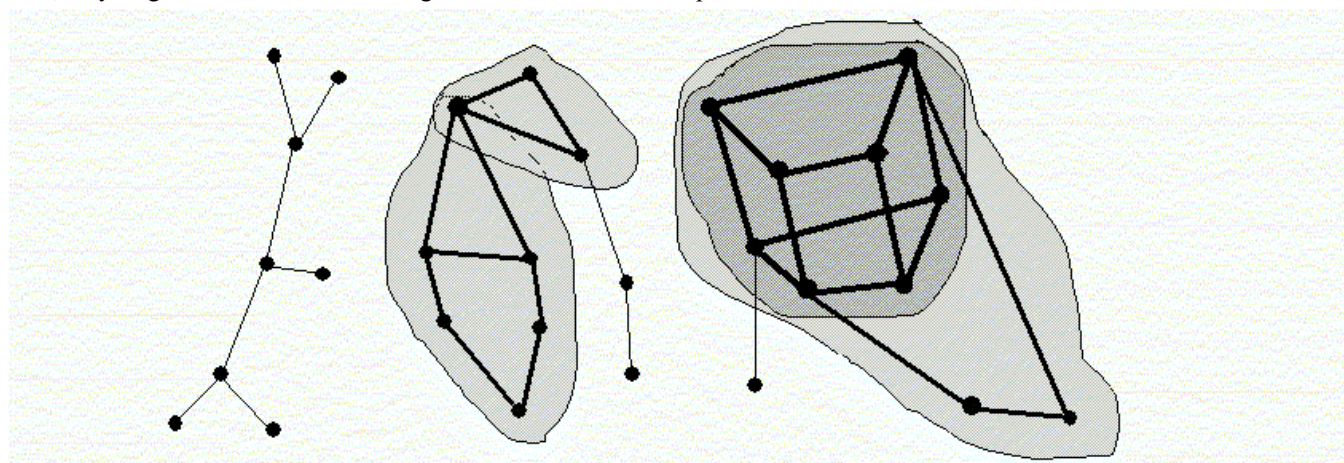
8.4

The p-graph is an empirical representation of the reproductive and marital structure of a population. Some parental information will always be missing or outside the population boundaries, hence the representation is finite. Empirically speaking, a p-graph has two kinds of nodes: *personal nodes* for single children and *marital nodes* for marital unions of two children (generally of opposite sex

and of different parents), and two kinds of arcs (directed edges): *male* and *female*, directed from parental nodes to child nodes. Formal speaking, a p-graph is an asymmetric and acyclic digraph with two kinds of arcs, and maximal indegree of 2, assuming arcs orient from parent to child (if the reverse, outdegree 2 is implied). In defining the boundaries of structural endogamy, however, the direction of the arcs in the p-graph is disregarded. Although parent-child links are directed, it is the undirected skeleton of the parent-child network among marriages that is relevant to structural endogamy. A *structurally endogamous block* of the skeleton of a p-graph is formally equivalent to a *bicomponent* of the graph since in a bicomponent two or more independent paths connect every pair of nodes.

8.5

Figure 2 illustrates the concepts of the components, bicomponents and tricomponents of graphs. A *component* of a graph is a subgraph of connected nodes that is maximal (as large as possible). A *bicomponent* (*tricomponent*) of a graph is a subgraph in which every pair of nodes is connected by two (three) or more independent paths. The figure shows a single graph that has three (disconnected) components, three bicomponents (two connected and one disconnected), and one tricomponent. In a bicomponent, every pair of nodes is necessarily connected by a cycle. The skeleton of a finite p-graph cannot be composed of tricomponents since this would imply that every node has at least one child (to reach the required degree of 3), which generates an infinite digraph. Hence *structurally endogamous blocks* of the skeleton of a p-graph are formally equivalent to *bicomponents*, never tricomponents. Two or more bicomponents can have at most one node in common, hence the same is true for structurally endogamous blocks. Thus, only single nodes or trees of linking nodes can connect bicomponents.



Three disconnected components, three bicomponents (light gray) and one tricomponent (gray)

Figure 2: Components, bicomponents and tricomponents of graphs, illustrating structural endogamy in graphs where marriages are the nodes and persons connecting marriages via parent-child links are the lines (direction of lines ignored)

8.6

The graph in **Figure 2** illustrates the concept of structural endogamy if we regard the nodes as marriages linked by undirected parent/child links. In the leftmost component of **Figure 2** there is no structural endogamy (no bicomponent), since the removal of any node (marriage) increases the disconnectivity of the graph. In the middle component there are two overlapping blocks of structural endogamy. They have one marriage in common whose removal increases the disconnectivity of the graph. The component to the right has a bicomponent, and within it, three or more independent paths connect every pair of nodes in a tricomponent. A finite tricomponent of a p-graph cannot possibly represent biological kinship, so this subgraph must necessarily have some fictive or sociological constructed element that is not based on biology. Note that in a graph of linked marriages, a cycle implies a marriage that relinks marriages already linked by some prior path of personal connections.

8.7

Structural endogamy, then, is uniquely well suited - both theoretically and empirically - as a starting point for a precise and unambiguous specification of the problem of identifying the largest, bounded empirical units of endogamy within a genealogical network. It yields an aggregate social unit at the most generic and extensive level when decomposing the partially ordered levels of marriage structure. It is within this largest structural unit that more specific rules or strategies of marital relinking operate, since, by definition, every relinking defines a cycle that is inside a bounded unit of structural endogamy. *All specific relational marriage rules and strategies*, such as consanguineal marriages, redoubling of alliances between lineages, dual organization, etc., of necessity, imply some form of relinking and hence *subblocks of structural endogamy*.

8.8

If some subset of marriages is strategic or rule-governed in some particular way and at some "level" in a partially ordered uniform marriage structure, we would expect this subset to have non-random characteristics in comparison to a uniform-probability model at that level. Marriages of similar-age spouses, for example, appear non-random against a uniform-probability model across all age groups. In a partially ordered uniform marriage structure model, each test of marriage structure at a given level needs to be made independently, but holding constant the marriage structures at a more basic level. If, for example, after identifying a specific age-bias in marriages, a uniform probability model predicts with high probability a narrow size-range for the largest structurally endogamous block, this does not imply the lack of other marriage rules or strategies that might be identified against this random-model backdrop. Sometimes small-scale rules and strategies may be masked in larger phenomena that resemble a near-random relinking model of structural endogamy.

8.9

What are some of the smaller-scale relinking patterns to be found within structurally endogamous blocks? One way to classify new relinkings between those already connected is by the type of prior personal connections. Personal connections may involve blood (parent/child or sibling/sibling connections) or marriage (husband/wife connection). A blood marriage (1-family) relinking is one where there exist prior personal connections between spouses involving only consanguinity (hence the spouses are blood related). An affinal (2-family) relinking is one where there exist prior personal connections involving only one prior marriage link. Multiple (k-) family relinkings involve prior personal connections with multiple (k-) prior marriage links. 1-, 2-, or k- family relinkings are *local structures*, in that they are defined by characteristics of a single, marital relinking cycle. One or multiple sets of cycles may be characterized by effective limits on the *genealogical depth* involved in strategic or rule-governed relinking, the *density limits* (high and low) of cluster of cycles, or *global properties* such as dual ([Houseman and White 1998b](#)) or segmentary dual organization ([White and Houseman ms.](#)). Other than the nodes or trees that connect blocks, all global structures need to be evaluated by the characteristics of the circuits within them. In dual organization, for example (see [White and Jorion 1992](#), [White and Jorion 1996](#)), circuits can be drawn as a bipartite graph where all the connections are between two supersets of nodes ^[2].

8.10

The partially ordered character of marriage structures, and appropriate methodologies such as hierarchical decomposition, derives from the network property that all marriage structures (blood marriage taken as 1-family relinking, redoubling of alliances taken as 2-family relinking, etc.) are contained within (1) the larger spheres of the structurally endogamous blocks of relinking, and (2) subblocks with higher densities or other identifiable structural properties; otherwise, there remains only (3) the tree structure of the paths of articulation among the structurally endogamous blocks.

8.11

The question posed here is: How to define the general phenomena of marriage rules and strategies empirically to make it possible to avoid mis-specification? That is, how to statistically decompose each of the possible levels of the problem and each of the possible "main effects" and "interaction effects," as it were, using the language of analysis of variance?



Canonical Representation of Kinship and Marriage Network Data

9.1

Circuits of matrimonial relinking have rarely been taken as canonical objects of study for marriage rules and strategies. To do so, one needs a representation of kinship and marriage networks in which matrimonial relinkings will always form identifiable circuits, and identifiable circuits are always and only associated with matrimonial relinkings. When such is the case, as with the p-graph representation, then graph theoretic analysis will be truly of value to the study of partner selection, population and demographic structure, marriage structures, kinship, and network approaches to social organization. The p-graph ([White and Jorion 1992](#), [1996](#)) is the only known graphic solution that fits these requirements. By taking as its nodes couples and single individuals, and as its arcs the concrete persons who link parental nodes to their descendants, there is no redundancy in the graph other than that created empirically by relinking marriages. All such redundancy then becomes a measure of cohesion related to "social structure" when patterns are recurrent and to "social organization" where new social choices or demographic constraints lead to diverse and potentially changing social structural outcomes. The p-graph is thus conceived as a *measuring system* for structural endogamy and other aspects of marriage systems, in which "relinking" and its recombinatory possibilities are major elements of structure.

9.2

The application of graph-theoretic algorithms to identify structurally endogamous bicomponents of nodes involved in matrimonial relinking represents a straightforward solution to the problem of precise decomposition of the aggregate social units potentially involved in marriage rules and strategies. These algorithms are capable, through depth-first search procedures, of identifying all bicomponents in a network in a computational time that is a linear function of the number of nodes in the network ([Gibbons 1985](#)). Hence, the bicomponent-finding methodology is applicable to networks of any size, and further structural analysis of marriage rules and strategies will be bicomponent-specific. Populations of extremely large size can easily be decomposed into bicomponents and marriage structure can be described within each such unit separately.

9.3

Bicomponent-decomposition thus solves the basic problem of contexts for global-structure specification of models for analysis, assuming that we know how to identify structure within bicomponents, which will not be the focus here. In the analyses that follow, I use programs for computing frequencies of local structures such as blood marriages (*Par-Calc*: described in [White and Jorion 1992](#)), for comparing actual structural endogamy versus simulated results (*Par-Bloc*: described in [Brudner and White 1997](#)), and for computing within-block global structures such as dual organization (*PGRAPH*: described in [Houseman and White 1998a](#), [1998b](#); [White and Houseman ms.](#); PGRAPH is the p-graph drawing program). For the statistical tests used, see White (1994) and White, Pesner and Reitz (1983). In addition, programs exist for analysis of 2-family relinking (*Par-Link*: described in [White and Skyhorse 1996](#)), and for estimating relatedness and inbreeding coefficients for individuals in a population (*Par-Coef*: forthcoming). These algorithms address the question posed of how to define the general phenomena of marriage rules and strategies empirically so as to avoid mis-specification of marriage models. The two problems remaining are: (1) How to establish meaningful simulations for comparison of these results against demographic and random baselines? and (2) How to evaluate statistically the computational findings about structural characteristics or frequencies of various types of marriages against demographic and random baselines?



Simulating Comparative Random Baselines

10.1

Hammel (1976a) and Lang (1995) developed population simulations that are sufficiently disaggregated so that we can evaluate outcomes at the individual level in terms of the frequencies of different types of marriage under a random mating regime by specifying a range of demographic parameters and constraints. Hammel (1976b), however, eventually used his simulations in an act of magical "handwaving" that dismissed alliance theory as a serious enterprise^[3]. Lang's (1995) simulation software, available for PCs, produces as output a population of men and women with birth dates and sibling sets through matrilineal links, where fatherhood is as yet unassigned. Hence, one could simulate a population under demographic constraints, and then assign marriage and/or paternity under another set of constraints (e.g., relative age, sibling or cousin avoidance, etc.). This approach, which requires a whole series of demographic parameters that would need to be matched to an empirical population for verisimilitude, is unnecessarily complex for the problems of marriage structure posed here.

10.2

There is an easier solution to the problem of simulation and to the complex problem of what constraints to use to establish random baseline "verisimilitude" to the empirical population under study. This is the approach of structurally controlled simulation, or the use of permutation tests. Say one has an observed network of parental links ordered by generation in a p-graph format. "Generation" is an empirical attribute of the marriage structure, and how generation is determined algorithmically is discussed below. How can one create a "control" population that shares as much structure as possible with this network but with one crucial difference, namely a random mating regime? Briefly, the idea of *structurally controlled simulation* is the following: Hold constant the ancestral tree generated by parental links through one gender, and then, within each successive generation, randomly permute the marriages that generate parental links through the other gender. Let us say that female descent lines will be held constant in the random baselines generated for the case studies in this article. Then, in each generation, one detaches the sons from their marriages, creating a marriage pool of potential mates who marry within this precise set of women. Husbands are then randomly reallocated from within this pool - they are by definition "marriageable" for that generation - to regenerate a total kinship and marriage network for this population with everything held constant (including sibling sets) except for a random marriage regime within each generation. One can also randomly reallocate both the son and the daughter marriages, keeping the sibling sets and marriage pools the same, but randomizing the ancestral structure in successive generations. The only additional parameters that need to be specified are the extent of prohibitions (e.g., brother/sister, and various prohibitions on first and second cousin marriages, for example). Because the simulated network is randomly constructed in order of successive generations, it is possible to specify rules, as each new generation is constructed, such as avoidance of certain kinds of cousins or other relatives (the network of relatives emerges from the random allocations of ties at earlier generations). Or, while not pursued here, one could use probability distributions defined in terms of classes of relatives, kinship distances from ego, and so forth^[4].

10.3

Figure 3 shows an illustrative p-graph of three generations and 18 marriages and a permutation of the male links between adjacent generations. Note that the sibling sets are unchanged. The upper left hand node, for example, has one female and two male children (descending lines) in both the original and the permuted graph. In the permuted graph, males have been randomly assigned new spouses in the appropriate generation, but the female links between nodes are unchanged, as are the female lineages (female lineages are deliberately simplified by having each marriage produce exactly one daughter in the hypothetical original graph). The permutation represents a random mating regime where the number of marriages in each generation, the female lineages, and the size and gender composition of sibling sets in each generation are held constant. Note that the kinship links among nodes have now been radically altered. The marriage in the lower left in the original graph, for example was a relinking between a man and his FaSiHuSiDa. After permutation, this marriage is one between a man and his FaBrDa.

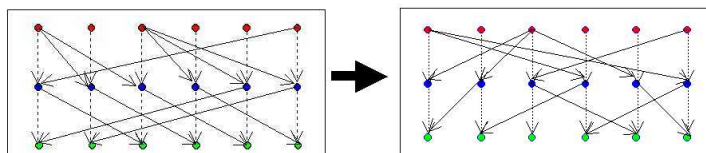


Figure 3: Illustration of permuting male links in a p-graph with 3-generations: left is the original graph, and right is the permuted graph. Top row is the first generation of marriages, solid arrows represent sons descending from parental marriages to form a marriage with a wife, the latter shown as a broken arrow descending from her parents.

10.4

Figure 4 illustrates how the permutation might differ if we permuted both male and female links. Note that again, the number of male and female children for every node in the original and permuted graphs is the same, since the permutations affect only the marriages of each person, not their parentage. This permutation, then, represents a random mating regime where the number of marriages in each generation, and the size and gender composition of sibling sets in each generation are held constant. The structure of female as well as male lineages has been permuted. It is preferable to do simulations permuting only the links of one gender, however, because one additional feature (lineage structure of the nonpermuted gender) is controlled since it mimics the original data.

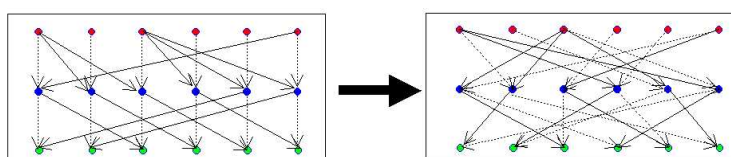


Figure 4: Illustration of permuting male and female links in a p-graph with 3-generations: left is the original graph, and right is the permuted graph

10.5

"Generation" is an empirical attribute of the p-graph marriage structure of a population because, unlike individuals (who have multiple marriages), each marriage is uniquely located in a partially-ordered generational structure defined by parent-child links. Because the p-graph is a partial order, it has a minimal number of generations. PGRAPH and the Pajek program ([Batagelj and Mrvar 1997](#)), both of which draw genealogical networks in p-graph format, use an algorithm for computing generations that minimizes the total sum of generational differences between the generational levels assigned to parental marriages and their children's marriages in the p-graph. In some societies, the average difference in generational level can be reduced to its minimum value of 1, in which case all marriages are unambiguously within the same generation. More commonly, there are some generational asymmetries in certain marriages, such as uncle/niece or FaFaBrWiDa marriage. Such marriages can still be placed within the overall minimum of distinct generations used to represent the marriage network, but they introduce a limited number of ambiguities as to where to place certain marriages higher or lower in the structure. There is no such ambiguity for an uncle/niece marriage, but for a FaFaBrWiDa marriage, there is some ambiguity as to where to place the FaFaBr's and FaFaBrWiFa's marriage relative to the others. The generational algorithms resolve this ambiguity by first locating the ambiguous children's marriages and placing them as close as possible to unambiguous parents' marriages; then any ambiguous parents' marriages that remain are placed as close as possible to their children's marriages. All such placements are made without violating the rule that parental marriages must be above - precede - those of their children. In most populations the marriage network is sufficiently dense that there is little ambiguity, and the variance in "random" placement within the minimal partial order constraint is very low.

10.6

Controlled simulation is done within the PGRAPH kinship analysis program (and a forthcoming stand-alone Par-Sim program) that provides a graph of a kinship and marriage network of a given population. Once an initial graph of a network is brought to the screen, the program will execute specified options. Options "G" for generations, followed by "P" for permutations, and further options for keeping male or female ancestries constant, allows for permuting parentage in the other gender within each generation, and saving the results to a file (P-xxx.ves).



The Case Studies

11.1

The case studies of "complex" systems selected to exemplify the statistical decomposition of marriage rules and strategies using random baselines are three farming villages located in Indonesia, Sri Lanka, and Austria. The Javanese village ([Schweizer 1989](#), [White and Schweizer 1998](#)) has been characterized as having "loose structure" and no particular marriage rules or strategies other than nuclear family incest avoidance and status endogamy. Rates of marriage amongst blood kin are very high among the elites. The Sri Lankan village of Pul Eliya was originally characterized by Leach ([1961](#)) as having various types of low frequency blood marriages but was later discovered to have a bipartite marriage structure or cognatic dual organization ([Houseman and White 1998a](#)). The Austrian village, with a proscription by the Catholic Church against blood marriages up to third cousins, was discovered by Brudner and White ([1997](#), using data from [Brudner 1969](#)) to have a high degree of matrimonial relinking related to a particular social class. Table 5 shows some of the characteristics of the case studies. Statistical identification of marriage patterns for these cases has been problematic since analyses have not been done against a random baseline.

Table 4: Case Studies and their Characteristics

Case Studies:	1A	1B	2	3
Village	Dukuh hamlet	Dukuh Elites	Pul Eliya	Feistritz
Country	Indonesia	Indonesia	Sri Lanka	Austria
Religion	Muslim/Hindu	Muslim	Hindu-Dravidian	Catholic
Descent	Bilateral	Bilateral	Bilateral	Bilateral
Residence	Dispersed	Clustered	Diga (patrilocal v. Binna (uxorilocal)	Stem
Inheritance	Equal Division, 2:1 male/female	Equal Division, 2:1 male/female	Agnatic	Impartible farmsteads
Class/Caste	Elites/commoners	Elites	Varna subcaste with	Heir/nonheir social class
Marriage Structure	Status endogamy	Status endogamy	Cognatic dual (sided) organization	Class position defined by matrimonial relinking
Known Incest Prohibitions	Brother-sister	Brother-sister	Brother-sister	Brother-sister and 1st, 2nd cousins



Decomposing Relinkings in the Case Studies in Structurally Endogamous Blocks, with Significance Tests of Departure from Randomness

12.1

We begin at the most general level by comparing simulation results with actual observations of the size of structurally endogamous blocks for each test case. In the simulations for each case, the female descent lines and the generational levels of the actual data are held constant. Then, in each generation, the sons in the actual datasets are detached from their marriages, creating a marriage pool

of potential mates who marry within the precise set of women whose husbands were detached. Husbands are then randomly reallocated (equiprobability sampling without replacement) from within this pool to regenerate a total kinship and marriage network for this population with everything else held constant, including sibling sets. A different parameter is set for each test case to prevent marriages from violating known incest prohibitions. For all four cases, brother-sister marriages are disallowed. For the last case, 1st and 2nd cousin marriages are disallowed.

12.2

Comparisons of the simulated and actual data for the first two test cases - both from Dukuh village in Indonesia - are summarized in [Table 5](#). The first case (A), a hamlet of Dukuh village ([Schweizer 1989](#)), is characterized as having a "loose social structure" with status endogamy but minimal, specific marriage rules and strategies beyond incest prohibitions. The simulation test shows close similarity between the relinkings in a random marriage regime and the actual marriage network, except for six marriages, that relink within two generations. Marriages such as these six (in column 1 of [Table 5](#)) are marked with asterisks to show that they occur more frequently in the actual than in the simulated and randomized marriage network. These are elite couples, with status endogamy ([White and Schweizer 1998](#)), who reside within the hamlet. For the second case (B) - the Muslim elites in the village containing the Dukuh hamlet - the simulated and actual results agree perfectly. The relinkings (through blood marriages) are random although the pool of potential mates is greatly restricted by status endogamy among the smaller group of wealthy families, thus forcing an essentially random distribution of marriages to include a much higher proportion of blood marriages than occurs with the Dukuh commoners, who have a larger marriage pool. This result confirms the argument made by White and Schweizer ([1998](#)) even though they did not have recourse to statistical tests for their hypotheses.

Table 5: Comparison of Relinking Frequencies for Actual and Simulated Data (*=greater than chance), for (A) Dukuh hamlet, Indonesia ([Schweizer 1989](#)), and (B) Muslim elite of the Village containing Dukuh Hamlet ([White and Schweizer 1998](#))

	Magnitude of Structural Endogamy with ancestors back 1, 2, ..., g generations					
Back:	1	2	3	4	5	6
(A) Dukuh						
Starting from:						
<i>Present generation</i>						
Actual	0	27	43	45	45	
Simulated	0	32	42	42	42	
<i>Back one generation</i>						
Actual	6*	6	17	17		
Simulated	0	14	14	14		
(B) Elites						
Starting from:						
<i>Present generation</i>						
Actual	0	4	9	10	10	
Simulated	0	4	9	10	10	
<i>Back one generation</i>						
Actual	0	7	8	8		
Simulated	0	7	8	8		

12.3

In [Table 6](#), the third test case based on Edmund Leach's ([1961](#)) Pul Eliya data and restudied by Houseman and White ([1998a](#)), we have a highly positive result regarding global "relinking" marriage rules. If we start one or two generations back from the last generation in Leach's genealogies, we have a surfeit of 12 marriages (8+4) that relink in the parental generation. All the relinked marriages such as these, in column 1 of [Tables 5](#) and [6](#) (and [Table 13](#)) are the result of sibling sets whose intermarriages form circuits. (One generation back is a circuit composed of eight sibling sets and two generations back is another circuit of four sibling sets. Since the "present" (most recent) generation has not completed its marriages, sibling marriage circles may possibly be formed here as well. The fact that sibling circuits do not occur three or four generations back is more likely due to missing data than to true absence of relinking.)

12.4

In five of the six generations studied in this case (all but the earliest generation), there are circuits of relinking among 1st and 2nd cousins (asterisked in columns 2 and 3) or even closer relatives (although not necessarily at the same generational rank, e.g., cousins "once or twice removed" generationally). The surfeit of actual over simulated relinkings, however, is much higher for relatives linked within the second degree (column 2 - 1st cousin or closer circuits), with a ratio of 71:41 (summing to Starting from "back four" generations), than for those linked within the third degree, where the ratio of 114:105 is close to a random regime (summing again to "back four"). Pul Eliyans have a two to one (83:41) non-random surfeit of "close" relinkings, i.e., within one or two degrees (summing columns 1 and 2 to "back four" generations). Since the relinkings occur through linking relatives who are only one or two generations back (hence likely to be alive or salient at the time of marriage), we can conclude that Pul Eliyans are

likely to be fully aware of, and knowledgeable about, affinal relinkings among their various families and compound groups. This is precisely what is argued by Houseman and White (1998a).

Table 6: Comparison of Relinking Frequencies for Actual and Simulated Data (*=greater than chance) for Pul Eliya (Houseman and White 1998)

	Magnitude of Structural Endogamy with ancestors back 1, 2, ..., g generations							
	1	2	3	4	5	6	7	8
Pul Eliya								
Starting from:								
<i>Present generation</i>								
Actual	0	34*	55*	62	73	81	94	94
Simulated	0	26	48	63	71	84	93	93
<i>Back one generation</i>								
Actual	8*	30*	33	45	54	67	67	
Simulated	0	15	40	46	60	69	69	
<i>Back two generations</i>								
Actual	4*	7*	7*	38	50	50		
Simulated	0	0	0	37	46	46		
<i>Back three generations</i>								
Actual	0	0	4*	25	25			
Simulated	0	0	0	29	29			
<i>Back four generations</i>								
Actual	0	4*	15	15				
Simulated	0	0	17	17				
<i>Back five generations</i>								
Actual	0	5	5					
Simulated	0	10	10					

Local Marriage Structures: Consanguineal Marriages

13.1

Table 7 moves from the global level of structural endogamy to the level of *local marriage structure* to examine Dukuh hamlet and the Muslim elite that crosscuts the various hamlets of the village. Here, the Par-Calc program (White and Jorion 1992) was used to calculate the frequencies of consanguineal marriages in the actual and simulated networks. What is especially important about these calculations is that for each kin-type, such as FBD for example, the program also computes the *number of relatives* that exist of this type. Hence, biases are controlled if the actual data have a different rate of availability for marriage of a given type of relative (i.e., what is controlled is how many relatives there are of each type, which can otherwise drastically and spuriously affect the raw frequencies of different consanguineous marriages). In addition, Hammel's (1976b) "matrilateral" and similar biases are fully controlled because the permutations within generations can only select, for example, those matrilateral cross-cousins who are actually married in one's generation when generating the simulated marriage rates. Hence, structurally controlled simulation provides an astoundingly simple solution to the problems that have plagued statistical inferences about marriage rules and strategies.

13.2

In Table 7 and the following tables, Fisher's exact significance test for dichotomous (2x2) tables is used to compare actual and simulated frequencies for the presence/absence of different types of marriage (White, Pesner and Reitz 1983, White 1994), except where the binomial test is appropriate (Tables 8-10). Table 7 also uses Bartlett's 2x2x2 test, a generalization Fisher's exact significance test, to compare the 3-way differences between two 2x2 tables. The simulated data from these tests are from a single simulation; hence there are no fractional numbers in the S or TS columns. A single run comparison is not only appropriate but also methodologically preferable for the use of the Fisher and Bartlett statistics. Two or more runs would double or triple the sample size of the simulated distributions, and where there are systemic (even if small) differences between the simulated and actual data, the inflation of sample size invariably yields greater significance. Hence the methodology of a single run is methodologically conservative, which is what we want for significance tests. If multiple simulations are averaged there is greater precision in the permutation results,^[5] but tests show that this will rarely affect accuracy at the integer level of measuring the frequencies expected by permutation, and rounding to the nearest digit will barely affect the significance tests.

Table 7: Test of Actual versus Simulated Marriage among Consanguineal Kin, Dukuh Hamlet and Village Elites (conclusion: no preferred marriages, only status endogamy)

	Javanese elites						Dukuh Hamlet						3-way Test
	A	S	TA	TS	p=	type	A	S	TA	TS	p=	type	
1:	1	0	4	3	.625	FBD	0	1	9	12	.591	FBD	1.00
2:	1	2	2	3	.714	MBD	1	0	11	16	.429	MBD	1.00
3:	2	1	3	2	.714	FZDD	0	0	11	0	-	FZDD	1.00
4:	0	1	6	7	.571	ZD	0	0	18	24	-	ZD	1.00
5	0	0	11	11	-	Z	0	0	36	43	-	Z	
6	0	0	4	4	-	BD	0	0	22	27	-	BD	
7	0	0	2	2	-	ZSD	-	-	-	-	-	-	
8	0	0	3	3	-	BDD	0	0	8	8	-	BDD	
9	0	0	3	3	-	ZDD	-	-	-	-	-	-	
10	0	0	4	4	-	FZ	0	0	21	27	-	FZ	
11	0	0	1	1	-	FZSD	-	-	-	-	-	-	
12	0	0	3	3	-	FZD	0	0	13	14	-	FZD	
13	0	0	3	3	-	FBDD	0	0	3	2	-	FBDD	
14	0	0	5	4	-	MZ	0	0	18	23	-	MZ	
15	0	0	2	2	-	MZSD	-	-	-	-	-	-	
16	0	0	4	4	-	MZD	0	0	13	14	-	MZD	
17	0	0	1	2	-	MBDD	0	0	6	5	-	MBDD	
18	0	0	2	3	-	MZDD	-	-	-	-	-	-	
19	-	-	-	-	-	-	1	0	1	0	-	FFBDD	
20	-	-	-	-	-	-	0	0	6	10	-	BSD	
21	-	-	-	-	-	-	0	0	5	6	-	FBSD	
22	-	-	-	-	-	-	0	0	6	7	-	FFZ	
23	-	-	-	-	-	-	0	0	4	5	-	FFBD	
24	-	-	-	-	-	-	0	0	3	2	-	FFBSD	
25	-	-	-	-	-	-	0	0	2	3	-	FFZD	
26	-	-	-	-	-	-	0	0	6	5	-	MBSD	
27	-	-	-	-	-	-	0	0	10	11	-	MFZ	
28	-	-	-	-	-	-	0	0	7	7	-	MFBDD	
29	-	-	-	-	-	-	0	0	4	3	-	MFBSD	
30	-	-	-	-	-	-	0	0	7	9	-	MFZD	
31	-	-	-	-	-	-	0	0	4	2	-	MFBDD	
32	-	-	-	-	-	-	0	0	10	11	-	MMZ	
33	-	-	-	-	-	-	0	0	5	4	-	MMBD	
34	-	-	-	-	-	-	0	0	3	1	-	MMBSD	
35	-	-	-	-	-	-	0	0	6	5	-	MMZD	
36	-	-	-	-	-	-	0	0	2	1	-	MMBDD	

Key

- A frequency of actual marriages with a given type of relative
- S frequency of simulated random marriages with a given type of relative
- TA total of actual relatives of this type
- TS total of simulated relatives of this type
- p probability (Fisher Exact)

13.3

Examining [Table 7](#) for Dukuh hamlet versus the Muslim elites, we see that FBD marriage occurs once among the elites in the 4 cases where a FBD is present (a 25% marriage rate!), but this does not differ significantly from chance ($p = 0.625$ by Fisher's Exact) from the simulated data, where no FBD marriages occur with only 3 such marriages possible. A second simulation to test this result (not shown here) obtained exactly the same rate in the random data as in the actual data, although the specific marriages resulting from permutation were different. Comparably, in Dukuh hamlet, while there were no FBD marriages (Dukuh contains only a segment of the total elite network for the village), only one was found in the simulated data, with a probability, given the simulated data, of $p = 0.591$ that fails to reject the null hypothesis. Further, using 3-way interaction tests ([White 1994](#)), there is no indication ($p = 1.0$) of a significant difference between the elite and hamlet frequencies. Similar conclusions hold for MBD and FZDD, that are the only other actual blood marriages, and for ZD, which occurs only in the simulated data. Results are also shown for kin-types that exist but do not occur as blood marriages either in the actual or the simulated data. Hence, we may conclude that (1) such

blood marriages as exist are not strategic or preferred but are either random or only a function of the status endogamy in smaller sized group of elites (in spite of their 25% and 50% rates of marriage with FZD and MBD relatives when they are members of the elite network!) and (2) controlling for status endogamy does not lead to any significant difference in rates of marriage with blood kin between Dukuh hamlet and the elites.

13.4

[Table 8](#) shows the blood-marriage analysis for Pul Eliya. Matrilateral cross-cousin marriage is the only type of marriage among consanguineal relatives whose frequency is sufficiently high relative to the simulation results to reject the null hypothesis ($p < 0.05$). This conclusion accords with Houseman and White (1998a), who consider MBD marriages as a conscious marriage strategy related to the consolidation of wealth among families who are politically influential in the village. Leach (1961), on the other hand, did not make much of MBD marriage as strategic alliances^[6]. Although MBD marriages are infrequent (where ego has a MBD, ego marries MBD 12.5% of the time, compared to 50% for the Javanese Muslim elites), this rate is sufficiently higher than expected in a simulated random marriage regime to qualify as strategic. FZD, which occurs with a 7.7% rate, does not differ significantly ($p = 0.32$) from the expected random rate. Many other blood marriages occur, but none may be regarded as differing from expected random rates when taken individually.

Table 8: Test of Actual versus Simulated Marriage among Consanguineal Kin for Pul Eliya (conclusion: MBD is a preferred marriage)

Type of Mar.	Actual Freq.	Simul Freq.	Total Actual	Total Simul	Fisher Exact	Blood Marriage		Viri-Sided?	
						Type	P-graph notation	Actual	Simul
12:	5	0	40	38	.042	MBD	GF=FG	yes	
2:	3	1	39	40	.317	FZD	GG=FF	yes	
1:	0	1	56	57	.508	FZ	GG=F		no
3:	0	1	6	6	.538	FFFZDSD	GGGG=FGFF		no
4:	1	0	3	1	.800	FFMZDSSD	GGGF=FGGFF	yes	
5:	0	1	5	3	.444	FFMBDSDD	GGGF=FFGFG		no
6:	1	0	18	15	.558	FMBSD	GGF=FGG	yes	
7:	0	1	17	12	.433	FMBDD	GGF=FFG		no
8:	2	1	18	12	.661	FMZDD	GGF=FFF	yes	
9:	0	1	9	5	.399	FMMBSSD	GGFF=FGGG		no
10:	0	1	4	5	.600	FMMFZSSD	GGFFG=FGGF		yes
11:	0	1	6	3	.400	FMMFZDSD	GGFFG=FGFF		yes
13:	0	1	25	27	.528	MBSD	GF=FGG		yes
14:	1	0	14	10	.600	MFZDD	GFG=FFF	yes	
15:	1	0	7	3	.727	MFFZDSSD	GFGG=FGGFF	yes	
16:	1	0	8	4	.692	MFFZDSD	GFGG=FGFF	yes	
17:	1	0	8	2	.818	MFMBDSSD	GFGF=FGGFG	yes	
18:	1	0	9	3	.769	MFMBDD	GFGF=FFG	yes	
19:	1	0	3	0	1.000	MFMBDDDD	GFGF=FFFFG	yes	
20:	1	0	8	2	.818	MFMFZSSD	GFGFG=FGGF	yes	
21:	1	0	3	0	1.000	MFMFZDDD	GFGFG=FFFF	yes	
22:	1	0	13	8	.636	MMZSSD	GFF=FGGF	yes	
23:	1	0	15	13	.551	MMBDD	GFF=FFG	yes	
24:	0	1	11	5	.352	MMZSDD	GFF=FFGF		no
25:	0	1	11	5	.352	MMBDDD	GFF=FFFFG		no
26:	1	0	11	4	.749	MMZDDD	GFF=FFFF	yes	

13.5

While the results of this section are based on analysis of consanguineal marriages, the analysis of local structures in marriage networks can also be extended to patterns of marital relinking with affinal relatives. Since there are many more combinatorial types of affinal relatives than consanguineal relatives, this involves greater statistical complexity, but appropriate models are under development (see [Appendix](#)).

14.1

There is, however, one highly significant feature of the blood marriages versus the simulated marriages at the global level. As shown in the last two columns of [Table 8](#) under the heading "Sided?" for actual and simulated marriages only, all of the 18 actual non-MBD marriages have an *even number of female links* whereas only half of the simulated non-MBD marriages do so. The probability of this occurring under a random regime whose character is estimated from this sample size is $p = 0.002$, but a better estimate is $p = 0.000004$, using the binomial test for a 50:50 expected distribution drawing 18 identical samples. Note that the simulation is performing exactly as expected for a random marriage regime since the chances of getting an even as opposed to an odd number of female links in a 1-family marriage relinking is exactly 50:50. But this also indicates that the non-MBD marriages, taken as an ensemble, are not "random" and correspond to a *marriage rule*, namely, *consistency with Dravidian viri-sidedness* defined as "marrying an affine" where blood relatives are converted to affines by the rule that *an odd number of female links* makes the relative an affine. The blood marriages, then, are strictly consistent with the Dravidian kinship terminology of Pul Eliya.

Table 9: non-MBD marriages, Correlating Actual versus Simulated with Dravidian Viri-Sided/Unsided Marriage ($p = 0.0004$; $p = 0.000004$ using the binomial test of 50%:50% expected)

	Viri-Sided	Unsided
Actual	18	0
Simulated	5	7

14.2

Can we test whether the marriage rule here is viri-sided (an *even number of female links*) as opposed to uxori-sided (an *even number of male links*)? We can do so by removing all those marriage with someone in one's own generation, where the two definitions of sidedness are necessarily identical (same generation blood marriages have an even number of linking relatives, and subtracting an even number of male links from an even number of total links always yields an even number of female links). [Table 10](#) shows that generationally "skewed" marriages which are uxori-sided, such as FZ, MMBDDD, MMZSDD, and FMMFZSSD, *never* occur in actuality, while unsided marriages in the uxori-sided sense (such as MFMBDD, MMZSSD, MMZDDD, MFMBDDDD, MFMFZSSD, MFMFZDDD, FFMZDSSD, MFFZDSSD, MFMBDSSD) do occur, but each is *sided in the viri-sided sense* ($p = 0.02$ and, using the binomial test of 50:50 expected, $p = 0.002$). Given the generational depth of up to four generations to the linking ancestors, we can say that Pul Eliyans are definitely aware of sidedness within their personal kindreds, and their marriages with blood kin are 100% compatible with viri-sidedness but 100% incompatible with uxori-sidedness where the two rules differ. Hence we can say that viri-sidedness is *prescribed* in blood marriages, not just preferred.

Table 10: non-MBD generationally "skewed" marriages, Correlating Actual versus Simulated with Dravidian Uxori-Sided/Unsided Marriage ($p=.02$; $>p=.002$ using the binomial test of 50%:50% expected)

	Uxori-Sided	Unsided
Actual	0	9
Simulated	4	3

14.3

Can viri- and uxori-sidedness be tested independently of blood marriages? The idea here is to identify the number of elementary cycles in each graph theoretic block of the network (in the Pul Eliya case there is only one such block). Since n nodes require $n - 1$ edges to be connected as a tree without cycles, each additional edge adds an extra elementary cycle, so that the formula for the number of elementary cycles is $k - n + 1$, where k is the number of edges in the block. Each elementary cycle has a 50: 50 chance of having an even or odd number of male links, and the same for the number of female links. Hence the likelihood of getting the observed number of sided versus unsided cycles can be computed from the binomial distribution ([White and Jorion 1996](#)) - the same formula used to test whether a given coin is fair with no preference for heads or tails. [Table 11](#) shows the results of the binomial test for the Pul Eliyan network, and gives $p = 0.008$ for rejection of the null hypothesis of no viri-sidedness. Note, however, that there are a number of errors to viri-sidedness that (as we have seen) do not come from blood marriages but from affinal relinking. Thus, we can say that the Pul Eliyans are not strict about a rule of viri-sidedness when it comes to affinal relinking between 2, 3 or more families. In fact, if we remove the blood marriages from the count of balanced cycles in [Table 11](#), we can accept the null hypothesis ($p > .30$) that Pul Eliyans disregard viri-sidedness completely when it comes to affinal relinking between 2 or more families, and choose spouses randomly in this respect.

Table 11: Test of Sidedness for Pul Eliya (Programs: PGRAPH and Par-Side) Number of Elementary Cycles: 4

A. Viri-sidedness	Actual	Expected
Balanced Cycles (Even length)	25	17.5
Unbalanced Cycles (Odd Length)	10	17.5
		$p = 0.008$

B. Ambilateral-sidedness (women adjusted by inheritance rules)	Actual	Expected
Balanced Cycles (Even length)	35	17.5
Unbalanced Cycles (Odd Length)	0	17.5
		p = 0.0000000003

14.4

Houseman and White (1998a) show that lacking brothers, Pul Eliyan female heirs to residential compounds and associated land and water rights take the place (and sidedness) of males in the marriage networks. The authors use this concept to identify what they call "ambilateral sidedness." Their criteria for ambilateral sidedness (see Houseman and White 1998a for a definition and discussion), gives a perfect 35:0 hit rate in predicting the sidedness of marriages (Table 11), which has an infinitesimally small probability by chance under the binomial hypothesis ($p = 0.0000000003$).

14.5

These results for Pul Eliya are especially interesting in that viri-sidedness is *prescribed* in blood marriages, but absent (and aleatory) in affinal relinking, yet there is an apparently determinate ambilateral pattern that follows inheritance rules linked to the affinal relinkings. The determinacy, however, is *post-hoc* in that while female inheritance in an agnatic line lacking a male heir "converts" the daughter from the side opposite her father to the father's side (where her brothers should be; a pattern associated with a special form of *binna* uxori-local marriage), there are some marriages whose assignment is indeterminate *a priori* but nonetheless consistent in the *emergent pattern* of sidedness. Hence, what might appear to be an "elementary" marriage system if viri-sidedness were followed rigorously, turns out to have a property of "semi-complexity." Indeed, this is not a unilineal descent system, and the Pul Eliya lack hereditary matrimonial moieties. Ambilateral sidedness here follows principles of cognatic inheritance. Hence, we cannot say that there is an ambilateral sidedness marriage *rule*, but rather a strategic motivational schema that is oriented to an "emergent" sidedness that keeps principles and pragmatics of inheritance in line, but is also consistent with Dravidian kinship terminology. But since there are violations of viri-sidedness in affinal relinking, there are adjustments of the viri-sided Dravidian kin terms (which apply the even-number of female links equally to affinal kin), where affinal relatives who are classified as siblings have their kin-terms readjusted to fit changing patterns of sidedness emergent in the marriage network through actual marriages that deviate from the viri-sided rule of affinal links. Leach (1961) describes numerous adjustments of kin terms to discrepancies that result when someone marries an affinal, classificatory sibling.

14.6

Sidedness in marriage systems is analyzed for Amazonian societies by Houseman and White (1998a), and for indigenous Australian societies by Houseman (1997). Houseman and White (1996) develop other concepts for emergent properties of marriage networks based on dual organization or bipartite marriage structures, such as a "dividedness" concept which applies to certain Polynesian societies in which the parents of every husband and wife can be said to come from one of two opposite affinal "divides," but there is no tendency for these emergent affinal groupings to follow principles of unilineal descent.

14.7

What about sidedness for Dukuh hamlet and Javanese Muslim elites? Table 12 shows the sidedness test, independent of blood marriage, for the elites (the Dukuh hamlet results are similar, and are not shown). There is no evidence for the statistical significance either of viri-sidedness ($p = 0.94$) or uxori-sidedness ($p = 0.31$).

Table 12: Test of Sidedness for Javanese Muslim Elites (Programs: PGRAPH and Par-Side) Number of Elementary Cycles: 4

A. Viri-sidedness	Actual	Expected
Balanced Cycles (Even length)	1	2
Unbalanced Cycles (Odd Length)	3	2
		P = 0.94
B. Uxori-sidedness	Actual	Expected
Balanced Cycles (Even length)	3	2
Unbalanced Cycles (Odd Length)	1	2
		P = 0.31

Fully Complex Marriage Systems

15.1

Finally, what of the application of this paradigm for analysis of marriage rules and strategies to fully complex marriage systems, such as in European societies? In the sections on "Defining the General Phenomena," this article began with "Difficulties of the Attribute Approach," (6.1) and went on to argue for a better specification of the entire problem of marriage rules and strategies in

"Network Terms," (7.1) namely through considering relinking as the "elementary" but *universal* form of endogamy, and *structural endogamy through relinking* as the universal form taken by marriage rules and strategies. What was proposed was basically a theory of kinship and marriage networks in which relinking lies at the root of much of what we call ethnicity, class, community, and other seemingly "categorical" variables that have traditionally - but ambiguously - been used to define some of the outer limits of endogamy.

15.2

As a theory - call it a "relinkage theory of social class and ethnicity" - this is a speculative idea because extensive network data (on networks of size 2,000 to 200,000, for example, as possible endogamous "demes" in urban societies) are neither easily available nor readily yield to analysis. What evidence do we have from European societies? The inspiration for relinkage theory comes from the findings of Brudner and White (1997) on an Austrian farming village where they argue *that structural endogamy tends to define the boundaries of an Austrian rural class system* that differentiates between principal heirs inheriting farmsteads and non-heir siblings who typically take up other occupations (workers, craftsmen, white collar) or emigrate from the village.

15.3

Table 13 examines Brudner and White's analysis of the evidence for non-random relinking within the Austrian village network of about 3,000 people. The construction of this table is identical with that of Tables 5 and 6 for Dukuh and Pul Eliya. What it shows is a surfeit of 42 marriages over the last three generations that relink within the depth of a single generation, whereas no relinkings occur in the simulated "random marriage" regime within such a short time span. In the last two generations there is a surfeit of 56 (total of 74) marriages over 18 expected. In the last generation there is a surfeit of 38 (total of 70) over 32 expected. Relinking with families where the links involve more than three generations depth, however, converge to randomness. From this it is apparent that shallow relinking (within 3 generations or less) is non-random and certainly "strategic," but not prescribed. Hence there is *marriage structure* within this community despite of a near-absence of any kind of blood marriage (9 out of 2491 marriages), at least by links within people's memory, which supply the major source of the data.

Table 13: Comparison of Relinking Frequencies for Actual and Simulated Data (*=greater than chance), from Brudner and White (1997)

Back:	Magnitude of Structural Endogamy with ancestors back 1, 2, ..., g generations											
	1	2	3	4	5	6	7	8	9	10	11	12
Starting from:												
<i>Present generation</i>												
Actual	8*	16*	70*	179	257	318	349	363	376	390	399	405
Simulated	0	0	32	183	273	335	365	382	388	397	397	403
<i>Back one</i>												
Actual	8*	58*	168	246	308	339	353	366	380	389	395	
Simulated	0	18	168	255	320	347	366	372	381	381	387	
<i>Back two</i>												
Actual	26*	115*	178	243	278	292	305	319	328	334		
Simulated	0	98	194	262	291	310	316	325	325	331		

15.4

Is there evidence of mild preference or avoidance, not only for proximal kin up to third cousins (proscribed by the Catholic Church), but for more distant kin? Table 14 analyzes the frequencies of actual blood marriages compared to the simulation model. The nine actual blood marriages, especially those that differ most from random expectations in terms of biases towards certain kinship types (Hammel's "handwaving" problem) in the actual data, show a tendency ($p=0.08$) are on the *father's side* (side here is used in an ordinary sense rather than that of Dravidian sidedness). Among these, one is with a first cousin, three with a second cousin once removed, and one with a third cousin. Similarly, the more significant *avoidances*, compared to expectations from the random model, are on the *mother's side* ($p=0.06$). This is in keeping with the common European idea that women often know more about kinship relations than men, and here it may be that women tend more to be the keepers of kinship prohibitions. There may, however, be a *strategic interest in relinking on the father's side* in light of the heavier inheritances that typically pass through males. These results are summarized in Table 14, showing that higher-significance actual blood marriages have a greater tendency to occur on the father's side while higher-significance simulated blood marriages, with fathers distributed more randomly, tend to occur on both the father's and the mother's side ($p=0.04$).

Table 14: Test of Actual versus Simulated Marriage among Consanguineal Kin for Austrian Village (conclusion: maternal-side blood marriages are avoided, paternal side not)

A	S	TA	TS	P=	
Type Actual	Simul	Total	Total	Fisher	Blood Marriage
of Freq.	Freq.	Actual	Simul	Exact	

Mar						type	degree
7:	1	0	32	34	.492	FFMBDD	2nd +
1:	1	0	165	144	.535	FBD	1st
14:	1	0	34	33	.514	FMMBSD	2nd -
8:	1	0	31	28	.533	FFMZDD	2nd +
17:	1	0	12	11	.541	FMMMBSDD	3rd + median
13:	1	0	6	5	.583	FMFMZSDD	3rd ++
16:	1	0	4	3	.625	FMMFZDSD	4th
23:	1	0	3	2	.666	MFMMBSDD	
24:	1	0	54	22	.714	MMBSD	
26:	1	0	8	3	.750	MMMBSDD	

The more non-random Actual Blood Marriages Favor the Fa's side

	Mo's side	Fa's side				
<.55 (median)	0	5				
>.55	3	2		p=.08		
25:	0	1	23	5	.206	MMFBSSD 3rd
21:	0	1	10	3	.285	MFMFBSSD 3rd +
20:	0	1	16	6	.304	MFMBDSD 3rd
19:	0	1	6	2	.333	MFFBDS 3rd +
5:	0	1	20	13	.411	FFFZSDD 3rd
18:	0	1	7	4	.416	MFBDDDD 2nd --
9:	0	1	5	3	.444	FFMFBDDSD 4th
15:	0	1	21	16	.447	FMMZSSD 3rd median
11:	0	1	46	37	.452	FMBSSD
2:	0	1	105	91	.467	FBSD
6:	0	1	17	16	.499	FFFZDDD
10:	0	1	4	3	.500	FFMFBDSDD
12:	0	1	10	10	.523	FMFFZSSD
3:	0	1	16	21	.578	FBSDDD
4:	0	1	10	13	.583	FFFBSDD
22:	0	1	1	1	.666	MFMFBDSDD

The more non-random avoidance of Actual Blood Marriages is more on the Mo's side

	Mo's side	Fa's side	
<.42	5	3	
>.42	1	7	P = 0.06

The more non-random Actual Blood Marriages favor the Fa's side while the more non-random simulated marriages favor the Mo's side

	Mo's side	Fa's side	
Actual	0	5	
Simulated	5	3	p=.04

key:

A = frequency of actual marriages with a given type of relative

S = frequency of simulated random marriages with a given type of relative

TA = total of actual relatives of this type

TS = total of simulated relatives of this type

p = probability (Fisher Exact)

15.5

Finally, can we answer the question of whether attribute endogamy or structural endogamy is a better indicator of class formation? [Table 15](#) attempts to do so by comparing the strength and the significance of the differences between two cross-tabulated predictors, one for farmer-farmer attribute endogamy ([White et al. 1983](#)), and the other for the correlation between farm heirs and structural endogamy. Although the heir/non-block cell in the latter table can only be estimated, the two correlations do not look all that distinct, although the network hypothesis may fare slightly better (the correlation between relinking and heirship, adjusted for

missing data, is $r = 0.74$, compared to correlations of 0.47 and 0.64 for attribute endogamy from language use and occupation, with $p = .000006$ and $p = .000007$ by Bartlett's exact test for significance of difference in correlations).

Table 15: Comparison of Magnitude of Attribute versus Structural Endogamy as Predictors

A. attribute endogamy: language

marriage	Wi bilingual	monolingual
Hu bilingual	96	16
monolingual	7	15
	$r = .47$	

B. attribute endogamy: occupation

marriage	Wi's fa: farmer	non-farmer
Hu's fa: farmer	80	7
non-farmer	15	34
	$r = .64$	

C. structural endogamy

Marriage	block members	non-block
Heirs	173	117 (adjusted est.40)
Residents	25	281
	$r = .55$, adj. $r = .74$	

3-way tests of difference A&B $p = .46$
 B&C adjusted, $p = .000006$ (greater correlation for structural endogamy)
 A&C adjusted, $p = .000007$ (greater correlation for structural endogamy)

15.6

There is support, then, for the idea that structural endogamy might provide a clue to marriage patterns, rules, and strategies in complex marriage systems. Richard's (1993) findings on French villages support this view, and he again finds occupational correlates of relinking that are probably also concomitant to differential social class formation.

 **Links between Kinship, Economics and Politics**

16.1

By identifying social units such as structurally endogamous blocks, matrimonial sides, or emergent groups in which certain patterns of marriage occur, the simulation methodology allows a better identification of the links among kinship, economics and politics on the one hand, and among positions in the kinship and marriage network, language categories, and verbal norms, on the other. Each of the studies examined here offers a case in point. Pul Eliya offers a dramatic example. Societies in the "Dravidian kinship" culture area of South Asia (numbering in the tens of millions of people) have "two-sided" kinship terminologies that set up a contrast between non-marriageable and marriageable kin as if there is in place a matrimonial system of dual exchange.

16.2

These "two-sided" verbal formulae of Dravidian kinship terminologies are thought by most South Asianists to be merely ego-centered perspectives that have little or nothing to do with a moiety social structure at a group level. The comparison of actual marriage patterns with the simulated case where marriages are uniform random within generations of the Pul Eliyan local subcaste, combined with the network analysis of Houseman and White (1998a), does show two features that exemplify a moiety-like structure at the group level. At the social structural level, viri-sided marriages among blood kin are strictly prescribed. This is not sufficient to produce moieties, however, since there are "discrepant" marriages outside the circle of blood kin that are not viri-sided. Here a second principle is asserted at the level of emergent social organization, where pragmatic social decisions are taken. Pul Eliyans "adjust" the sidedness of the non-blood kin "discrepant" marriages to bring them into alignment with a form of sidedness that is not associated with a strict rule of descent, but instead is associated with a variable rule of inheritance in which a household "successor" may be women if the current generation in the household lacks an appropriate male heir. Decisions about the variable "sidedness" of female heirs gives rise to an emergent dual organization at the group level that correlates perfectly with elements of Pul Eliyan ideology that are widespread in the Dravidian culture area, namely the value placed on exchange marriages as an expression of the political equality among different household and lineage groups. The substantiated preference for MBD marriage further cements the behavioral expressions of these economic and political values. Hence, the fit among positions in the kinship and marriage network, language categories, and verbal norms is far greater than previously thought to be the case. Certain aspects of the kinship system are strictly prescribed, however, such as appropriate marriages among blood kin, while others are indeterminate and emerge only through decisions and behaviors taken among variable alternatives. Some of the verbal formulae in play are not strictly models "of" behavior but models "for" behavior and may include adjustments for departures from norms that apply in one domain (blood kinship) but not another. Internal variability turns out to be a key factor for understanding the connection between marriage patterns, kinship ideology, economics and politics.

16.3

The Dukuh hamlet and elites and the Feistritz village are cases where marked social stratification is in play. This allows for much simpler statements of fit among kinship, economics and politics. In the Dukuh case, elites and commoners behave very differently but do not consider themselves to differ culturally and they operate under a more general norm of moral equality (any one family, for example, may have rich and poor relatives, with the wealthier helping and often taking as clients their poorer brethren). A general norm of status endogamy is found to apply at each level of the status hierarchy, and the simulation results show that the apparent difference in marriage behavior - that the elites are more likely to marry close blood relatives - are due only to the smaller size of their social circles where there is less chance of not marrying a relative. In the Feistritz case, the connections among kinship, economics and politics operate with a very different hierarchical inflection of status and property. Whereas the Dukuh have equal division of property among sons (and also among daughters, who receive half that of their male counterparts under Islamic norms), the Feistritz farmers pass their farmsteads to single heirs, paying quitclaim inheritances to other children.

16.4

Here, in the Austrian village of Feistritz, the structurally endogamous unit of the village defines a social boundary containing those marrying within, yet multiply connected through kinship links to the entire Slovenian farming community of the Gailtal valley. The connection between marriage structure and economics is striking. Those within the structurally endogamous core of the village - emergent from marriage choices - belong to a social class of propertied farmers, and those outside this core, even if they are the siblings of heirs, rarely belong to this social class. The farmers constitute an economic block, a political block, a social class (as is well documented in other studies), and a kinship unit constituted not by consanguinity but by an emergent pattern of structurally endogamous marriages.

Models: Systems, Rules, Strategies and Emergence

17.1

Looking at marriage structure models from the long view, Lévi-Strauss is credited with assimilating both rules and strategies to a Von Neuman-Morgenstern game theoretic conception of society. "Structure" defines the rules and constraints of the games and strategies are taken accordingly. His classification of marriage system models as elementary (= generalized prescriptive rules, 0/1 probabilities constraining strategies) or complex (= limited proscriptive rules, variably probabilistic strategies; semi-complex where the proscriptive rules are maximally generalized to nearly prescribe a distributive structure) does not do justice to cases like the Pul Eliya ([Houseman and White 1998a](#)) which are semi-prescriptive (for blood relatives) with dependence on strategy for the emergence of global structure out of networked interaction. Nor does it do justice to cases like Feistritz ([Brudner and White 1997](#)) where an apparent complexity of open ended marriage strategies (with proscriptions against blood marriages) masks a nearly prescriptive community-level demand with institutional sanctions that causes heirs to farmsteads to marry into a self-defining, and thus a structurally emergent endogamous group -- a strategy that assures farmstead continuities in knowledge and property rights for both heir and spouse.

17.2

Santa Fe Institute perspectives on complexity, while not the subject of discussion here, are more compatible with the findings of the present study that social processes generate emergent structural forms and that some of the stability of living and social systems derives from processes and forms - to use Stuart Kaufmann's analogy - hovering, ever changing, between deterministic order and aleatory chaos.

Conclusions

18.1

The approach to marriage rules and strategies presented here has applications to, and implications for, the study of social class, community organization, wealth consolidation, transmission of political office, elite structural endogamy, ethnic integration, and the testing of alliance theories and specific alliance models in different ethnographic cases. Four such cases were used to exemplify the approach. Characterized as a network problem, and using structurally controlled simulation techniques (using permutation methods) for generating random baseline comparison models for individual cases, the analysis of marriage rules and strategies becomes analogous to log-linear or multiple regression analysis with interaction terms: a statistically decomposable problem.

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Notes

- ¹ It is the phrasing of these prohibitions in terms of lineages that is seen as the link to Crow-Omaha "lineage-skewed" kinship terminologies.
- ² Paths that are not contained in circuits are trees which can always - trivially - be mapped onto a bipartite graph by assigning a simple alternation of connected nodes to supersets.
- ³ There is a consequent dearth of current applications of his programs to the issues of marriage rules and strategies, partly caused by a failure to supply a personal-computer version of the software and perhaps also through lack of motivation given Hammel's (1976b) finding.
- ⁴ This approach is being pursued through a working group at the Santa Fe Institute.
- ⁵ The more standard approach of Monte Carlo estimation is to run many simulations, build a statistical distribution empirically, and then locate where the observed sample is located in this distribution to give a probability estimate. While studies such as that of White et al (1999) used this approach, it is computationally cumbersome and, as in the present case, unnecessary. The computer programs used here can, of course, be used to verify that the present approach converges with Monte Carlo results, but that will not be undertaken here.
- ⁶ If Leach was later stung by Hammel's (1976b) critique, with its mocking title, of the Leach 1951 arguments about MBD as a strategic alliance among the Kachin, structurally controlled simulation using permutation tests provides a means of refuting Hammel's argument concerning particular cases of MBD marriage.
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Appendix: A List of Relevant Computer Programs

A web-site at <http://eclectic.ss.uci.edu/~drwhite/pgraph.html> provides guidance about program availability and documentation:

- PGRAPH - graphs and simulations, sidedness, segmentary dual organization, etc.
- Par-Sim - generates simulated data for p-graphs (available in 2000)
- Par-Calc - frequencies for marriages of blood relatives
- Par-Link - frequencies for two-family relinkings
- Par-Comp (incorporates Fisher tests) - for outcomes based on types (blood or relinking)
- Par-Bloc - analysis of structurally endogamous blocks of marital relinkings
- Par-Side (binomial test) - computes likelihood of sidedness
- Par-Coef - computes inbreeding and relatedness coefficients for individuals in a population

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