

Structural Endogamy and the network *graphe de parenté*

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SUMMARY -- This article, one of a series, approaches the topics of marriage and kinship through a revitalized kinetic structural approach that shifts the primary focus from abstract models of rules, terminologies, attitudes and norms to exploration of concrete relations in a population, analyzed graph-theoretically in their full complexity as networks. Network representation using the *graphe de parenté* (see below) serves as the basis for examining marriage alliance theory, population structure (such as endogamy and exogamy, inbreeding, subgroups), as well as other possible concepts of general sociological interest, including social formations such as classes, strata, ethnicity, and elites (Schweizer and White 1997). This type of potentially multi-layered structural approach extends to the study of structures and processes of actual marriage and kinship *practices* and other forms of social linkage that build off of them. Identification of structure and processes which occur in such networks is enhanced by mapping attributes or dynamic variables onto the armature of the kinship graph. Any number of theoretical questions concerning kinship and marriage may be posed or restated to address questions of the structure of kinship networks, and thus depend upon such analysis for deeper critical insights. The focus in this discussion is specifically on the connections between graph-theoretic analysis and various substantive theoretical questions concerning kinship and marriage networks.

In their very construction, *graphes de parenté* embody a temporal dimension that then provides a processual orientation for the analysis of culturally constructed kinship relations. They lend themselves, using established methods of graph-theoretic analysis, to precise conceptualization and measurement of various aspects of endogamy and marriage structure as they unfold over time. A notable benefit of graph-theoretic representation of kinship and marriage networks -- specifically the *graphe de parenté* -- is their ability to provide a simultaneous and dynamic, yet parsimonious representation of descent and alliance, their interrelations and constituent structures, as well as the structure of a total network of a universe of empirical relations of *parenté* (kinship and marriage). To the extent that kinship alliances are at the heart of group and class formation they tend to provide essential clues to the development of structure and to processes of change. Further, the *graphe de parenté* permits the use of various one-to-one or isomorphic relations between circuits in such graphs and various concepts of theoretical interest. Isomorphisms are the most useful type of mappings with which to explore relationships

between models or representations (as in a graph of a network of relationships) and the phenomena they represent.

I. Structural Background: P-graphs, Structural Endogamy, and Network Structure

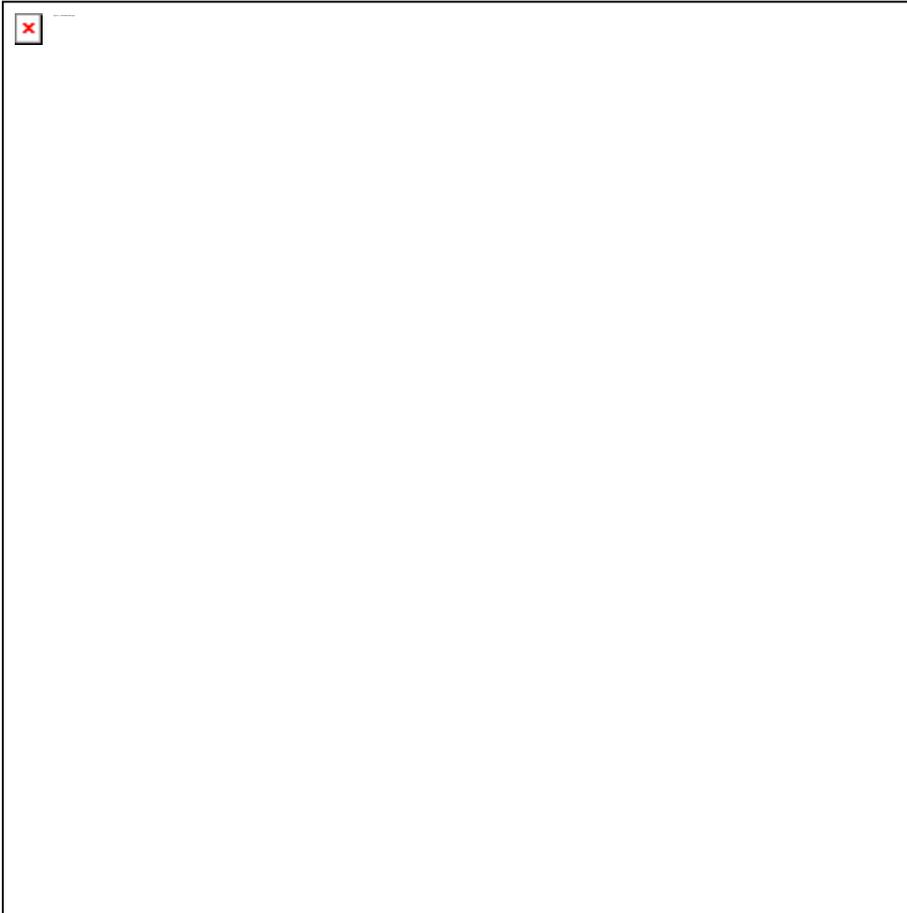
Two basic structural conditions, posed in Lévi-Strauss's (1969) theory of alliance, are fulfilled by the *graphes de parenté* invented by Guilbaud (1970) and much later, following other developments (see Héran 1995), by a more generalized conception of p-graphs (parental or partnership graphs: White and Jorion 1992) as representations of marriage and kinship networks. In the p-graph, where gendered lines for individuals descend from their parental unions and may converge to form new unions, vertices represent states (including absence) of sexual union (marriage, co-habitation, or other coupled states; or uncoupled states of an individual) and lines represent the individuals who connect them either as partners or offspring. Circuits in such graphs (closed paths or semi-cycles that ignore direction of links) satisfy Lévi-Strauss's two conditions, ones that are required for development of alliance theory using the theory of graphs. First, their circuits are suitable to represent *elementary alliances*, while second, except for such exceptional cases as sibling marriage, such circuits are normally absent within the nuclear family. Thus circuits are not ordinarily formed in such nuclear family triads as father-mother-child, as is the case with ordinary egocentric graphs of kinship. Hence, circuits in p-graphs are isomorphic with (always and only found when) one or more of any of the following three alliance conditions (see Bourdieu 1962, 1976; Jola et al. 1970; LaMaison 1979; Segalen 1985; Richard 1993) are present:

- marriage of consanguines, where two persons of common ancestry form a new union,
- *redoublement d'alliance*, where unions linking two co-ancestral lines are redoubled,
- *renchaînement*, where two or more intermarried co-ancestral lines are relinked by a new union.

The cultural contents of kinship, marriage, communication and exchange networks, as dealt with in alliance theory, vary across cultures. However local networks are defined, a part of their structure and temporal dynamic may be compared in terms of p-graphs, which provide a skeletal framework for mapping the field of social relations that derive from sexual partnerships and/or parentage. One series of questions that can be addressed by p-graphs is taken up by Héran (1995) in terms of the structural equivalence of individuals in different groups and kinship positions, and of representing relational parallels (homomorphisms) in marriage structure. Another series of fundamental questions about structure and dynamics, taken up here, is that of how and how much the network of kinship and marriage turns in upon itself in terms of endogamy. Structural endogamy turns out to be a crucial concept for many of the concerns of alliance theory.

Structural Endogamy: The Concept

Structural endogamy is a concept with a series of properties that follow from identifying all the circuits, each isomorphic with an elementary alliance, involving links between people's families of origin and their families of procreation, and defining endogamous units in terms of maximal subsets of such circuits. An exemplary p-graph of Old Testament genealogy, in figure 1, illustrates both the prototype for construction of a network representation of kinship and marriage, and a prototype for the analysis of marriage circuits in such a graph-theoretic representation.



[Figure 1:](#)

[Canaanite marriages](#)

We can read or calculate variable types of marriage structures and study their relationships by analysis of the graph itself. Figure 1 is historically ordered from Terah's marriage at the top to Jacob and Esau's at the bottom: female lines between marriages are dotted to contrast with male lines that are shown as solid if only to emphasize patriliney while not losing sight of bilateral connections. Down-intersections of lines are read as sexual unions or marriages and up-intersections as sibling sets linked to parental couples. It is evident that a union occurred between two children (Abraham and Sarah) of Terah, whose two lines by different wives are shown by a connecting horizontal bar. This marriage (point 1 on the graph) completes a circuit of relationships, and we read from the graph that the marriage was between half-siblings. There are two overlapping circuits at the left where a man produced daughters (issuing from point 2) with whom he mated (Lot

and his daughters coupling at points 3-4). Between these circuits is another where a man married his niece (Haran's marriage-5). The latter's granddaughter married, at point 6, the son (Isaac) of the couple uniting at point 1, Abraham and Sarah. Isaac's son Jacob, at points 7-8, married sisters who, as we read from the circuits above them, are his matrilineal cross-cousins. Finally, in the circuit above point 9, Jacob's brother (Esau) marries a more distant lineage-mate (the daughter of Isaac's half-brother Ishmael).

Figure 1 has two maximal circuit sets, one for the lines representing Lot and his daughters, and the other containing the remaining lines in the graph. These two sets intersect only at point 10, a cutpoint or point of articulation in the graph; the maximal circuit sets contain no such cutpoints. Alliance theory is aided by the fact that maximal circuit sets are discrete and contain all of the elementary alliances of a kinship graph. Structural endogamy thus defines the endogamic blocks of a kinship network, a series of social units each having a complex internal structure.

Within a given kinship network, an endogamic block or endogam is a maximal set of individual-level linkages between couplings such that every pair of couplings are connected by multiple independent paths (none using the same edges) within the endogam. Uncoupled people without children and those whose parent-child ties do not form circuits are isogams, solitary links possibly embedded in chains but not circuits. Endogams and isogams are mutually exclusive, and together make up the graph-theoretic blocks of the network. Isogams may be bridges in a chain of links between endogams, without forming circuits. All the individual-level links (rather than individuals, who may have multiple partnerships) of a kinship network can thus be partitioned into mutually exclusive blocks, each being either an endogam (containing more than two couplings and multiple linkages between them) or isogam (an individual's line that is not part of any larger circuit).

Blocks and endogams, constituted out of kinship links, draw out a concept of precisely defined endogamous social units from what have been thought to be merely statistical or aggregate tendencies towards endogamy. Sociologically, these social units are unusual since structural endogamy generates a partition of the procreative links of individuals but not of individuals themselves. Since the procreative links of an individual may be singular, as in a single marriage, or multiple, as in polygamy or serial marriage, it is possible that the different procreative links of a single individual may belong to different endogamic blocks.

The Graph, its Circuits, and its Blocks

P-graphs are canonical graphs for kinship and coupling. One of their fundamental properties, noted above, is that circuits of ties are formed within individual families only in the case of brother-sister marriage, so that circuits are not a general property or "given" of the kinship graphs. In the p-graph, circuits always represent structural endogamy, or the formation of social units through the "relinking" of families.

Graph theoretically, let H be a connected graph or component. If the removal of a point v disconnects H (or results in a single disconnected point), then v is a cutpoint or articulation point of H. If H contains no articulation point, then H is a block (Hage and Harary 1983:28; Gibbons 1985: 5). A block with three or more points is a bi-component or endogamic block. Two distinct bi-components may share a single articulation point (as in figure 1), but cannot share two or more points without becoming a single block. The graph-theoretic blocks of a p-graph of kinship and couplings (where we consider semipaths of connections, disregarding their direction) partition its lines (or edges) into maximal sets such that any line in a given set is either circuit-connected to all other lines in the set (an endogam or bi-component) or is the sole member of the set (an isogam).

The circuitry properties of p-graphs are of considerable significance. To summarize, first, circuits formed beyond the level of the nuclear family become the "atoms" of kinship, as proposed by Lévi-Strauss (1949), and their concatenations (such as blocks and their substructures) the "molecular structures." Second, graph-theoretic blocks are equivalent to a partition on the edges of p-graphs, leading to unique identification of structurally endogamous units. Third, since graph-theoretic blocks are easily computable in linear time by depth-first search algorithms (Gibbons 1985: 24-30), large-scale kinship networks -- of virtually any size -- can be analyzed and decomposed into their endogamic blocks or constituent units of structural endogamy.

Order and Depth of Endogamy

Kinship networks offer an indefinite social space that connects any pair of people in the world to common ancestors at varying time depths and to matrimonial relinkings of varying orders. To establish relative limits in this space, we define the depth of a kinship circuit as the length of its longest path from descendant to ancestor:

- · Depth-one endogamy is a circuit whose completion is formed with only 1 generational step back to ancestors.
- · Depth-two endogamy is a circuit whose completion is formed within 2 generations of links back to ancestors.
- · Depth-three endogamy is a circuit whose completion is formed within 3 generational steps back to ancestors.
- · Endogamy of depth d is a circuit whose completion is formed with d or fewer generational steps back to ancestors.

The order of a kinship circuit is the number of marriage links that connect all of its common-ancestor groups into a circuit:

- · First-order endogamy is a circuit whose completion is formed by a ("blood") marriage within "family" lines.
- · Second-order endogamy is a circuit whose completion is formed by two marriages relinking or redoubling links between two "families."
- · Third-order endogamy is a circuit whose completion is formed by three marriages relinking three "families."

- o'th-order endogamy is a circuit whose completion is formed by o marriages relinking o "families."

Any connected graph with k edges and n vertices will have $k - n + 1$ elementary circuits (not necessarily unique) which when added together pairwise (with deletion of common edges) will generate all circuits of the graph (Gibbons 1985). The depth d^* of an endogamic block is the (least) longest path from any descendant to any ancestor in some set of its elementary circuits. Its order o^* is the highest number of marriage links among the elementary circuits in some set of elementary circuits having the least depth.

Substantive Meaning of Structural Endogamy

Circuits of relinking of lower-order and lower-depth are more likely to reinforce patterns of consensus or cleavage --ordered structures-- in social behavior. Within a structurally endogamous block composed of living kinship and marriage links, gossip travels through multiple paths from every source to every other node as potential receiver. Multiple paths for the transmission of information that stems from the same source allow divergent lines of transmission to be compared, thus helping to sort out potential lines of friendship and enmity, accuracy and distortion, bias and reliability. A high degree of social 'ordering' is possible within an endogamic block.

Endogamic blocks, moreover, are typically made up of links of kinship and marriage whose concatenations (such as brother of father, father's brother's daughter, etc.) are typically known and labeled not just as individuals, but in terms of roles and expected behaviors. If we contrast the 'stronger' ties of nuclear family or co-resident social units from the 'weaker' ties (Granovetter 1973) concatenated out of intermediary links operative through individuals who were close in times past, then the web of kinship and marriage is one in which relatively distant and 'weak' ties likely to exert a relatively high degree of supervisory sanction.

The nature and strength of ties is also relevant to the present context. Friends of friends of friends, for example, are often unknown (unless they also happen to be friends through transitivity) and unlabelled as a particular kind of alter, and as such, exert relatively little direct influence on one's life, except as a rather impersonal source of diffusion. Chains of close relatives of close relatives of close relatives, such as Fa Br So for example, in contrast to friendship chains, are usually known and labeled, and exert direct interpersonal influences. It follows, then, that structural endogamy -- chains of kinship links reinforced by relinking -- will constitute a social arena in which considerable social influence and drive to consistency or divisiveness is exerted. If we are looking to construct a theory of social practice in the field of kinship and marriage and of the consequences of practice, it is with circuits of endogamously reinforced kinship ties that we might begin to make more precise some of our notions about social influences in kinship networks.

The Problem of Partiality of Endogamic Structure

Kinship networks, if studied empirically, are necessarily partial and incomplete. They are individually and culturally constructed and can be observed from various points of view that embody particular interests. An historian, anthropologist, or demographer might have specific data on a particular community, social strata, class, linked biographies or occupations, from a particular site or set of linked places and time period. The selection of kinship "links" -- of blood and marriage -- so constituted is necessarily truncated, snipped out of a larger context, and is often the result of various types of culturally constructive processes whereby the links in question are manufactured. It is almost impossible to encounter a kinship network in a purely "natural" form, unless we were to identify a population on which we had complete data and which was totally isolated over a long time period. Yet even in these rarefied conditions, kinship links, being defined by culturally constructive processes, would still fail to satisfy a "natural" form.

Yet it is precisely this -- the cultural constructions of kinship relations in a selective setting -- that we are interested in examining. The construction of a p-graph representation of what is known or sampled of a cultural construction of kinship does not assume that the links so named be biologically grounded, but that such relations as are culturally constructed can be cross-checked by multiple methods. Different links may also be imputed by different actors or different sources. There may be multiple alternate constructions of kinship networks in a given setting, and the links may include imputed biological maternity or paternity, adoption, sociological parenting, etc. Nor need we assume that kinship links are purely ascribed ones: indeed, not only marriage but the imputation of culturally valid kinship links of all types may change over time, may be achieved, performative, etc. Hence, in the remarks that follow, we will begin with questions of structure, but return later to consider questions of selectivity, partiality, and comparability of analytic results.

Structure in the Endogam

The kinship networks we are interested in are dynamic ones, with considerable internal variability over time. Here, amid this flux of constructive activity, including the imputation of links by different actors, the utility of being able to identify shifting units of structural endogamy and their emergent structural properties -- endogam structure, substructure and dynamics -- becomes all the more apparent (noting, of course, that high-consensus kinship links might have different structural implications than contested ones).

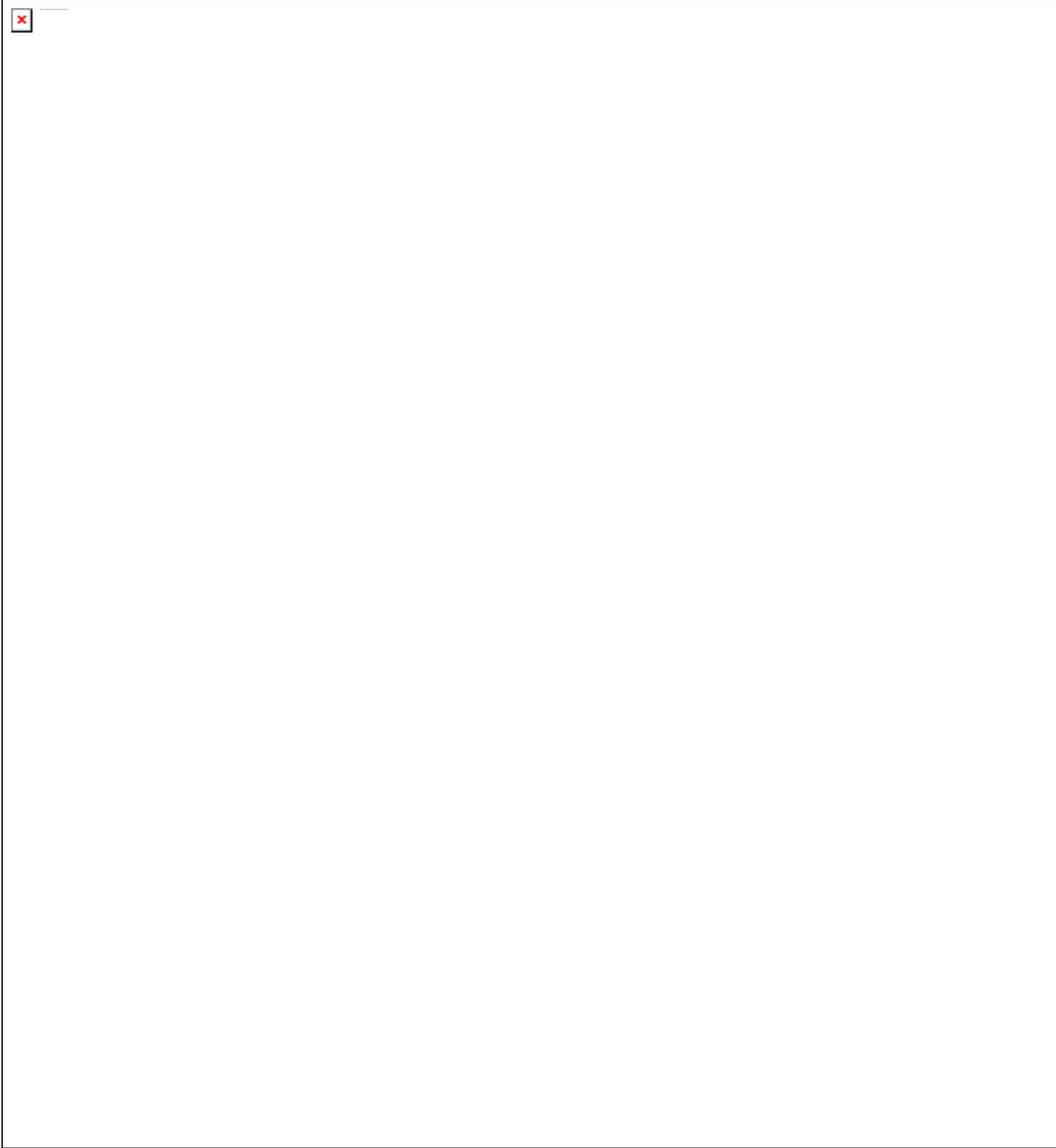
Within the endogamic block there may be additional structural properties that are significant to theories of marriage exchange, alliance, or population structure. Dual organization, for example, may exist in a wide variety of forms that are discernible only with the aid of network concepts of social structure. Dual organization in the matrimonial realm has hitherto been thought to be equivalent to hereditary unilineal moieties, where two halves of a society intermarry while men are prohibited from marrying women of their own half, and moiety membership is either by descent from the father or the mother, or a function of both (as in section systems). White and Houseman (in review; also White and Jorion 1996), however, show that descent principles are unnecessary in that more general forms of dual organization occur that are non-unilineal. Their results are achieved

by definitions of marriage structure that are dependent on the network structure within endogamic blocks rather than on rules of descent. Several examples are given below.

Bipartite and Tripartite Endogamic Blocks

As Houseman and White (1996) define it, an endogamic block is bipartite if couples can be divided into two sets (divides) such that the two parental-couple nodes -- those of husband and wife -- of every couple belong respectively to opposite divides. An endogamic block is tripartite if couples can be divided into three sets such that the two respective parental nodes for every couple never belong to the same set. Tripartiteness is an almost universal property of p-graphs: for it to be violated, four sibling sets must all intermarry. For bipartiteness to be violated, any odd number of sibling sets only need to be remarried in a circle. Bipartiteness is often satisfied vacuously, where there are no circuits at all of marriages among sibling-sets. Where there are such circuits, and the circuits all involve an even number of links, linked couples, or linked sibling sets, bipartiteness is an indicator of matrimonial dual organization, and is a significant property of a social system (White and Houseman, in review). Houseman and White (1996: 71) identify an ethnographic case in which divides (*structure à partage*) are evident in a kinship and marriage network independently of the form of hereditary moieties that dual matrimonial organization is conventionally assumed to take. In this case, a bipartite division of siblings-in-law into opposing sets is politically significant (Houseman and White, in review), but membership in the divides of one generation is not inherited in the next.

A stronger concept of dual matrimonial organization is that of sides (White and Jorion 1996, Houseman and White 1996: *structure à coté*), where the p-graph tends to be bipartite in one set and hereditary in the other. An example is shown in Figure 2 for (virilocal) sides (hereditary in the male line) among the Makuna (Arhem 1981; see also White and Houseman 1997). Sidedness can exist as a tendency in an empirical network, independent of the existence of named descent groups and moiety organization.



[Figure 2: Makuna marriages as a bipartite structure](#)

The strength of the evidence for network concepts such as sides or divides can be evaluated only within a particular structurally endogamous block of relinked marriages, and depends on the number of relinkings within the block as well as their type. Here, as

elsewhere in our discussion of concepts, it is particularly helpful to have a significance test to determine how likely are the observed relative frequencies of different types of relinkings in a random series of equal size.

II. Statistical Refinement and Simulation

The Coefficient of Inbreeding: First Order Endogamy

Biologically speaking, every individual necessarily represents the inbreeding of ancestral stock, and every couple has common ancestral relatives at some depth of remove. This is easily demonstrated for all sexually reproducing populations. At any ancestral generational depth n , the number of distinct ancestral lines is 2 to the n 'th power. At some finite k , this number will exceed the number of members of the ancestral population, hence not all the ancestors in this generation could have been distinct. Assuming a common evolutionary origin of species, it is easy to adapt this proof to the case of any given couple, such as the parents, having ancestors in common.

The coefficient of inbreeding of an individual is equal to the coefficient of consanguinity of the person's parents (Hughes 1988: 23), and weights consanguinity by the degree of relatedness to common ancestors. Thus, first order structural endogamy is measured for any given individual as a weighted composite of circuits of procreative links formed by blood marriage or inbreeding. For any given endogamic block, first order structural endogamy can also be computed in the aggregate. The coefficient of consanguinity between two individuals i and j represents the probability (given common ancestral circuits) that any two alleles at a given locus, one drawn randomly from i and the other at random from j , are identical by descent. This coefficient is measured by a sum of probabilities of inheriting the same allele from each of the couple's common ancestors.

Higher Order Endogamies

Endogamous groups descended from M independent founder couples can breed for $M-1$ generations (for example, each couple producing a son and daughter who themselves live to reproduce) without any inbred (consanguineous) marriages as reckoned from the founder couples. The endogamic order of such a breeding population can also be as high as $M-1$. Structurally endogamous social units can thus be operative at a high order for many generations without generating any biological inbreeding beyond that already present in the founder generation.

Not only does every couple in the p -graph have a coefficient of consanguinity, but every pair of couples has such a coefficient, the average of the consanguinities between the two persons in one couple with the two in the other. The matrix of consanguinities among couples is suitable for analysis of the combined effects of consanguinity and affinity in a population. Hughes (1988) shows how to make use of principal components analysis of matrices of consanguinities among individuals; p -graph consanguinity matrices extend his techniques to the more general problem of clustering of consanguineal groupings that overlap through marriage.

To define a generalized (or structural) coefficient of endogamy for a population, consider structurally endogamous circuits of order k between two individuals i and j , each made up of $m \leq k$ pairs of related individuals who are married in a circuit. Each such pair has a given coefficient of consanguinity, and the *coefficient of endogamy* may be defined as the product of these probabilities, times $1/2$ for each marriage, summed over a set of elementary circuits with a minimum sum of orders. The marital weighting combines affinal linkage in a way analogous to genetic linkage, but extends the idea of linkage from genetic to cultural transmission. Thus, if marriage partners were able to imitate $1/2$ of the common-allelic behaviors of relatives (to give more weight to interfamily transmission where the relinking couples have greater numbers of children we could take as the multiplier the j 'th root of $1/2$ where j is the number of children), then this coefficient would represent the probability of relinked couples sharing a behavior that was partly inherited and partly shared through coupling and learned diffusion. Because the coefficient of k -th order endogamy incorporates lower order endogamous transmission (including that of inbreeding), it will necessarily be higher than the coefficient of inbreeding, and the ratio of the two could represent a potential for cultural reinforcement of learned behavior through social interaction, or paths of potential cultural diffusion through endogamy. We can also partial out the effects of 2nd order endogamy, 3rd order, and so forth.

Exact Tests for Endogamic Bipartiteness

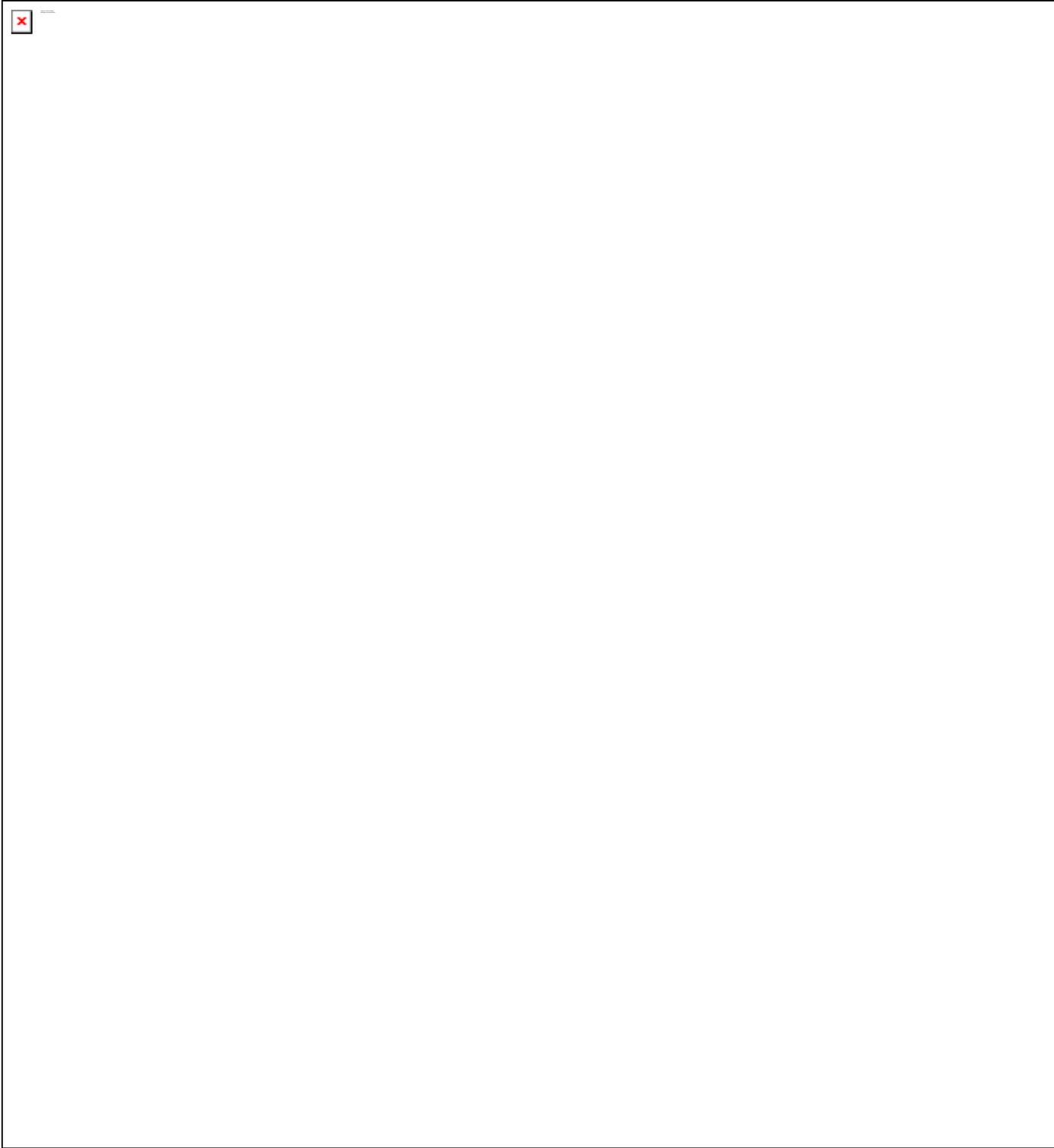
Bipartiteness is an example of matrimonial network structure where an exact probability can be calculated of an observed outcome occurring by chance alone. Each endogamic block of k cross-set marriages among n sibling-sets, for example (or: lineages: in the case of sides), has $k - n + 1$ elementary circuits, and the chance of an even or odd number of links in each circuit is $1/2$. The probability of getting m circuits with an even number of links out of $k - n + 1$ can be determined by a simple binomial test, directly analogous to the probabilities of different observed outcomes of getting a certain number of heads and tails in the experiment of tossing a fair coin. For the Makuna diagram in figure 2, the probability of the observed level of bipartiteness occurring by chance is $p < .0000000002$.

Descent Line Prestation Orderings and Permutation Tests of Prestation Orderings

Figure 3 shows a tripartite graph of Dukuh village marriages (Schweizer 1989; White and Schweizer 1997), but unlike the bipartite graph, the groupings of marriages are not unique, and the structure has little substantive significance. A more interesting model of generalized exchange is a series of descent lines which establishes a directed order for the giving of wives (or husbands) among them. Figure 4 reorganizes the male descent lines of Dukuh village (from figure 3) into a series such that, with one exception (marriage 20: a reciprocal redoubling of links between two lines), there is a consistent direction to the giving of wives (from left to right), and all the marriage circuits (ignoring the direction of links) but for the one exception are of diameter > 2 .



[Figure 3: Dukuh village marriages as a 3-compartment structure](#)



[Figure 4: Dukuh village marriages as a partial order](#)

What is the likelihood p that K marriages among N descent lines will form a partial order, given the distribution of in- and out-degrees of descent lines? It is the likelihood that no directed cycles will form among the descent lines. To consider the independent

combinatorial possibilities, we take every non-cyclic directed path P_d , $d=1, L^*$ (L^* equals the number of all non-cyclic directed paths) of varying lengths ($L=1, N-1$), with endpoints i and j and path length L from i to j for each P_d . For each P_d we calculate the likelihood that a random assignment of j 's descent line outdegree (O_j) will exclude the cycle completed by j linking to i 's descent line, where I_i is i 's descent line indegree. This likelihood of not reaching i 's descent line by one of its I_i indegrees is $(K-L-I_i)/(K-L)$ raised to the power of j 's outdegree O_j , or $[(K-L-I_i)/(K-L)]^{O_j}$. Multiplying these probabilities for each separate P_d , we have:

L^*

$p = [(K-L-I_i)/(K-L)]^{O_j}$, where L , i and j are a function of P_d .

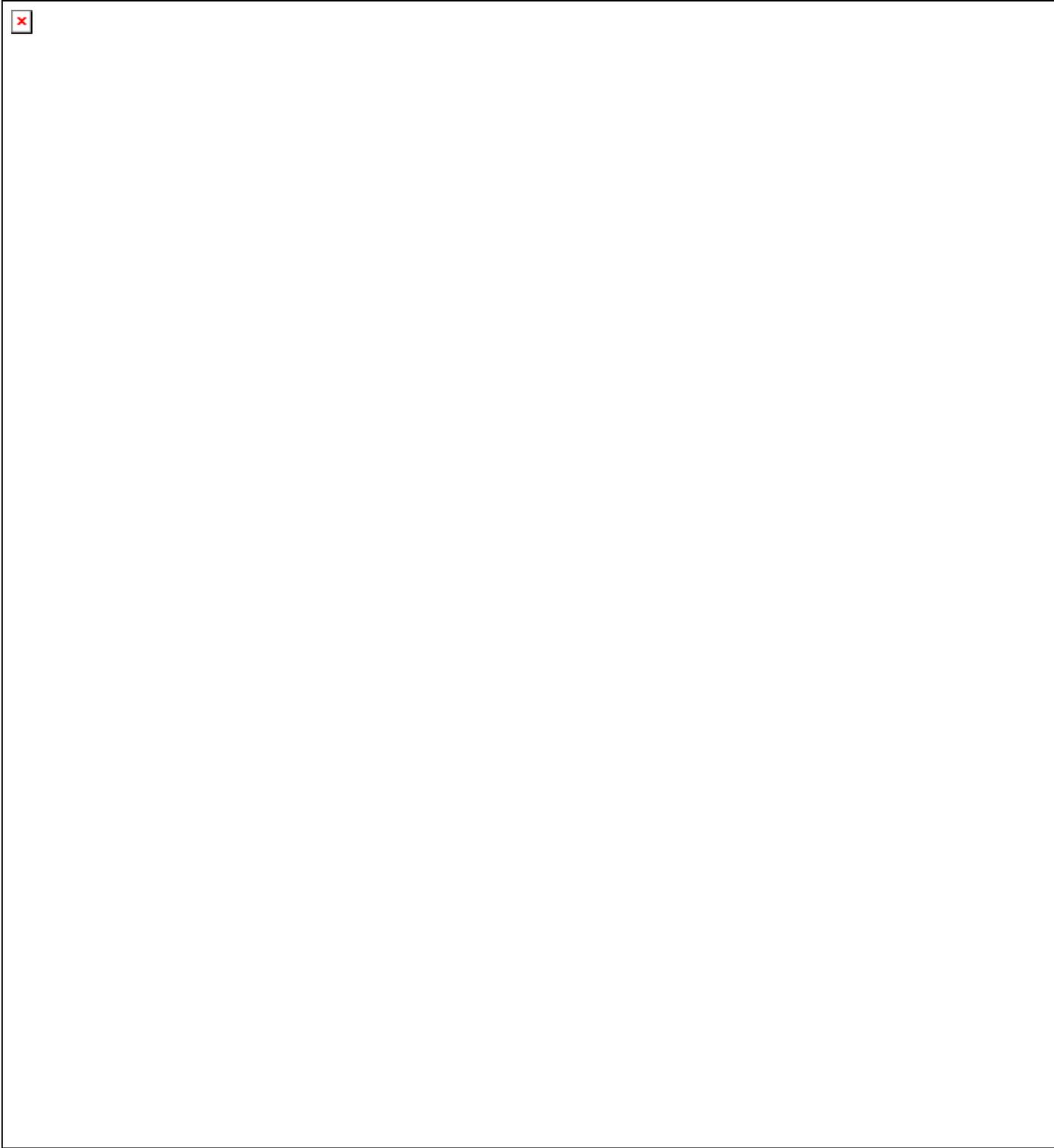
$d=1$

For Dukuh, $p = .15$ for no directed cycles, and the structure has little statistical significance.

Marriage Rules and other Structural Characteristics in the Endogam

While marriages outside of endogamic blocks may satisfy attributional constraints (e.g., relative age, wealth, gifts, payments, etc.) the problem of characterizing "marriage rules" in a social network in relative terms -- as a reflex of social structure, as put by Lévi-Strauss -- is one of evaluating the different types of circuits in endogamic blocks. Different varieties of bipartiteness (realized at a certain level of fit in comparison to an ideal model and of statistical rejection of the null hypothesis in comparison to appropriate stochastic models), for example, can be used to characterize different concepts of matrimonial dual organization (Houseman and White 1996, White and Jorion 1996). What of various tendencies towards certain kinds of blood marriage, favored types of relinking, or tendencies towards tighter or looser endogamic constructions? Certainly, a generic census of all the relative frequencies of all such types of marriage can be made, and their relative incidence can be indexed as percentages of the total number of potential spouses available of each specified type. But given that the network itself is biased in its construction, and that outcomes are potentially biased by certain attributional constraints, how can we identify what might be marriage "structure" against a background of statistical noise?

Consider figure 5, showing kinships among Central American Presidents and politicians, for example, as compiled by Samuel Z. Stone (1990). These data were collected with the intent of showing how the descent of politically important figures of Central American countries such as their Presidents and Congressmen -- indicated by P or C on the p-graph representation by White (1996) in figure 5, from Stone's data as entered for computer analysis by Fabio Flouty -- traces back to a *conquistador* governing elite. Thus, the upward links are all towards linking ancestors, so that the existence of numerous relinking marriages falls out of the method of data collection, but also reflects some degree of structural endogamy among these elites.



[Figure 5: Conquistador and colonial elites of Central America](#)

Controlled Simulation in and of Endogamic Blocks

How can we compare networks, each of which is a potentially different cultural construction of kinship in a setting that is selective according to different criteria, different types of missing data, or different boundary conditions? One way to do so is to normalize comparisons by fitting the number of observed marriage relinkings to observational parameters for different samples of a population, as done by Richard (1993), using the exponential family of curves. The parameters of these fitted curves then become more comparable across populations because they are adjusted to the network "contexts" that may result from differences in methods of data collection. The approach taken here, however, is to compare observed structures in terms of how they differ from a random baseline model that takes the constructive and selective criteria as constants. This strategy is able to evaluate how the occurrence of different kinds of circuits differs from random baseline expectations.

In evaluating structural tendencies by comparative simulations, validity is improved where a maximal number of observed empirical features are controlled in the simulation model. The simplest way to do this is to use permutations to randomize a feature under study, while holding other features constant, that is, to compare actual distribution to permutation tests. A general strategy of "self-simulation" for kinship networks, for example, is to hold constant the numbers of couples and the female links that connect them, and within each generation of sibling sets (defined by the generational level of parental nodes), to permute the male links holding constant the size and makeup of sibling sets and the distribution of multiple marriages. We might also choose to impose other constraints to improve the validity of the comparisons required. This strategy simulates the potential pool of marriage partners within each generation, at least of those recalled or constructed by the methods of data collection. Constraints might include different rules of exogamy or attributional preferences, comparing outcome distributions with those observed. Another strategy is to constrain the observed pool of potential mates only by attributional preferences. By comparison of these two types of simulations against observed outcomes, the relative importance of relational constraints versus attributional constraints could be determined. More "elementary" as opposed to more "complex" systems might be defined as those with more weight on relational over attributional constraints.

Randomization by this means of Samuel Stone's (1990) Central American data, compared to the actual data shown in figure 5, provides a means of testing whether the actual relinkings among these political elites occur in fewer generations than expected by chance, given the method of data collection. Relinkings through the few apical ancestors chosen to demonstrate kinship linkages are not of direct interest here. Rather, the other relinkings that occur within shorter generational spans may be seen to be either a product of a random process, or of a real social bias within this group of elites towards structural endogamy. Hence, if the number of these relinkings exceeds those of the random-linkage simulation, then we have definite evidence of a tendency towards social closure through marriage among the political elites. Given the bias of the data collection exclusively towards ancestries (where data on siblings or ancestors' siblings and their spouses were not collected unless they were prominent politicians), however, the data on relinking within a single generation (which would require sibling and sibling-in-law data) will not

have been assessed. Similarly, within a few generations, many actual relinkings through siblings of ancestors have been eliminated. The pattern of 'excess relinking' needed to establish evidence of structural endogamy among these elites would only be expected to show up in examining relinkings through linking ancestors three or more generations back.

Table 1 shows the results of the comparisons between patterns of actual and randomly simulated marital relinking of the Central American political elites. The results conform to methodological expectations about the effects of ancestor-only biases in the data collection: there are no relinkings within one, two, or three generations, either in the actual OR the simulated data. This does not mean that there would not be such relinkings if complete genealogical data were collected, but is an artifact of the data collection method. For relinkings within 4, 5, 6 or 7 generations, there is evidence of non-random relinking, irrespective of which generation is taken as a reference point to assess relinkings within a certain number of generations ancestral to it. Over all reference generations, as shown under the "Totals" of the data in Table 1, relinkings within 4 or 5 generations occur at more than twice the rate (213 to 227 percent of that) expected by chance. At 6 and 7 generations the rates of relinking fall back to 24-37% higher (124-137%) than expected by chance. Beyond this (9-12 generations back), the actual relinkings fall back at or below (e.g., 95-96%) the rate expected by chance.

Table 1: Comparison of Relinking Frequencies for Actual and Simulated Data (*=greater than chance), from White, 1996 'Enfoque de Redes,' Estudios Demográficos y Urbanos

			1	2	3	4	5	6	7	8	9
10	11	12									
Starting from:											
Present generation											
Actual			0	0	0	0	15*	58*	66*	141*	162
197	236	261									
Simulated			0	0	0	6	11	31	43	105	175
215	231	263									
Back one generation											
Actual			0	0	0	5	28*	36*	115*	125	153
192	217	233									
Simulated			0	0	0	5	5	30	92	149	196
212	244	261									
Back two generations											
Actual			0	0	0	13*	24	89*	99	132	171
199	215	236									
Simulated			0	0	0	0	23	77	104	161	179
219	236	266									
Back three generations											

Actual			0	0	0	7*	11*	55*	70*	99	142
170	187	208									
Simulated			0	0	0	0	4	34	54	129	147
188	205	223									
Back four generation											
Actual			0	0	0	4	12*	17	53*	100*	
122*	142*	167*	185								
Simulated			0	0	0	4	4	31	45	69	115
136	158	186									
Back five generations											
Actual			0	0	0	5*	10*	10*	29*	78*	
107*	133*	151	152								
Simulated			0	0	0	0	0	0	11	63	92
115	145	149									
<hr/>											
TOTALS			1	2	3	4	5	6	7	8	9
10	11	12									
Actual (A)			0	0	0	34	100	265	432	675	857
1043	1173	1275									
Simulated (S)			0	0	0	15	47	203	349	676	
904	1085										
Ratio A/S-			n.a.	n.a.	n.a.	2.27	2.13	1.31	1.24	1.00	.95
.96	.96	.95									

It does not seem plausible that members of an elite would consciously, by some preference for endogamy, choose to marry others just because they were descendants of conquistadors: the set of such descendants is too large, would hardly be restricted to elites, and would be difficult in any case for people to know. Nor would people be likely to marry so as to relink with other elite families where the relinking ancestors only occur 4 or 5 generations back. People would probably not be cognizant of such ties: they are too far back. The method of data collection in this case, however, suppresses the occurrence of 'close' relinking marriages within 1-3 generations by systematically neglecting to collect genealogical data on the siblings of the reference population. The methodological suppression of evidence for 'close' relinkings, however, would not displace relinkings through more distant linking ancestors. This is exactly what the simulation comparisons show. Hence, the argument about elite endogamy in this case is that these results show by implication that these elite circles are highly likely to be relinked in fact (if the data were complete) within 2-3 as well as 4-5 generations, but also that the true rates of relinking would be much higher than those observed. People in an elite social circle are very likely to know precisely if and how they are related to others by genealogical ties (blood or marriage) within the past few generations, hence a preference for relinking is plausible as the only reasonable explanation for the results in Table 1. Hence, it is entirely reasonable to infer from these results that there is strong evidence for preferential structural endogamy among Central American political elites.

A Generalized Measure of the Order and Depth of Structurally Endogamous Relinking

Statistics for the assessing how marital relinkings are organized within a population can be further refined by extending the approach shown in Table 1, in which the number of marriages are computed that are in structurally endogamous blocks of varying generational depth, and starting at different generational reference points. Each of these varying structurally endogamous blocks, differing by reference generation (the rows of Table 1) and by generational depth (in the columns of the table), has a distinct number C of elementary cycles (computed, as above from $k-n-1$, where k is the number of links in the block and n is the number of marriages in the block) and a certain number R of relinking marriages. Hence the ratio R/C is the average number of relinking marriages per elementary cycle, or average relinking order (see section I, Order and Depth of Endogamy) of the block. If this average were close to 1 it would mean that most of the relinking is through blood marriages. If it were close to 2 it would mean that the average relinking order is that of relinking (redoubling ties) between two families; if 3 then that between three families, and so forth. Similarly, for each relinking marriage in a block, we can compute the distances linking or apical ancestors for that block, and hence the average generational depth of such distances for a given block.

The average of relinking orders (O) and generational depths (D) of different structurally endogamous blocks define the size of the 'structural holes' inside the circuits of kinship and endogamy. The average circuit diameter is $2*O*D$. If O is close to 1 and D is small, then the block has high inbreeding. If O is between 2 and 3 and D is 4 or less (as with the Central American data), inbreeding is low but relinking is preferential if it departs from a random model. The parameters O and D , along with their departure from randomness (which can be precisely determined, but is not taken up here), and the number and size of structurally endogamous blocks, can be used to characterize the gross morphology of marriage systems in different populations.

III. Importance of Structural Endogamy for Class, Ethnicity, and Complex Societies

Social Class

Social class, as "a general way of life, a sub-culture, tends to be hereditary because (a) individuals from the same sub-culture tend to intermarry, and (b) parents bring up their children to imitate themselves" (Leach 1970). Yet to this same author: "The endogamy of English social classes is a tendency only and the groups so formed are ill-defined and unnamed." What if, however, we were to examine the extent to which particular social class formations were concomitant with structural endogamy of a certain order and depth, as a precisely defined conceptual unit? We would expect that families involved by this route in social class formation would have an idea of "good families," "suitable matches," etc., that reflect some notion of affinities among a potential intermarrying set of families, but that not all the children of the class would be "required" to marry within the class. Rather, social class inscription would take place through the diffuse agency of relinking by marriage, which could both validate the social standing of the individual and

constitute the diffuse but relinked social unit -- endogamic block -- of class formation. How would it be possible to validate or verify such an hypothesis? One way is by showing a match between the selection of certain children to be heirs -- e.g., by inheritance -- to class standing, as correlated with relinkings through marriage. Simulation within the endogam might show the internal marriage distribution to be close to a perfectly randomized marriage "market," while simulated permutation tests across distinct endogamic blocks would show a marked divergence from randomness contrasting with distinct memberships that correlate with "class standing." The first two steps in this sort of validation (but not the third, since data were lacking) were taken by Brudner and White (1997) in their study of Austrian intra-village class stratification.

Simulating Complexity: Exploring Structural Endogamy Hypotheses

The class system of Slovenian farmers in Carinthia studied by Brudner and White (1997) encourages by its particular character the selection of appropriate marriage partners through relinking families holding the heirships to farms. Since people can build on knowledge of past to shape their social network, is relinking itself a strategic variable, and a type of preferential marriage? If so, would such a case undermine the understanding of European marriage alliance systems as *complex* in Lévi-Straussian terms: based only on norms that *prohibit* certain marriages, such as the Catholic ban upon blood marriages up to cousins of depth three in collaterality, rather than defining ideal categories of marriageable persons as a reflex of kinship and social structure?

To test the hypothesis that rates of structural endogamy might depart from random expectations, the sizes of structurally endogamous blocks at varying generational depths, starting from different generations in the actual population, are compared to random baseline simulations, taking care to exclude sibling and first and second cousin marriages to simulate the actual population constraints in terms of proscriptive marriage norms. Table 2 shows the results starting from each of the last three generations. Starting from the present generation in which data were collected (ca. 1970), and examining blocks from one to 12 generations in depth, these comparisons show that the size of the core in the actual network is significantly larger than in the baseline models, but only within blocks with a generational depth of 3 or less. Starting one generation back, where the ancestral data is thinner, we find a similar result but only up to a generational depth of 2. Starting two generations back, in spite of the thinning of the retrospective data, the absolute numbers of marriages in the endogamic blocks are higher, and include a good deal of relinking within a single generation; again the results differ from simulated data to a depth of 2 generations. Summing the results from these three reference generations (the Totals in Table 2) there is a very high degree of relinking among sibling sets in a single generation, and actual relinkings within two generations occur at 63% over the expected rate under random simulation, dropping to 14% excess within three generations and to random levels thereafter.

Table 2: Comparison of Relinking Frequencies for Actual and Simulated Data (*=greater than chance), from Brudner and White, 1997 'Visualizing Networked Histories,' Theory and Society

			1	2	3	4	5	6	7	8	9
10	11	12									
Starting from:											
Present generation											
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									
Back one generation											
Actual			8*	58*	168	246	308	339	353	366	380
389	395										
Simulated			0	18	168	255	320	347	366	372	381
381	387										
Back two generations											
Actual			26*	115*	178	243	278	292	305	319	328
334											
Simulated			0	98	194	262	291	310	316	325	325
331											
<hr/>											
TOTALS			1	2	3	4	5	6	7	8	9
10											
Actual			42	189	416	678	843	949	1007	1048	
1084	1113										
Simulated			0	116	364	700	884	992	1047	1079	
1094	1109										
Ratio				1.63	1.14	.97	.95	.96	.96	.97	.99
1.00											
			42/0								

These results (from Brudner and White 1997) help to show that structural endogamy in this case plays a central role in heirship and class formation. The structurally endogamous couples tend to be highly correlated with farmstead heirs in the actual data. Relinking of marriages with close generational depth is important as an emergent variable in terms of who qualifies for heirship in a potential group of siblings. Here, then, is support for the idea that structural endogamy might provide a clue to marriage patterns, rules, and strategies in marriage systems whose demarcation as "complex" is called into question. Richard's (1993) assumption that relinking is significant only within people's memory of actual genealogical links, say within a depth of four generations, is borne out by the Austrian study: both studies are indicative of strategic agency towards relinking by preference, if not a prescriptive ideal. While he examines only second-order relinking, whereas the latter study includes relinkings of higher orders, he also finds occupational correlates of relinking which are likely concomitants to differential social class formation in French villages.

Alternately, we might examine the family-dominance hypothesis of heirships as a strategic variable that translates into certain families placing their descendants in farmsteads in subsequent generations in excess of the distribution of ancestral dominance expected in a random marriage market. Since people are not generally able to shape the future for successive generations of descendants, one might expect this hypothesis not to be confirmed. Indeed, when the distribution of differential genetic contributions of couples to the population (the sum of their fractional contribution through their descendants to the genetic makeup of individuals in the population) is compared to the distribution expected under the hypothesis of a random marriage market, the dominant-family hypothesis supported. Comparisons to the actual distribution were made for two random baseline models, one where females are held constant, and male links randomly permuted, the other where female links were permuted. In either case, the genetic dominance distribution acts as a random variable.

Ethnicity

Many of the markers of ethnic identities -- foods, distinctive behaviors, symbolic loyalties, etc. -- are strongly reinforced by diffuse kinship networks and intermarriage. If models of class formation can be provided or validated in some historical contexts by the construct of endogamic blocks, what about models of ethnic-group formation? In network terms, the mapping of endogamic units onto alternate and potentially cross-cutting types of social constructions is a highly complex undertaking. Principal components analysis of p-graph consanguinity matrices (see "Higher Order Endogamies" above) may prove a useful technique for identifying social aggregates that share various degrees of endogamy. By using the measurement of the pairwise coefficients of endogamy between couples, zones of intensification of endogamy may be identified that are not only marked by local spikes for groups or couples, but by patterns of cleavage and intensification across the matrix of couples. A multivariate dimensional analysis may map more easily onto alternate social constructions.

Elite Networks: Governors, Owners, Traders

Kinship and marriage are largely ignored as dynamic and causal phenomena in modern society given the myth that industrial society has reduced the role of the family and that the state has crumbled extensive kinship structures. Families, however, do not operate in isolation, but in networks: networks of weak as well as strong ties, ties that overlap in other institutional contexts. As Robertson (1991) demonstrates, networks of families use other institutions to do their work. Opposed to the myth of kinship's demise are innumerable studies of elites (see Baltzell 1989, Domhoff 1983, Lundburg 1940, Mills 1956, Myers 1911) and social class formation, in which family networks tie into institutional settings involved in the reproduction of family, social class, and other network structures. Stone's (1990) example for the region of Central America shows the operative strength of family networks in governance, ownership and trade as a holdover from the precapitalist period, and the present analysis of his data (Table 1) shows a definite preference towards close relinking among political elites. Curtin (1984) demonstrates the dependence of mercantile trade on family networks in the classic

civilizations up to the modern era. His thesis that the role of kinship networks in international trade terminates after 1800 is eminently arguable. Berkowitz (1975), building on elite studies such as cited above, goes further to provide an analysis of the nineteenth century transformation of "family capitalism" via the incorporation of elite family networks into the modern institutional banking and corporate structures. His recent work with colleagues (see Berkowitz and Fitzgerald 1995) shows how to trace contemporary corporate ownership back to large scale enterprises that may be linked as networks of economically dominant families.

IV. Conclusions

If concepts such as structural endogamy offer an analytic framework for examining empirical networks of interest not only to alliance theory but to contemporary study of large-scale political, economic and kinship networks, care clearly must be taken not to sidestep the issues of the content of cultural constructions such as the relations of kinship, family, economics or politics. There is no suggestion here that one single approach replaces another. Schneider (1984), however, critiques the imposition of a naturalizing biological ontology to the "kinship" constructions of "other cultures" and ends with asserting the non-existence of kinship as a valid comparative category or substantive universal. White and Jorion (1996) respond by an extensive critique of Schneider's conceptual confusions, but argue that the full cross-cultural panoply of culturally constructed concepts and relations of kinship can be variously and validly represented for comparative purposes as well as for case-by-case analysis within a comparative framework.

In some basic sense, however, the advantage of network analysis as a starting point is that it allows the much vaunted relations between form and content, structure and function, to be explored within a theoretical framework that can view structure as emergent and dynamic, constituting locally and temporally variable contexts for social actions and further decisions for social actors. Linkages and patterns of linkages within the network can provide a basis for explaining how action is organized, how resources are transmitted, how outcomes are shaped by shifts in the historical social context. Within this context, a grounded theory of practice can be developed in which the specific role of social context and linkages are taken into account as a basis for social action.

Can the approaches outlined here and in the related series of studies aimed at the revitalization of kinship studies (Brudner and White 1997, Houseman and White 1996, 1997, White and Houseman in review, White and Jorion 1992, 1996, White and Schweizer 1997 -- but see also Richard 1993, Leach 1961, Turner 1957) actually achieve this goal? The elements developed in this approach are similar to those of social networks more generally, but they also go a step further in enriching our understandings of complex systems of network embedding. These elements are briefly reviewed below.

First, the graph-theoretic structural approaches taken here open up the study of social structure and organization in a way that allows us to keep in focus the relations between population structure, patterns of marriage alliances that shape that structure, and resultant

social formations such as classes, strata, ethnicities and elites. In doing so, we can focus as well on actual kinship and marriage *practices* as well as the abstract models of rules, attitudes, symbolic structures and norms that have been the hallmark of structuralist approaches to the subject matter through the simplifying codifications of mentally abstracted models. The approach taken here, in contrast, starts with concrete relations in a population, in their full complexity as networks. It allows us to study both culture (e.g., the formation of norms and the broader processes of cultural transmission) and agency (e.g., non-random and purposive behavior such as the local tendency towards population closure through marital relinking) within the variable and shifting local contexts of larger social networks (see Emirbayer and Goodwin 1994 on "networks, culture and agency") whose *concrete form* is represented at the level of a population (with both internal and external linkages). The network approaches discussed in this article are well suited to analysis of kinship and marriage alliance components of large-scale networks of various sorts. They represent a start at a joint mapping of aspects of social structure that are too often kept apart.

Second, the representation of the phenomena of kinship and marriage as a network is itself significant, in that the p-graph unifies into a single graph-theoretic framework a study of the relations of alliance and descent, their constituent structures and their interrelations, and a total network of a selective universe of empirical relations of kinship and marriage. The p-graph, however, is merely an armature for the study of emergent *structural form* in a network of relations which are necessarily ordered in their temporal sequence (e.g., "parents" preceding "children"; parental couplings preceding those of their children). The analysis of such networks proceeds on a practical and analytic basis rather than on a structural "mental architecture." The graph-theoretic analysis is of complex networks that are isomorphic with inter-individual relationship. Cultural assumptions about or constructions of the content of kinship or coupling are not implicit within the graph but are external to it: the contents of kinship and marriage vary cross-culturally and intraculturally, but their relations can be mapped onto the graph for an inspection and analysis of the larger patterns or forms of the *relations among their relations*. Hence, the graph itself represents a higher order of abstraction concerning "social structure" even while representing the empirical complexity of a full network of relations in a population. Further, the p-graph armature can serve as a basis for mapping other relations and attributes in a dynamic of processual representation of social structure in its full complexity, where simplification of form and process is achieved analytically rather than *a priori* as in some of the earlier structuralist approaches (e.g., both by Radcliffe-Brown through role relations and by Lévi-Strauss through mental templates).

Third, as in network studies generally, the graph-theoretic framework allows formal concepts and measures to be defined that tap different aspects of social structure and process. The present discussion has not been concerned with such concepts as centrality, position, group cohesion, etc., that typify network studies (see, for example, Wasserman and Faust 1994), but with isomorphisms between structural forms and certain concepts fundamental to the study of social structure in human populations: particularly, structural endogamy and its component forms of relinking (dual and tripartite organization,

prestation orderings, marriage rules, covariational structures of inbreeding and endogamy) through kinship and marriage.

Fourth and last, these concepts, and the array of statistical tools provided, allow a complete analytical evaluation and statistical decomposition of the sources of structure in kinship and marriage networks: a spectroscopy for identifying the generational depths and orders of relinking by which structurally endogamous units are generated by purposive social action that departs from expected random baselines in populations having characteristic reproductive constraints. Within this "structural spectroscopy" we can identify, as particular subtypes of structural endogamy, the tendencies for different kinds of proscriptive marriage norms on the one hand, and for purposive agency to be oriented towards different types of marriage strategies or preferred or prescriptive marriage rules on the other. The simulation methods outlined above are particularly important for testing statistical hypotheses and for establishing comparability across different cases where the types of population and methods of data collection vary radically (see also Richard 1993). P-graph permutational methods offer a much simpler approach to simulations than conventional methods. Among the important empirical results established in the present paper are concrete demonstrations of marriage preferences towards close relinking (structural endogamy) among political elites in Central America and among a farmstead rural elite (heirs and their spouses) in an Austrian village with single-heir inheritance of half of the farmstead value, but where reductions of the value of estates through inheritance are partially compensated by wealth reconsolidation through relinking marriages. A significant new means of establishing comparability among case studies of marital relinking is added -- beyond those provided by Richards (1993), and even when data collection methods differ radically -- by the present simulation methodology.

Structural endogamy, among the concepts for an analytic and statistical decomposition of the networks linking marriage practices in a population, is crucial as a means of identifying relevant social units within a given social field of study. It emphasizes identification of sub-units in networks whose properties have substantive relevance to the social sciences as in the study of class and social strata, ethnicity, and elites. Structurally endogamous social units are not closed social compartments, but fundamentally open structures which at any point may link to other units or to an exterior social environment. Hence they are themselves dual structures, with both an interior structure and a pattern of external linkages. Structural endogamy and the *graphe de parenté* may help us radically to reconstruct the conceptual bases of social structure. Thus, it is important to examine how the population units identified by structural endogamy differ from conventional social classifications. Blocks of structural endogamy can be identified that take into account only those circuits of relinking that are within a generational depth and order of relinking established statistically as non-random outcomes of social agency. Once the rules governing the construction of blocks through social agency are identified, the blocks partition the *relations* in a total network into precisely identified, discrete and non-overlapping units. These units, however, are not like those of social groups as conventionally classified. In a p-graph, the relations categorized into blocks represent the different reproductive alliances of individuals, not the individuals themselves. Hence, an

individual could be a member of more than one block (or social class) by virtue of different marriages. Further, certain marriages may be pivotal in that they connect different blocks (or classes) through their constituent family members. Thus, if we are able to understand certain social formations -- such as classes, strata, ethnicities or elites - - through an analysis of the structural endogamy of blocks and circuits, it will not be along the lines of conventional typology-building but by understanding much more complex forms of relational embedding and overlap in social contexts.

Acknowledgments

All of the software used in these analyses is available as MS-DOS shareware with a manual at the distribution web site <ftp://eclectic.ss.uci.edu/pub/drwhite/pgraph>. Ego2cpl.exe converts raw genealogy and social attribute data to pgraph format. Pgraph.exe creates graphics, does analysis and simulation (and creates simulated datasets), and outputs data in usable formats for UCInet software, HPGL printers, and HGL files that can be converted into word-processor graphics by PaintShop Pro. Par-Calc.exe produces statistical output on kinship structure and frequencies of different types of marriage. Par-Comp.exe compares actual and simulated datasets in order to compute the statistical significance of deviations between them for different types of marriages. Par-Side.exe computes binomial tests for evaluating bipartite structures. Par-Bloc.exe computes relinking frequencies for actual or simulated datasets (as in Tables 1 and 2). Much of the software was written under a Bourse d'Haute Niveau from the Ministère de la Recherche et de la Technologie to work with Alain Degenne and others at CNRS-LASMAS, a NSF BNS93 research award, or with support from a Leibnitz award to Professor Thomas Schweizer. Special thanks to William Fitzgerald, Thomas Schweizer, Patricia Skyhorse, Lilyan Brudner and John C. Welchman for suggestions in revising the manuscript.

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