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RING COHESION THEORY IN MARRIAGE AND SOCIAL NETWORKS

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RÉSUMÉ – Théorie de la cohésion par les renchaînements d'alliance dans les mariages et les réseaux sociaux

Une théorie de la cohésion sociale peut être développée à partir d'une approche structurale : « Les recherches structurales sont apparues dans les sciences sociales comme une conséquence indirecte de certains développements des mathématiques modernes, qui ont donné une importance croissante au point de vue qualitatif, s'écartant ainsi de la perspective quantitative des mathématiques traditionnelles. Dans divers domaines : logique mathématique, théorie des ensembles, théorie des groupes et topologie, on s'est aperçu que des problèmes qui ne comportaient pas de solution métrique pouvaient tout de même être soumis à un traitement rigoureux. Rappelons ici les titres des ouvrages les plus importants pour les sciences sociales : Theory of Games and Economic Behavior, *de J. von Neumann et O. Morgenstern (1944);* Cybernetics, etc. *de N. Wiener (1948) ;* The Mathematical Theory of Communication, de *C. Shannon and W. Weaver (1950). »* [*Lévi-Strauss,* Anthropologie structurale, *chapitre XV : « La* notion de structure en ethnologie *»*, *1958, p. 310*].

MOTS-CLÉS – Réseaux de parenté, Renchaînement d'alliances, Cohésion sociale, Endogamie.

SUMMARY – *Ring cohesion, as a theory relevant to social cohesion, offers itself in the analysis of matrimonial relinking as an outgrowth of a structural approach: "Structural studies are, in the social sciences, the indirect outcome of modern developments in mathematics which have given increasing importance to the qualitative point of view in contradistinction to the quantitative point of view of traditional mathematics. It has become possible, therefore, in fields such as mathematical logic, set theory, group theory, and topology, to develop a rigorous approach to problems which do not admit of a metrical solution. The outstanding achievements in this connection – which offer themselves as springboards not yet utilized by social scientist - is to be found in J. von Neumann and O. Morgenstern, Theory of Games and Economic Behaviour; N. Wiener, Cybernetics; and C. Shannon and W. Weaver, The Mathematical Theory of Communication".* [*Lévi-Strauss,* Structural Anthropology, 1963, *Chapter XV*, Social Structure, section on "Structure and Measure", p. 283].

KEY-WORDS – Kinship network, Family relinking, Social cohesion, Structural endogamy.

1. INTRODUCTION

What are the basic forms of reciprocity by which strong ties and structural forms of social integration are constructed through marriage? Lévi-Strauss (1969 [1949]) classified forms of elementary marriage cycles created by cousin marriage in terms of their implications for social cohesion, that is, how patterns of marriage integrate social groups. Reciprocity can take the form of a cycle of direct exchange, either delayed, as in

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A _ B _ A, or immediate, as in A _ B. Alternately, it can take the form of a cycle of indirect or generalized exchange, A _ B _ C _ … _ A. This kind of question leads to examining actual patterns by which marital links between families create some of the observable social network patterns of cohesion, especially those involving cycles.

Noting Goldenweiser's [1913] complaint of the impossible complexity of kinship networks, Lévi-Strauss [1969, p. 125] argued that because human beings cannot cognize this "apparent and impossible complexity" in the network patterns of kinship systems, they must formulate their models of social structure, like the analyst of social organization, in terms of rules. Rules, and the strategies for using them, could thus form a game in which social structures are seen to evolve by transformations of rules and how they are employed or applied. "Structure" defines the rules and constraints of the games and strategies are taken accordingly [White, 1999]. This remains a powerful model of social structure and evolution. This study shows how to use network analysis to account for marriage preferences that are not necessarily based on discrete rules, and how to give a more useful and more powerful statistical account of preferences that incorporates discrete rules as well as probabilistic preferences. It offers a more precise and conceptually intuitive accounting of the complexity that underlies kinship networks and their formation, and of the forms of cohesion that result from kinship dynamics.

Elementary structures were for Lévi-Strauss those formulated by rules that took a closed form: a marriage rule for a class of relations that one should marry. "Semi-complex" structures were those that specified a class of proscriptions for whom one should not marry that were sufficiently broad and organized as to entail as an effect a class of marriageable relations, also of closed form. The "complex systems" were those with merely statistical tendencies, preferences or avoidances as to whom to marry or not.

Studying cycles in a network reopens questions about complexity in a very different way than the presupposition of structural analysis that complexity lies in the nature of the rule, mechanical, statistical, or intermediate. Network analysis applies statistical analysis to the network itself as a complex entity, regardless of how the 'rules of play' are apprehended by the anthropologist or articulated by the players. Very different results about types of complexity are the result. This approach – developed by Houseman and White [1998(a,b); White and Houseman, 2002] in a 'theorie de la pratique' applied to kinship networks – is also a requirement of any study of statistical effects of different variables on marriage choices.

One way to study the contribution of marriage cycles to social integration and the forms of reciprocity – and to how prior relations affect actual marriages – is by developing a calculus for the occurrence of such cycles in a marriage network. Early attempts to do so, such at the analysis of Purum marriage cycles by Das [1945], failed to develop an adequate calculus, and were critiqued by Schneider [1965][2]. One of the goals of the present paper, embedded in a theory of ring cohesion, is to develop a calculus appropriate to kinship and marriage networks.

[2] Empirically oriented Anglo-American anthropologists tended to shy away from such studies following Schneider's critique or in avoidance of structuralist assumptions, while French anthropologists continued to study kinship and marriages networks using the vocabulary of a logico-deductive framework of structural thinking and without adopting a network framework for the empirical analysis.

1.1. DEFINITIONS AND THEOREMS

To pose basic research questions, graph theoretic definitions are required. A *digraph* D = <V, P, T> is a set V of nodes (vertices) and a set P of ordered pairs in V classified by a set T of types of pairs. The different types $k = 1,t$ of pair relations P in (V x V) are called *edges* if all pairs of this type are undirected ties (e.g., siblings) and as *arcs* if any of its type are directed (e.g., parent/child)[3]. A *graph* G = <V, P, T> is a digraph with the restriction that all relations P in (V x V) are edges. A *subgraph* of a graph G is a graph having all of its nodes and edges in G. An *induced subgraph* <S> of a graph G is a subgraph of G having the set S of nodes in G plus all the edges in G in the subset of pairs <S x S>. A *path* and a *cycle* are two types of series of alternating nodes and edges in which each edge connects the two nodes to which it is adjacent in the series: in a *path* no nodes are repeated*;* in a *cycle*, the first and last nodes are identical but no other nodes are repeated. A *semicycle* of a digraph is a cycle in which arcs are treated as edges, connecting nodes in either direction. A *directed cycle/path* of a digraph is a cycle/path whose order of connected nodes is consistent with a uniform direction of arcs. A cycle in an *induced graph* of digraph – in which edges are substituted for arcs – is equivalent to a semicycle. A graph G is *connected* if every pair of nodes is joined by a path. A *component* of G is any of its largest connected subgraphs. The *degree* of a node in a graph G is the number of edges incident to the node. A *simple cycle* in a graph is an induced subgraph <S> that contains a single cycle; and all nodes in S have degree two. A *tree* is a graph with no cycles.

Representing the data of a given kinship and marriage network in this framework, a *p-graph* is a digraph in which marriages are taken as nodes and the arcs are those between parents in an ascending generation and their children or children's marriages in a descending generation. Arcs are distinguished by sex of the child[4]. Inventories of marriage types that occur in a p-graph are taken by defining each type as a distinctive type of *ring*, or simple labeled semicycle in the p-graph <V, P, T>. Each ring type identifies an empirical marriage of that type as an induced subgraph, or type of *fragment*, within the empirical network. A ring may be composed of several different kinds of elements in <V, P, T> that form a semicycle. A corresponding fragment of G must consist of an induced subgraph that is isomorphic to the ring. The *null ring* is one in which the cyclic closure of the ring is a null link, indicating a marriage in which there is no prior p-graph link between spouses. Except for the null ring, an empirical marriage or ring type that creates a semicycle is called a *relinking* or relinking marriage[5].

A single empirical marriage may be of one or more ring types and many – but not all – different types of ring can co-occur. An example is shown in figure 1, a

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[3] Terms given formal definition are in italics, and generally follow those of Harary [1969], although these digraphs, assuming that a pair of nodes has only one type of edge or arc (e.g., one does not marry a parent), add a classification of types of arcs and edges.

[4] The p-graph convention of marriages as nodes was adopted by Weil [1949] for algebraic representation of kinship models, generalized by Bertin [1983] to genealogies, continued by Jorion [1984] for broader classes of kinship models, and regeneralized by White and Jorion [1992, 1996] to genealogies. P-graphs do not distinguish half-siblings because when the same parent is in two different marriages the half-sibling relationship resembles that of cousins. Half-siblings are distinguished in the bipartite p-graph format, in which individuals are one set of nodes and couples another, and in more conventional graphs with individuals as nodes and the arcs from parents to children. The latter include the marriage calculus format described here and by Hamberger *et al.* [2004], and the more primitive Ore [1960] graph that lacks links for marriages.

[5] Jola, Verdier and Zonabend [1970].

genealogical diagram with triangles for males, circles for females and squares for unspecified parents. To convert this to a p-graph, each couple is drawn together into a single node, as in figure 2. The marriage labeled A in diagram (a) in both figures is of two different types: sister exchange with B and FaBrDa. This combination of two relinking marriages, one consanguineal and one not, entails a second consanguineal marriage for B, also of the FaBrDa type. Alternately, the two FaBrDa marriages (A, B) entail sister exchange. Another example is shown in p-graph (b): marriage A is a sister exchange for B, and a second marriage C is a repeated sister exchange with D. The consequence is that marriages C and D are also of both types MoBrDa and FaSiDa. In p-graph (c), marriage A is a sister exchange for B, and a second marriage C is of types MoBrDa and FaSiDa, each entailing the other given the prior sister exchange.

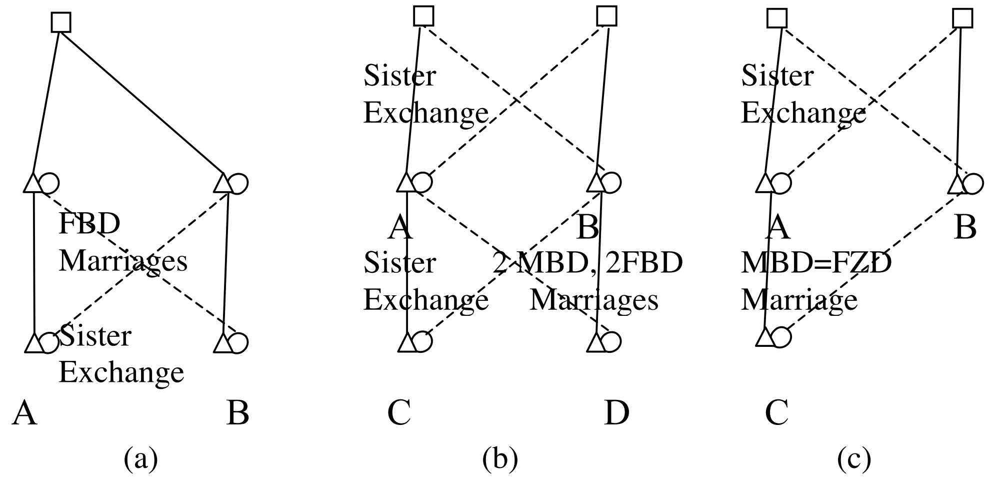

Figure 1. Relinking marriage types with two or three independent cycles

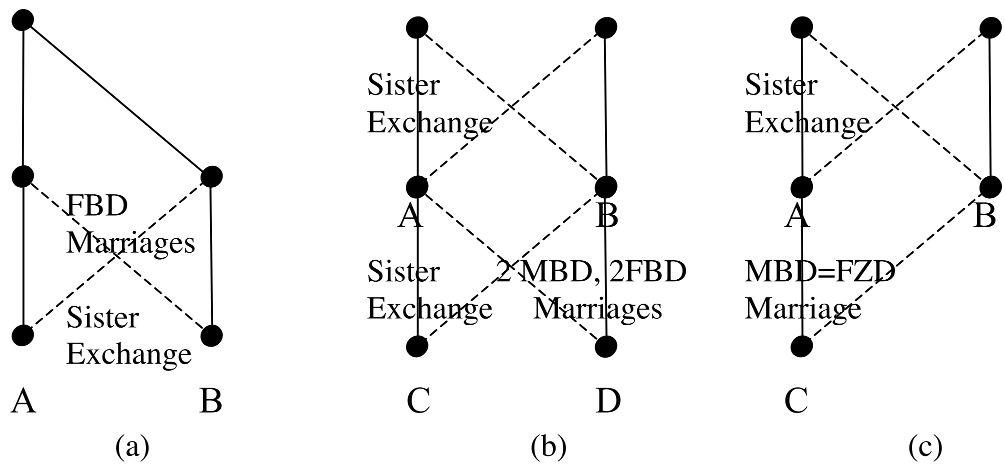

Figure 2. The relinking marriage types of figure 1 drawn as p-graphs

In figure 2, all the couples are replaced by single nodes for marriages, and the types of lines – solid for male and dotted for female – differentiate the genealogical relationships. The beauty and simplicity of this (di)graph, whose lines are time-directed arcs, is that all the marriage types can now be identified strictly in terms of rings or types of marriage cycles (semicycles in a digraph). Sister exchange, for example, is a bow-tie graph for antecedent and precedent generations with links of one sex in the vertical and those of the other sex in the crossover.

Different types of graph fragments can now be defined, such as the sister exchange bow-tie pattern of cycle, and these ring fragments can be searched for and enumerated in a network database. How this is done efficiently with network software will be discussed below. This produces a frequency distribution for the occurrence of different types of marriage. In the examples of figures (a), (b) and (c), there are three, six and three different types of marriage, respectively[6].

Graph theoretic definitions thus simplify certain problems of analysis prior to posing research questions. In these examples, it is evident that the cycles in a graph are not independent. Figure (a), for example, has three marriage types or cycles (digraph semicycles): two FaBrDa marriages and one sister exchange (SiHuSi marriage). When any two of these cycles are present, the third is entailed.

In graph theory, *a set of independent cycles* is any set of cycles in which each cycle contains at least one edge that is not present in any of the other cycles. Because a p-graph contains no directed cycles, the term *cycle* used in this and similar contexts will refer to its semicycles, leaving the time dimension implicit (but identified with appropriate labeling). In example (a), any two of the cycles are independent, but all three are not independent because all the edges in the graph are used by any two cycles.

THEOREM i. *Independent cycles (ring cohesion)*. The *largest possible* number of independent cycles for a graph G with k edges, n nodes, and d disconnected components is $k - n + d$. This applies to any graph G (see [Harary, 1969] for proof)[7]. In a kinship network represented by a connected p-graph G, there are a maximum of $r = k - n + 1$ independent cycles. For a comparable genealogical graph with individuals as nodes and arcs running from parents to children (Ore graph)[8], the formula for the maximum number of independent marriage cycles is $r = k - n + 1 - \sum_{k=1,s} (n_s - 1)$ where subscript s is the number of sibling groups with two parents and n_s is the size of each.

If these formulae are tested on figure (a), $r = 2$, while for (b), $r = 3$, and for (c), $r = 2$: there are a maximum of two independent marriages in examples (a) and (c) and three in (b). Conversely, while not immediately evident, the minimum number of nonindependent marriage cycles is one in (a) and (c) and three in (b)[9].

Given the way that relinkings are computed, because the fragment frequencies are computed for induced subgraphs that are simple cycles, nonindependent cycles in an induced subgraph with $r = 2$ cannot result from the conjuncture of two consanguineal marriages, or from that of two nonconsanguineal marriages, but only by the combination of one of each type, as in examples (a) and (c). A given marriage cannot be both a FaBrDa and a MoBrDa, for example, unless (1) one's parents are siblings, or (2)

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[6] Sister exchanges, like many symmetric 2-family relinkings, could also be counted as two marriages of the same type. The counts used here eliminate such symmetries.

[7] The proof is simple, in that n-1 nodes are the minimum required to connect a graph, additional edges will by definition create $k - (n-1)$ independent cycles, and any arbitrary number of cycles greater than $k - n + 1$ will be nonindependent. Starting from d (disconnected) components of a graph, $n - d$ edges will be required to connect the nodes in each component, so the formula will be derived from $k - (n-d)$ independent cycles.

[8] A primitive Ore [1960] graph may also be embellished by distinguishing individual nodes by sex.

[9] The computation of the total number of cycles in a graph is complicated, but can be determined from how pairs of cycles overlap in a maximal set of cycles. If two independent cycles share an edge, they create one dependent cycle. If they share two nodes but no edge they generate four dependent cycles, and so forth. There is no easy formula.

a person has more than one father and/or mother. Under these restrictions, a man can marry both a FaBrDa and a MoBrDa only if they are different wives.

Ring cohesion theory uses calculation of independent cycles to solve problems of how to explain a complex marriage structure in terms of preferences whose maximal extension to some number of independent marriage cycles is of size r. Suppose a model for a network with r independent cycles, in which $k = r$ marriages are posited that occur because of a preferential marriage rule and the preferential marriages create k cycles. If $k = r$ preferential marriages are identified, their presence in the network accounts for all other cycles, although the ways they concatenate into nonindependent cycles is open to further study of second-order structure[10]. The nonindependent cycles are necessarily concatenated from some set of marriage cycles whose maximal extent is r.

In graph theory, accounting for other cycles corresponds to taking the union of the subgraphs for two cycles, and then subtracting the edges they have in common. This will generate a new, nonindependent cycle. In figure (a), for example, the graph-addition of the two FaBrDa marriages leaves as the outcome the sister exchange. Similarly, the graph-addition of one of the FaBrDa marriages with the sister exchange leaves the other FaBrDa marriage, and so forth. Using these procedures allows us to give a reckoning of independent cycles in a graph, provided the model identifies those types of marriages that are either preferential or that are not disallowed by a marriage proscription.

Now suppose that a model in which a certain number m of marriage types can be ranked in order of preferences. Let f_i be the empirical frequency of the first and any successive marriage type (i=1,m). If we remove each of these marriages from the network, we will typically observe a reduction of the frequency of other types of marriage for cases in which the marriages of this type overlap with marriages of other types. Let $F = \sum_{i=1,m} f_i$ be the total number of marriages removed by this process. If $F = r$, no cycles will remain. The removals, that is, reduce the genealogical graph to approximate a tree (with no cycles)[11]. This model will have succeeded in accounting for all the cycles in the network. By accounting for the independent cycles and, further, *how* they concatenate, an account is given as well for the nonindependent cycles.

2. RESEARCH QUESTIONS AND FURTHER DEFINITIONS

Research Questions

Questions of interest that derive from ring cohesion theory apply to any genealogical network in which individuals have at most two parents (however defined and thus not necessarily biological), and parental and ancestral relations are temporally ordered (parents preceding children, so that no directed cycles occur where one is one's own ancestor):

1. What are the sources of marital cohesion in the community?

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[10] In a bicomponent of a p-graph with m marriages, every marriage with two parental nodes is a relinking, and $m \geq r$, but as (b) in Figure 3 shows, m does not always equal r, and the total number of cycles may be much greater than m.

[11] The proof is obvious: remove $r = k - n + d$ edges from a graph with k edges, and $k - r = n + d$ edges remain; if both the initial and final graphs are connected, then the final graph is a tree if $d = 1$ and a set of d trees otherwise.

2. Can ring cohesion calculus be used to help give an account of the sources of cohesion in a kinship network that are due to relinking marriages?
3. Can the frequencies of matrimonial types be accurately enumerated up to the limit of the investigators' knowledge as coded in the database?
4. Is there a valid means for identifying which sets of marriages in any given community are more preferential than the rest? What are the statistical signatures of sets of preferential marriages?
5. What will remain of a given empirical network when those marriages posited as preferential are subtracted, and how is this accomplished?

Answers to these questions require further definitions and theorems constructed from the logical basis of ring cohesion theory. Footnotes in the following sections address these questions and refer to operations of the network analysis program Pajek [Batagelj, Mrvar 1998, 2002] used for computational purposes.

2.1. OVERALL COHESION AND SOURCES OF COHESION

To return to the initial theme, that of social cohesion, cycles created by marriage in genealogical networks create the boundaries of *structural endogamy* [White, 1997], in which every marriage connects with every other through two or more independent paths. A p-graph representation of marriage networks lets this definition be operationalized so as to entail social cohesion created by marriage. Two or more paths from one node to another are defined as (*node-*) *independent* if they have no intermediate nodes in common. The *level of cohesion* of the induced graph of a p-graph*, measured by an integer k,* is defined as the number k of nodes that must be removed in order to disconnect it. This is the *cyclomatic number* or *connectivity k* of a graph.

THEOREM ii. *Multiconnectivity (ring cohesion).* If a graph or subgraph has connectivity k, then every pair of its nodes has k node-independent paths between them [Menger, 1927; Harary, White 2001], and vice versa.

A p-graph is *regular* if no individual has more than two parents and no marital node has more than two parental couples, one for a male, one for a female; if married or coupled the male and female are members of the same node in the p-graph. A *bicomponent* of a p-graph P is a maximal (largest possible) subgraph of P in which every pair of nodes is joined by two or more node-independent paths and is contained in a (semi) cycle[12]. No p-graph may have connectivity 3 or higher if it is regular. A bicomponent of a regular p-graph is therefore a maximal unit of structural endogamy and isomorphic to a maximal unit of social cohesion for a genealogical network.

[12] Pajek computation of bicomponents is done by Net/Component/Bicomponents. The results are posted in the Hierarchy window that must be clicked at the root number of the display in order to see the hierarchy of possibly overlapping bicomponents. Two bicomponents may share at most one node in common and cycles of overlapping bicomponents are disallowed because they must, instead, constitute single bicomponents. The Net/Component/Bicomponents command also generates multiple partitions in the partitions window. The first identifies vertices belonging to exactly one bicomponent by their number, with nodes that are not in any of the bicomponents assigned to partition zero and with nodes of intersection (articulation points) between bicomponents assigned to partition 99998. The second partition identifies articulation points, assigning each the number of bicomponents in which they are members. To select the subgraph consisting of nodes in any of the bicomponents, Operations/Extract from network/Partition, and then entering a minimum value of 1 and a sufficiently large maximum value, will result in the reduced subgraph shown in the network window.

Regular p-graphs thus provide a natural means of recognizing structurally endogamous and genealogically cohesive groups within genealogical networks of kinship and marriage. A sexually reproductive community will typically have a single large bicomponent or structurally endogamous unit. Alternately, a sexually reproductive community may be defined by the local limits of structural endogamy, that is, discounting the marriages of those who have permanently emigrated from the local area and whose descendants have not returned.

Typically, analysis of cohesive structures is done on a single maximally large bicomponent or structurally endogamous unit of a regular p-graph, referred to as a cohesive 'community' subgraph of a genealogical network. It is only within such a community or bicomponent of the kinship graph that rings will be found.

2.2. RING COHESION CALCULUS

Marriages between people who are previously related come in two basic forms, with subvarieties. One is consanguineal marriages. The other is marriage between in-laws, extended generically to all those who are linked, prior to their marriage, by one or more paths that combine blood relations and prior marriages. Both are called relinking marriages. Any type of relinking marriage, when defined by a simple cycle, will involve 1, 2, 3, or a higher number of marriages, including the relinking marriage that is last in the time sequence. The minimum number of marriages involved (discounting those of ancestors to other nodes in the ring) is identical to the number of families who are relinked, where families are defined as the number of (disconnected) components that remain after the marriages that give rise to cycles are deleted.

To employ the marriage-removal method of ring cohesion as it applies to genealogical networks, the graph theoretic representation must include marriage as a type of link and, thus, individuals as the nodes of the graph. P-graphs no longer suffice. In the type of graph that is needed, when all marriage links that are embedded in a given type of marriage cycles or ring are removed from the graph, the individuals connected by the marriage must remain[13]. Formats for genealogical networks that conform to this structure also make possible the following definition, which assumes that a matrimonial relation (marriage, union, couple) may exist without children but when children of a couple do exist they are considered for analytic purposes to be "married".

Matrimonial rings[14]. A *matrimonial ring* in a genealogical digraph with edges for marriage links among individuals and arcs from parents to children is a simple (semi)cycle such that after removal of the edges all components are rooted trees with a single ancestral node. A tree is *minimal* if it consists of a single node.

The rings in a genealogical digraph together with their trees and branches allow the statement that a matrimonial ring corresponds to a cycle of marriages within or among families defined by members of a rooted tree of consanguineal relatives with a common ancestor or ancestral couple. Note that "within or between families" is relative to a particular ring and not to an ensemble of rings. In figure 2(a) there were three rings

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[13] In Pajek, Nets/First network is used to select the main network and Nets/Second network the network with edges or arcs to be subtracted. Nets/difference will subtract the arcs and edges in the second from the first, leaving all the nodes.

[14] This section and the final definition of matrimonial rings is a joint work with Klaus Hamberger and others in the ongoing collaboration of the Parisian research group TIME.

within a single family: two FaBrDa marriages and one sister exchange. The sister exchange is a simple cycle because there are no additional parent-child or husband/wife links among the actors in the cycle, and this ring, taken by itself, is a relinking marriage between two nuclear families.

In a further example, in figure 3(a), there are only the two rings for the FaSiDa marriages. The FaBrSoWiSi marriage is not a ring because of the "line 1" link between the woman in the center to her parents. This link prevents the FaBrSoWiSi marriage from being a relinking between two families. Had it not existed, as in 3(b), the FaBrSoWiSi marriage would be a ring, one relinking two families. The algorithm that finds fragments as simple cycles recognizes this difference. The subgraph induced by the nodes in the cycle on the outer perimeter of figure 3(a) fails to constitute a ring because it contains, in addition, the "line 1" link. Recall that an induced subgraph <S> of a digraph is a subset S of its nodes plus *all* the edges and arcs that are in the subset of pairs <S x S>. In a subgraph of a larger network induced by its isomorphism to a ring, the degree of every node must be two because the ring is a simple cycle. Figure 3(b) qualifies as a ring by this criterion, but not figure 3(a), which instead contains two such rings.

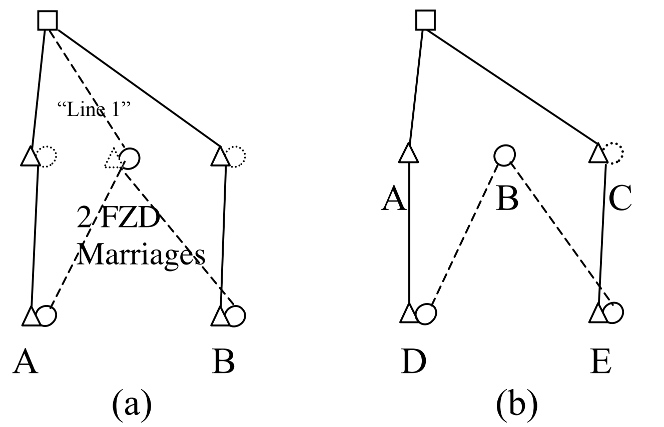

Figure 3: Genealogical networks with (a) two rings and (b) one ring

THEOREM iii. *Branching (ring cohesion)*[15]. As can be proven in general, and as shown in these examples, there are no more than two branches in any of the rooted trees in a matrimonial ring. In the network in figure 3(a) there are four branches and two marriages relinking two rings within a single family. Each individual single ring, however, has only two branches. Each FaSiDa ring in 3(a) has two branches; and each of the FBD and sister exchange rings in 1(a) has two branches to the relinked subfamilies. Theorem iii can be restated in a form that is more intuitive:

A matrimonial ring corresponds to a cycle of marriages within or among families defined as members of a rooted tree of consanguineal relatives having a common ancestor and at most two branches.

[15] Given that a matrimonial ring is a set of one or more two-branch rooted family trees linked and relinked by marriage ties to form a simple semicycle, there must be exactly two nodes within each tree connected by marriage. If a marriage occurs within a family, that closes a ring, and the tree must have two branches to reach those nodes. If a marriage ring occurs between families, each family must have two branches to reach the two nodes that connect it in the circle of family trees.

A minimal matrimonial ring may even consist of a cycle of marriages with minimal rooted trees consisting of single nodes and no branches. Four individuals, for example, may form a matrimonial ring if a man marriages his WiHuWi. As a further example, if individuals A and B in figure 3(b) happened to be the parents of D and E, then 3(b) would no longer be a matrimonial ring because couples A-C-E would form a FaBrDa marriage ring among themselves of which D is not a part.

3. ENUMERATION

Many ethnographers have noted the importance of the full versus half sibling relation in human societies. Given that couples and not solitary individuals typically engender offspring, the ancestral nodes of the rooted trees within matrimonial rings may be either individuals (male, female) or couples without violating the simple cycle criterion of rings. By theorem iii (branching), two branches at most are possible without violating the simple cycle criterion. As a corollary, the ancestral node is the only type of node in a matrimonial ring that generates branching[16]. Whether the branching is that between full, paternal or maternal siblings, or undetermined (with a corresponding parental couple, father, mother, or unknown parent) will be evident if sibling relations are properly coded from the database. Then, when rings of all four types are computed and compared, the branching types can be distinguished.

4. STATISTICAL SIGNATURES OF PREFERENTIAL MARRIAGES

Short cycles. Rules of incest prohibition – for brother-sister, mother-son, father-daughter, or other dyads – typically lengthen the minimal cycle lengths that will be found in marriage networks. Communities differ in their rules proscribing marriage with various kinds of near or distant cousins, uncles, aunts, and other relatives and affines, including such proscriptions as not marrying a WiBrWi, for example [White, n.d.].

Preferences. Among permitted marriages, we would expect to find many communities in which there are preferences for closer relatives, that is, marriages that involve greater preference for short over long cycles in marriage, after excluding incest and marriage proscriptions.

Raw frequencies. The frequencies of observed marriages classified by type may provide a first-order indication of marriage preference, but the evidence for preference must be carefully assessed.

Percentages. For each type of relative that can be taken in marriage (e.g., FaBrDa, BrWi), the percentages of those relatives who are actually taken in marriage also need to be calculated. This can be done with Pajek by creating fragments for each type of marriage ring but removing the marriage link itself, leaving only a path to define the fragment (as a null ring) and not a cycle. To obtain this percentage for the FaBrDa relation, for example, the number of FaBrDa marriage rings is divided by the number of

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[16] This can be proven as follows. Because every family in a marriage cycle has an even number of marriage links and thus at most two branches, if the ancestrally rooted tree for a family with a branch that is not generated by two children of the root, then the only way the ancestor can be involved in a matrimonial cycle is by a marriage: if that marriage is within the same family tree, there can only be one branch; if it is with another family then only one node on a single descent line from the ancestor can be the other marriage involved in the matrimonial rink and hence that tree also has only one branch. In either case a contradiction results, hence the theorem is proven.

FaBrDa paths. These types of percentages were already computed for consanguineal kin in the Par-Calc program for analysis of p-graphs [White and Jorion 1992, 1996], but can now, using Pajek, be computed for affinal kin.

Frequency distributions. Here, we consider three methods of showing frequency distributions:

1. Rank order the marriage types by their *frequencies or percentages*, with frequency on the y-axis of the plot and the *rank order of these quantities* (allowing ties) on the x-axis. Use of ring cohesion calculus may show that only a limited number of high-frequency types (with few ties among their frequencies) are needed to account for the independent cycles in the marriage network.
2. Nominate the x-axis as a *frequency descriptor for types*, starting with 1 for those types with lowest frequency or percentage and running up to the largest value. In this case the *number of types that have this nominated value* is put on the y-axis. Hence, if there are 200 types with frequency 1, the number of marriages involved is 1x200=200, while if there are 100 types with frequency 2 these also represent 200=2x100 marriages. At the extreme there will be very few types with high frequency, but these will represent many marriages. When the ring cohesion calculus is used, and only a certain number of high-frequency types are sufficient to account for the independent cycles, this method will result in discontinuities in the graph of x-y values. To look for continuous relationships between the x-y values, we may use a cumulative measure of frequency as follows.
3. Nominate the x-axis as the cumulative frequency of all types having *successively less frequent occurrence* and the y axis as the *cumulative number of types*. This plot allows continuous interpolation among the plotted x,y values and consideration of the shapes and slopes of the curve under various transformations of the x-y axes (linear, logged on one axis, and log-log plots).

When the distributions are constructed in one of these three ways, but preferably the third, we may observe various types of empirical relationships among the pairs of values on the x-y axes as follows:

- *Discrete stairstep relationship*. Here, in plot method 1, several of the most frequent types will show as roughly tied in rank, with possibly a second or third echelon of tied ranks.
- *Linear relationship*. One or several of the plot methods shows a linear relationship between unlogged x and y values. This indicative of a preference for “more” of the most frequent items, with less frequent items as partial substitutes.
- *Exponential or logarithmic relationship*. Here the x-y relationship is linear when one but not both of the axes are logged. The clearest interpretation will result when method 3 is used. This is not necessarily indicative of a preferential order because this may also occur with randomly generated frequencies for different types. The question here, as with a) and b), is whether the ordering is predicted by a certain preferential logic that can be predicted in advance from some independent characteristics of individuals in the community.
- *Power-law relationship*. Here the x-y relationship is linear when both of the axes are logged (possibly only for the first *r* independent cycles). The clearest interpretation will result when method 3 is used. This suggests that there are differentially self-amplifying elements in the ordering. The appropriate model is to look for independent components that go into the ordering, each weighted differentially to

produce both the power relationship (the higher the product or sum of weights the more the self-amplification) and the ordering itself.

5. MARRIAGE CALCULUS FORMAT AND ANALYSIS

The definition and methods for enumeration of marriage types allow us to identity all marriages in a genealogical network of each given type, and these frequency distributions can be analyzed for evidence of preferential marriages. Once the actual identification of marriages by type is completed, a new question arises from ring cohesion theory: if we remove marriages in order of presumed preferences, regarding them as within the set of independent cycles, what happens to the frequencies of the remaining marriage types? The independent cycles theorem i requires that these will include types that are nonindependent of the preferential types, and hence these frequencies will diminish. When few or no cycles remain after a series of removals, it is valid to say that an account of the total ensemble of cycles in the network has been rendered in terms of the preferential and independent cycles.

In the marriage-removal method proposed here and operationalized by Hamberger *et al.* [2004], a minimum of five relations need to be defined, and a sixth is optional[17]. Five are primitive in the sense that they are not the logical result of any composition of other primitives (e.g., child of grandparent=parent of parent). The sixth, siblingship, is a relationship that is not primitive but derived from having common parents. These six relations in the marriage calculus format are:

F-D (arc)	M-D (arc)	Marriage (arc)
F-S (arc)	M-S (arc)	Siblings (edge)

If only the five primitive kinship relations are used to define search fragments for use with a kinship network coded in the same format, the ring fragments may be coded to include individual ancestors or ancestral couples in the family tree components of the ring. Rings of complementary types may be designed to include only female ancestors, only male ancestors, only ancestral couples, or unspecified. These distinctions are important for the types of sibling branches that occur from the ancestral nodes.

An alternative network format introduces the sibling relation and deletes the ancestral node parental to a sibling branch in a family tree. This introduces cycles in the graph that are not due to marriage, but occur within nuclear families with two or more children. The appropriate formula for the maximum number of independent marriage cycles given above is $r = k - n + 1 - \_{k=1,s} (n_s -1)$ where subscript s is the number of sibling groups with two parents and n_s is the size of each[18].

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[17] A bipartite p-graph is alternative network formalization for this purpose since it has individuals as well as marriage nodes, and removal of a marriage consists of replacing the marriage node with descent lines from individual parents to individual children. As this is done, however, cycles are created which do not correspond to marriage cycles, so a variant of the correction formula for Ore [1960] graphs must be applied to compute the number of remaining marriage cycles.

[18] An approximation of this number is computed in an Ore graph by deleting sibling edges and spousal links and then computing the indegree of each node, which is saved as a partition, and then computing sibling links using Net/Transform/Add/Sibling Edges/Input. Then, using Net/Transform/Remove/all Arcs, all arcs are deleted. Now the previously saved indegree partition, already positioned in the partition window, is used to do Operation/Extract – selecting Network/Partition/values from 1 up – and Net/Partition/Degree/Input degree is used to compute the numbers of sibling links on the edges. Finally, Operation/Extract from Network/Partition/values from 1 up and again will produce for each individual in

5.1 METHODS AND MEASURES

Samples. Hundreds of coded genealogical samples are available for analysis [White, Houseman, Schweizer, 1993] and thousands of anthropologists have collected complete genealogies for the communities they have studied. Project TIME (see [Hamberger *et al*., 2004])- has converted many of these and other genealogical networks into the marriage calculus format.

Software. From the first year of its implementation in 1996, the Pajek program for large networks analysis provided and has since updated a series of algorithms for kinship networks and genealogies [Batagelj, Mrvar 1998, 2002, 2004; White, Batagelj, Mrvar 1999]. The index of relinking, a measure of the extent to which a graph with k independent ancestors has the maximal possible number of relinkings, was implemented in 1998. A definitive version of Pajek (1.01, 2004), released with an instructional manual [de Nooy, Mrvar, Batagelj, 2004], provides for the marriage calculus data format and method in studying ring cohesion. Macro commands for kinship analysis come with the Pajek installation.

Fragments. Search and identification of fragments in graphs was implemented in Pajek in 1997. In 2003, I developed a set of kinship fragments for identifying different types of consanguineal marriages in p-graphs. The Pajek count of fragments eliminates isomorphisms (e.g., two brothers marrying two sisters is counted as a single fragment), which allows counting of marriage types by number of subgraphs or by number of marriages. For example, HuSiHi rings have isomorphic transformations between the two marriages involved in the ring. Knowing the number of isomorphisms of each graph, e.g., the two isomorphisms for sister exchange, fragment counts are easily converted to frequency counts for individuals. Hamberger *et al.* [2004] develop an improved set of kinship fragments in marriage calculus format for identifying different types of relinking, including blood marriages. This approach uses software by Jürgen Pfeffer (FAS-Research, Vienna) to convert a kinship file in Excel format (Ego, Sex, Fa, Mo, Spouse) into a Pajek genealogical file in the new format. Sibling links must then be added and resultant loops removed, which are simple operations in Pajek[19]. To find marriage types as fragments in the network, the genealogical file is scanned for successive fragment types, now a standard Pajek option[20]. The fragments found of a given type may be saved without renumbering nodes so that marriages of a given type can be subtracted from a given network[21]. This feature is used for the marriage removal method of ring cohesion analysis[22].

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the partition a sibling count. These sibling sets must be counted for each size group, labeling them k=1 to (s-1), where s is the largest number of siblings, and adding the products of each frequency by its index k. The reason this is approximate is that there may be half-siblings in the network.

[19] The procedure is to make an *.xls file with Ego#, Name, Sex (H=homme, F=femme), Fa#, Mo#, Spouse#, sort by sex, delete all the spouse numbers for males (to make the spousal relation directed), then run the Gen2Pajek program to create a Pajek *.net file. This file requires the addition of sibling links, which is a Net/Transform/Add operation (Input option for equivalence of siblings) in Pajek.

[20] The procedure is to read the fragments as a *.paj file (File/Pajek Project file/Read), then load the genealogy file made with Gen2Pajek, and use option Nets/Second network to load it for comparison. The network window is clicked to reselect the first fragment, and option Nets/First network is used to enable the fragment (first network) to be found in the (second) larger network by using option Nets/Find (1 in 2). Options must be set in Nets/Find, before this last step, to check [x] values of lines, [x] Extract subnetwork and [x] Retain all vertices after extraction. These will allow the found marriages to be subtracted from the genealogy. If rings are wanted then the option must be checked for [x] induced subgraph. Otherwise, if [ ] induced subgraph is left unchecked then the cycle in the fragment will be found whether or not the subgraph identified as containing this cycle has additional links that are not in the fragment.

[21] Because the marriages have line value 1, it is only necessary in the extracted subnetwork to use option

5.2. HYPOTHESES

White and Houseman [2002, p. 78-79] posited a tricotomy of community types with respect to sources of marital cohesion:

- H1. Communities with many blood marriages may have power-law preferences on blood marriages, but will be neutral on multifamily relinkings, that is, with differences that are exponentially distributed. The appropriate ring cohesion model to test here is that the independent cycles that generate structural endogamy are the blood marriages.
- H2. Communities with few blood marriages may have power-law preferences on multifamily relinkings. These may exhibit one of two subtypes:

  Power-law preferences on two-family relinkings.

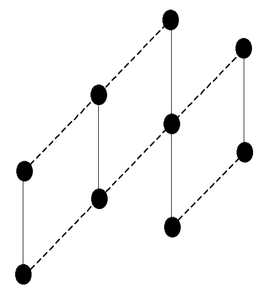
  Power-law preferences on three-family relinkings

Independence partition principle (ring cohesion). Ring cohesion theory helps to explain the basis for White and Houseman's [2002] hypotheses 1 and 2. When uniqueness of parents and restrictions against sibling marriage apply for a given genealogical database, it is convenient to think of either the entire set of consanguineal marriages as constituting the bulk of a set S of independent cycles, with nonconsanguineal marriages constituting the bulk of the complementary set of nonindependent cycles, or vice versa. This is because among the consanguineal marriage set, for any induced subgraphs with $r = 2$ independent cycles, found in a fragment search, there can be no nonindependent cycles[23], and the same is true for the nonconsanguineal marriage set. Nonindependence for $r \geq 3$ induced subgraphs will involve combinations of consanguineal and of nonconsanguineal relinkings: two MoBrDa marriages entail two FaBrDa marriages, as in figure 1(b), for example, only if there is sister exchange in the first generation. In general, the major restrictions on the types of relinking that can co-occur are within the consanguineal and nonconsanguineal classes of relinking [White, 1997]. Complex cases such as example 1(b) might involve combinations of one nonconsanguineal and two consanguineal types, or vice versa.

Net/Transform/Remove/lines with value/more than [1] and Net/Transform/Remove/all edges in order to create a network file with the marriage links only. This is then subtracted by loading the genealogy file with option Nets/First network and loading the marriage file to be subtracted with Nets/Second network, so that Nets/difference subtracts the marriages from the network.

[22] Hamberger [Hamberger *et al.*, 2004] developed an additional series of Pajek macros to calculate from this file into a 3-mode dataset with individuals, marriages, and marriage types.

[23] In the p-graph below, for example, there are three independent cycles, and while graph addition for the two that share an edge would form a MoMoBrDaDa marriage ring, this ring would not be found as a ring-fragment of the graph because of the requirement that the search is for a simple cycle, not a pair of cycles.



What the independent cycle theorem i and the independence partition principle jointly imply is that if a community has preferences oriented towards types of consanguineal relatives, a preferential ring distribution of consanguineal marriages will normally imply an exponential (nonpreferential) distribution of nonindependent affinal relinking cycles. The converse will apply if a community has preferences oriented towards types of nonconsanguineal relinking. The distribution of nonindependent cycles would normally be expected not to be preferential because they are not independently formed. This provides a third hypothesis as a derivation from ring cohesion theory.

- H3. Few communities will have power-law preferences on both consanguineal and affinal relinkings.

It may be unlikely but not impossible, however, that both distributions could be optimized and preferentially structured. This would involve a second-order of systematic and preferential concatenation of rings into larger cohesive structures.

White and Houseman's [2002, p. 78] hypotheses (H1 and H2) were initially a report of an empirical pattern of investigative results concerning kinship networks generally. Ring cohesion theory identifies the derivation of these hypotheses from network and mathematical principles that hold for kinship systems generally. H3 holds because kinship has a hereditary component (descent) and an elective component (affinity). Biological and other kinds of networks also have internal contrasts of this sort for certain subtypes of network relations, so further generalization of H3 to other sciences would be expected from first principles. More generally:

- H4: Whatever the method of detecting marriage preferences, there will be some statistical tendencies for preferences of the consanguineal sort to reduce those of nonconsanguineal relinkings, and vice versa.

This takes into account the possibility that a preference ordering on a small subset of consanguineal marriages would not rule out additional affinal preferences, and vice versa. It is only when a preference ordering is over a larger range of marriage types that H3 is likely to be operative.

5.3 ILLUSTRATIVE RESULTS FOR KINSHIP NETWORK ANALYSIS

The ring cohesion approach is exemplified here from the Turkish Aydınlı nomad data studied by White and Johansen [2004; Johansen, White, 2002]. Results in the following tables and figures are illustrative of tests of hypotheses about the Turkish nomads, with an Arabic type of kinship system and rights to FaBrDa marriage.

Preferences

Evidence for consanguineal marriages as preferential and thus as the appropriate set of independent cycles in the network is considered first. If both these conditions were true, it is possible that the affinal relinkings, considered as nonindependent cycles, would require no further explanation in terms of preference. The supporting evidence that consanguineal marriages are preferential (and nonconsanguineal relinkings are not) comes from White and Johansen [2004, p. 275-278], as shown in the following figures, some of which are discussed in White and Houseman [2002].

Figure 4 uses plotting method 2 to break out the frequency gradient for all types of consanguineal marriages, regardless of kinship distance[24]. Here the *x* axis is a variable for the number of spouses whose marriage fits one of the 234 types of blood kinship within the range of fifth cousins (7 generations to a common ancestor). The *y* axis is the number of those types of marriage with exactly the number *x* of related spouses.

From the graph we can read that 156 of the 234 types of marriage have a marriage frequency of one in the dataset. This number drops to 36 of the 234 types for which there are two marriages. If the graph were exponential it would keep dropping by a constant fraction, such as from 156 to 36 to 10 to ~2 and quickly to zero. Instead, the graph follows a power law, and drops from 156 to 36 to ~18 to ~10 to ~5, showing the extended tail of a power-law distribution. The long tail indicates that a few types have much higher frequencies than would occur if types of marriage partner were chosen randomly. The extreme outlier in this breakdown of frequencies by type is FaBrDa marriage, for which there are 32 instances, nearly twice that of the next most frequent marriage, of the MoBrDa marriage type. The distribution has a fixed exponent ca. 2, an inverse square power law whose equation is approximately $y=156/x^2$, with y the number of types whose frequency x is between 1 and 32. The fit of the power-law curve to the data and is $r^2=.83$ with an estimated slope of 1.97. Because a power-law distribution is not what we expect at random, this is one indicator of a preferential distribution. Power laws of this sort are suggestive of networks that operate as self-organizing systems having fractal properties, where the frequencies of cohesion-generating behaviors are self-scaling, for example, with the diameters of cohesive cycles formed. Self-similar behavior at different scales tends to play out so that the more diffuse the form of marital relinking, the lower its frequency. The types of Aydınlı marriage with the highest frequencies (FaBrDa, MoBrDa, FaSiDa) also tend to follow a frequency ordering that reflects kinship distance reckoned from a perspective of patrilines. For marriage cycles of greater length, the frequency ordering tends to scale fractally according to level of patrilineal corporate solidarity scaled by distance to the common ancestor.

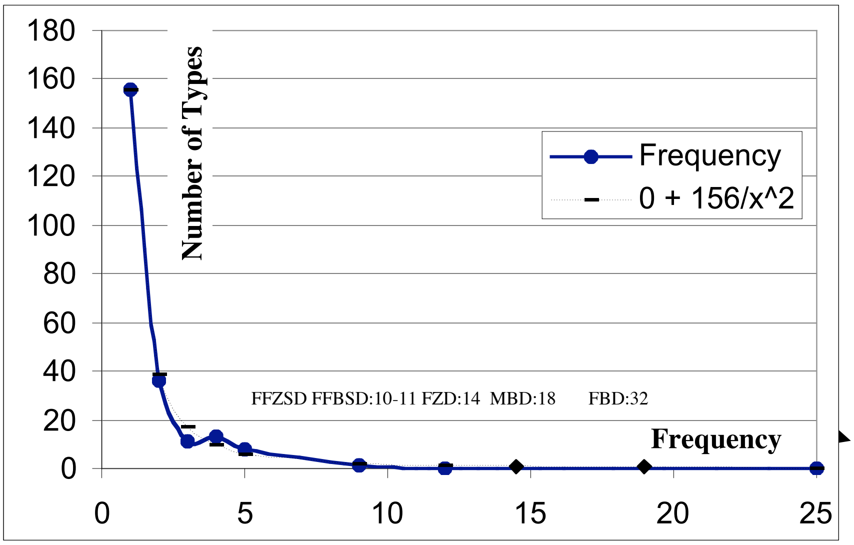


Figure 4. Power-law Fractality of Marriage Frequencies

[24] Kinship distance can be reckoned in various ways, one of which is the shortest path from individual A to B in the marriage calculus kinship format. Other measures are more culturally specific.

Figure 5 repeats the analysis in figure 4, this time taking the log of values on the x and y axes, and fitting a straight line to the plot. The fit approximates a power-law distribution. The statistical signature of this relationship is discussed under that heading in section 4 – the hypothesis being that of differentially self-amplifying elements in the ordering. The amplification process resulting in these frequencies is greatest the closer the link-distance when male links are weighted higher than female, so that FaBrDa comes out highest in the ordering.

Fractal marriage patterns function rather like Granovetter's [1973] strong and weak ties, which have complementary strengths at complementary distances. The stronger and more frequent ties (of many fewer types) work at closer distances, in this case concentrically oriented toward close and patrilineal relatives, while the weaker ties of each type are individually less frequent but work as an ensemble in a distributed manner over longer distances. Unlike the way that marriage preferences are usually formulated as discrete rules, the fractal pattern is continuously scaled rather than a simple dichotomy of preferred marriage types.

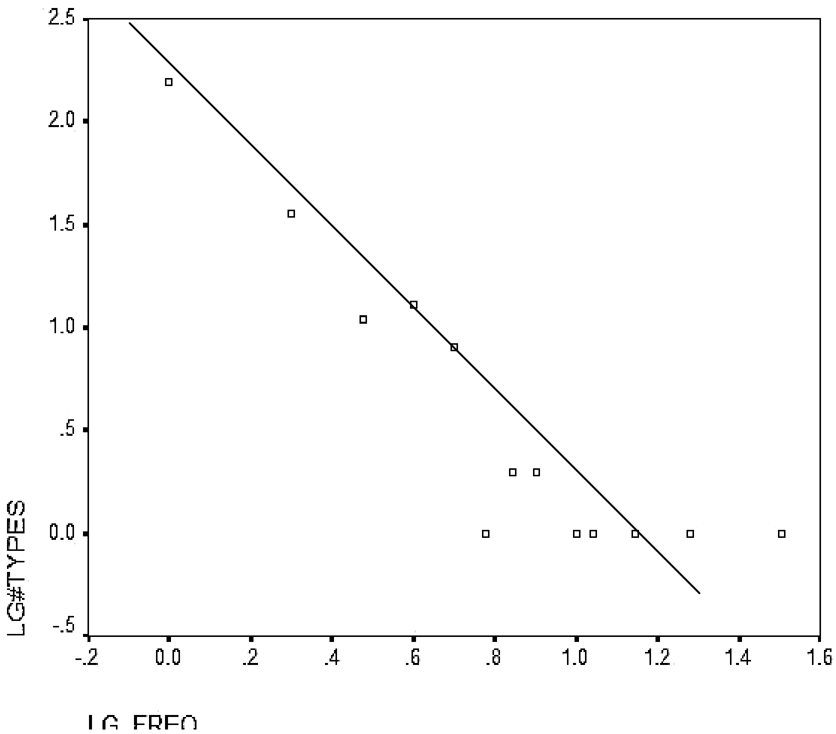


Figure 5: Power Law for Marriage Frequencies - Log-log plot for Figure 4 with fitted line, slope ~ 2

These results can be compared with those of plotting method in 4.1, as shown in figure 6. Here the raw frequency line shows the outcome of graphing the frequencies of all the 234 types of consanguineal marriages up to seventh cousins ordered by rank with logged frequencies on the y axis and the logged number of observations for this type and frequency on the x axis. The distribution of raw frequencies is linear in the log-log graph and thus approximates a power-law distribution, fitting our overall observation about a fractal marriage pattern. The other aspects of consanguineal marriage distributions graphed by this method are the number of possible spouses of each type in the upper part of figure 6 and the percentage married of each type in the lower part.

The upper curve for frequencies of types of possible spouses (all those available in a given category) shows an exponential decay or logarithmic distribution. Here FaBrDa is the most frequently available type of relative, and MoBrDa the next. The curve for percentage married of each type of those available is also a logarithmic distribution, unlike figure 4, again with FaBrDa as the highest percentage and MoBrDa the next. The logarithmic shape is due to the fact that there are many fewer *types* of consanguines at each kinship distance as we move closer to ego (four types of first cousins). Also, in a limited network, as we move to very distant relations these thin out if there are few apical ancestors. This is because many of the vast number of combinatorial possibilities do not occur, and the closer relationships have already used up many of the relatives in the network. Only the raw frequencies fit the power-law distribution that is characteristic of fractality. This is as it should be in a system that is behaviorally self-organized. In this society, FaBrDa is not only a preferred marriage but a relative whose proximity is more likely because of the preference for brothers and their children to live together, stay together and work together.

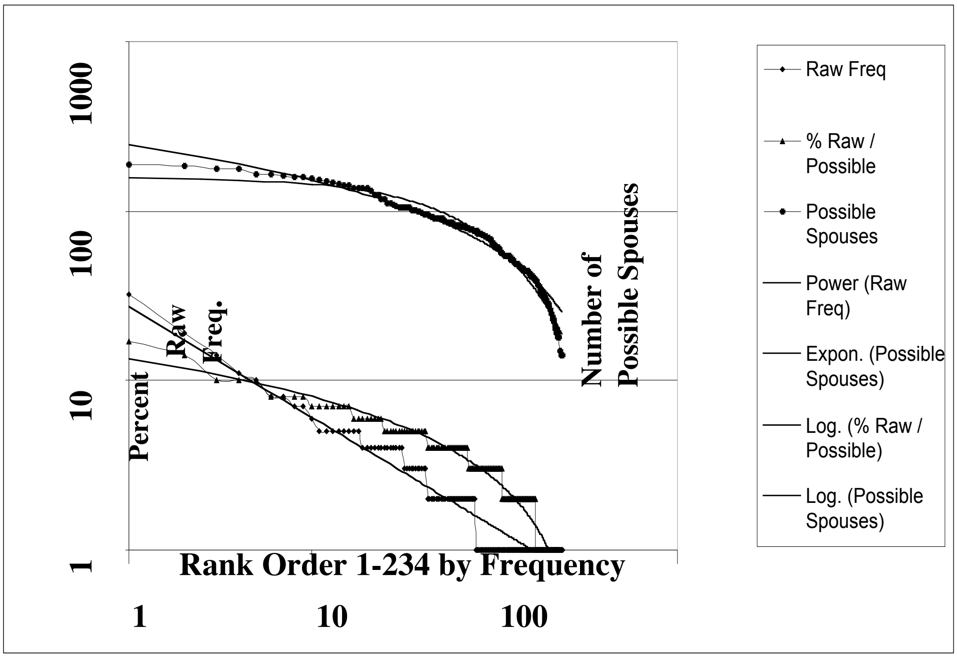


Figure 6: The Fractality of Consanguineal Marriage Frequencies

Analyses of relinking marriages that are nonconsanguineal for the case of the Aydınlı nomad clan, comparable to those of consanguineal marriages, do not show power-law tendencies, consistent with H1 and H3.

Ring Cohesion Results for the Aydınlı Turkish Nomads

The ring cohesion results on preferential distributions for the nomad clan show that, although the most frequent consanguineal marriage is FaBrDa marriage, these marriages are not essential to the cohesion of the clan. It is the larger class of consanguineal marriages that generate this cohesion; they are hypothesized to be the set of cycles we should consider as independent. This is stated in hypothesis 5 and tested in Table 1.

- H5 (Aydınlı)**:** The elimination of FaBrDa marriage does not reduce structural endogamy, but structural endogamy is generated by the larger class of consanguineal marriages.

For the data in Table 1, the structurally endogamous bicomponent was computed prior to adding sibling links as edges. The size of the bicomponent is 960. The ring cohesion calculus was used to make Table 2 by finding FaBrDa marriages in the same database and deleting only the FaBrDa marriage links while retaining the rest of the graph used for Table 1. The bicomponent is then recomputed, but its size is again 960. Aydınlı FaBrDa marriages, then, are between relatives cohesively linked independently of their relatedness as FaBrDa/FaBrSo.

Table 1

nodes in bicomponent = 960	Arcs	Edges
Number of lines with value=1	248	2573 (p-tur-bico)
Number of lines with value#1	1749	0

Table 2

FaBrDa: 34 marriages found and deleted
After removal of FaBrDa and sibling edges:

nodes in bicomponent = 960	Arcs	Edges
Number of lines with value=1	214	2573
Number of lines with value#1	1749	0

Table 3 shows calculations of the independent cycles in the marriage graph for close cousin marriages compared to the total genealogical network. There are 116 independent cycles accounted for by these consanguineal marriages out of a total of 266, leaving 150 unaccounted for, as suggested as well by examining figure 4 for consanguineal marriages with frequencies of one or two per type. First and second cousin marriages, then, although they occur between patrilineages, also fail to account for Aydınlı clan cohesion.

Table 3. Independent Cycles in the Cousin Marriage
Graph (first and second cousins) compared to the Total graph

In the cousin fusion graph

Number of lines		315 - (no edges)
Number of nodes		176
--------	139 - 11 - 11	independent cycles = 116

In the total graph

Number of lines		1997 (no edges)
Number of nodes		960
--------	1037 - 1 - 771	independent cycles = 266
difference		150 unaccounted for

What if all consanguineal marriages are eliminated?

- H6 (Aydınlı): The elimination of all consanguineal marriages eliminates as well almost all of the two-family and other affinal relinkings.

H6 holds for all systematic affinal relinkings except for 11 marriages between pairs of siblings: once consanguineal marriages are eliminated, the sibling relinkings (sister exchanges and BrWiSi marriages) are reduced from a frequency of 135 to 11, and none of the other two-family relinkings have any significant frequency.

The ring cohesion calculus in the illustrative case of Turkish nomads is consistent with the class of consanguineal marriages as the source of preferential relinking between spouses and almost fully accounts for the structural endogamy in the network without having to take into account multifamily relinking except for some of the marriages between pairs of siblings. FaBrDa marriage per se accounts for none of the structural endogamy, which is almost entirely due to a variety of other consanguineal marriages, most of which are between lineages. In this case, these results speak to the fact that there are two major poles to the marriage structure, one being widely distributed consanguineal marriage choices within the clan, many of them with distant consanguineals. The other is that close marriages that reinforce lineage cohesion, such as FaBrDa, are easily available with the high frequency of such coresident women available, and these also account for the highest percentage of marriages with those in any given marriage type. Given that the number of consanguineal marriage cycles is sufficient to account for nearly all the independent marriage cycles, the nonconsanguineal relinkings may be considered for the most part as nonindependent cycles and by-products of the concatenation of consanguineal marriages, as exemplified in figure 1. However, because there is some independent evidence for independently cohesive marriages between pairs of siblings (the 11 exceptions to H6) and the very high number of concatenated blood marriages that produce such marriages, like those in figure 1(b), there is also good reason to consider that these concatenations, as second-order cohesion structures, are also preferential among the Aydınlı.

CONCLUSIONS

The term ring cohesion is used to convey the possibility of finding the micro-macro connections between individual behavior that generates elementary cycles in networks and the largest level of cohesive groupings are created in a network. The first creates the second, and the second (the structural cohesion of groups) has important sociopolitical, economic and other consequences that include the creation of the context for microbehavioral choices. The structure within and extent of cohesive networks at the macro level are part of what gives communities and social groups their distinctive structure and dynamics. To understand explicitly how these micro-macro linkages work across different community and social structure may come eventually to constitute part of new foundational theories related to social organization, structure, and dynamics.

For the analysis of networks generally, ring cohesion theory provides a solution to problems of studying cycle formation and the relation between local cohesion through behavior that leads to relational cycles and more global properties of network cohesion. For the analysis of marriage networks in particular, ring cohesion theory provides a solution to problems that have long plagued this field [Schneider, 1965]: How to count cycles? How do marriage cycles contribute to social cohesion? How to measure cohesion in a genealogical network? How to define the boundaries of a cohesive community? How to determine preferential marriages? How and to what extent do preferential marriages contribute to structural endogamy? What is the relation between social cohesion and structural endogamy? Predictive cohesion theory, as formulated and tested by Moody and White (2003), for example, answers some of the other questions as to: So what? Why is structural cohesion important in the first place? What are its predictable consequences? Ring cohesion theory gives an important extension to predictive cohesion theory, linking micro individual behavior to macro structure and dynamics.

The Pajek network analysis software, now equipped with our suggestions for ring cohesion analysis, provides operational procedures to address these issues, some of which have been exemplified and examined in the Turkish nomad example of an Arabic type of kinship and marriage system. In that case a preferential marriage gradient is evident for consanguineal but not for nonconsanguineal relinking. Removing the consanguineal marriages as a set of marriages large enough to constitute the total independent set of marriage cycles gives a confirmatory result in that nonconsanguineal relinking cycles are removed as well, consistent with ring cohesion theory. The theory is useful, then, in bounding the problems of explanation and prediction in developing social theory for marriage networks, and may be easily extended to networks in general for the study of sources of cohesion.

As a more general theory applied to social networks, the problem of ring cohesion is one of behavioral gradients: what are the local contexts in which individuals make choices that affect the larger issues of social cohesion by the formation of cycles in networks? This is a micro-macro problem: choices made locally in a network to form links either do or do not form cycles. Pairs of cycles, when concatenated, form additional cycles indirectly, out of the view or intent of the local actor, sometimes strategically, but usually not as a direct result of local action. What ring cohesion offers is a set of measures and theorems that allow independent sets of cycles to be hypothesized for any given network and matched against actual behavior generating them, while the nonindependent set of cycles (typically longer) that necessarily occur in the larger network are a by-product of that behavior, although how a set of simple independent cycles concatenate into the second order structure of nonindependent cycles is an additional question posed, formalized and analyzed in several ethnographic examples by Hamberger *et al.* [2004] for marriage networks.

Nonindependent cycles, however, while formed ‘behind the backs’ of local actors, are equally a part of the larger cohesive structures embedding actors and subgroups in the network. These larger macro structures and the concatenation of nonindependent cycles may require additional statistical testing and explanation if the concatenations are nonrandom given the framework of the independent fragment preferences. They cannot be analyzed in the same statistical frame as the first-order cycles, and need to be analyzed in a special frame for second-order analysis. Accounting for both the first- and second-order construction of a network may be required to study micro-macro linkage.

Except for unusual circumstances, however, it is toward the independent set of cycles of *shorter length* that analysis of first-order cycle formation must be focused [Vismara, 1997; Batagelj and Zaversnik, 2003]. Which specific set of cycles should be considered independent is a matter of identifying preferential or gradient-driven social action directed towards the simplest building blocks of social structure. It is only then that second-order questions can be considered: what are the ways, strategies, and benefits of combining these building blocks, if any exist beyond random concatenations?

The guiding hypothesis of ring cohesion is that cohesive cycles form as a result of local action. In the general case, they should be easily recognizable and localized rings, within the perceptions of social actors (see [Brudner, White, 1997]). These locally definable contexts are the first places one should look from gradient-driven or preferential behavior. In addition, for exceptional individuals or processes that involve exploiting large structural holes in networks [Burt, 1995] in order to form long but simple cycles, one might look for intentional behavior in the larger diameter rings of cohesion, which are otherwise and more typically nonindependent of the smaller rings. It is the inner/outer ring differentiation that helps to understand how history – in the sense of the effects of cohesive groupings – is made behind the backs of individual actors, as a result of the first-order micro-macro linkages, but again, sometimes strategically. The ideas of rules and strategies can thus be assimilated to the same analysis.

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