

A reticular approach to kinship

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Regardless of how marriage is locally defined, most people in most places marry (and/or have children with) people who are neither too close (immediate family members) nor overly distant (total strangers). As a result, many members of a given community are linked to each other by multiple direct or indirect ties of consanguinity and/or affinity. A reticular or network approach to kinship is concerned with the nature of these interconnections, the way they combine to form patterns, and how these patterns relate to other types of social phenomena: kinship terminology, residence, religious or political formations, economic transactions, and so forth.

Marriage relations, however they are locally defined, are taken to play an essential role. While consanguineal ties link individuals into open-ended family trees, marriage acts not only to link these trees together, but also to *relink* the individuals in them to each other in a variety of additional ways. Such marriage-based connections give rise to closed circuits of kinship and marriage ties, thereby generating cohesion within the genealogical field. Members of different families can thus come to be appreciated as part of a single kinship network unfolding through time. From this point of view, a network approach to kinship builds on Lévi-Strauss' (1967) (and Tylor's [1889]) insight into the structural properties of affinal ties: consanguineous groups, and relatively isolated individuals, are integrated into higher order totalities through marriage. However, whereas Lévi-Strauss sought to grasp the relational properties of matrimonial alliance synchronically, by appealing to reductive "elementary" structures deriving mainly from classificatory schemes and normative precepts, a reticular approach proceeds directly from the analysis of actual marriage choices. Indeed, perhaps the most distinctive aspect of a network perspective is the emphasis it lays on the systematic treatment of empirical kinship and marriage data. A reticular approach is inherently practice-based.

The development of kinship network analysis

With its emphasis on actual (marriage) behaviour, the study of kinship networks may be said to derive, within anthropology, from a number of different sources. One overarching antecedent is the work of researchers affiliated with Max Gluckman's "Manchester school" of anthropology who, seeking to distance themselves from normative models of social structure, undertook detailed analysis of interaction in particular situations in order to infer their underlying rules and assumptions. John Barnes (1954) introduced the notion of "social network" to describe and analyze systems of relations (kinship, friendship and neighbourhood in a Norwegian parish) which do not cluster into clearly delimited groups. His idea of treating interacting individuals and assemblies as a set of nodes some of which are joined by lines, was adopted and developed by others: Elizabeth Bott in her treatment of kinship and friendship in Britain (1957), S.F. Nadel in his theoretical treatise on "field theory" (1957), and especially Clyde Mitchell and his colleagues who used network analysis to visualize and understand the workings of personal, organizational and inter-ethnic networks in urban settings in Africa (Mitchell 1965). This promising approach disappeared from anthropology in the 1970s. However, the network paradigm was taken up elsewhere to become the foundation for a major field of inquiry in the social sciences, increasingly dominated by quantitative concerns and resulting in a slew of innovative concepts and analytical procedures such as structural cohesion, centrality, balance, block modelling, etc. Insofar as kinship studies are concerned, foremost among the contributions to this more mathematically oriented

development was Harrison White's *Anatomy of Kinship* (1963) which expands on Lévi-Strauss' and especially Weil's (1949) work to provide an algebraic account of kinship relations along network lines, in the absence, however, of actual marriage data. Mention should also be made of Per Hage and Frank Harary's (1984, 1991) use of graph theory to study exchange patterns, an approach which was subsequently applied to the modelling of actual marriage data (Harary & White 2001).

Another important influence was undoubtedly Edmund Leach's ambition to develop a more dynamic, pragmatic alternative to the idealised accounts of social structure that had become the hallmark of British structural functionalism (Leach 1954, 1961). While clearly attracted by the possibilities of formal modelling, and admittedly influenced both by the Manchester school and by Lévi-Strauss, Leach increasingly stressed the importance of tracing out detailed empirical patterns of networked relations – kinship ties but also land ownership, inheritance, and political affiliations – as the basis for studying social organization. It is indeed no accident that Paul Jorion, one of Lévi-Strauss' former students, after having worked in Cambridge under Leach and then with him on “multifunctional kinship networks” among Australian Aboriginal populations (Jorion 2000), commissioned Elaine Lally to write “an algorithm for the analysis of genealogies as to prior kin connection between spouses.” This algorithm, revived by Douglas White and Jorion (1992), and implementing Jacques Bertin's (1967) and Georges Th. Guilbaud's (1970 [1961]) convention of representing marriages as points and individuals as lines (applied by Jorion and De Meur [1980], albeit not to empirical marriage data), was the basis of White's *Pgraph* software which became the first operational instrument allowing for the systematic analysis of kinship networks.

Finally, a third source is Françoise Héritier's work (1974, 1981) on “semi-complex” alliance systems. The latter are characterised by ego-centric marriage prohibitions that apply to broad kinship categories, marriage being impossible, for example, with members of one's grandparents' clans, with those of one's lineage brothers' wives' clans, between individuals having a grandparental clan in common, and so forth. This research, directly motivated by Lévi-Strauss' (1967) conjecture that such systems might be best approached computationally, set out to analyze the patterning of empirical marriage choices among the patrilineal Samo (Burkina Faso) with the help of computer software (cf. Selz 1994). Héritier's data allowed her to propose an multilateral alliance model entailing ongoing exchanges between alternating patrines and the regular occurrence of marriages between distant kin – “consanguineous bucklings” –as soon as prohibitions allowed. By suggesting that such structural models might be found in the absence of “elementary” alliance systems, her research provided the initial impetus for a body of French work looking to identify recurring marriage patterns within empirical kinship networks (e.g., Guignard 1984, Segalen 1985 [also Richard 1993], Delille 1985, Cazès & Guignard 1991, Collard 1997, Houseman & White 1996, Barry 1998).

Within kinship studies, these various developments prompted a move away from “closed” algebraic models derived in large part from kinship terminology (Weil, H. White, Tjon Sie Fat) to describe *possible* alliance patterns, to an emphasis on more open, multi-levelled aspects of matrimonial connectivities as revealed by actual kinship data. Marriages are seen as taking place within a genealogical landscape composed of the circuits resulting from antecedent ties of kinship and marriage, whose properties play a significant role in determining the nature of subsequent marriage choices and the circuits they create. This relational landscape is thus not a static configuration but a set of statistical regularities built up and changing over time. It varies from one region of the kinship network to the next, fitting itself to local demographic and historical contingencies and leaving room for both strategy and happenstance. Nonetheless (at least this is the working hypothesis of kinship network analysis), it also has a number of general characteristics and recurrent features – particular qualities of extension, shape and texture – such that demographic, historical, strategic and

probabilistic considerations tend to be accommodated in certain ways rather than others. These general characteristics and recurrent features are the reticular alliance structures that kinship network analysis sets out to model and explain.

The genealogical circuits that compose the kinship network of a given community do not occur in isolation. Because individuals and/or the links between them can be implicated in any number of circuits, the latter invariably intersect, overlap, or encompass each other. As a result, identifying the circuits that compose a kinship network, determining how exactly they are related to each other, economically representing the morphology of these inter-connexions, and analysing these morphologies so as to account for reoccurring patterns, are not trivial tasks. They require the use of computer software, and in this respect, a reticular approach to kinship is a very recent development. While twenty years of research has resulted in a number of significant conceptual and methodological advances, this new-founded field remains largely programmatic.

Analytical instruments such as computer software are not conceptually neutral. The various packages that exist for kinship network analysis have been developed within the framework of specific research projects addressing particular issues and emphasizing certain ideas and questions over others. It is thus hardly surprising that certain operations are more easily done with some software than with others. Reciprocally, the development of these tools has resulted in a number of different, complementary theoretical contributions regarding the relational composition of kinship itself. *Pgraph*, and its attendant modules (*par-calc*, *par-side*, *ego2cpl*, etc.) that together compose the *Parente Suite* written by Douglas White (White & Skyhorse 1997), at present largely superseded by *Pgraph*-inspired algorithms implemented for *Pajek* (White, Batagelj & Mrvar 1999), draws on Weil's algebraic network-of-families approach to represent the network of actual marriages as signed graphs (Harary & White 2001), making empirical kinship networks particularly amenable to analyses using graph-theoretical concepts such as balance, centrality, cohesion, etc. (White 2011). *Genos*, written (and unfortunately since abandoned) by Laurent Barry (Barry 2004), introduced an innovative "positional" notation as the basis for the identification of kinship linkages, thereby providing an exceptionally rigorous foundation for the systematic computation of actual genealogical connections. *Puck*, written by Klaus Hamberger (Hamberger, Houseman & Grange 2009) with its emphasis on the complete and coherent enumeration of marriage types, allowed for a strict definition of the matrimonial circuit as represented by characteristic vectors, thereby opening the way for an arithmetic approach to the algebra of circuit composition (Hamberger 2011). All three efforts have been instrumental in developing the analysis of kinship networks as a specific branch within social network studies, defined by its own axioms and described by its own theorems (Hamberger, Houseman & White 2011), and in making available a large number of historical and ethnographic data-sets for kinship networks from societies around the world (<http://kinsource.tge-adonis.fr/kinsource/bin/view/KinSources/WebHome>).

Substantive advances in kinship network studies can be usefully grouped around four major issues: (1) identifying and counting marriage circuits, (2) determining and analysing the higher-order kinship networks composed of the interconnections between these circuits, (3) detecting structural patterns within such networks, and (4) simulating these patterns, notably as a means of evaluating the significance of observed regularities.

Matrimonial census

Even a fairly modest kinship network, of several hundred marriages over, say, three or four generations, contains an impressively large amount of matrimonial circuits that can be sorted into a smaller but still considerable number of marriage types. A matrimonial census

identifies these circuits, the particular kinship and marriage ties that compose them, and the types to which they belong.

Being able to make such a census so as to acquire a complete list of circuits, by marriage type, by couple, etc., is important first of all as a means of assessing the viability of a given data set. A genealogical network that serves as the object of analysis is a reconstituted entity. Providing an incomplete and partial image of the real kinship network, it invariably incorporates any number of distortions relating to genealogical depth, lateral extension, degree of completeness, and so forth. In many data sets, for example, some types of circuits (such as certain consanguineous unions) may be over-represented and certain lines of descent may be given pride of place over others. It is essential to be able to determine the nature of such biases, and to evaluate their sources: methods of data-collecting, informants' genealogical "amnesia," etc. Laurent Barry & Michael Gasperoni (2008), for example, have addressed the issue of agnatic and uterine bias in both ethnographic and historical kinship networks, showing how unbalanced data regarding paternal and maternal ascendants may affect the kinship census and give rise to misleading results. They also suggest various methods for dealing with such biases. [Relative frequency in the circuit census for different types are married of relatives against the raw number of each type of relative \(White and Jorion 1992\)](#) is a useful controlled comparison in drawing conclusions about marriage preferences, as is [comparison of circuit census frequencies against randomized marriages in each generation, holding constant its numbers of families and offspring, married and unmarried \(White 1999\)](#). Another the chronological or generational segmentation of the kinship network into genealogically more homogeneous sub-networks. A fourth consists in reducing the kinship network according to criteria of completeness, by taking into account only those marriages, for example, for which all four of Ego's and Alter's grandparents, or all eight of Ego's and Alter's great-grandparents have been recorded.

It is also worth emphasising that because marriages often bring together people between whom some sort of consanguineal or affinal connexion already exists, the presence of circuits within the network is of little significance in itself (their absence is indicative of missing data). It is above all the relative frequency of different types of circuits in relation to each other that can provide the grounds for speculations regarding marriage preferences and avoidances. Raw frequency rates of particular marriage types as a proportion of the total number of marriages easily lead to erroneous conclusions. Radically different pictures emerge when unions of a given type are considered within the context of the other types marriages to which these same marriages also correspond. Matrimonial circuits typically intersect or overlap, some circuits encompassing and/or being encompassed by others, such that the frequency of a given marriage type is to be evaluated not only with respect to the number of potential partners of this type that exist within the kinship network, but also in light of the other marriage types with which it is regularly combined. These issues are usefully reviewed in Hamberger & Daillant (2008).

Circuit censuses have also proved useful as an instrument for evaluating the applicability of alliance models derived from classificatory schemes or stated preferences and norms. Gabail & Kyburz (2008), for example, reconsidered the kinship networks of two Tuareg populations, the patrilineal Iwellemeden of Mali studied by André Chaventré (1983) and the matrilineal Udalen studied by Erik Guinard (1984), whose expressed preference for unions between a man and his maternal uncle's daughter (MBD) led their ethnographers to analyze their marriage practices in the light of Lévi-Strauss' notion of "generalized exchange," in one case positing an asymmetrical circulation of spouses between patrilineages, and in the other seeing individual unions as being organized into oriented affinal "spirals" (a closed series of oblique marriages). A careful scrutiny the collected data suggested that in both cases the proposed models, relying among other things on questionable extensions of the

category of “cross-cousin” – including in the first case individuals such as father’s brother’s wife’s brother’s daughter (FBWBD), and in the second, the children of the classificatory sister of Ego’s classificatory brother’s wife – were empirically unwarranted. On the one hand, asymmetrical flows of spouses between (largely endogamous) lineage groups among the *Iwellemeden* proved to be statistically insignificant, and more than half of the recorded marriages with mother’s brother’s daughter were at the same time between agnatic kin. High frequencies of mother’s brother’s daughter marriage among the *Iwellemeden* was thus shown to be an artefact of a preference for lineage endogamy with little connection to the structural model of “generalized exchange.” On the other hand, the ability to interpret Udalen marriage practices *a posteriori* as organized into affinal spirals turns out to be a consequence not only of an overly generous understanding of cross-cousinhood, but also of the extreme density of their marriage network: such spirals can be shown to exist to the same degree in any number of other extremely dense kinship networks for populations with radically different marriage preferences and prohibitions.

Another, more theoretical and as of yet largely unexplored consequence of a systematic and exhaustive matrimonial census, is that it leads to a renewed appreciation of the role played by classificatory kinship ties. Most circuits within most kinship networks do not involve close kin marriages, even in those communities where such unions are allowed and may be said to be preferred. Indeed, from a kinship network perspective, in which marriage structures are envisaged as genealogical landscapes whose recurrent, self-organizing features orient the aggregation of particular marriage choices, close kin marriages may be appreciated as largely peripheral phenomena. They appear less as the generative “hard core” of the matrimonial system than as the reduced, limiting-case expressions of its more comprehensive reticular dynamics. In other words, it may be that the emblematic pre-eminence of close kin marriage obscures its structurally marginal role.

Finally, a matrimonial census reveals that most of the circuits that comprise a kinship network correspond to marriages not between kinsmen (e.g., unions with MBD, FMZSD, etc.), but between affines (unions with ZHZ, MBWBD, etc.) or affines of affines (unions with ZHZHZ, MBWBDHZ, etc.). One of the challenges of kinship network analysis had been to account for these non-consanguineous marriages –globally called affinal “relinkings” (*renchainements* in French, cf. Jolas *et al.* 1970)– in a systematic fashion, as providing the possible basis for a given population’s matrimonial system. Such a perspective implies a considerable departure from the emphasis alliance theory places on close kin marriage, and opens onto the modelling of “complex” alliance structures in their own right.

In this respect, and other research on marriage strategies among European populations notwithstanding (e.g., Lamaison 1979, Delille 1985), Martine Segalen’s (1985) study of matrimonial relinkings in Lower Brittany (cf. also Richard 1993) was groundbreaking in that it demonstrated, on the basis of extensive community-wide genealogical data (1720-1980), the existence of a generalized marriage system founded upon repeated relinking. The local community was composed of a set of bilateral kindreds matrimonially relinked through widow remarriage and ongoing exchanges of spouses between family lines. Consanguineous unions were avoided and kin ties systematically overlaid with affinal connexions such that four spouses typically had two ancestral couples in common (Figure 1). At the price of a high degree of mobility of domestic groups (exclusive of emigration), this practice allowed for the continuous recomposition of economically viable properties fragmented by a strict principle of egalitarian inheritance. All else being equal, a family line’s wealth varied with the intensity of its relinking arrangements. A similar marriage system, but characterized by a vertical inflection due to the presence of “house” properties inherited by a single heir, and entailing the systematic emigration of a section of the population, has been documented and analyzed by Brudner & White (1997) for the Austrian village of Feistritz. Here again, although

villagers often stated that they were “all blood related,” no consanguineal unions were recorded over the hundred year period of 1860-1960. Interfamily relinking, occurring at a rate significantly greater than random for connexions up to three generations back (White 1999), defined cohesive blocks composed of couples who inherited “houses” and their associated farmlands. The non-inheriting individuals were often given quitclaim inheritances to family property. This system thus acted to divide the members of each generation into two social classes corresponding to the economic classes of the village: on the one hand, a cohesive core of wealth-holding heirs who married and remained within the farming community, and on the other, non-inheriting parties who typically married outside or moved elsewhere.

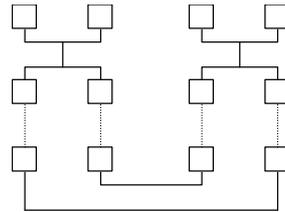


Figure 1. Affinal relinking between two consanguineous families

Circuit interconnection

As mentioned, matrimonial circuits typically occur not in isolation, but in close conjunction with others as part of an ever-emerging genealogical “landscape.” As a result, one of the central concerns of a network approach to kinship is understanding how circuits combine with each other to give rise to statistical patterns that define reticular alliance structures. A particularly simple yet theoretically far-reaching example of the role played by circuit aggregation in the emergence of matrimonial regularities is found in Laurent Barry’s study of endogamous marriage between parallel patrilineal cousins among the Fulani of Cameroon (Barry 1998). By taking into account all of the genealogical circuits linking the spouses of each union, he was able to show that certain “affinal combinations” of Ego’s and Alter’s marriage with those of Ego’s and of Alter’s ascendants were favoured over others. Barry discovered two rules of prohibition, which are logically equivalent: 1) A man does not marry a first cousin when his father married a FBD (b and d) and 2) does not repeat the same patrilineage alliance as his father (b and d in the Figure). Combinations a and c in Figure 1 occur frequently (in 12 and 15 cases) while b and d occur not at all, although all are of equal probability. Similarly, overall, FBD marriages occur twice as frequently as MBD. Whereas “Arab marriage” (FBD) had been classically interpreted as an agnatic “preference,” e.g., as in each senior generation in Figure 1, which could follow for the junior generation (c, d) but does not occur as in d. Considering the zero occurrence of MBD in b but its high frequency in c but not d and elsewhere these various types of “Arab marriage” are demonstrated to be the consequence of avoidance of repeated (“uterine”) alliances from the wife’s patrilineage.

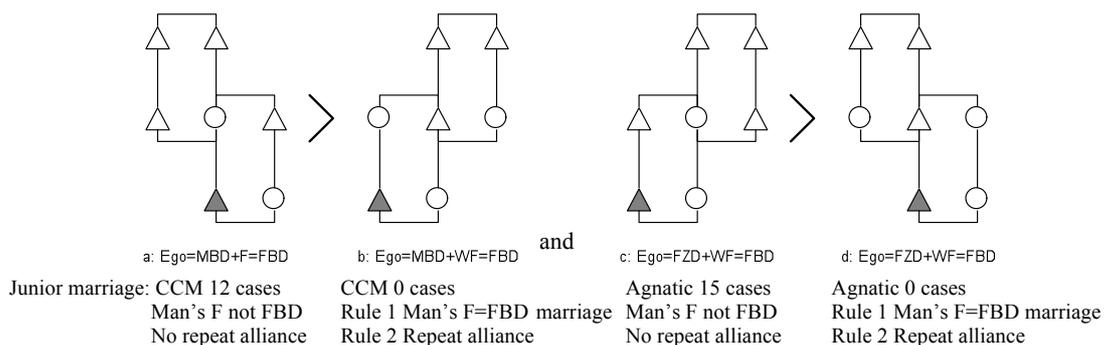


Figure 2. Relative frequencies of different affinal combinations (Barry 2008: 27-30)

Another, less egocentric approach deriving from block modelling and the notion of “cohesion” in social networks was developed by Douglas White (2004, 2011). Here, the favoured object of analysis is not the entire kinship network as such, but that part of the network that is composed of marriages that are connected to each other by at least two independent genealogical paths. The result is a matrimonial bi-component (MBC), a cohesive cluster of “structurally endogamous” marriages (White 1997), linked together by a set of interdependent marriage circuits. A given kinship network may contain several such (autonomous or linked) MBCs that comprise the “core” of the network, and whose size, number and modes of connexion provide valuable indications regarding the composition of the data set as a whole. It is best to treat a data set containing two large, unconnected or little-connected MBCs as two different kinship networks, as most viable data sets have a core of either a single MBC or one overwhelmingly large one, called the network’s “kernel,” which becomes the privileged object of analysis. As a general rule, a network’s kernel is about one third the size of the kinship network as a whole. Reducing kinship networks to their kernels (or cores) has many advantages: it makes disparate networks formally comparable and facilitates their study with the tools of social network analysis. It also paves the way for multi-levelled analysis in which a networks of relations can be embedded within the nodes of another network at a higher level, or what Harary & White (2001) p-systems: thus marriage relations (e.g., “couples”) can be treated as nodes linked by individuals as descendants (as in p-graphs; White and Jorion 1992); types of marriage circuits can be treated as higher-order nodes linked by frequencies of affinal connection (as in the second-order graphs produced by *Puck*, see Hamberger, Houseman & Grange 2009), etc. Further, White & Johansen, in their study of Aydınli nomads in Turkey (2005), demonstrated the usefulness of identifying “structurally cohesive” (k -connected) groups identified by the maximal set of couple in interfamily networks are linked to each other by two or more two independent paths. These may overlap, as where separate genealogical bi-components (MBCs) of couples or individuals (each connected by two or more independent paths between them; p-graph networks do not have k -connected groups higher than 2 assuming children to have only 2 parents) may have a single node in common. These build “strong ties” (Granovetter 1973) that for the Aydınli were found to navigable (White and Houseman 2002, White and Johansen 2005) so as to connect allies to allies to allies outward throughout the community. “Extracohesive” extensions to cohesive units may contain pairwise k -connected sets (White & Newman 2001) where two nodes are connected by k independent paths. Cohesive units in networks of kinship or other associative ties are usually predictive of the kinds of cooperative outcomes that groups can accomplished by redundancy of information and links or chains of mutual support. Among the Aydınli, for example, those individuals or families that were not in the network bi-component (2-connected cohesion or structural endogamy) and thus lacking multifaceted support within the community, tended very strongly to be those that emigrated out to resettle in towns or villages.

Segmenting the kinship network according to genealogical or other criteria applied to the individuals or collectivities involved provides another, complementary approach to the issues of circuit combination and the delimitation of theoretical objects of research. For some areas of investigation, the matrimonial bi-component, comprised as it is of *all* of the network’s interconnected marriage circuits, whatever their length might be, including those whose sociological relevance is far from evident, may be deemed to be too encompassing. Grange & Houseman (2008), taking the kinship network of bourgeois Jewish families in finance and industry installed in Paris at the end of the 19th century as an example, have

explored various ways in which sub-networks can be extracted from the kinship network as a whole. One way, implemented by *Puck*, is to produce “restricted” censuses and sub-networks composed of only those matrimonial circuits falling within predetermined limits of height (maximum length of successive parental links) and width (maximum number of consanguineal chains, where blood marriages = 1, first order affinal relinkings, that is, marriages between affines = 2, second order affinal linkings or marriages between affines of affines = 3, etc.). A typical restricted sub-network, for example, might be composed of all consanguineous marriages of maximum height 3 (up to and including unions with second cousins), all marriages between affines of maximum height 2 (up to and including unions between two sets of first cousins) and all marriages between affines of affines of maximum height 1 (up to and including unions between siblings and the siblings-in-law of their siblings-in-law). Other, exogenous criteria can be used as well to produce sub-networks composed of all those circuits connecting persons who were born or whose marriages took place during particular a period, all those circuits connecting individuals born in a particular area, or who migrated, or who share the same religious affiliation, income level or set of names, etc. Using these procedures separately or together with formal discriminations of “cohesiveness” (for example, by reducing such “restricted” sub-networks to their matrimonial bi-components) allows for a fine-grained, sociologically and historically anchored analysis of the genealogical “landscape” and its incidence on the ordered aggregation of marriage choices.

Emergent patterns

One of the ambitions of a reticular approach is to identify matrimonial structures characteristic of the organisation of kinship network as a whole. Such statistical properties are emergent: they are generated through the coordinate integration of a variety of different marriages types in accordance with certain overarching principles. While resulting from the combination local ego-centric initiatives, such structures are not easily accounted for by synchronic, ego-centric models.

One particularly well-attested, global structure of this nature is what has been termed “sidedness”: a pattern of matrimonial dual organisation that is not determined by named moieties or principles of descent, but derives from the convergence of a variety of different processes (terminological distinctions, parallel reckoning, diametric ordering of social interaction, etc.), realized in the patterning of the network as a whole (Houseman & White 1996). A viri-sided network, for example, is one in which marriages between genealogical patriline are such that the latter can be ordered, to a statistically significant degree, into two exogamous sets (viri-sides). Viri-sidedness automatically implies uxori-sidedness (and vice-versa) in the absence of oblique unions (White 2010). Sidedness has been shown to exist among cognatic, “Dravidian” groups in Amazonia (Houseman & White 1998a) and in South Asia (Houseman & White 1998b), and among “settled” Australian Aboriginal populations (Houseman 1997); it would also seem to “go without saying” in other places as well (e.g., Bloch 1995). Another, less constraining bipartite structure, found in Polynesia (Houseman & White 1996), is “dividedness,” characterized by a succession of generation-deep, unnamed matrimonial moieties, in which marriages between sibling sets are such that these sets can be divided into two exogamous groupings (divides).

Denham and White (2005) and White (2011:140) summarize graphically their work on the Alyawarra where a large structurally endogamous bicomponent in the kinship network divides according to both patriline and matriline, which necessarily intersect (White 2010) to form the alternating generations typical of many section-system Australian societies. Denham’s data on actual ages show that due to an average age of females that is 1/3rd younger than men the siblings-in-law links within generations, excluding G^{+2} and G^{-2} marriages, are

age slanted. A spiral model was done for the Alyawarra in 1979 (Denham, McDaniel, and Atkins), analyzing the pattern of the network of combined kin terms and marriages but it also showed that 14% of the marriages did not follow a double-helix for alternate spiraling lines of women across vertical lines of men (or vice versa, each entailing the other). This is not a mental model of individuals but a product of kin term proscriptions on marriage behavior: 98% or more for all kin terms except for one subsections, D1, out of eight, with 15% exceptions, the errors being where ego uses M and MB terms for *both* sections of the opposite patrimoiety, equating MBSD=MBD=M, which by use of an Omaha type usage *prevents* certain possibilities MBD marriage. About 1/3rd of the marriages links between proper classificatory kin, however, violate the spiral model, by marrying gerontocratically with G⁺² men.¹

Taking an alternative, more micro-oriented line of approach, Daillant & Hamberger (2008) have accounted for differences between three dense Amazonian kinship networks as structural variations of the same underlying, Dravidian principle whereby the genealogical field is exhaustively divided into two classes: “crossed” kinship relations with whom marriage is authorised, and “parallel” relations with whom marriage is theoretically prohibited. Given the fact that spouses are typically connected to each other by a multitude of different, pre-existing genealogical paths, and given the variety of mechanisms capable of producing any given path, it becomes problematical to assume, as is often the case, that it is enough to count the frequencies for certain marriage types (“crossed” unions) to confirm or invalidate stated or implicit marriage norms. By taking not some but all of the empirical connections between spouses into account, their aim was to characterise the global morphology of the kinship networks as ongoing self-organising systems grounded in a particular binary logic whose limits they set out to explore. Specifically looking at the relational spaces created in each case by the interconnections between the multiple pre-existing genealogical chains linking spouses together, they found that whereas among the Bolivian Chimane (753 married couples), *all* of the kinship connections between a man and his wife must be “crossed,” among the Brazilian Parakaña (192 marriages) characterized by the practice of oblique marriage (and have a preference for close kin marriage), *at least one* of these connections must be “crossed,” and among the Arawete, also of Brazil (197 marriages), with a specific institution of formal friendship whose “anti-dravidian” logic impacts significantly and negatively on bipartite marriage patterning, even if none of these prior connections is “crossed,” the marriage itself, by transforming kin into (marriageable) non-kin acts to legitimize the union as “crossed” after the fact. In this way, these kinship networks are revealed as concrete transformations of a model, ideal types within the Dravidian landscape.

Simulation and analytic models

With the availability of large-scale kinship networks and the development of analytical tools capable of exhaustively identifying the matrimonial circuits they contain, simulation techniques have become increasingly important as a means of reliable interpretation of empirical results. Adequate simulation methods can provide the grounds not only for the

¹ This is often forced because helical same-generation marriage often works less well for one of the two alternating spirals of women with few daughters in some classificatory lineages and generations, leaving the same-generation men they might normally marry men to seek G⁻² women in the proper section above and to their upper left in the diagram rather than those at upper right (See White 2010). Demography may thus deflect these women from same-generation to gerontocratic marriage when taken as wife by an older classificatory MB or FMDD. Conversely, men may marry a widow who is a classificatory FFBDD and much older than him. Such is the complexity that can be represented by p-graphs and inspected visually.

neutralisation of data set biases, but also for evaluating the statistical significance of observed marriage type distributions.

One approach has been to take actual kinship networks as providing their own baseline for random simulations that test whether a the observed pattern of marriages has elements that would be expected at random, given the population structure, as opposed to elements that are significant departures from randomness. White's (1999) "controlled simulation" or permutation method holds the numbers of marriages and family compositions (male and female offspring) in each generation constant, and permutes who marries whom in each generation. Constraints on the simulation can specify that marriage permutation cannot violate certain rules (e.g., no marriages between siblings, no adjacent-generation unions, etc.). Since the number of offspring of each member of a couple are held constant in the permutation, generational composition will not change, but random marriages within this constraint may change the distribution of marriage-type frequencies for number of available relatives of each type. This method, although not without problems ([while the minimal number of generations for a p-graph is determinate, the level assigned to a parent in some cases can be indeterminate, and although parent-child distances can be minimized, the Pajek algorithms generally used to compute generations do not include this feature, and do not deal with slanted generations among siblings-in-law due to average age-of-marriage differences between men and women as in our Alyawarra example](#)), does away with the need to independently calculate demographic factors and allows both for an evaluation of the significance of observed marriage patterns and for the exploration of the organizational consequences of modifications in simulation rules.

More recently, a probabilistic version of the permutation principle has been applied to the analysis of alliance networks. The permutation of alliance networks, simpler than that of (genealogical) kinship networks, corresponds to a random re-distribution of marriages between groups. Roth *et al.* (2012) have developed an analytical model that, given the number of marriages and intermarrying groups and assuming that the number of married men and women in each group remains constant (within expected deviations), mathematically predicts certain characteristic morphologies of the resulting alliance network: degree of endogamy (the proportion of unions between members of the same group), degree of matrimonial concentration (the recurrence of unions between the same groups) and degree of symmetry (the proportion of same-sex vs. different-sex relinkings between groups). The next step is to develop such predictive models for the distribution of genealogical circuits within kinship networks, [controlling also for generation \(White 1999\)](#).

Another direction of research is the simulation of virtual fieldwork, a prototype of which has been implemented in the software Puck. Applying this idea to alliance networks, the SimPa project research team set out to model genealogical datasets by a two-step process. The first gives the "real" network generated by the marriage choices of the agents themselves (groups), as determined by varying degrees of preference for endogamy (proportion of marriages within a group) and for relinking (proportion of marriages between groups already connected by marriage). The second transforms this network into the "observed" network resulting from biases introduced by the ethnographer, as determined by research strategies entailing varying degrees of immobility (additional informants chosen from the same group) and of snowball sampling (additional informants chosen from an allied group). One clear result of this work has been to show the crucial role played by observational bias – typically resulting in an overestimation of the concentration of marriage relations – in the composition of genealogical data sets (see Hamberger *et al.* 2012). Generalizing this method, Gargiulo *et al.* (2012) have profitably studied the impact of different data-mining algorithms on weighted network exploration.

Obvious advantages of the multi-level reticular approach to kinship are the actual measurement of network features that we have defined and illustrated: structural endogamy, bicomponents, embedded levels of multicohesive components, uniquely defined; sidedness and dividedness components and network theorems about the antecedents and concomitant causes of balance properties in subnetworks; generational levels and demographic structure by generational levels of the distribution of family sizes and genders of children; and a host of other features. These advantages multiply when other data are overlaid for further analysis on the scaffolding of the kinship networks. Approaches that use these measures are far superior to impressionistic interferences from limited features about how “kinship systems” are constituted. Kinship and kinship networks are not as problematic as they seemed to be in the period that Schneider wrote “Some Muddles in the Models” (1965), or *A Critique of the Study of Kinship* (1984). Most of the many egregious errors that Schneider identified have been repealed and his critiques of the positivism and ethnoscience of the 1960s have been vindicated.

In one of the most formidable of these developments, Padgett (2010) used White’s (1997) bicomponent measure of structural endogamy and Moody and White’s (2003) measure of structural cohesion:

to measure the prestige, or status value, of a lineage in the Florentine marriage market, and hence its change over time... [i.e.,] to assess the degree to which a family with a last name was in the core or on the periphery of the Florentine intermarriage network. In particular, the statistical concept of *structural cohesion* [defines the network core] as the set of nodes in such deeply integrated and hard-to-remove network positions.... Social mobility in this marriage context means movement of a family, through its pattern of marriages with other families, into or out of the core of the city’s marriage network.... Movement into or out of the core can be interpreted as movement of families into or out of the Florentine marriage elite. (Padgett 2010:374-375)

Movement into or out of the weaker *structurally endogamous bi-component*, notes Padgett, represents “movement of families into or out of the Florentine marriage market itself.” Thus, Padgett is using the multi-level properties of the kinship network first for measuring structural endogamy (bicomponent structure) in the network of families and second for measuring structural *k-cohesion* at the higher level of the network of lineages.

As an example of the power of the multi-level reticular approach, the analysis of these data changes the understanding of Florentine social, economic, and political history. For Padgett (2010:391): “What difference did these mobility and marriage dynamics make for the demographic success and failure of Florentine families? ... The overall picture is that three factors drove the demographic growth and decline of Florentine families during the Renaissance: wealth, political factional success, and being within the marriage-network core” defined by White’s “structural cohesion” (Moody and White 2003).

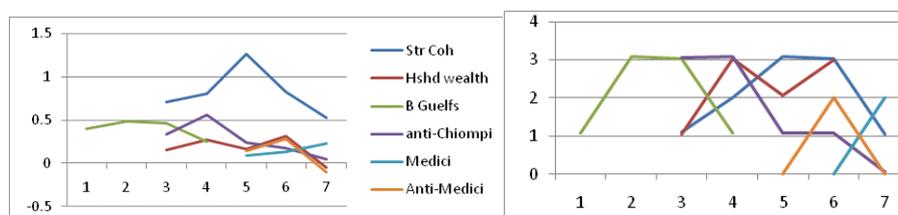


Figure 3. Growth or decline in Florentine family size during the Renaissance, 1282-1317 (period 1) through 1458–80 (period 7) is predicted by structural cohesion (White and Harary 2001). Graphs at the left show predictive regression coefficients, and, at the right, the statistical significance of the predictions (N=1,697 distinct families). The Black Guelf faction, after winning the struggle in 1301 (X) between Blacks and Whites, were endogamous for a century, and the anti-Chiampi faction, after putting down the Ciompi revolt in 1378 (X) between Blacks and Whites, were also endogamous for a century. Average household wealth predicts a small fraction of the variance in family growth or decline, compared to marriage-network structural cohesion between

families. The negative effect of family size (larger families, lower growth in size) has less effect than household wealth, except for period 4 (1379-1403).

The Florentine structural cohesion, wealth, and winning political faction predictions of growth/decline in family size reach as high as $R^2 = 0.42$ and $R^2 = 0.29$ in periods 4 and 6 in Fig. 3, but these graphs show high regression coefficients and significance for inter-family cohesion in periods 4-6 prior to the Medici takeover of the state and as the power of winning factions declines.

Conclusion

The multi-level reticular approach has had effects in unexpected ways, including 80+ kinship network databases generated by ethnographic publications recently posted by anthropologists at the Kinsources (2009) open archive website. Any of these databases can be analyzed by any of the software discussed here. Using the current software, it is now possible to analyze large kinship networks of 200,000 or more family nodes. We have emphasized ways forward, given new databases and software, as well as paths of previous development in the field of kinship. These began in one form in England (Rivers 1910), took logico-deductive and mathematical form in France (Weil 1949, Lévi-Strauss 1949) and a more empirical network-oriented form in Britain (Leach 1961), given Jorion as a crossover from Lévi-Strauss to Leach, switched from idealized models to empirical networks (White and Jorion 1992), were developed further by Americo-Slovenian informatics (White, Batagelj and Mrvar 1999), and then by Anglo-French teams (Hamberger, Houseman and White 2011) and others, and has opened new historical findings for Renaissance Florence using the multi-level reticular approach. These developments represent a successful international effort in anthropology and the historical sciences.

A significant area of anthropological and evolutionary study where the reticular and multi-level approaches to kinship can be newly applied is to the many cases in the Kinsources data files where the genealogies of foragers have been provided (often by W.W. Denham) from numerous ethnographic studies, while 339 forager societies, overlapping with those with sociocentric genealogies have been extensively studied by Binford (2001). Binford's meticulous codings of band, subgroup and family sizes, and the spatial and environmental distributions have been analyzed by complexity scientists (Hamilton, Milne, Walker, Burger and Brown 2007) who have shown a fractal organization of family and successive sizes of embedded groups that is uniform at all levels except for continental differences. Here, differences in fractality coefficients at the continental level (as between Australia, Africa and other regions) could well be put into correspondence with multi-level network genealogical structures.

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