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A tutorial on methods for the modeling and analysis of social network data

Garry Robins

Melbourne School of Psychological Sciences, The University of Melbourne, Australia

HIGHLIGHTS

- A tutorial review of some fundamental ideas and important methods for the modeling of empirical social network data.
- Basic concepts from graph theory and central elements from social network theory.
- Recent methodological developments in social network analysis.

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ABSTRACT

This article provides a tutorial review of some fundamental ideas and important methods for the modeling of empirical social network data. It describes basic concepts from graph theory and central elements from social network theory. It presents models for the network degree distribution and for network roles and positions, as well as algebraic approaches, before reviewing recent work on statistical methods to analyze social networks, including boot-strap procedures for testing the prevalence of network structures, basic edge- and dyad-independent statistical models, and more recent statistical network models that assume dependence, exponential random graph models and dynamic stochastic actor oriented models. Network social influence models are reviewed. The article concludes with a summary of new developments relating to models for time-ordered transactions.

1. Introduction

It is now widely argued that human social networks are central to the structure and dynamics of our contemporary social world (Barabási, 2012). In keeping with this new enthusiasm, "network science" is claimed as a distinctive, emerging research discipline. Brandes, Robins, McCranie, and Wasserman (2013), in the first editorial of a new journal *Network Science*, pointed to familiar statements that "networks are everywhere", but argued that a science requires more than this. Rather, network science is based on a conceptual unity across many disciplines: an ontological commitment to the primary importance of relationships between entities. The encroaching disciplinary spread of network science is very wide indeed, with networks given increasing notice in, for instance, information and computer science, mathematics, communication, engineering, management and organizational science, economics, political science, psychology, anthropology, public health, medicine, physics, statistics, sociology, animal behavior, biology and history.

Social science disciplines feature prominently on this list, psychology among them. Network perspectives are perhaps most relevant to social, organizational, developmental and educational psychology. Yet, as noted below, there was something of a divorce between network and psychological research in the 1970s. This historical gap – related to differences between individualized and system-based research designs – is only just being bridged.

It is certainly the case that in a globalized world, connected by the internet and social media, it is easier than in the past to accept a paradigm that emphasizes social systems and social connections. Examples abound. Different types of networks serve as channels through which knowledge is diffused, opportunities are recognized, influence is exerted, support is offered, stereotypes are formed, disease is spread, and actions are coordinated. Networks of organizations govern our environmental systems and respond to human and physical disasters. Organizations structure and restructure internally to obtain efficiencies, building new formal systems at the same time that they inadvertently create informal networks through which collaboration actually occurs. Health behaviors spread across social systems, crime is conducted through illicit networks, and community movements are prompted by social media. Social connections are crucial to each of these phenomena.

Human social systems

Yet these examples also illustrate the inherent complexity of social systems: the macro-level behavior of a social system, such as an organization or a community, critically depends on the precise nature of self-organizing network-based social processes occurring at local levels of interaction. In order to understand and manage

E-mail address: garrylr@unimelb.edu.au.

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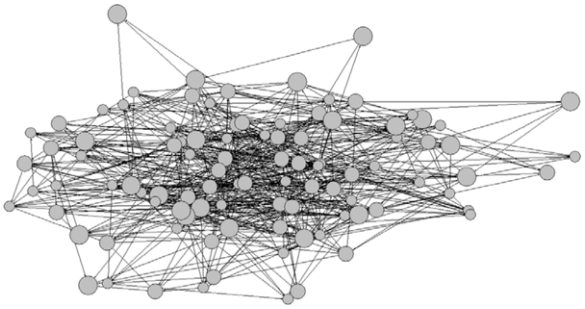

Fig. 1. A friendship network of undergraduate students.

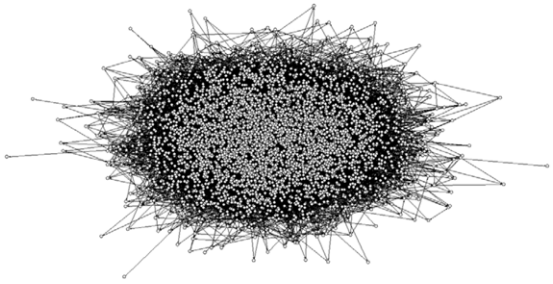

Fig. 2. A simulated network of social contacts for a community of 5000 derived from a snowball sample.

such social systems, we need a precise appreciation of the nature of these local interactions and of the ways in which they cumulate to determine system-level properties. We need to do this in ways that fully take into account important features of observed human social systems.

Social systems – whether large scale communities or smaller scale organizations – are arenas of cooperation, coordination and conflict that necessarily involve relationships among individuals. These relationships structure into regularities and patterns that can be understood in terms of networks. But once we take this conceptual step, it becomes more difficult to pull apart the system and study aspects of it in isolation. This is a picture of complexity, not of reductionism (Barabási, 2012).

This has led to tensions with traditions in psychological research based on individualized research designs that include randomized control, random sampling and general linear models. Robins and Kashima (2008) argued that this tension can be resolved, but there needs to be a recognition that networks require different methods.

To illustrate the complexity that network analysis can present, consider the two network visualizations in Figs. 1 and 2. Fig. 1 depicts empirical data from a study of 102 undergraduate students in a university college. The nodes represent participants and the links between them are friendships. The size of each node reflects the strength of alcohol usage. A typical network-based research question would be whether alcohol usage is associated with friendship among these students. With longitudinal data, one can proceed further to ask whether participants choose their friends based on common alcohol usage, or whether participants are influenced by their friends to increase their alcohol intake (or both). Fig. 2, on the other hand, represents social connections in a suburb of 5000 inhabitants. This data is a simulated network derived from a statistical model with parameters estimated from a snowball sample of participants in that community (Daraganova et al., 2012). The primary research question was to understand the precursors of urban unemployment and to determine to what extent the relevant factors were social, geographic or individual phenomena. Another application would be to understand the likely spread of a highly infectious disease such as bird flu across an urban community. As can be seen from the figures, it is not possible to address these different issues simply by inspecting the network visualizations, nor is it obvious how they would be analyzed with standard statistical approaches commonly used in psychology.

So, it is important that the network-based modeling of social systems is making rapid progress. We have reached the methodological point where we can construct network models that reproduce a very wide range of important local and global features of a network: for instance, variations in local connectivity of each network actor, the degree of local clustering among actors, and the general distribution of connectivity (e.g. Goodreau (2007)). Models for social network processes are now embedded within time (Snijders, van de Bunt, & Steglich, 2010), social settings (Schweinberger, 2003) and space (adams, Faust, & Lovasi, 2012). Analyses that include local interactions between network processes and individual characteristics (including psychological variables such as beliefs and attitudes) are standard. There are exciting new advances in event modeling involving social relationships (e.g. systems of email or social media exchanges), some of which are in articles in this special issue. Methodologically, network science is flourishing.

Networks and psychology

Empirical social network research goes back at least to the 1930s with the ground-breaking introduction of sociometry by Moreno (e.g. Moreno and Jennings (1938)). In his history of social network analysis, Freeman (2004) observed that, although sociology and anthropology drove many of the early methods, psychological researchers were prominent. For instance, the 1930s Hawthorne studies (Roethlisberger & Dickson, 1939), famous in organizational psychology, included a network analysis of the Bank wiring room, a major component in the Hawthorne research program but one that eludes description in most modern psychology texts discussing the Hawthorne effect. This gap reflects the theoretical and methodological tensions described by Robins and Kashima (2008), tensions that led to fading interest in social network methods with the rise of social cognition studies in the 1970s. Even today, the dramatic growth in network-based research and methods, including new ideas from physics and other disciplines (Freeman, 2011), does not always receive attention in psychology (Mason, Conrey, & Smith, 2007). So it is timely for a special issue of the Journal of Mathematical Psychology to review social network methods and to give a flavor of the most recent methodological developments.

It is important to understand why the standard analytic approaches typically used in psychology are not always applicable in network-based research. There are a variety of reasons but the most fundamental lies in the nature of dependence in social network data. Brandes et al. (2013) argued that dependence was at the heart of the network paradigm. A standard assumption of general linear model techniques, on the other hand, is that observations are independent. A network perspective overtly assumes complex dependence among observations. In particular, as Brandes et al. point out, it is a structuring among the domain of a variable that is different. In individualized designs, a variable can be seen as a function that assigns a set of numbers (the range) to a set of entities (the domain); and while the range may be structured (e.g. by different measurement scales), it is expressly assumed that the domain is not. Networks, however, place a complex dependence among the entities in the domain. The importance of this dependence assumption is not just that it has methodological implications; more to the point, it is a basic theoretical claim about appropriate ways to aggregate or

combine socially-based observations (Robins & Kashima, 2008; White, Boorman, & Breiger, 1976). Analytic methods that attempt to 'compensate' for observational dependence miss the point. A network-based social system has dependence at its heart. To wish away dependence in order to apply standard techniques is to undermine the theoretical basis of a network conceptualization.

As Robins and Kashima point out, the gap between psychology and network is two-way: network analysts have been a little too reluctant to accord motivations and other psychological features to the nodes in their graphs. So, social network research often under-theorizes individuals; while social psychological research often under-theorizes social contexts, structures and systems. Yet, there is no need for psychologists and network researchers to abandon what they already do so well. Rather, there needs to a richer intersection of psychology and networks in productive ways. Hence, this special issue of the Journal of Mathematical Psychology.

This tutorial

This article provides a tutorial review of some fundamental ideas and important methods for the modeling of empirical social network data. The emphasis is on the analysis of data, so the article does not focus on the extensive work on simulation and other models not specifically designed for data fitting. Given the frequency of new analytic developments, this review concentrates on selected major methodological themes in current social network research and does not aim to cover everything in this rapidly growing field. Motivated readers will find much detail of interest in the older text by Wasserman and Faust (1994) and in more recent volumes such as Carrington and Scott (2011), Carrington, Scott, and Wasserman (2005), Jackson (2010), Kolaczyk (2009), and Newman (2010). Butts (2008a), Snijders (2011) and Wasserman and Robins (2012) provide shorter reviews of current social network methodologies.

The article begins with a review of some basic network terminology and concepts. Lists of definitions can be a little dry, but those wishing to undertake network studies need to be familiar with these fundamental ideas, so they are included for the sake of completeness. I go on to describe a number of popular methods specific to different types of network data.

1.1. Terminology and notation

Social network

A *social network* comprises a set of social entities, called *actors*, and at least one but possibly several social relationships of different types among them. A *relational tie* is a social connection of a particular type between two actors (two actors and the possible tie between them are referred to as a *dyad*). The types of relationship studied in social network research vary enormously: communication, collaboration, enmity, friendship, acquaintanceship, trust, business partnerships, marriage, kinship, and so on.

Graphs

A social network can be represented and visualized as a graph. Network and graph terminology is frequently used interchangeably.

A *graph* $G(N, E)$ is a mathematical object with a *node set* $N = \{1, 2, \ldots, n\}$ and an *edge set* E comprising edges between pairs of nodes. Sometimes nodes are called *vertices*. An edge may be *undirected* in which case it is a property of an unordered pair of nodes $\{i, j\}$; or *directed*, in which case the edge is a property of the ordered pair and is directed from the *sender* node i to the *receiver* node j. For a directed graph, the term *edge* is usually replaced by *arc*. An induced *subgraph* of a graph G comprises a subset of node set N and the edges that exist in G among those nodes.

A graph can also be represented as an $n \times n$ *adjacency matrix* with a cell representing the presence or absence of an edge by 1 or 0, respectively. By convention, in much social network analysis the diagonal entries are forced to be zero, representing that actors do not have relational ties with themselves. For undirected and directed graphs, the adjacency matrix is symmetric and asymmetric, respectively. The adjacency matrix may also be valued, representing the strength of a social relationship. For the most part, this article will concentrate on binary edges.

A convenient statistical notation is to specify binary variables X_{ij} to denote the presence or absence of a tie between i and j (undirected) or from i to j (directed). An instantiation is denoted x_{ij}. The full set of variables may be denoted $\mathbf{X}$ with instantiation $\mathbf{x}$.

Attributes

Actors may have attributes of various types to represent individual-level properties. In this article, we use the notation Y_i to denote a variable pertaining to the attribute Y of node i with an instantiation y_i. An attribute variable may be binary, categorical or continuous. Of course, in any one study, a number of different attribute variables may be measured.

Other types of social network data

The description above pertains to a *unipartite* network which has one type of node and (usually) one type of relational tie. A *bipartite* network has two types of node with ties possible between nodes of different types but not between nodes of the same type. A bipartite network can represent membership or participation (for instance, persons participating in events). In this case, the adjacency matrix is rectangular rather than square. There are a range of methods for analyzing bipartite networks (see Latapy, Magnien, and Vecchio (2008) and Wang, Sharpe, Robins, and Pattison (2009)), many of them analogues of methods used for unipartite networks. In this article, we will concentrate on unipartite methods.

We refer to a *multiple network* as having one type of node but with more than one type of relational tie, so that dyads may have different types of relationships among them. When different types of relational tie occur simultaneously in a dyad, the dyad is said to have a *multiplex tie*.

Recent attention has been directed to *multilevel networks* with a bipartite network structure (i.e. two types of nodes) but with relational ties (usually of different types) possible within the two sets of nodes (e.g. Lazega, Jourda, Mounier, and Stofer (2008) and Wang et al., (in press)—see Iacobucci and Wasserman (1990) and Wasserman and Iacobucci (1991), for earlier work).

Dynamics

Longitudinal network data is typically collected in a panel design on the same set of nodes. There may be some small changes to the node set, but most of the nodes are assumed to remain active in the network across the time period of data collection.

In some cases, the network is fixed across time and the diffusion of attribute change through processes of social influence is studied dynamically. This approach is often taken in studying the spread of disease through contagion. Of course, attributes and ties frequently co-evolve so the assumption of fixed network may be inappropriate. Again both attribute and tie data may be collected on the one set of nodes.

These approaches assume that the relational tie is the appropriate concept. A relational tie is viewed as changeable but of indefinite duration, possibly long-term. A *relational transaction*, on the other hand, refers to a time-delimited exchange within a dyad. A transaction is time-stamped, of relatively short-term duration, with a specific beginning and an end. Examples include a purchase, an email, and a specific contact that might permit disease transmission. One of the exciting new areas in network analysis is the study of systems of relational transactions. This is the focus of several of the articles in this special issue.

2. Social network concepts and theories

2.1. Some basic graph and network concepts

In this section, a number of simple graph and network concepts are defined.

Network activity and substructures

Density: The density of a (binary) network is the proportion of observed to possible edges. For directed and undirected graphs, the density is calculated as $L/n(n-1)$ and $2L/n(n-1)$, respectively, where L is the number of arcs/edges in the observed graph. A graph is *complete* if all possible edges are present (density $= 1$), and is *empty* if no edges are present (density $= 0$).

Degrees: In an undirected graph, the degree of a node is the number of edges incident to it (i.e. the degree of i is $\sum_j x_{ij}$). For a directed graph, the outdegree of a node is the number of ties directed away from the node, and the indegree the number of ties directed to it ($\sum_j x_{ij}$ and $\sum_j x_{ji}$, respectively). For a social network, the outdegree and indegree of a node are sometimes termed the *activity* and the *popularity* of the actor.

The *degree distribution* for an undirected graph is the distribution of counts of nodes with given degrees across all nodes in the graph: that is, $(d_0, d_1, d_2, \ldots, d_{n-1})$, where d_k is the number of nodes with degree k. For directed graphs, there are both indegree and outdegree distributions.

A *k-star* is a network subgraph centered on one node i, with k edges from i to k other nodes. (The degree of i may be greater than k, as a star is only a subgraph, not a maximal subgraph.)

In an undirected graph, a *triangle* is a complete subgraph of three nodes. In a directed graph, a *cyclic triad* is a cycle of length three (a subgraph on three nodes, i, j and k, such that $X_{ij} = X_{jk} = X_{ki} = 1$). A *transitive triad* is a subgraph on three nodes, i, j and k, such that $X_{ij} = X_{jk} = X_{ik} = 1$.

In a directed graph, if $X_{ij} = X_{ji} = 1$, the tie x_{ij} *reciprocates* the tie x_{ji} (and vice versa) and the dyad is *mutual* (M); if $X_{ij} \neq X_{ji}$, the dyad is *asymmetric* (A); and if $X_{ij} = X_{ji} = 0$, the dyad is *null* (N). The count of M, A and N dyads constitutes the *dyad census*. There is also a *triad census* based on the counts of different types of triads in both undirected and directed graphs.

Network connectivity

Paths: A path is a connected sequence of edges across a number of nodes (e.g. edges between nodes i_1 and i_2, i_2 and i_3, i_3 and i_4, and so on). The number of ties is the *length* of the path. A path of length k is sometimes referred to as a k-path. For a directed network, a path requires that the directionality is consistent across all ties (that is, there is an arc from i_1 to i_2, from i_2 to i_3, from i_3 to i_4, and so on). In a directed network, a *semipath* is such a sequence of arcs linking two nodes but disregarding directionality, so inconsistent directionality is possible.

A *cycle* is a path of length greater than two for which the first and last nodes are the same.

A *geodesic* is the shortest length path between two nodes, and the *geodesic distance* is the path length of the geodesic. If there is no path between the two nodes (i.e. they are not connected or *reachable*), the geodesic distance is said to be infinite.

Centrality

The *centrality* of a node is its prominence in the network. There are several types of centrality (Freeman, 1979), the most familiar of which is *degree centrality*, simply measured by the degree of each node.

However, degree centrality focuses on the activity of a node, not necessarily on how important a given node might be in maintaining the connectivity of the network. *Closeness* and *betweenness* centrality are measures relating to connectivity and involve, in different ways, the presence of the node on geodesics. *Closeness centrality* of node i is the reciprocal of the sum of the lengths of geodesics from i to all other nodes in the network. In this case, closeness is best used for a connected graph with no infinite geodesics. An alternative definition is the sum of reciprocated geodesic distances whereby infinite geodesics count as zero. *Betweenness centrality* is a measure of how frequently a node sits on geodesics between other nodes. If g_{jk} is the number of geodesics between nodes j and k, and if $g_{jk}(i)$ is the number of those geodesics that pass through i, then the betweenness centrality of i is the sum over j and k of $g_{jk}(i)/g_{jk}$.

Cohesive subsets of nodes

A cohesive subset of nodes is a subset of nodes whose induced subgraph has substantially greater density than other parts of the graph. The basic idea is to determine a graph-theoretic concept that can be interpreted as a distinct group in a social network, hence the notion of *cohesion*. There are a number of ways to implement this idea.

A *clique* is a complete subgraph. However, for empirical purposes, the definition of a clique is often seen as too restrictive, so there have been a number of generalizations proposed as a better representation of cohesive subgroups within the social network. Some of these have included notions of connectivity, not just density, in their definition, and so do not require that the induced subgraph be complete. For instance, an n-clique (Luce, 1950) is a maximal subset of nodes, each pair of which is connected by a path of length two or less. For further generalizations, see Wasserman and Faust (1994, chapter 7).

These various notions of cohesive subsets of nodes are not too commonly used in analysis, despite the appealing nature of the general concept. However, they lead into an important idea, that a network may be modeled by aggregating subsets of nodes into various categories based on graph-theoretic ideas. Some methods based on network position are summarized below.

2.2. Important elements in social network theory

This section briefly outlines some important elements in social network theory that motivate some of the methods described below.

Closure

A feature of many social networks is a tendency toward triangulation (Cartwright & Harary, 1956; Davis, 1970). This is often termed *network closure* where a 2-path tends to *close* with the addition of an extra edge into a triangle. Other terms that have been used to describe triangulation include network *clustering*, *transitivity* or *balance* (following Heider (1946)—see Cartwright and Harary (1956)). Simmel (1908) observed that triads of individuals had distinctive properties that could not just be derived from their constituent dyads. Granovetter (1973) argued that strong social ties tended to close into clique-like structures, but weak ties did not, so that weak ties provided connectivity across the system. Burt (1992), drawing on Simmel, proposed *structural hole* theory, whereby an individual in a non-closed triad (e.g. at the center of a non-closed 2-star) was in a position to obtain advantage by acting as a *network entrepreneur* or *broker*.

Small worlds

Milgram (1967) originated small world research by studying the connectivity of individuals in the United States. He conducted an experiment whereby he asked participants to forward letters to acquaintances in order to locate a stranger with certain characteristics. When these paths reached the desired destination, the median path length was six, hence the popular attribution of *six degrees of separation*. Most popular descriptions ignore the fact that the majority of paths did not reach the desired destination. There was some follow-up work (Kochen, 1989; Pool & Kochen, 1978) but the idea attracted renewed attention when Watts and Strogatz (1998) investigated small world issues with computer simulations. Watts's (1999) definition of a small world was a

graph with low density, highly clustered (high closure) but with short average geodesic lengths, where low clustering and short average geodesics were defined relative to a simple random graph (see below). Watts conducted simulation studies to show that the addition of a small number of randomly generated ties to a highly clustered graph with long geodesics could result in a phase transition to a small world graph. In other words, the addition (or "re-wiring") of ties to a long-path graph reaches a point whereby there are sufficient "short-cuts" to shorten average geodesics dramatically and suddenly, while the strong clustering is retained. It is only with further rewiring that the clustering in the graph is considerably reduced.

Small world ideas focus attention on the nexus between closure and connectivity, between clustering and geodesic length. The extensive subsequent work, particular in the physics literature, is reviewed by Schnettler (2009). He argues that future directions in this area might focus more on processes of diffusion and search on network structures. This could even affect the definition of "smallness". As Schnettler (p. 177) concludes, "with regard to infectious diseases, the whole world could be small—but with regard to solidarity, and mutual support, six degrees might be a whole universe apart".

Selection

Social selection occurs when individuals select certain network partners based on individual attributes. A commonly considered selection process is *homophily* whereby individuals form a relational tie because they share one or more individual qualities, such as age, sex, attitudes or interests (McPherson, Smith-Lovin, & Cook, 2001). It is also possible that individual factors might lead to individuals obtaining certain social positions, irrespective of the attributes of partners. For instance, certain individual attributes might predispose individuals to greater activity or popularity, or individuals with certain motivations or personality traits may choose to occupy structural holes (Kalish & Robins, 2006).

Influence

For social selection, ties come into existence due to individual-level factors: that is, attribute values affect the presence of ties. *Social influence*, on the other hand, occurs when individuals might change some of their individual attributes (e.g. attitudes) because of influence from their network partners (Mason et al., 2007). The paradigmatic case is of network-based disease transmission (Morris, 2004), so this process is also referred to as *network contagion* or *diffusion*. In influence processes, ties do not change but attribute variables do. In contrast to selection, the presence of ties affects the distribution of attribute values across the nodes.

There has been considerable work on influence and contagion in health behaviors, such as smoking (Ennett & Bauman, 1993) and, more recently, obesity (Christakis & Fowler, 2007; De la Haye, Robins, Mohr, & Wilson, 2010). Diffusion of innovations (Valente, 1995) and attitude agreement (Goel, Mason, & Watts, 2010) have also been of research interest.

Of course, individuals occupying certain network positions may also experience effects on attributes irrespective of the attributes of network partners. This is one of Burt's (1992) principal ideas in terms of network brokerage, that individuals who occupy structural holes will gain individual advantage, a form of *network social capital*.

Network self organization

Social selection leads to the formation of network ties because of the distribution of attributes across actors. However, network ties may also occur because of the presence of other network ties. The simplest example is reciprocity where the presence of a tie from i to j may increase the chances of a tie from j to i, irrespective of nodal attributes. Network closure is another example: as noted above, Granovetter's (1973) argument was that closure could occur because of the nature of ties (i.e. that they were strong), irrespective of attributes. Of course, the presence of homophily among a triple of nodes may also lead to the formation of ties, so it is not always a simple matter to determine whether a triangular structure arises due to triadic closure processes themselves or to dyadic attribute homophily.

The formation of ties due to the presence of other ties can only arise if there is dependence among the network tie variables. Below we describe several theories of tie dependence. With tie dependence, the network takes on the features of a complex system with feedback effects among the tie variables. In this sense the network *self organizes* through *endogenous structural processes* (Wasserman & Robins, 2012) to create certain patterns of ties that can give clues to the underlying social processes. This theoretical argument is an important motivator in several of the modeling approaches outlined below.

3. Probability models for the degree distribution

Let K be the degree of a *randomly chosen person* in the network. Then a statistical model for the degree distribution is represented by: $P(K = k) = f(k)$ where $f(k)$ is a probability distribution.

3.1. Degree distributions for simple random graphs

Simple random graph distributions (i.e. Erdös–Renyi graphs or Bernoulli graphs—see below), where edges occur independently with a fixed probability, produce graphs with approximate Poisson degree distributions. Unfortunately, these graph models do not fit empirical social network data well: social networks often exhibit a high level of closure (triangulation) and positive skew on the degree distribution.

3.2. Positively skewed degree distributions

Positively skewed degree distributions imply a greater variation of activity of actors in the network than would be expected by chance. For instance, in directed networks, it is not unusual to see some actors who are highly *popular* (indegree) and/or highly *active* (sometimes referred to as *expansive*—outdegree). Sometimes, but certainly not universally, empirical networks may exhibit outliers in the degree distribution with particularly high degree, often referred to as *hubs*. Such degree distributions indicate high centralization in the network, with network activity centered on a few high-degree nodes.

Inverse power law degree distributions ("scale free")

Barabási and Albert (1999) proposed the following degree model for networks with highly skewed degree distributions.

$P(K = k)$ is proportional to $k^{-\rho}$ (at least for large k)

where ρ is a scaling parameter (greater than 1). Newman, Strogatz, and Watts (2001) argue that an exponential cut-off for the degree distribution is more typical, and so prefer:

$P(K = k)$ is proportional to $k^{-\rho}e^{-k/\kappa}$

where ρ and κ are constants and $k \geq 1$.

Networks with such a degree distribution are referred to as *scale free networks*. Albert and Barabási (2002) proposed that scale free networks could be the outcome of the *preferential attachment model*. New nodes are added to an existing network with the probability of a new connection related to the degree of the existing nodes. In this way hubs are created as popular nodes become more popular. The preferential attachment model was originally proposed by Simon (1955) and is represented by the Yule distribution (Yule, 1924). The intuition behind preferential

attachment is that popularity itself may attract further popularity, so that nodes with high degrees are most likely to obtain ties from new nodes. The notion is that popularity may arise from structural position (in this case high degree centrality), irrespective of any characteristic of the nodes.

Whether a network is scale free is often assessed by checking linearity through a simple plot on a log–log scale, with ρ estimated using ordinary least squares regression. Handcock and Jones (2003) criticized this simple approach as statistically unsound and recommended likelihood-based approaches (Handcock & Jones, 2004).

A critique of claims about scale-free networks has been presented by Li, Alderson, Tanaka, Doyle, and Willinger (2005), who argued that scale free networks did not even apply to the supposed paradigm case of the internet. Li et al. proposed some firm definitions and a systematic approach to this body of research. The supposed universality of scale free networks is not supported. Some networks may be scale free but in each case this is an empirical question that needs to be investigated rather than presumed. Handcock and Jones (2003) have shown that careful fitting of the degree distribution against a variety of possible statistical models shows that scale free networks are not always the best fitting model. It is also sometimes claimed that degree distributions determine all other features of the network, so that only knowledge of the degree distribution is necessary to understand the properties of the network. This claim does not stand in the face of plenty of counter-examples (Goodreau, 2007; Li et al., 2005; Robins, Pattison, & Woolcock, 2005; Snijders & van Duijn, 2002).

In short, the scale-free idea is appealing in its relatively simple model of the degree distribution. It directs attention to the importance of nodal degrees and the frequent observation of long-tailed distributions. However, when precision is required, there should always be an understanding that scale-free degree distributions imply a very specific shape to the distribution and simply observing some high degree nodes or some apparent linearity on a log–log plot is not sufficient. The data can be tested against a number of different distributions, as shown by Handcock and Jones (2003), to check whether scale-free is indeed the preferred inference.

Controlling for degree distributions

Newman et al. (2001) developed an approach to calculate a variety of graph properties for graph distributions that are random except for an arbitrary degree distribution. This is an approach that takes the degree distribution into account, rather than models it and follows a long tradition within social network analysis of using uniform graph distributions controlling for certain graph features as null models, as discussed below.

4. Models for social position

An important theme in social network research is that nodes may be categorized into subsets that reflect structural positions. If this can be achieved, then the network structure may be collapsed into a simpler representation, so there is a long history in such methods.

4.1. Equivalence

Structural equivalence

In order to categorize nodes on the basis of structure, the general notion of *equivalent* positions in a network needs to be defined. Lorrain and White (1971) essentially defined *structural equivalent* nodes as a pair or subset of nodes connected to the same other nodes. Put simply, in an undirected network, nodes i and j are structurally equivalent if $X_{ik} = X_{jk}$ for all k (see Borgatti and Everett (1992), for a more detailed definition). A *position* is a set of structurally equivalent actors. Obviously under this definition, an actor can be in one and only one position. Note that a position may be different from a cohesive subset of nodes (see above), for there is no requirement that the equivalent nodes need be linked directly to each other. However, there are some important properties of structural equivalence that do relate to cohesive subsets (Borgatti & Everett, 1992). Lorrain and White (1971) noted that structural equivalence is a purely local property, in that the equivalence for a pair of actors can be determined simply from their ties to others. Moreover, as Borgatti and Everett (1992) pointed out, two nodes cannot be structurally equivalent if they are more than two ties apart, that is, structurally equivalent nodes are part of a 2-clique.

The idea of structural equivalence is useful empirically when the n actors can be categorized into a substantially smaller number of m positions, each preferably containing several actors. As it is rare in most empirical social networks to find strict structural equivalence classes, there has been a search for good methods to find approximately structural equivalent subsets of nodes. Basically, this approach is achieved by some form of clustering applied to a distance measure derived from pairs of rows (and columns for directed graphs) in the adjacency matrix. For instance, in an undirected adjacency matrix, the Euclidean distance or correlation (or some other distance or proximity measure) between rows i and j can be taken as the "distance" between i and j and the matrix of distances clustered to produce categories of approximately structurally equivalent nodes. An early version of such a technique based on correlation, still often used, is the CONCOR algorithm (Breiger, Boorman, & Arabie, 1975). More recent clustering methods can of course be utilized, including methods based on optimization procedures such as the TABU search algorithm implemented in the network software suite UCINET (Borgatti, Everett, & Freeman, 2002).

Generalizations of equivalence

Structural equivalence has been generalized in several ways. Two nodes are *automorphically equivalent* (Everett, 1985) if there exists a mapping of the node set onto itself which preserves the network structure (i.e., an automorphism), such that one node is mapped onto the other. *Regular equivalence* partitions nodes into classes whereby nodes of the one class are connected in the same way to other classes of nodes (for a formal mathematical definition, see White and Reitz (1983); for algorithms to determine regular equivalence classes, see Borgatti and Everett (1993)). Because these generalizations step away from the local nature of structural equivalence, they do not carry with them the proximity/cohesion implications. Borgatti and Everett (1992) argued that these different versions implied quite different notions of position: position in structural equivalence is based on the identity of network partners, whereas in the other forms it is based on the way in which actors are connected. Regular and automorphic equivalence are well suited to extracting what are called *role systems* where actors in different positions are assumed to take different social roles derived from the pattern of network connections within and between positions.

4.2. Blockmodels

Given that the network nodes are partitioned into a set of positions, then the set of all ties from actors in one position to those in another forms a *block*. A *blockmodel* simplifies the network into an *image matrix* containing only positions and blocks (White et al., 1976). The image matrix can be determined in various ways, by using the density of the blocks or various approximations or numerical summaries. In this way, a simplified version of the empirical network structure can be developed, further analyzed and interpreted. The basic idea is that the blockmodel describes an underlying fundamental structure compared to the "surface

structure" of the observed networks (Ferligoj, Doreian, & Batagelj, 2011).

Generalized blockmodeling

Doreian, Batagelj, and Ferligoj (2005) proposed a method of *generalized blockmodeling* whereby there is a comparison of an ideal blockmodel based on structural equivalence with an empirical blockmodel with the same number of positions (Ferligoj et al., 2011). Inconsistencies between the two are minimized through an optimization criterion. Regular equivalence blocks may also be incorporated into the generalized blockmodels.

Stochastic blockmodels

Statistical methods for blockmodeling have been proposed as *stochastic blockmodels*. Here the positions are taken to be latent classes for the nodes, referred to as the *colors* of the nodes. The conditional distribution of dyads is assumed to be independent conditional on the node colorings and the goal is to determine the latent classes, and thereby to define the blockmodel. This approach was first proposed by Holland, Laskey, and Leinhardt (1983) and further developed by Nowicki and Snijders (2001) who presented an algorithm for node classification. Airoldi, Blei, Feinberg, and Xing (2008) extended this approach to mixed membership models.

Other latent space approaches

These latent class models suggest a natural extension to continuous latent spaces, even though the latter are not strictly a blockmodeling approach. The basic idea is that the network nodes are embedded in a latent space where the probability of a tie decreases with distance between nodes in the latent space. Both Euclidean (Hoff, Raftery, & Handcock, 2002) and ultrametric (Freeman, 1992) spaces have been proposed but these methods have not been frequently adopted to date in empirical work. See Snijders (2011) for a review of these models.

4.3. Community structure

More recently, approaches have been developed principally among physics researchers to identify *community structure*. Newman and Park (2003) proposed that social networks differed from many other types of networks in having denser regions of the network that may be interpreted as social *communities*. Girvan and Newman (2002) presented a well-known algorithm to allocate nodes to communities determined from the data, but since then a large number of other algorithms have been proposed as extensions. For a summary of these and associated methods, see Newman (2010).

5. Algebraic approaches

Relation algebras arose in part from the analysis of kinship systems (e.g. Boyd (1969) and White (1963)). An algebraic system was considered a good representation of the quite strict familial rules that can exist in complex kinship structures. Subsequently, such algebraic methods were applied to more general social networks, with a goal of representing regularities in network structure. For instance, Boorman and White (1976) built on the then new concept of blockmodels to represent role systems in algebraic form.

Pattison (2011) noted that algebraic constructions can provide a language for expressing regularities in social forms, and thereby assist with their identification in empirical data. For instance, reciprocation and triangulation can be represented within a relation algebra. Pattison summarized some basic algebraic operations that would provide for these network features, establishing conditions for a partial order and axioms that would constitute a proper algebra. These axioms reflect properties that are familiar from standard algebraic systems, including appropriate commutativity, associativity and distributivity properties as well as the existence of an identity.

Algebraic methods are not as commonly applied as in the past. Pattison (2011) noted several ways that relation algebras have been used in the literature. Firstly, for small networks, it is feasible to analyze the full algebra, just as Boorman and White (1976) proposed to do for blockmodels. Pattison (1993) developed partially ordered semigroups derived from blockmodels. This enables comparison of relation algebras across distinct sets of actors to compare structural regularities.

Secondly, in larger empirical contexts where the full algebra might itself be complex or difficult to determine, it may be helpful to construct *partial algebras* that are subsets of full algebras with restrictions placed on the number of times the operations may be applied (see Pattison (2009)). Thirdly, approximate algebraic representations may be obtained through statistical techniques, thereby permitting statistical analysis of the structural properties of relationships that can be expressed in algebraic form (Pattison & Wasserman, 1995; Pattison, Wasserman, Robins, & Kanfer, 2000). This approach can indicate structural patterns that occur in observed data.

6. Statistical methods for cross-sectional network structure

6.1. Conditional uniform graph distributions

The question of whether a particular network pattern might be more prominent than expected in empirical data goes back to the very beginnings of modern network analysis. For instance, in many directed networks, we expect to see tendencies toward reciprocation in ties. Moreno and Jennings (1938) calculated the expected number of mutual ties for a graph with randomly occurring arcs, to compare with the observed number of mutual ties ($\sum_{i,j} X_{ij}X_{ji}/2$) in a graph with the same node set, in order to infer whether a distinctive reciprocity effect is present.

Of course, some network properties are not so readily calculable, and especially their standard deviations for the purposes of a significance test. Katz and Powell (1957) proposed a number of conditional uniform graph distributions, where for a fixed node set the ties are randomly generated conditional on some other network property. The simplest and most common of these is $U|L$, the uniform graph distribution conditional on a fixed number of edges or arcs L. For a given node set, all graphs where $\sum_{i,j} X_{ij} = L$ have equal probability and all other graphs have zero probability. It is simple enough to simulate graphs with these properties and so to obtain a sample of graphs from the distribution. For each graph in the sample, the network property of interest (e.g. the number of mutual ties) can be calculated, providing a bootstrapped null distribution against which to compare the observed data. If the observed statistic is extreme in this distribution, then there is evidence for a distinct effect (i.e. reciprocation) that cannot be adequately explained by the conditioning (i.e. the presence of L arcs).

Holland and Leinhardt (1976) showed how to condition on the triadic properties of the network (see also Wasserman (1977)). Snijders (1991) was the first to show how to condition on in- and out-degree distributions but there have since been a number of elaborations (McDonald, Smith, & Forster, 2007; Rao, Jana, & Bandyopadhyay, 1996; Roberts, 2000; Verhelst, 2008). Pattison et al. (2000) extended the general inferential approach to combine it with conditioning on algebraic constraints (see above). The general method was rediscovered in different contexts by Milo et al. (2002).

In short, this approach provides a means to test hypotheses about network data. One can select any graph property, simulate a graph distribution conditioning on selected marginal properties reflecting some social process, and then locate observed data in this distribution to see whether it is extreme or not. If the observed data

is extreme, then the inference is that the graph feature cannot be explained by the processes embodied in the marginal properties.

Snijders (2011) noted that the method is not in much current use for two reasons: conditioning on any but simple properties is combinatorially complex, and the rejection of the null hypothesis does not enable the construction of a model for the network being studied. The first objection is not necessarily pertinent. Wang et al. (2009) conditioned on an exponential random graph model (ERGM) in order to infer further network effects that could not be readily parameterized in the ERGM. But of course this approach does require the development of a model for the network.

6.2. Quadratic assignment procedure

Quadratic assignment procedure (QAP) is another bootstrapping approach, designed to make inferences comparing different networks on the same set of nodes. Mantel (1967) originally used QAP to investigate the geographical clustering of diseases. Hubert and Schultz (1976) coined the phrase "quadratic assignment" and proposed it for a number of different data analytic contexts (see also Hubert (1987)). Basically, the idea is to test whether a pair of matrices is correlated, so the network application follows naturally (Krackhardt, 1987) to test multiplexity in observed multiple network data.

The method can be described simply. For the cells of the two matrices, a correlation or some other suitable association statistic is calculated in the usual way. The issue is whether the value of the statistic is significant. A permutation is applied to the node labels of one of the two matrices and the statistic recalculated. The permutation produces a matrix with identical structure but the node relabeling implies that any multiplex associations between network ties of different types will be lost. If a large number of permutations are applied, and the test statistic calculated in each case, we have a distribution against which to test the observed statistic.

QAP has been extended beyond the original form to a version of network regression (MRQAP), whereby multiple matrices are used to predict an outcome network (Krackhardt, 1988). The regression coefficients are calculated in standard ways, using the respective cells as data points. The significance of each regression coefficient is determined by a QAP-like procedure between the relevant matrix and the outcome network, conditioning on the other matrices. This is a somewhat controversial method because permutation within this multiple regression framework may be problematic. Dekker, Krackhardt, and Snijders (2007) proposed new permutation procedures for QAP to resolve some of these issues, but concluded that further work was needed to establish MRQAP using binary data.

6.3. Erdös–Renyi graphs

In terms of a model for an entire network, the simplest is of course one where ties occur randomly. The most famous version of this model is the *simple random graph model* of Erdös and Renyi (1959), referred to as the Erdös–Renyi graph or Bernoulli graph distribution (Frank & Nowicki, 1993). A similar model, akin to $U|L$, was also proposed by Gilbert (1959), although as noted above, ideas about random graphs go back to the beginnings of network analysis. Erdös and Renyi suggested that for fixed N, network ties occur independently and with a fixed probability p. For an observed network, p is easily estimated as the density. The properties of this model have been extensively examined, but as noted earlier a model based solely on randomness is not a good representation of empirical social networks. The model is still seen at times, however, usually as a null model against which to compare more complex effects, as with the discussion of conditional uniform graph distributions above.

Very early on, Rapoport and colleagues understood that "biases" away from pure randomness were necessary to represent empirical networks (Rapoport, 1953), especially biases toward reciprocity and closure. The development of *biased net theory* (Rapoport, 1957; Rapoport & Horvath, 1961) was limited by the elusiveness of a complete mathematical treatment (Pattison & Robins, 2008) but this can be seen as a forerunner of exponential random graph models.

6.4. The p_1 and p_2 models

For directed networks, Holland and Leinhardt (1981) extended simple random graph models by assuming independence between dyads, rather than tie variables. This permitted the parameterization of effects for reciprocity and for differential node-level activity (out-degree) and popularity (in-degree). The dyad-independence assumption enabled estimation through standard loglinear models. Holland and Leinhardt called this model p_1, the subscripted '1' implying a program of further research, with progressively enlarged dependence assumptions (within arcs, within dyads, within triads, etc.).

The p_1 model is an important historical step in network model development, but is seldom used nowadays. A more sophisticated extension, the p_2 model, still has dyadic independence at its heart, but conditional on random node-level effects (van Duijn, Snijders, & Zijlstra, 2004). When node variables are of principal research interest, especially across multiple research contexts when the multilevel random node-level effects come into play, the p_2 model can be a valuable method.

6.5. Dependence graphs

Extending Holland and Leinhardt's (1981) dyadic independence approach, Frank and Strauss (1986) took a crucial step in focusing on *conditional* dependence (Dawid, 1979). All tie variables may be dependent on each other, but only some pairs of tie variables may be dependent after conditioning on the values of other ties. These are "neighboring" ties. So, a tie variable X_{ij} is a neighbor of X_{kl} if the two variables still affect one another, given the state of all other tie variables, that is, conditional on the rest of the network.

These notions are common in the graphical modeling literature (e.g. Lauritzen (1996)). In a similar fashion to that literature, Frank and Strauss (1986) introduced a *dependence graph* to represent possible dependencies among network variables X_{ij}. The nodes of the dependence graph are the network variables X_{ij} and an edge between two nodes indicates a *neighborhood* relationship. The cliques of the dependence graph can be thought of as *local social neighborhoods* of the tie variables (Pattison & Robins, 2002). If an edge in the dependence graph is absent, the two variables are conditionally independent and their interaction is not included in a model based on local social neighborhoods. (See Koskinen and Daraganova (2013), and Robins et al. (2005), for a more detailed description of dependence graphs.)

6.6. Exponential random graph models (ERGMs)

ERGMs are models for network structure and are underpinned by the dependence graph literature. They are typically used with cross-sectional network data, although longitudinal versions exist. There are various classes of ERGMs, each with different dependence assumptions. In all cases, however, the models are parameterized in terms of patterns of network ties, termed network *configurations*. For instance, a mutual tie may be a configuration, or a triangle of ties. In this way, the model represents a network as an accumulation of small local network subgraphs that build the overall, global structure of the network.

The parameter values indicate the relative force of the different configurations in this accumulation. Because the configurations may be indicators of network processes – for instance, a triangle may indicate network closure – the parameters provide information about the social processes that may underpin the network.

So, while my exposition here follows the dependence graph argument, much applied network research simply uses an ERGM as a means to model the network in terms of configurations, while eschewing mathematical antecedents and dependence graphs (see, for instance, the first section of Lusher, Koskinen, and Robins (2013), for a more intuitive, less statistical description of ERGMs). Nevertheless, it is important to note that the use of any ERGM implicitly carries assumptions about dependence between tie variables. Even when used implicitly, a dependence assumption amounts to network theory at a rather deep level (Brandes et al., 2013).

The general ERGM form follows from the Hammersley–Clifford theorem, first published by Besag (1974) in the context of spatial statistics. Analogous models exist in statistical mechanics (Park & Newman, 2004). The theorem states that the probability distribution for a set of interacting variables relates solely to the neighborhood structure (or clique structure) of the dependence graph. For networks, the neighborhoods are in effect possible configurations that could be observed in a graph $\mathbf{x}$, so once we start thinking in terms of configurations we can move away from dependence graph considerations (although they are still there implicitly). For a binary network on a given node set N, once a dependence hypothesis is specified, it follows from the Hammersley–Clifford theorem that:

$$\Pr(\mathbf{X} = \mathbf{x}) = (1/\kappa)\exp\{\Sigma_A \eta_A g_A(\mathbf{x})\} \quad (1)$$

where:

(i) the summation is over all configurations A;

(ii) η_A is a parameter corresponding to the configuration A;

(iii) $g_A(\mathbf{x}) = \prod_{x_{ij}\in A} x_{ij}$ is the *network statistic* that defines configuration A;

(iv) κ is a normalizing quantity to ensure that (1) is a proper probability distribution.

Frank and Strauss (1986) proposed a homogeneity assumption whereby parameters would be equated across configurations. In that case, the model retains the same form as in expression (1), but now the parameters relate to the different types of configurations and the sufficient statistics are counts of the configurations.

In short, the LHS of (1) states that this is a probability distribution of graphs, with the RHS stating that the probability of graph $\mathbf{x}$ in this distribution is determined by the linear sum of configuration counts $g(\mathbf{x})$ weighted by parameters, within the exponential.

Bernoulli random graph models

With no dependencies within the network (an empty dependence graph), we revert to simple random graph models, as above. The cliques of the dependence graph are single nodes (i.e. single tie variables). With parameters equated for single ties, Eq. (1) becomes:

$$\Pr(\mathbf{X} = \mathbf{x}) = (1/\kappa)\exp(\Sigma_{i,j}\theta x_{ij}) = (1/\kappa)\exp\theta L(\mathbf{x})$$

where $L(\mathbf{x})$ is the number of edges (arcs) in $\mathbf{x}$ and θ is a *density* or *edge* parameter. This graph distribution is equivalent to an Erdös–Renyi graph with $p = \exp\theta/(1+\exp\theta)$.

Dyadic independence models

For directed networks, dyadic independence requires edges between variables X_{ij} and X_{ji} in the dependence graph with neighborhoods in the form of single edges and dyadic pairs $\{X_{ij}, X_{ji}\}$. With one density parameter θ for all single edge neighborhoods and one *reciprocity parameter* ρ for all dyadic neighborhoods, Eq. (1) then becomes:

$$\Pr(\mathbf{X} = \mathbf{x}) = (1/\kappa)\exp(\theta L(\mathbf{x}) + \rho M(\mathbf{x}))$$

with $L(\mathbf{x})$ the number of arcs and $M(\mathbf{x})$ the number of mutual dyads ($X_{ij} = X_{ji} = 1$) in $\mathbf{x}$. Slightly more relaxed homogeneity constraints result in the p_1 model.

Markov random graphs

Frank and Strauss (1986) proposed Markov dependence, where ties X_{ij} and X_{kl} are conditionally independent if and only if $\{i,j\} \cap \{k,l\} \neq \emptyset$, that is, two tie variables are conditionally independent unless they share an actor. With this dependence assumption, configurations for undirected graphs include single edges, k-stars and triangles. There is a wider range of possibilities for directed graph models (Wasserman & Pattison, 1996). An undirected Markov graph model then has the form:

$$\Pr(\mathbf{X} = \mathbf{x}) = (1/\kappa)\exp(\theta L(\mathbf{x})\Sigma_{r=2,n-1}\sigma_r S_r(\mathbf{x}) + \tau T(\mathbf{x}))$$

with θ a density parameter, and $L(\mathbf{x})$ the number of edges in $\mathbf{x}$, as before; σ_r is a parameter for a *star of size* r, and $S_r(\mathbf{x})$ is the number of stars of size r in $\mathbf{x}$; τ is a triangle or closure parameter and $T(\mathbf{x})$ is a count of the number of triangles in $\mathbf{x}$. The expression $\theta L(\mathbf{x}) + \Sigma_{r=2,n-1}\sigma_r S_r(\mathbf{x})$ completely parameterizes the degree distribution, so the τ parameter represents the strength of closure conditional on the degree distribution of the graph. There are still too many star parameters in this model for it to be identified and it is common to include only 2- and 3-star parameters. In that case, the θ, σ_2 and σ_3 parameters control for the first three moments of the degree distribution.

Wasserman and Pattison (1996) popularized Markov random graphs as p^* models. Extensions included models for multivariate networks (Pattison & Wasserman, 1999), for valued networks (Robins, Pattison, & Wasserman, 1999), and for bipartite networks (Skvoretz & Faust, 1999). For a review of the general formulation of ERGMs and of Markov random graphs, see Robins, Pattison, Kalish, and Lusher (2007).

Model degeneracy

Despite the appeal of Markov random graph models, they are frequently beset by problems of model degeneracy. Handcock (2002) termed a graph distribution as *near degenerate* if only a very few (possibly only one or two) distinct graphs had substantial non-zero probabilities. Certain parameter values for Markov random graph models place almost all of the probability mass on either the empty or the full graph, or at least two quite separate regions (one of low density and another of high density), with a phase transition from one region to the other as parameter values change very slightly. Such properties of Markov random graph models have now been well studied (e.g. Handcock (2002), Jonasson (1999), Park and Newman (2004), Robins et al. (2005) and Snijders (2002)). Issues of degeneracy call into question whether Markov random graph models can adequately represent most network data. Intuitively, what happens to Markov graph models when there are heterogeneities in the network (e.g. a long tailed degree distribution or areas of greater density, i.e. many triangles) is that the relatively simple Markov parameterization cannot deal with the heterogeneity well. For instance, one triangle parameter cannot deal with regions of low and high triangulation simultaneously.

Social circuit dependence: partial conditional dependence

Pattison and Robins (2002) proposed *partial conditional dependence* as an extension beyond Markov dependence, where dependence was created by the presence of certain network ties, and showed how to incorporate this type of dependence into the Hammersley–Clifford theorem. Snijders, Pattison, Robins, and Handcock (2006) used this approach to define *social circuit dependence*, where two tie variables are conditionally dependent if their observation would lead to a 4-cycle.

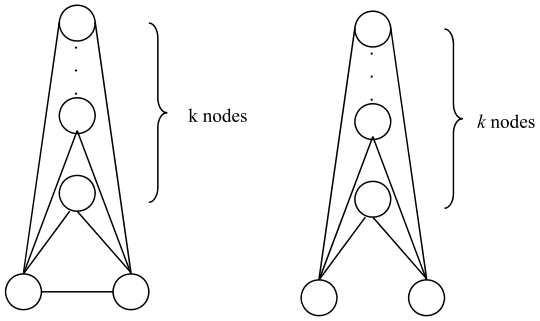

Fig. 3. A k-triangle (left panel) and a k-2path (right panel).

Theoretically, 4-cycles have been argued to be collaborative structures in networks, leading to forms of generalized exchange (Lazega & Pattison, 1999). Lusher and Robins (2013) provide an intuitive explanation of social circuit dependence with an example of two couples meeting at a party. If one partner from each couple (i and j) begin to talk, then the other pair (k and l) may also begin to talk. Here, the presence of existing relationships (i and k, and j and l) means that the presence of a tie across relationships (i, j) affects the probability of the other tie (k, l) occurring.

Using both social circuit and Markov dependence assumptions, Snijders et al. (2006) proposed three new ERGM statistics for undirected networks: *alternating k-stars, alternating k-triangles*, and *alternating independent two-paths*. These statistics used a non-linear functional form to combine counts of related configurations into the one statistic, the so-called *alternating* form. For instance, all Markov star parameters are included in the model but with the constraint that for all $k \geq 2$, $\sigma_{(k+1)} = -\sigma_k/\lambda$ for some λ greater than 1. It is common to set λ to a fixed value such as 2, but it can also be estimated (Hunter & Handcock, 2006). Hunter (2007) proposed a mathematically equivalent version of this parameter, the *geometrically weighted degree parameter*, explicitly modeling the degree distribution but with weights decreasing geometrically as the degrees increase.

Snijders et al. (2006) showed that with both social circuit and Markov dependence assumptions, configurations such as a *k-triangle* and a *k-2path* are possible in the model (Fig. 3). The alternating form of the statistics was also applied to counts of these configurations. Hunter (2007) again proposed equivalent geometrically weighted versions, the *geometrically weighted edgewise shared partner* (GWESP) statistic and the *geometrically weighted dyadwise shared partner* (GWDSP) statistic, modeling the distributions of shared partners across dyads. The alternating triangle/GWESP parameter captures closure effects, and the 2path/GWDSP parameter relates to local connectivity, akin to structural equivalence.

So for undirected networks, a standard social circuit ERGM can be parameterized parsimoniously with edge, alternating star, alternating triangle and possibly alternating 2path parameters. For directed networks, the choice is larger, but the general approach is the same (Robins, Pattison, & Wang, 2009). Social selection effects can be included, for instance, with homophily and sender/receiver effects. While social circuit models do not entirely avoid degeneracy, the alternating statistics offer sufficient control over the higher order stars and triangles so as to perform dramatically better than Markov models.

Because of the complex dependence, estimation from data utilizes Markov chain Monte Carlo Maximum Likelihood estimation (Hunter & Handcock, 2006; Snijders, 2002). Earlier methods of pseudo-likelihood estimation (Strauss & Ikeda, 1990) should be avoided. Simulation from the parameter estimates to compare non-fitted features of the observed graphs against the simulated graphs provides information on how well the model explains these additional features (Hunter, Goodreau, & Handcock, 2008).

Recent discussions of social circuit models include Lusher et al. (2013) and Robins, Snijders, Wang, Handcock, and Pattison (2007). ERGMs have been extended to other forms of relational data, such as bipartite networks (Wang et al., 2009). Research on the use of ERGMs to resolve issues of missing network data and on snowball sampling of network data is very promising (Handcock & Gile, 2010; Koskinen, Robins, & Pattison, 2010).

7. Methods for network influence

Mason et al. (2007) noted that social psychologists have studied the psychological processes involved in various forms of social influence but typically in tightly controlled laboratory settings, and without consideration of larger scale social contexts, especially how influence processes develop with multiple sources and multiple targets over time. Social network researchers have been less interested in the specific cognitive processes involved in social influence and more about how influence might spread across a networked social system.

For influence processes on social networks, the structure of the network $\mathbf{x}$ is typically taken as exogenous and fixed and the focus of interest is on the distribution of attributes $\mathbf{Y}$ given that network. The simple insight is that actors may be influenced by their network partners, so that variable Y_i may depend on the interaction effect $Y_j X_{ij}$ (that is, the presence of a network tie between i and j together with the attribute of j). But of course there is no reason to privilege i or j, so similarly Y_j may depend on the interaction effect $Y_i X_{ij}$. This simple idea leads naturally to various autoregressive and autologistic-type models. Autocorrelation approaches have a long methodological background (e.g. Winsborough, Quarantelli, and Yutzky (1963)), are familiar in spatial statistics (e.g., Anselin (1982, 1984), Cliff and Ord (1973, 1981) and Ord (1975)), and were introduced to network approaches through Doreian and others (Doreian, 1982, 1989a,b; Doreian, Teuter, & Wang, 1984; Erbring & Young, 1979; Leenders, 2002).

The *network effects model* (Doreian, 1982; Erbring & Young, 1979; Friedkin & Johnsen, 1990; Marsden & Friedkin, 1994) is one such approach. The model is expressed as

$$\mathbf{Y} = \alpha\mathbf{Yx} + \mathbf{Z}\boldsymbol{\beta} + \boldsymbol{\varepsilon}$$

where, as above, $\mathbf{Y}$ is a vector of attribute variables, $\mathbf{x}$ the association matrix for the observed network, $\mathbf{Z}$ a matrix of exogenous attribute variables that may be influential in shaping the attitudes, and $\boldsymbol{\varepsilon}$ a vector of residuals. Here α is a parameter for the effect of the network in transmitting attitudes, and $\boldsymbol{\beta}$ a vector of parameters for the effect of exogenous attributes on an individual's attitude. Friedkin and Johnsen (1997) summarized a discrete time version of this model and discuss the results emerging from different balances between the network and exogenous variables. Friedkin (1998) developed these models further into what he termed a structural theory of social influence. The association matrix $\mathbf{x}$ was replaced by a weighting matrix $\mathbf{w}$ that can incorporate a number of different effects, including effects derived from $\mathbf{x}$.

Robins, Pattison, and Elliott (2001) introduced an autologistic model using an exponential random graph approach. This has recently been extended (Daraganova & Robins, 2013) as the *autologistic actor attribute model*.

These autocorrelation methods continue to be popular and have been developed and applied in a variety of ways (Valente, 1995, 2005). Similar approaches have been studied in economics, where influence processes are often referred to as peer effects (An, 2011; Durlauf & Young, 2001; Jackson, 2010; Manski, 1993). There has been growing interest in social influence effects in public health (e.g. Christakis and Fowler (2007)).

One of the difficulties, of course, is precisely identifying a social influence effect as distinct from a social selection effect. Certainly, it is not easy to distinguish causal direction without some form of longitudinal data. A longitudinal version of network effects model can be obtained with panel data where the attributes **Y** are measured at various time points t while the network **X** is assumed constant, so that:

$$\mathbf{Y}_t = \alpha \mathbf{Y}_{t-1}\mathbf{x} + \mathbf{Z}\beta.$$

Friedkin and Johnsen (1990) showed that in equilibrium this can be solved as:

$$\mathbf{Y}_e = (\mathbf{I} - \alpha\mathbf{x})^{-1}\mathbf{Z}\beta$$

where $\mathbf{Y}_e$ are the equilibrium attitudes.

In their extensive recent work on social influence, Christakis and Fowler (2013) use a similar longitudinal approach, but typically with binary variables and a logistic link. They argue that influence effects can be parsed from selection effects if the direction of ties is taken into account, but there has been considerable debate about when and if this is possible (e.g. Lyons (2011)). Accordingly, for suitable longitudinal data there is advantage in modeling both selection and influence effects simultaneously.

8. Longitudinal modeling

8.1. Statistical methods for the coevolution of ties and attributes

Stochastic actor-oriented models (SAOM—also known as stochastic actor based models) were originally designed for the dynamics of network self organization (Snijders, 1996, 2001). The models use panel network data, so that each network is measured at discrete time points. The models assume that unobserved changes to network ties occur one at a time between the measurement points and that these changes arise because actors direct their ties toward other actors to optimize their network environments. To do this, the model includes an *objective function* whereby actors may change their choices of other actors according to network structural statistics similar to those of exponential random graph models. For instance, if actors prefer reciprocated ties, then there will be a positive parameter in the objective function expressing preferences for tie choices that increase reciprocity in the graph. Parameter estimates are obtained by simulation. Based on a current estimate, a chain of changes is simulated and the resulting new graphs are compared to the observed data. The estimate is then adjusted based on any discrepancy until all parameter estimates converge. It should be noted that SAOMs condition on the first observation point, and so explicitly model only the process of change, not the structure at a particular time point. There is a close relationship to ERGMs, with the equilibrium distribution of an SAOM equivalent to a suitably specified ERGM (Snijders et al., 2010).

These actor-oriented models are now a major method to model the co-evolution of network structures and individual behaviors. The basic idea remains as before, but now the panel data includes changeable network ties and actor attributes. Network ties are assumed to affect attributes (influence) at the same time that attributes affect ties (selection), and there are separate objective functions for ties and attributes. So these models provide a principled method whereby both influence and selection parameters are included in the one model at the same time (Snijders, Steglich, & Schwienberger, 2007; Steglich, Snijders, & West, 2006). As with ERGMs, SAOMs are computationally intensive in estimation, so they are not readily applicable to very large network networks. But, for many longitudinal network datasets, they are now the preferred method and they are increasingly popular in the social networks literature. A recent (2010) special issue of the journal *Social Networks* covers the detail of these models very well and we direct interested readers to the articles therein (e.g. Snijders et al. (2010)). The popularity of these methods resulted in the publication of a second special issue in 2012 (e.g. Snijders and Doreian (2012)).

8.2. Methods for time ordered transactions

Models for transactions or events on networks are starting to be introduced. Unlike a long-standing relational tie of indefinite duration, a transaction or event occurs at a specific time and so together form a time-ordered sequence of events. Recent work has focused on models to explain the structuring of events: e.g. event-based actor oriented methods (Stadtfeld & Geyer-Schulz, 2011); and models drawing on event history analysis including the *Relational Events Models* (Butts, 2008b) and extensions by Brandes, Lerner, and Snijders (2009) and de Nooy (2010).

These approaches are among the most interesting and novel of recent social network methods. Notably, they provide a means to model sequences of exchanges among individuals without aggregating across time, so they are well suited to understanding communication structures such as email. At the same time, structural dependencies among communication exchanges can be modeled (e.g. reciprocity in email exchanges).

Time sequencing complicates network analytic methods. To represent the specific exchanges of diffusion and influence directly it is necessary to take time into account, implying the static analysis of network structure is not necessarily sufficient. Paths in a network representation aggregated across time may not properly represent paths that do not violate the forward movement of time (Moody, 2002).

One of the features of this special issue is a number of papers that deal with time ordered transactions and the time sequencing of network-based exchanges.

9. Conclusions

While this review has focused on some important approaches in the modeling of network data, it is not intended to be exhaustive. There has been an enormous methodological development over the last decade alone. Nevertheless, it will be obvious from the work examined in this article that network methods have developed to cover a wide range of distinctive data analytic challenges. Moreover, methodological research continues at a fast pace, even for approaches that have a long network analytic tradition. There remain a number of difficult problems to be solved, and many methods can be considered as at an early stage of development. Given another decade, the field may well look quite different in the sophistication and capability of what can be done, although the basic directions of research interest are likely to remain fairly constant.

There is a growing understanding that for certain important social science questions, a social network perspective is central, not just an add-on to previous theories and methods. This implies that methodological development must not simply occur in isolation of good social science. Good social network theory (as a form of social science) needs to be associated closely with methodological advance. As theory develops to produce novel hypotheses, methods will follow. At the same time, new methods open the possibility of examining new theories in novel ways. The most fruitful approach will be a proper combination of social network theory and method, and applied within specific disciplinary domains to address specific empirical challenges.

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