An Introduction to Exponential Random Graph (*p**) Models for Social Networks

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Abstract

This article provides an introductory summary to the formulation and application of exponential random graph models for social networks. The possible ties among nodes of a network are regarded as random variables, and assumptions about dependencies among these random tie variables determine the general form of the exponential random graph model for the network. Examples of different dependence assumptions and their associated models are given, including Bernoulli, dyad-independent and Markov random graph models. The incorporation of actor attributes in social selection models is also reviewed. Newer, more complex dependence assumptions are briefly outlined. Estimation procedures are discussed, including new methods for Monte Carlo maximum likelihood estimation. We foreshadow the discussion taken up in other papers in this special edition: that the homogeneous Markov random graph models of Frank and Strauss (1986) are not appropriate for many observed networks, whereas the new model specifications of Snijders, Pattison, Robins and Handcock (2006) offer substantial improvement.

In recent years, there has been growing interest in exponential random graph models for social networks, commonly called the *p** class of models (Frank & Strauss, 1986; Pattison & Wasserman, 1999; Robins, Pattison & Wasserman, 1999; Wasserman & Pattison, 1996). These probability models for networks on a given set of actors allow generalization beyond the restrictive dyadic independence assumption of the earlier p_1 model class (Holland & Leinhardt, 1981). Accordingly, they permit models to be built from a more realistic construal of the structural foundations of social behavior. The usefulness of these models as vehicles for examining multi-level and multi-theoretical hypotheses has been emphasized (e.g., Contractor, Wasserman & Faust, in press).

There have been a number of major theoretical and technical developments since Anderson, Wasserman and Crouch (1999) presented their well-known primer on *p** models. We summarize these advances in this paper. In particular, we consider it important to ground these models conceptually in their derivation from dependence assumptions, as the underlying basis of a model is then made explicit and more readily linked with hypotheses about (unobserved) social processes underlying network formation. It is through such an approach that new models can be developed in a principled way, including models that incorporate actor attributes. Recent developments in model specification and estimation need to be noted, as do new technical steps regarding setting structures and partial dependence assumptions that not only expand the class of models but have important conceptual implications. In particular, we now have a much better understanding of the properties of Markov random graphs, and promising new specifications have been proposed to overcome some of their deficiencies.

This article describes the models and summarizes current methodological developments with an extended conceptual exposition. (More technical recent summaries are given by Wasserman & Robins, 2005; Robins & Pattison, 2005; and Snijders, Pattison, Robins & Handcock, 2006.) We begin by briefly describing the rationale for analyzing social networks with statistical models (section 1). We then provide an overview of the underlying logic of exponential random graph models and outline our general framework for model construction (section 2). In section 3, we discuss the important concept of a *dependence assumption* at the heart of the modeling approach. In section 4, we present a range of different dependence assumptions and models. For model estimation (section 5), we briefly summarize the pseudo-likelihood estimation (PLE) approach, and review recent developments in Monte Carlo Markov

Chain maximum likelihood estimation techniques. In section 6, we present a short example of fitting a model to network data. In conclusion, we note the importance of the new model specifications that are the focus of attention in other papers in this special edition.

1. Why model social networks?

There are many well-known techniques that measure properties of a network, of the nodes, or of subsets of nodes (e.g., density, centrality, cohesive subsets.) These techniques serve valuable purposes in describing and understanding network features that might bear on particular research questions. Why, then, might we want to go beyond these techniques and search for a well-fitting *model* of an observed social network, and in particular a *statistical* model? Reasons for doing so include the following:

(1) Social behavior is complex, and stochastic models allow us to capture both the regularities in the processes giving rise to network ties while at the same time recognizing that there is variability that we are unlikely to be able to model in detail. Moreover, as Watts (1999) has cogently demonstrated, "adding" a small amount of randomness to an otherwise regular process can dramatically alter the properties of the possible outcomes of that process. It is therefore important to allow for stochasticity if we believe that it best reflects the processes we aim to model. Perhaps most importantly, a well-specified stochastic model allows us to understand the uncertainty associated with observed outcomes: we can learn about the *distribution* of possible outcomes for a given specification of a model, or we can estimate, for given observed data, the parameters of the hypothesized model from which the data may have been generated (and also obtain quantitative estimates of the uncertainty associated with estimation).

(2) Statistical models also allow inferences about whether certain network sub-structures – often represented in the model by one or a small number of parameters – are more commonly observed in the network than might be expected by chance. We can then develop hypotheses about the social processes that might produce these structural properties.

(3) Sometimes, different social processes may make similar qualitative predictions about network structures and it is only through careful quantitative modeling that

the differences in predictions can be evaluated. For instance, clustering in networks might emerge from endogenous (self-organizing) structural effects (e.g. structural balance), or through node-level effects (e.g. homophily). To decide between the two alternatives requires a model that incorporates both effects and then assesses the relative contribution of each.

(4) The more complex the network data structure, the more useful properly formulated models can be in achieving efficient representation. It is notable that there are a variety of deterministic approaches for analyzing single binary networks, but many of these are not appropriate, or are too complex, for more complicated data. To understand network evolution (Snijders, 2001) or multiple network structures (Lazega & Pattison, 1999), models can be of great value.

(5) Several longstanding questions in social network analysis relate to the puzzle of how localized social processes and structures combine to form global network patterns, and of whether such localized processes are sufficient to explain global network properties. It is difficult to investigate such questions without a model, as in all except rather simple cases the global outcomes resulting from the combinations of many small-scale structures are not immediately obvious, even qualitatively. With good *locally-specified* models for social networks, it may be possible to traverse this micro-macro gap, often through simulation.

We particularly emphasize the value of developing plausible models that are estimable from data and hence empirically grounded. There are many models in the network literature that are important tools for simulation, hypothesis generation, and "thought experiments". But our principal goal is to estimate model parameters from data and then evaluate how adequately the model represents the data. These complementary approaches serve useful but different purposes, with the distinctive value of the data-driven approach clearly being its capacity for empirical interrogation of the assumptions underpinning model construction.

2. The logic behind *p** models for social networks – an outline[1]

We describe as the *observed network* the network data the researcher has collected and is interested in modeling. The observed network is regarded as one

[1] For other introductions to the logic of *p** modeling, see Monge and Contractor (2003), and Contractor, Wasserman and Faust (in press).

realization from a set of possible networks with similar important characteristics (at the very least, the same number of actors), that is, as the outcome of some (unknown) stochastic process. In other words, the observed network is seen as one particular pattern of ties out of a large set of possible patterns. In general, we do not know what stochastic process generated the observed network, and our goal in formulating a model is to propose a plausible and theoretically principled hypothesis for this process

For instance, one of our research questions may be whether in the observed network there are significantly more, or less, structural characteristics of interest than expected by chance. We might see these characteristics as the outcomes of local social processes. For example, we might ask – as Moreno and Jennings (1938) did in one of the first applications of statistics to social networks – whether the observed network shows a strong tendency for reciprocity, over and above the chance appearance of a number of reciprocated ties if relationships occurred completely at random. In other words, do actors in the observed network tend to reciprocate relationship choices? Here the structural characteristic (reciprocated ties) is the outcome of a social process (individuals choosing to reciprocate the choices of others.) Thus, as a simple example, we might posit a stochastic network model with two parameters, one that reflects the propensity for ties to occur at random and one that reflects an additional propensity for reciprocation to occur.

In general, the structural characteristics in question help to shape the form of the model. An assumption of a reciprocity process leads us to propose a model in which an index of the level of reciprocity is a *parameter*. The assumption also reflects an expectation about what sort of networks are more likely. A statistical model for a network on a given set of actors assigns a probability to all possible networks on those actors. For instance, since reciprocity of ties is a commonly observed feature in friendship networks, a good model is likely to imply that networks with reciprocation are more common and networks without reciprocation are rather improbable.

As is usual, we represent networks as *graphs* of *nodes* and *edges.* For a given model, the node set is regarded as fixed. The range of possible networks, and their probability of occurrence under the model, is represented by a *probability distribution* on the set of all possible graphs with this number of nodes. In this distribution of graphs, those graphs with substantial levels of reciprocation are likely to have higher probability than graphs with little reciprocation, with the precise probabilities depending on the value of relevant parameters, such as a reciprocity parameter. Note that the

observed network is a particular graph in this distribution and so it also has a particular probability.

Of course, at the outset, we do not know which parameter values to use in assigning probabilities to graphs in the distribution. Our goal, rather, is to find the best values (by *estimating model parameters*) using the observed network as a guide. The essential *maximum likelihood* criterion is to choose parameter values in such a way that the most probable degree of reciprocation is that which occurs in the observed network. If the model has a reciprocity parameter (defined to be zero when reciprocal ties occur by chance), and if there are many reciprocated ties in the observed network, then a model that is a *good fit* to the data in terms of degree of reciprocation will have a positive reciprocity parameter. If we estimate a reciprocity parameter for the observed network, and if we can be confident that this parameter is positive, we may infer that there is more reciprocity in the observed network than expected by chance.

Once we have defined a probability distribution on the set of all graphs with a fixed number of nodes, we can also draw graphs at random from the distribution according to their assigned probabilities, and we can compare the sampled graphs to the observed one on *any* other characteristic of interest. If the model is a good one for the data, then the sampled graphs will resemble the observed one in many different respects. In this ideal case, we might even hypothesize that the modeled structural effects could *explain* the emergence of the network. And we can examine the properties of the sampled graphs in order to understand the nature of networks that are likely to emerge from these effects.

As an example, consider friendship in a school classroom. The observed network is the network for which we have measured friendship relations. There are many possible networks that could have been observed for that particular classroom. We examine the observed friendship structure in the classroom in the context of all possible network structures for the classroom. Some structures in the classroom may be quite likely and some very unlikely to happen, and the set of all possible structures with some assumption about their associated probabilities is a probability distribution of graphs. We are placing the observed network within this distribution, rather than comparing the observed network to friendship networks in other classrooms. (Of course, our model for the observed network may also be a good model for other classrooms but that is not the issue at this point.)

Note that the assumption is that the network is generated by a *stochastic process* in which relational ties come into being in ways that may be shaped by the presence or absence of other ties (and possibly node-level attributes). In other words, the network is conceptualized as a *self-organizing* system of relational ties. Substantively, the claim is that there are local social processes that generate dyadic relations, and that these social processes may depend on the surrounding social environment (i.e. on existing relations). For example, we can assume that actors with similar attributes are more likely to form friendship ties (homophily), or that if two unconnected actors were connected to a third actor, at some point they are likely to form a friendship tie between them (transitivity). Note that in addition to the assumption of stochasticity, this description is also implicitly temporal and dynamic.

2.1 A general framework for model construction

In positing an exponential random graph model for a social network, a researcher implicitly follows five steps. While the focus of research is on the final step of parameter estimation and interpretation, it is through all the five steps that a researcher makes explicit choices that connect theoretical decisions to data analysis. And as shown below, it is through these earlier steps that we can locate certain earlier network models within the rubric of exponential random graph models.

Step 1. *Each network tie is regarded as a random variable.*

This step implies a stochastic framework with a fixed node set. By assuming that a tie is a *random variable* we do not imply that people form relations in an *ad hoc* fashion: some relationships might be highly probable. Rather, we are simply stating that we do not know everything about relationship formation, that our model is not going to make perfect deterministic predictions, and that as a result there is going to be some statistical "noise", or lack of regularity, that we cannot successfully explain.

With possible network ties established as random variables, it is timely to review some basic notation. For each i and j who are distinct members of a set N of n actors, we have a random variable Y_{ij} where $Y_{ij} = 1$ if there is a network tie from actor i to actor j, and where $Y_{ij} = 0$ if there is no tie. We specify y_{ij} as the observed value of the variable Y_{ij} and we let $\mathbf{Y}$ be the matrix of all variables with $\mathbf{y}$ the matrix of observed ties, the observed network. Of course, $\mathbf{y}$ can also be construed as a graph on the node set N, with the edge set specified by those pairs (i,j) for which $y_{ij} = 1$. $\mathbf{Y}$ may be *directed* (in which

case Y_{ij} is distinguished from Y_{ji}) or *non-directed* (where $Y_{ij} = Y_{ji}$ and the two variables are not distinguished.) It is also possible for **y** to be valued, although for this article we will restrict attention to binary ties.

Step 2. *A dependence hypothesis is proposed, defining contingencies among the network variables*.

This hypothesis embodies the local social processes that are assumed to generate the network ties. For instance, ties may be assumed to be independent of each other, that is, people form social connections independently of their other social ties. This is not usually a very realistic assumption. In the example of the school classroom with reciprocity processes in place, if student A likes student B, then student B will quite probably like student A implying some form of dyadic dependence. Ties may also depend on node-level attributes (see section 4.4 below), with for instance possible homophily effects in the classroom. Notice that each of these processes can be represented as a small-scale graph configuration: for instance, a reciprocated tie, or a tie between two girls.

Step 3. *The dependence hypothesis implies a particular form to the model.*

It can be proven that well-specified dependence assumptions imply a particular class of models (the *Hammersley-Clifford theorem,* Besag, 1974). Each parameter corresponds to a *configuration* in the network, that is, a small subset of possible network ties (and/or actor attributes – although that is for later). These configurations are the structural characteristics of interest (e.g. reciprocated ties), referred to above. The model then represents a distribution of random graphs which are assumed to be "built up" from the localized patterns represented by the configurations. For instance, a single tie is a configuration, as may be a reciprocated tie (in a directed graph), a transitive triad and a two-star. Parameters related to the presence of each of these configurations in the observed graph may be included in a model.

Dependence assumptions and the general form of the model are discussed in section 3 below. Particular dependence assumptions are presented in section 4.

Step 4. *Simplification of parameters through homogeneity or other constraints*.

In order to define a model clearly, we need to reduce the number of parameters. This is often done by imposing homogeneity constraints. In effect, we ask whether some

parameters should be equated or related in other ways. For instance, we usually propose one parameter for a reciprocity effect across the entire network, by assuming that the reciprocity parameters for each possible reciprocated tie are all equal. Parameter constraints for particular models are illustrated in section 4.

Step 5. *Estimate and interpret model parameters*:

Of course, estimation and interpretation are usually a focus of particular research applications, but reaching this step implies that the other four have already been undertaken, even if only implicitly. This step is complicated if the dependence structure is complex, as it probably needs to be for any realistic model. Having obtained parameter estimates, as well as estimates of the uncertainty of estimation, we may then take full advantage of having a statistical model for the network that is constructed from specifiable dependence assumptions and that is estimated from observed network data. For example, we can explore the range of network outcomes predicted by the model, a step that can be very helpful in assessing how good the model is, and we can make inferences about model parameters. For instance we can infer whether any model parameter is significantly different from zero and so whether the corresponding configuration is present in the observed graph to a greater or lesser extent than expected by chance, given other parameter values. We discuss parameter estimation in section 5.

3. The general form of the exponential random graph model: Dependence assumptions and parameter constraints

Exponential random graph models have the following form:

$$\Pr(\mathbf{Y} = \mathbf{y}) = (1/\kappa) \exp\{\Sigma_A \eta_A g_A(\mathbf{y})\} \qquad (1)$$

where:

(i) the summation is over all configurations A;

(ii) η_A is the parameter corresponding to the configuration A (and is nonzero only if all pairs of variables in A are assumed to be *conditionally dependent*)[2];

(iii) $g_A(\mathbf{y}) = \prod_{y_{ij} \in A} y_{ij}$ is the *network statistic* corresponding to configuration A; $g_A(\mathbf{y})$ = 1 if the configuration is observed in the network **y**, and is 0 otherwise[3];

[2] i.e. conditional on the rest of the graph.

(iv) κ is a normalizing quantity which ensures that (1) is a proper probability distribution.[4]

All exponential random graph models are of the form of equation (1) which describes a general probability distribution of graphs on n nodes. The probability of observing any particular graph **y** in this distribution is given by the equation, and this probability is dependent both on the statistics $g_A(\mathbf{y})$ in the network **y** *and* on the various non-zero parameters η_A for all configurations A in the model. Configurations might include reciprocated ties, transitive triads and so on, so the model enables us to examine a variety of possible structural regularities.

So why are dependence assumptions important here? Dependence assumptions have the consequence of picking out different types of configurations as relevant to the model. Note from point (ii) above, parameters are zero whenever variables in a configuration are conditionally independent of each other. In other words, the only configurations that are relevant to the model are those in which all possible ties in the configuration are mutually contingent on each other.[5]

It is worth noting that if a set of possible edges represents a configuration in the model, then (1) implies that any subset of possible edges is also a configuration. Thus, single edges are always configurations, as demonstrated in section 4.

So the dependence assumption is crucial in constraining which configurations are possible in the model. We will discuss particular examples in section 4. A configuration A refers to a subset of tie variables, and corresponds to a small network substructure. For instance, if for a directed network we apply a dyadic dependence assumption (see section 4) it will follow that reciprocity parameters will be in the model. In this case, one configuration in the model is the set of variables $\{Y_{12}, Y_{21}\}$,

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[3] We write $g_A(\mathbf{y})$, rather than g_A, to remind ourselves that the statistics relate to the graph **y**.

[4] It is possible to assert a model of the form of (1) by incorporating more general statistics than configuration and subgraph counts (see Wasserman & Pattison, 1996). But then dependence assumptions may not be clear. Our preference is for an explicit dependence structure in order to be able to link the model to interpretations regarding local social processes.

[5] More technically, the dependence assumptions may be represented in a *dependence graph*, first introduced into the network literature by Frank & Strauss (1986), following the approach described by Besag (1974). The configurations A are represented by the cliques of the dependence graph. Interested readers should consult Frank and Strauss (1986) for further details; see also the review by Robins and Pattison (2005).

another is $\{Y_{13}, Y_{31}\}$, and so on, with every dyad providing its own configuration. Obviously for any of these configurations, if both of the ties are present in the observed graph, we see a reciprocated tie, so the configuration represents a type of network substructure that may be observed in the graph **y**. We can think of this configuration diagrammatically as that substructure, i.e. a reciprocated tie.

But of course there is no guarantee that all possible edges in a given configuration will be present in a realized graph **y**, so we will observe some of these possible substructures but not others. Some ties will be reciprocated, some will not. Configurations represent possibilities. The graph statistic, $g_A(\mathbf{y})$, on the other hand, tells us whether the configuration A is in fact observed in the network **y**. For a reciprocity configuration A, that statistic simply tells us whether there are reciprocated ties between the relevant pair of nodes or not.

We can think of the graphs in the distribution as being generated by these potentially overlapping configurations. For instance, suppose there is a reciprocity effect at work in the process generating the network. If we could observe the evolution of the network, and if the network started with few reciprocated ties, we might expect to see more reciprocated ties emerge over time. In thinking this way, though, we need to bear in mind that as a particular tie emerges through an imagined process of generation, its presence may affect other potential neighboring ties. So there is an implicitly dynamic and self-organizing quality to this hypothetical construction process: as one tie emerges or disappears, other neighboring ties are likely to emerge or disappear as well, and there may be no natural endpoint to this ongoing stochastic process. Nonetheless, the strength and direction of any particular parameter value will affect how frequently the corresponding configuration is observed. If the parameter is large and positive, we expect to observe the corresponding configuration in graphs in distribution (1) more frequently than if the parameter were zero. So if a reciprocity parameter were large and positive, we would expect to see many reciprocated ties in the observed network. Likewise, when a parameter is large and negative we expect to see the configuration (e.g., reciprocated ties) relatively less frequently than if the parameter is zero.

Because (1) has an exponential term in the right hand side, such distributions have been referred to as *exponential random graph models*. The *Markov random graphs* of Frank and Strauss (1986) are one particular class of exponential random graph models. The network analytic community also refers to the exponential random graph

model class as p^* models because they are a generalization of dyadic independence models, of which p_1 models (Holland & Leinhardt, 1981) were a popular early example.

3.1 Constraints on parameters

Notice that equation (1) refers to different configurations for sets of different nodes. For instance, for models with reciprocity there is a separate configuration for $\{Y_{12},Y_{21}\}$, for $\{Y_{13},Y_{31}\}$, and so on. In this general form, then, the model implies many parameters. For instance, there are $n(n-1)/2$ parameters relating to reciprocity alone.

This is simply too many parameters and the model cannot be estimated from a single network observation. Some parameters need to be set to zero, equated or otherwise constrained. Following Frank and Strauss (1986), we often impose a *homogeneity assumption* by equating parameters when they refer to the same *type* of configuration. For instance, in considering reciprocity, Paul may tend very strongly to reciprocate friendship offers from others, but Mary might be more cautious. For the purpose of constructing a simpler model, however, we may assume that there is a single tendency for reciprocity shared by both Mary and Paul. The resulting error is then consumed into the model as statistical noise. This approach assumes that certain regularities are the same for the entire network, for example, that there is a single tendency for reciprocity across the network, irrespective of which nodes are involved. We term this *homogeneity of isomorphic network configurations*, where parameters are equated if the configurations are the same when we ignore the labels on the nodes (in which case the configurations are said to be *isomorphic*). A less radical assumption is also possible: for instance, if we were able to measure whatever characteristics of individuals incline them to reciprocate ties, we could allow the reciprocity effect to depend on those node characteristics.

When we make this homogeneity assumption, we produce a model with the same form as equation (1) but now the (isomorphic) configurations refer to generic effects (e.g. the overall reciprocity effect.) The statistics then become the counts of the corresponding configurations in the network (e.g. the number of reciprocated ties).

But there are several other ways in which constraints on the parameters may be applied, and different constraints result in different models. Another method of applying constraints may be to equate parameters for isomorphic configurations involving similar types of actors. For example, in the case of reciprocity in classroom friendship

networks, we could propose one reciprocity parameter for girl-girl configurations, one for girl-boy configurations and another for boy-boy configurations.

Even with sensible homogeneity constraints in place the model may still have too many parameters to be estimable. In that case, we might consider limiting the number of configurations by setting some parameters to zero (see section 4.3), or by introducing hypothesized constraints on the values of parameters associated with larger configurations (as proposed by Snijders et al, 2006 – see section 4.8).

4. Dependence assumptions and models

4.1 Bernoulli graphs: the simplest dependence assumption

Bernoulli random graph distributions are generated when we assume that edges are independent, for instance if they occur randomly according to a fixed probability α (see Erdös & Renyi, 1959; Frank & Nowicki, 1993). The dependence assumption is simple in this case: all possible distinct ties are independent of one another. We noted above that the only configurations relevant to the model are those in which all possible ties in the configuration are conditionally dependent on each other. When all possible ties are independent, the only possible configurations relate to single edges $\{Y_{ij}\}$. So from (1) the general model is:

$$\Pr(\mathbf{Y} = \mathbf{y}) = (1/\kappa) \exp(\Sigma_{i,j}\, \eta_{ij} y_{ij})$$

Note that compared to (1) every set A comprising a single possible edge Y_{ij} is a configuration in this model, and there is a parameter η_{ij} for each of these configurations. The network statistic $g_A(\mathbf{y}) = g_{ij}(\mathbf{y}) = y_{ij}$ tells us whether that configuration is observed or not. If we impose a homogeneity assumption so that the effect for each tie is identical we equate parameters such that $\eta_{ij} = \theta$ for all i and j, hence:

$$\Pr(\mathbf{Y} = \mathbf{y}) = (1/\kappa) \exp(\theta L(\mathbf{y})) \qquad (2)$$

where $L(\mathbf{y})=\Sigma_{i,j}\, y_{ij}$ is the number of arcs in the graph **y,** and the parameter θ is related to the probability of a tie being observed.[6] The parameter θ is called the *edge* or *density* parameter.

[6] Specifically, $\alpha = \exp\theta/(1+\exp\theta)$. The homogeneity assumption means that there is a fixed probability for all possible edges across the graph, i.e. that there is a single α.

There are other possibilities for imposing homogeneity. Suppose we have actors in two *a priori* blocks and we impose *block homogeneity*, so that $\eta_{ij} = \theta_{11}$ if both i and j are in block 1, $\eta_{ij} = \theta_{12}$ if i is in block 1 and j in block 2, and so on. Then it is simple to show that

$$\Pr(\mathbf{Y} = \mathbf{y}) = (1/\kappa) \exp(\theta_{11} L_{11}(\mathbf{y}) + \theta_{12} L_{12}(\mathbf{y}) + \theta_{21} L_{21}(\mathbf{y}) + \theta_{22} L_{22}(\mathbf{y}))$$

where $L_{11}(\mathbf{y})$ is the number of arcs within the first block, $L_{12}(\mathbf{y})$ is the number of arcs from block 1 to block 2, and so on.

4.2 Dyadic models: the dyadic independence assumption

A somewhat more complicated (but not usually very realistic) assumption for directed networks is that dyads, rather than edges, are independent of one another. With this dependence assumption we have two types of configurations in the model, single edges and reciprocated edges. With homogeneity imposed, the model then becomes:

$$\Pr(\mathbf{Y} = \mathbf{y}) = (1/\kappa) \exp(\theta \Sigma_{i,j} y_{ij} + \rho \Sigma_{i,j} y_{ij} y_{ji}) = (1/\kappa) \exp(\theta L(\mathbf{y}) + \rho M(\mathbf{y})) \qquad (3)$$

where $L(\mathbf{y})$ is the number of ties in $\mathbf{y}$ and $M(\mathbf{y}) = \Sigma_{i,j} y_{ij} y_{ji}$ is the number of mutual ties in $\mathbf{y}$. A slightly more complex homogeneity assumption results in the p_1 model of Holland and Leinhardt (1981).

Related but more complex and realistic models include the p_2 model (Lazega & van Duijn, 1997; Van Duijn, Snijders & Zijlstra, 2004) which assumes dyadic independence but conditional on node-level attribute effects. The p_2 model is appropriate when structure is expected to arise from attributes. It is an extension of the p_1 model with sender and receiver effects treated as random effects and with actor and dyadic effects included. The more complex assumptions underpinning this model make it more realistic for actual network data, especially when attribute effects are expected to be strong. It differs from usual exponential random graph models in the incorporation of random effects.

Of course, in the case of non-directed networks, Bernoulli and dyad dependence models are identical: for non-directed networks, the reciprocity parameter ρ in equation (3) is irrelevant and the model reduces to that of equation (2).

4.3 Markov random graphs

Bernoulli and dyadic dependence structures are unrealistic assumptions in many circumstances, both empirically and theoretically. Frank and Strauss (1986) introduced

Markov dependence, in which a possible tie from *i* to *j* is assumed to be contingent on any other possible tie involving *i* or *j*, even if the status of all other ties in the network is known. In this case, the two ties are said to be *conditionally dependent*, given the values of all other ties[7]. Markov dependence can be characterized as the assumption that two possible network ties are conditionally dependent when they have a common actor. For instance, the relationship between Peter and Mary may well be dependent on the presence or absence of a relationship between Mary and John (especially if the relationship is a romantic one!) We can express this more formally by assuming conditional dependence between the possible ties Y_{pm} and Y_{mj}. These two possible ties are conditionally dependent because they share the node *m* (Mary).

If we also assume homogeneity, we obtain the Markov random graph model, with configurations (and associated parameters) for directed and non-directed networks presented in Figure 1. These parameters relate to some well-known structural regularities in the network literature. For directed networks, we have already seen the edge (τ_{15}) and reciprocity (τ_{11}) parameters from the Bernoulli and dyadic independence models. There are various two-star effects: the two-out-star parameter (τ_{12}) can be thought of as relating to expansiveness, the two-mixed-star parameter (τ_{13}) relates to two-paths, and the two-in-star parameter (τ_{14}) relates to popularity. Note the important transitivity and cyclic configurations (τ_9 and τ_{10}). The inclusion of these parameters is a strength of these models because there is a paucity of network models that incorporate these effects (Newman, 2003), and very few indeed that are estimable from data. The full parameter set includes all possible higher order stars as well, although if all such stars are included there are too many parameters for the model to be estimable. Although some early applications of the Markov random graph model included only two-star effects, it is now known that it may be important to include a non-zero parameter for at least the three-star effect in models for many social networks (Robins, Pattison & Woolcock, 2004, 2005). An alternative approach (see below) includes all higher-order star parameters but imposes constraints on the relationships between higher-order star parameters and lower-order ones.

For example, a Markov random graph model for a non-directed network with edge, 2-star, 3-star, and triangle effects is:

[7] If two ties are conditionally dependent, then if the value of one tie changes, the probability of the other tie is affected, *even if all other ties in the network remain the same*.

$$\Pr(\mathbf{Y} = \mathbf{y}) = (1/\kappa) \exp(\theta\, L(\mathbf{y}) + \sigma_2\, S_2(\mathbf{y}) + \sigma_3\, S_3(\mathbf{y}) + \tau\, T(\mathbf{y})) \qquad (3)$$

where $S_2(\mathbf{y})$ and $S_3(\mathbf{y})$ are the numbers of 2-stars and 3-stars, respectively, in the network **y**, and $T(\mathbf{y})$ the number of triangles in **y**. Note that for Markov random graphs, it is also possible to include parameters for stars of higher order than 3 (4-stars, 5-stars, etc.). The model in equation (3) is an example of how we might set certain higher order parameters to zero (section 3.1). In this case, we are assuming that the distribution of stars (in effect, the degree distribution) can be adequately explained by the 2- and 3-star effects.[8]

Insert Figure 1 about here

It should be noted that the statistics in the Markov model are often related to each other, in the sense that some are higher-order to others. For instance, suppose there is a 3-star in a non-directed network centered on node *i*. Then it is also the case that there are three 2-stars (and 3 edges) also centered on *i*. This is analogous to higher order interactions in more familiar general linear model procedures. This is an important feature of the model that assists interpretation. If, for instance, a network has many 2-stars present, then some will form triangles just by chance. But if there is a substantial triangle effect in a Markov random graph model, this is over and above any 2-star effect, and we can infer that the level of triangulation did not occur simply because of the chance overlapping of many 2-stars (or indeed of many edges). In that case, we would infer that triangulation was an important process in this network, independently of other effects.

Several elaborations of this basic Markov random graph model have also been developed: for multivariate networks (Pattison & Wasserman, 1999); for valued networks (Robins, Pattison & Wasserman (1999); and for affiliation networks (Skvoretz & Faust, 1999; see also Pattison & Robins, 2004).

[8] To be confident about this, we could simulate a distribution of graphs from a fitted model and inspect the degree distributions as compared to the observed network. Examples of such goodness of fit diagnostics are presented in other papers in this special edition.

4.4 Dependence structures with node-level variables

There are various ways of introducing node-level effects (actor attributes) into Markov and other exponential random graph models. We assume a vector **X** of binary attribute variables with $X_i = 1$ if actor i has the attribute and $X_i = 0$, otherwise. The vector **x** is then the set of observations on **X**. It is possible to generalize to polytomous and continuous attribute measures but we will restrict the current discussion to binary attributes. Here, as an example, we briefly describe social selection models where attributes are assumed to be exogenous predictors of network ties (Robins, Elliott & Pattison, 2001).[9] We can investigate a similarity or homophily hypothesis as a basis for social selection – that social ties tend to develop between actors with the same attributes – by looking at the distribution of ties given the distribution of attributes. In other words, as distinct from equation (1), our interest is in the probability of the graph **y** given the observations of attributes **x**, that is, $\Pr(\mathbf{Y} = \mathbf{y} \mid \mathbf{X} = \mathbf{x})$.

A simple dependence assumption between the attribute and network variables is that the attribute of i influences possible ties that involve i (i.e., Y_{ij}), referred to as a *Markov attribute* assumption. For example, in an organizational setting, an actor's seniority (say, senior management versus junior management) may influence the possible ties of that actor. If we consider Markov attributes along with Markov network dependencies, for a non-directed network the model contains the configurations (up to three-stars) shown in Figure 2, with a filled node representing an actor who has the attribute *seniority* (i.e., the actor is a senior manager), and an empty node (with dotted line) just representing an actor, irrespective of whether junior or senior. In other words, the configuration (A) represents tendencies for senior managers to have ties with each other; whereas the configuration (B) represents the tendency for a senior manager to have many ties, and so on. A large positive parameter estimate for configuration (A) is evidence for homophily effects in the network.

It is notable from Figure 2 that the only higher order configuration with attributes is that of a two- or three-star, with the actor with the attribute at the centre of the star. To produce triangle configurations with attribute variables requires additional dependence assumptions.

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[9] Another method to incorporate actor attributes is through social influence models, where network ties were taken as exogenous predictors of attributes (Robins, Pattison & Elliott, 2001).

Figure 2 about here

4.5. More complex dependence assumptions

Elaborations of exponential random graph models that go beyond Markov random graphs have been developed. Pattison and Robins (2002) presented two innovations. With *setting structures*, they confined dependencies within social settings. Drawing on Feld (1981), they suggested as possible examples settings based on a spatiotemporal context, such as a group of people gathered together at the same time and place; settings based on a more abstract sociocultural space, such as pairs of persons linked by their political commitments; and settings that reflect external "design" constraints, such as organizational structure.

An additional motivation to introduce settings is that Markov dependence seems unrealistic for large networks, where individual actors may not even be aware of each other, and have no means to come into contact, yet their possible tie still is taken to influence other possible ties. If the setting structure hypothesis is well founded, there are implications for the type of data that needs to be collected for a full understanding of a social network. For further elaborations, see also Schweinberger and Snijders (2003).

A second direction presented by Pattison and Robins (2002) was to propose non-Markov dependencies among ties that did not share an actor but might be interdependent through third party links. For instance, Y_{ij} may be conditionally dependent on Y_{rs} for four distinct actors if there is an observed tie between either *i* or j and either r or s. These *realization-dependent models* can be developed through what Pattison and Robins (2002) described as *partial dependence structures.* These models also permit the introduction of triangles involving attribute effects.

4.6 New model specifications

There is mounting evidence that homogeneous Markov random graph models are not good models for many observed social networks (see section 5.2 below), so these models are not always useful in practical terms. Based on realization-dependence structures, Snijders et al (2006) developed new specifications for exponential random graph models that include new higher order terms. These models introduce constraints on *k*-star parameters, as well as new higher-order *k*-triangle configurations which allow for the measurement of highly clustered regions of the network where two individuals may be connected to a large number of *k* others (a *k*-triangle). For these models, many

higher order star and triangle effects are included (rather than set to zero) but they are constrained in the form of a weighted sum with alternating signs. The motivation behind these innovations, and the success of these new model specifications, are discussed in other papers in this special edition.

5. Estimation

Anderson et al. (1999) in their *p** primer used pseudo-likelihood estimation introduced by Strauss and Ikeda (1990) in order to estimate the parameters of Markov models. We now know that, depending on the data, there may be serious problems with pseudo-likelihood estimates for these models. But for Markov random graph models, standard maximum likelihood estimation is not tractable for any but very small networks, because of the difficulties in calculating the normalizing constant in equation (1). What this means is that standard statistical techniques cannot be applied to these models. These problems have been overcome in recent times by the development of new Monte Carlo maximum likelihood techniques. We begin by making some rather brief comments about pseudo-likelihood and then introduce the new estimation approaches.

5.1 Pseudo-likelihood estimation: an approximate technique

The use of maximum pseudo-likelihood to estimate interactive models was first proposed by Besag (1975), and was suggested for Markov random graph models by Strauss and Ikeda (1990). In the general statistical community, pseudo-likelihood has given way to Monte Carlo techniques where feasible, although it still has its adherents (see Wasserman & Robins, 2005, for some of the literature.) The advantage of pseudo-likelihood estimation in the context of exponential random graph models is that it is relatively easy to fit even complicated models. The disadvantage is that the properties of the estimator are not well understood and it is known that for many data sets pseudo-likelihood estimates are not accurate.

Pseudo-likelihood estimation is best understood by transforming equation (1) – the *joint form* of the model – into the following equivalent *conditional form* (see Strauss and Ikeda, 1990, for more detail):

$$\log\left[\frac{\Pr(Y_{ij}=1\,|\,\mathbf{y}_{ij}^{C})}{\Pr(Y_{ij}=0\,|\,\mathbf{y}_{ij}^{C})}\right]=\sum_{A(Y_{ij})}\eta_{A}d_{A}(\mathbf{y}) \qquad (4)$$

where:

(1) The sum is over all configurations A that contain Y_{ij};

(2) η_A is the parameter corresponding to configuration A;

(3) d_A (**y**) is the *change statistic*; the change in the value of the network statistic z_A(**y**) when y_{ij} changes from 1 to 0;

(4) $\mathbf{y}_{ij}^{C}$ is all the observations of ties in **y** except the observation y_{ij}.

The calculation of the change statistic has been discussed extensively by a number of authors (Anderson et al, 1999; Pattison & Robins, 2002; Wasserman & Pattison, 1996; Wasserman & Robins, 2005), so we do not go into it further here. With the change statistics calculated, to produce the pseudo-likelihood estimates, each possible tie Y_{ij} becomes a case in a standard logistic regression procedure, with y_{ij} predicted from the set of change statistics (Anderson et al, 1999).

This procedure looks like a logistic regression – or indeed, a loglinear model – but it is not. Logistic regression assumes independent observations, an assumption we explicitly do not make with Markov and higher order models. So the parameter estimates may be biased; and the standard errors are approximate at best, and may be too small. One should not rely on the Wald statistic as a means to decide whether a parameter is significant or not. As well, one cannot assume that the pseudo-likelihood deviance is asymptotically distributed as chi-squared (which would be the case in normal logistic regression). When the dependence among observations is not so strong, it is generally the case that PL estimates will be more accurate. Pseudo-likelihood estimation has been used to date as a pragmatic convenience (given that alternatives have not hitherto been readily available) and the method does not have a principled basis. Whenever possible, the preferred option is to use Monte Carlo estimation procedures.

5.2 Markov Chain Monte Carlo maximum likelihood estimation (MCMCMLE)

Important recent developments in Monte Carlo estimation techniques for exponential random graph models have been presented and reviewed by a number of authors (see Snijders, 2002; Handcock, Hunter, Butts, Goodreau & Morris, 2004; Snijders et al, 2006; Wasserman and Robins, 2005), and are further discussed in other articles in this special edition, so we include only a brief summary here.

To begin, we note that simulation of these models can be implemented in a relatively straightforward way. Without going into details, simulation of the graph distribution for a given set of parameter values can be achieved through a number of algorithms (e.g. algorithms well-known in statistics more generally, such as the Metropolis algorithm). Simulation is at the heart of Monte Carlo maximum likelihood estimation. Procedures for simulating exponential random graph distributions have been described by Strauss (1986), Snijders (2002), and Robins, Pattison and Woolcock (2005).

Although there are variations between different Monte Carlo estimation techniques (Snijders, 2002; Hunter & Handock, 2006), they are based on the same central approach: simulation of a distribution of random graphs from a starting set of parameter values, and subsequent refinement of the parameter values by comparing the distribution of graphs against the observed graph, with this process repeated until the parameter estimates stabilize. Recent software that implements Monte Carlo maximum likelihood estimation for exponential random graph models is reviewed in other papers in this special edition.

Both estimation and simulation studies have raised issues of model specification for Markov random graphs. Handcock (2003) defined *near degeneracy* as occurring when a model implied that only a few graphs had other than very low probability (often these were the full graph or the empty graph). If a model implies only these rather uninteresting outcomes, it will not be useful for modeling real networks. Simulation studies suggest that Markov graph models that contain at least non-zero three-star parameters tend to exhibit less near degeneracy than those with two-stars as the highest order non-zero star parameter (Robins et al, 2005). But the inclusion of three-star parameters often is not sufficient to remove near degeneracy behavior in Markov graph models, particularly when attempting to find models that reproduce the high levels of transitivity often observed in human social structures (there is an extended discussion in Snijders et al, 2006). The fact that these problems may not occur for pseudo-likelihood estimation simply means that for near degenerate models, pseudo-likelihood estimates may be particularly misleading. The primary problem in these cases is that the model is not well-specified.

The bottom line is that various Monte Carlo estimation techniques are now available and, wherever practicable, are to be preferred. These new approaches highlight certain inadequacies in Markov random graph models when, for instance, transitivity

effects are strong. If this does happen for a given data set, researchers fitting Markov random graph models will notice that it is impossible to obtain consistent parameter estimates with Monte Carlo maximum likelihood estimation (technically, the estimation process does not *converge*.) This means that the Markov graph models are inappropriate for the data. It is for such reasons that Snijders et al (2006) introduced their new specifications for exponential random graph models, mentioned in section 4.6, and discussed in other papers in this special edition.

6. A short example: A Markov random graph model for Medici business network

Other papers in this special edition provide examples of fitting exponential random graph models to data, so here we present a very short example. We fit a Markov random graph model for the well-known non-directed network of business connections among 16 Florentine families, available in UCINET 5 (Borgatti, Everett, & Freeman, 1999). (For a fuller description of the context of the data, see Padgett and Ansell, 1993.) The model includes edge, two-star, three-star and triangle parameters as in Equation (3). This model is not degenerate for this data set and parameter estimates successfully converge. MCMCMLE parameter estimates are presented in Table 1. We see that the density and triangle parameters are substantial in magnitude in comparison with their standard errors.[10] Interpretation is therefore relatively simple. The negative density parameter indicates that edges occur relatively rarely, especially if they are not part of higher order structures such as stars and triangles. The positive triangle parameter can be interpreted as providing evidence that the business ties tend to occur in triangular structures and hence to cluster into clique-like forms. The star effects are not significant, so perhaps do not merit interpretation. But the parameter values suggest that there is a tendency for multiple network partners (the positive 2-star estimate) but with a ceiling on this tendency (the negative 3-star parameter). So, while there is tendency for network actors to have multiple partners, there are few actors with very many partners.

Table 1 about here.

[10] The distribution of the statistic formed as the ratio of the estimate to its standard error is not known, but likely to approximate a *t* distribution (Snijders, 2002). As a result, ratios exceeding two in absolute magnitude suggest non-zero effects.

7. Conclusion

This article provides an introductory exposition of the formulation and application of exponential random graph models for social networks. We have concentrated on presenting the underlying logic and derivation of these models. Given the limitations of space, we have only given summary attention to more recent developments which will be discussed in other papers in this special edition.

Recent work on the Markov random graph models of Frank and Strauss (1986) shows that they may be inadequate for many observed networks. In reviewing developments in these models to this point, we have deliberately made no more than very summary comments on improved model specification. The new specifications of Snijders et al (2006) offer substantial improvement in the practical use of exponential random graph models. They also indicate a way forward to developing other innovative specifications. One of our aims in this paper has been to lay the groundwork for an understanding of these new developments, which are given a fuller exposition in other papers in this special edition.

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Figure 1

Configurations and parameters for Markov random graph models

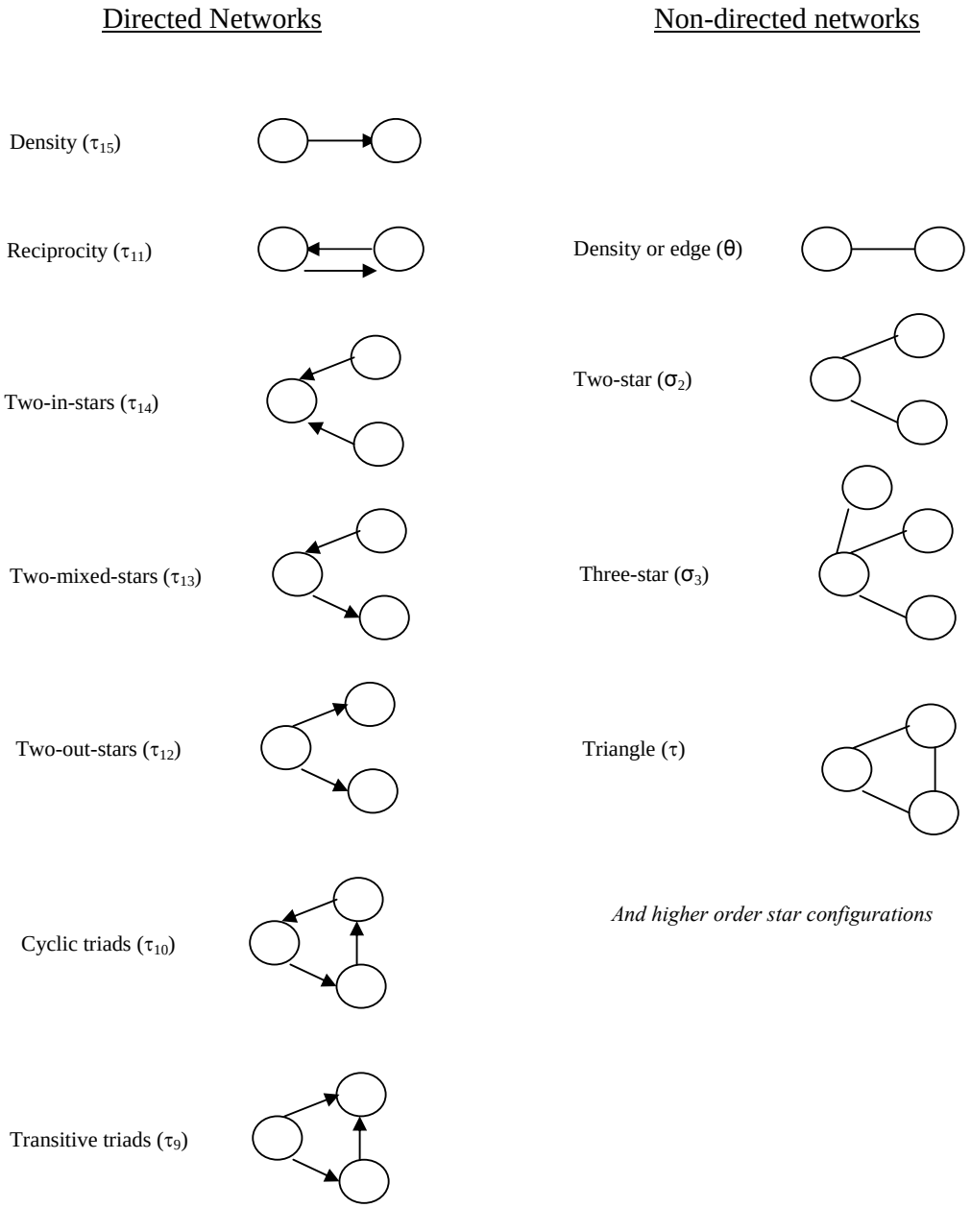


Figure 2

Configurations for a Markov attribute-Markov graph social selection model

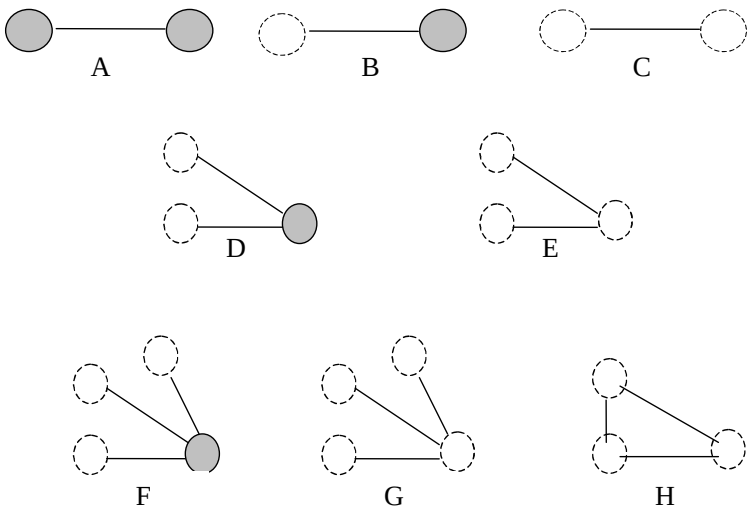
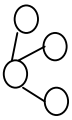


Table 1

Parameter estimates for Markov graph model: Florentine families business network

(Maximum likelihood estimates with standard errors in brackets)

Parameter	Configuration	Estimate (standard error)
θ		-4.27 (1.13)
σ_2		1.09 (0.65)
σ_3		-0.67 (0.41)
τ		1.32 (0.65)